

ORTEC[®]

Renaissance[®] Supervisor

**Whole-Body Counter Software for
Microsoft[®] Windows[®] 8.1 Professional, 7 Professional,
and XP Professional SP3**

REN-P-BW

Software User's Manual

Software Version 7.0

Advanced Measurement Technology, Inc.
(“AMT”)

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NOTE!

If you are not fully acquainted with the Windows environment, we strongly urge you to visit the Microsoft website as well as familiarize yourself with a few simple applications before proceeding.

The convention used in this manual to represent actual keys pressed is to enclose the key label within angle brackets; for example, <F1>. For key combinations, the key labels are joined by a + within the angle brackets; for example, <Alt + 2>.

1. INTRODUCTION

ORTEC's Renaissance® Whole-Body Counter software is primarily designed to provide a rapid screening device using sodium iodide (NaI) or germanium (HPGe) detectors. It works in either stationary detector or scanning mode. In typical environments such as those found in a nuclear power plant, the expected and normal result is to find no activity in the subject or objects being monitored. In this situation, the primary purpose of the count is to confirm the lack of any radioactive contamination within a reasonable count time. In the scanning mode, a plot of activity vs. position (MCS mode) can be displayed. The spectra are saved at up to 128 different detector positions.

The Renaissance software reduces the collected spectrum from the detectors (see Section 1.4) to a list of nuclide activities or concentrations in the person or objects. A spectrum file contains all the necessary information for the analysis and can be archived. A record is created each time a person or object is counted, and is stored in a database; one person can have many records over a period of time. A composite report can be made, if desired, by retrieving the information from the Microsoft Access®-format database. The exact details of the report depend on the options selected, the spectrum, the calibration, and the libraries. This report — which can include data such as nuclide activities, library energy, actual energy, percent uncertainty, peak area, total activity, and alarm and warning limits — can be automatically viewed and/or printed.

Renaissance combines two programs in one package, the *supervisor* program, Renaissance Supervisor; and the *operator* program, Renaissance Operator. These programs fulfill the need to separate the tasks performed by the operator from the duties of the supervisor. The supervisor controls the setup, initialization, calibration, quality assurance (QA), reporting, alarm and warning limits, and password security from the extensively interactive supervisor program. The supervisor thereby controls the operator program. The operator only has access to the data-acquisition and record-creation features of Renaissance.

Renaissance can collect inputs for and produce outputs that can be used by any dose-calculation program.

The Supervisor software provides extensive menus and toolbars for the operation of all acquisition and analysis functions such as control of acquisition, setting of analysis parameters, calibration, and library editing. Graphical displays of the spectrum data and calculated data or functions are used to present the data and results in easy to understand formats. Multiple windows allow you to view several spectra at once for easy comparison or to monitor the acquisition of several sample spectra.

The details of the spectrum files are described in the *ORTEC Software File Structure Manual for DOS and Windows Systems* (P/N 753800; hereinafter called the *File Structure Manual*), available on the Renaissance start menu.

1.1. MCA Emulation

A *multichannel analyzer* (MCA) is an instrument that sorts and counts events in real time. This sorting is based on some characteristic of these events, and the events are grouped together into bins for counting purposes called *channels*. The most common type of multichannel analysis, and the one that is of greatest interest to nuclear spectroscopists, is *pulse-height analysis* (PHA). PHA events are signal pulses originating from a Detector,¹ and the characteristic of interest is the pulse height or voltage, which is proportional to the particle or photon energy. An *analog-to-digital converter* (ADC) is used to convert each pulse into a channel number, so that each channel corresponds to a narrow range of pulse heights or voltages. As pulses arrive over time, the MCA will collect in memory a distribution of the count of pulses with respect to pulse height (a series of memory locations, corresponding to ADC channels, will contain the count of pulses of similar, although not necessarily identical, height). This distribution, arranged in order of ascending energies, is commonly referred to as a *spectrum*. To be useful, the acquired spectrum must be available for storage and/or analysis, and is displayed on a graph whose horizontal axis represents the height of the pulse and whose vertical axis represents the number of pulses at that height, also referred to as a histogram.

Renaissance, combined with *multichannel buffer* (MCB) hardware and a computer, provides an MCA with considerable power and flexibility. The MCB performs the actual PHA, while the computer and operating system provide the display and data-archiving hardware. The Renaissance software is the vital link that integrates these components to provide meaningful access to the MCB via the user interface provided by the computer hardware.

In the scanning mode, a different type of spectrum is acquired. This spectrum is a record of the counts per time or counts per position in the scan. This is similar to a multichannel scaling (MCS) spectrum. The MCS spectrum can be saved and viewed.

The Renaissance Supervisor program MCA emulation shows the acquired spectrum, operating conditions, and available menus. All important operations that need to be performed on a spectrum, such as peak location, insertion of *regions of interest* (ROIs), display scaling, and sizing are implemented with both the keyboard (accelerators) and the mouse (menus and toolbars). Spectrum peak searching, report generation, printing, archiving, calibration, and other analysis tools are available from pull-down menus. Some menu functions have more than one accelerator so both new and experienced users will find the system easy to use.

¹In this manual, the term “Detector” is in some cases used interchangeably with MCB, and means the transducer (sodium iodide or germanium) plus all the electronics including the ADC and histogram memory. The transducers are referred to by their complete name; e.g., sodium iodide detector.

Renaissance maintains one or more *buffers* in the computer memory, to which spectra can be moved from the MCB memory for display and analysis while another spectrum is collected in the MCB. As much as possible, a buffer duplicates in memory the functions of the MCB on which a spectrum was collected. Also, data can be analyzed directly in the MCB memory, as well as stored directly from the MCB to disk.

1.2. Accessing Renaissance Across a Network

Renaissance uses the network features of Windows so it can be used to control ORTEC MCB hardware anywhere on the network. In this way, the results from all counters can be added together making it possible, for instance, to generate a composite report from all of the MCBs. However, Renaissance on one computer cannot access the Renaissance database on other computers. In a facility where more than one computer is used to run Renaissance (each controlling its own whole-body counter), an experienced programmer can copy the necessary information from the individual Renaissance databases into a master database. The format of the master database is often determined by the needs of the other reporting programs at the facility.

1.3. Computer Requirements and Operating System Cautions

Renaissance is designed for use on computers that run 64-bit Windows 8.1 Professional, 64- and 32-bit Windows 7 Professional, or Windows XP Professional SP3. In 32-bit Windows operating systems, the Renaissance program files are installed in the `\Program Files` folder; in 64-bit Windows, Renaissance is installed in the `\Program Files (x86)` folder.

1.4. MCB Support in Renaissance v7

Renaissance can control from 1 to 250 ORTEC MCBs, using any combination of NaI and HPGe detectors, at one time. The MCBs are configured by the supervisor and assigned unique identification numbers and names. The MCBs can be divided into *groups* for ease of use. The supervisor can display the data from any of these available MCBs, or can open spectra from disk into buffer windows. The operator can display the data from available MCBs. Several Renaissance windows can be open in the program at one time, displaying Detectors, buffers, spectrum files from disk, and data analyses.

Your computer's processor and operating system will determine which MCBs, instrument-to-computer interfaces, and network protocols can be used. For detailed information, see the accompanying CONNECTIONS Driver Update Kit Instruction (P/N 932721) or consult your ORTEC representative. For setup of pre-2005 MCBs, the legacy *ORTEC MCB CONNECTIONS-32 Hardware Property Dialogs Manual* (P/N 931001) is available in our online library.

Adding more MCBs to your system is fast and easy; see the accompanying CONNECTIONS Driver Update Kit Instruction (P/N 932721) for instructions.

2. INSTALLING RENAISSANCE

You must have Administrator access in Windows to install Renaissance.

2.1. Step 1: Installing CONNECTIONS

The Renaissance CD is accompanied by a CONNECTIONS Driver Update Kit (Part No. 797230). *You must install CONNECTIONS before Renaissance will install.* If you attempt to install Renaissance before CONNECTIONS, an error message will be displayed. If a “program compatibility assistant” dialog then opens saying “this program may not have installed correctly,” click **Cancel** to close it, install CONNECTIONS, then install Renaissance.

Be sure to read the Update Kit instruction guide completely! It describes how to install CONNECTIONS, enable/disable the drivers for your ORTEC MCB(s), share ORTEC instruments across a network, and control the MCB Configuration program. It also points you to information on selecting the proper network protocol for older, direct-to-Ethernet units. At the end of installation, you will be directed to restart the computer.

2.2. Step 2: Installing Renaissance

- 1) If you are upgrading from an older version of Renaissance and have modified your `b30winds.ini` or `g30winds.ini` file (see Sections A.2.2 and A.2.3), be sure to make a backup copy of your modified `.ini` file(s) before installing the new version of Renaissance or your files will be overwritten.
- 2) Insert the Renaissance CD, then navigate to the CD drive and open `\Disk1\Setup.exe`. One or more security dialogs will open. Choose the “continue” or “install anyway” option, then the installation wizard will start. Click **Next** to begin moving through the wizard screens.
- 3) File installation locations are as follows:
 - A folder of example files, including spectra, calibrations, libraries, analysis results files, etc., is installed in `C:\User\Ren V7 Examples`.
 - The `\Renaissance` folder contains the Renaissance executable, all analysis engines, user manual PDFs, help files, language support files, and the `b30winds.ini` and `g30winds.ini` analysis engine parameter files.
 - The QA database is installed in `C:\User` and all context files are in `C:\User\Cxt`.
 - WinPlot, CONNECTIONS, and the library editor are stored in the program files folder under `\Common Files\ORTEC Shared`.

- The default storage folder for all spectrum, analysis, report, and graphics files generated by Renaissance is `C:\User`. You can change this on the Directories tab under **File/Settings...** as discussed in Section 5.1.1.4.

2.3. Step 3: Establishing Communication With Your ORTEC MCBs

- 1) If you have purchased new ORTEC spectroscopy hardware, connect it and power it on according to its accompanying hardware manual.²
- 2) Connect and power on all local and network ORTEC instruments that you wish to use, as well as their associated computers. Otherwise, the MCB Configuration program will not detect them during installation. Any instruments not detected can be configured at a later time.

- 3) To start the software, enter the letters `mcb` in the “*search programs and files*” box at the bottom of the Windows Start menu, then click the **MCB Configuration** search result; or open the Windows Start menu and click **Renaissance**, then **MCB Configuration**. The MCB Configuration program will locate all of the powered-on ORTEC MCBs on the local computer and the network, and display the list of instruments found

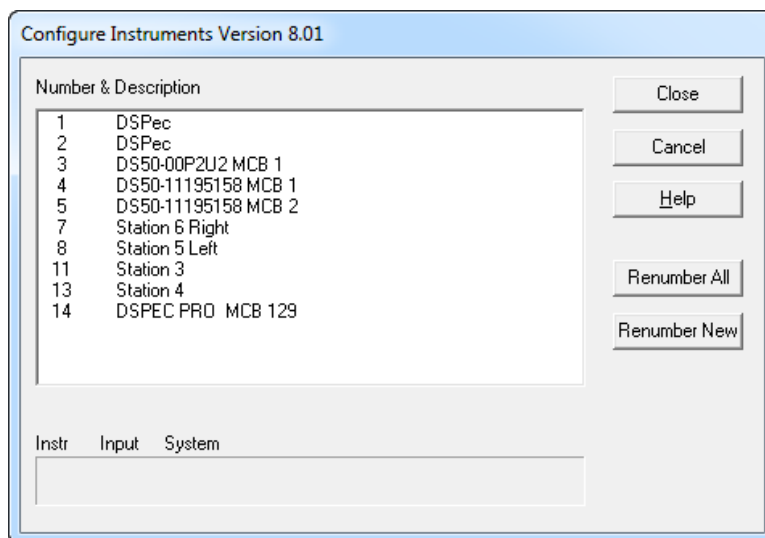


Figure 1. Detector Numbering and Descriptions.

(the *Master Instrument List*; Fig. 1). If you wish, you may enter customized instrument ID numbers and descriptions (Section 2.3.2). When you close the dialog, any changes you have made to an ID number or description will be written back to the corresponding Detector.

²The first time a particular MCB model is connected, a “found new hardware” wizard will start up. Choose *not* to “search the internet for a driver” option, then choose to automatically search for the driver.

2.3.1. Configuring a New Instrument

The first time a new instrument is detected, the dialog shown in Fig. 2 will remind you that all new instruments must be assigned a unique, *non-zero* ID number.³ Click **OK**. You can either manually change the ID Number and Description as described in the next subsection, or you can click the **Renumber New** button to renumber only the new instruments.

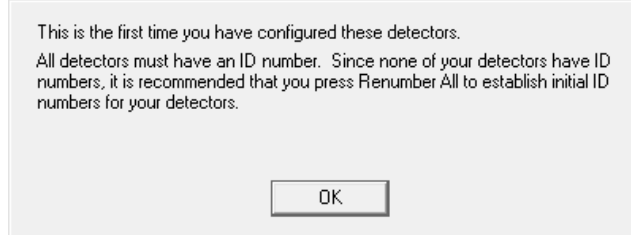


Figure 2. New Instruments Must Have a Non-Zero ID Number.

NOTE *We recommend not using the **Renumber All** button.* In addition, we strongly recommend *not* renumbering Detectors that “belong” to other users, as this could affect the interaction between their Detectors and their ORTEC software, for instance, if they control their Detectors with .JOB files (e.g., the .JOB file command `SET_DETECTOR 5`), or use the Renaissance or ISOTOPIC spectroscopy applications. See also the following NOTE and the NOTES in the next section.

NOTE FOR MULTIPLE USERS ON A NETWORK

There are two ways to reduce the chance that other users will renumber your Detectors:

- Add the `-I` flag to their MCB Configuration command line, as described in Section 2.4.3. This will allow you to assign whatever ID Numbers you wish, regardless of the numbers assigned by other users on your network. (Ideally, everyone using ORTEC instruments on your network should make this change.)
- To prevent others from renumbering your Detectors (or performing any other actions except read-only viewing), password-lock your Detectors with the **Lock/Unlock Detector** command (Section 5.7.5). If you lock a detector that will be controlled by a JOB stream, remember to include the proper password-unlock commands in your .JOB file (Section ?).

³If this is a first-time installation of ORTEC products, all your instruments will be “new.”

2.3.2. Customizing ID Numbers and Descriptions

If you wish, you can change the instrument ID Numbers and Descriptions by double-clicking on an instrument entry in the Configure Instruments dialog. This will open the Change Description or ID dialog (Fig. 3). It shows the physical Detector location (read-only), and allows you to change the **ID Number** and **Description**.

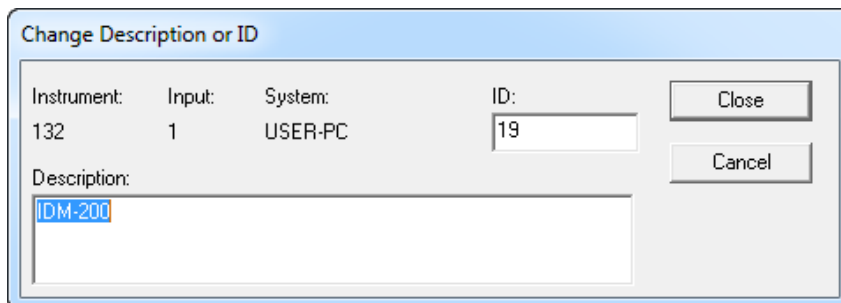


Figure 3. Change Detector Number or Description.

Make the desired changes and click **Close**. Any changes you have made to an ID number or description will then be written back to the corresponding Detector.

If a modified description has already been applied to a particular instrument, you can restore the default description by deleting the entry in the **Description** field and re-running MCB Configuration. After MCB Configuration runs, the default description will be displayed.

2.4. Caution: Running the MCB Configuration Program Can Affect QA, Detector Groups, and Scan Type Definitions

Detector identification in Renaissance is based on the *instrument ID number and description* assigned to a Detector by the MCB Configuration program. Instrument **ID** number and description are assigned when MCB Configuration polls the local computer and network for attached ORTEC MCBs and then builds a Master Detector List of the instruments found. This instrument identification is then used for all quality assurance (QA) measurements; when you identify specific detectors as either germanium or sodium iodide; assign one or more of these instruments to *detector groups*; then associate these detector groups with the specific *scan types* that will be used for making measurements in the Renaissance Operator program.

Once you have created — and subsequently *used for measurements* — detector groups, scan types, and quality assurance settings for those detectors, if you then re-run the MCB Configuration program for any reason, you must ensure each instrument is still assigned its previous instrument **ID** number and description *before collecting any more data*. Allowing the MCB Configuration program to assign a new instrument identification to a detector, and then *using* that new identification, breaks the connection to existing detector groups and scan types. In addition, it interrupts the orderly accumulation of QA records because Renaissance treats the renumbered detector as new, with zero “previous QA measurements” and potentially incorrect QA settings.

If you must re-run the MCB Configuration program, you can avoid any renumbering problems either by not renumbering instruments or by manually editing the instrument numbers for all of the Detectors on the Master Detector List for your computer. Doing so requires that you keep a separate record of the ID and Description for each MCB on your system. **Note spelling, spacing, and uppercase/lowercase; these details will be necessary when recreating the Description text string.** Let us use the following example to illustrate the process.

2.4.1. Manually Restoring Instrument ID Number and Description

Suppose you are using two MCBs for your Renaissance measurements and in your original MCB Configuration you configured them as **1 DSPEC PRO 1** and **4 DSPEC PRO 4**. This is depicted in Fig. 4. The numerical prefixes **1** and **4** are the **IDs** and the corresponding text strings are the **Descriptions**.

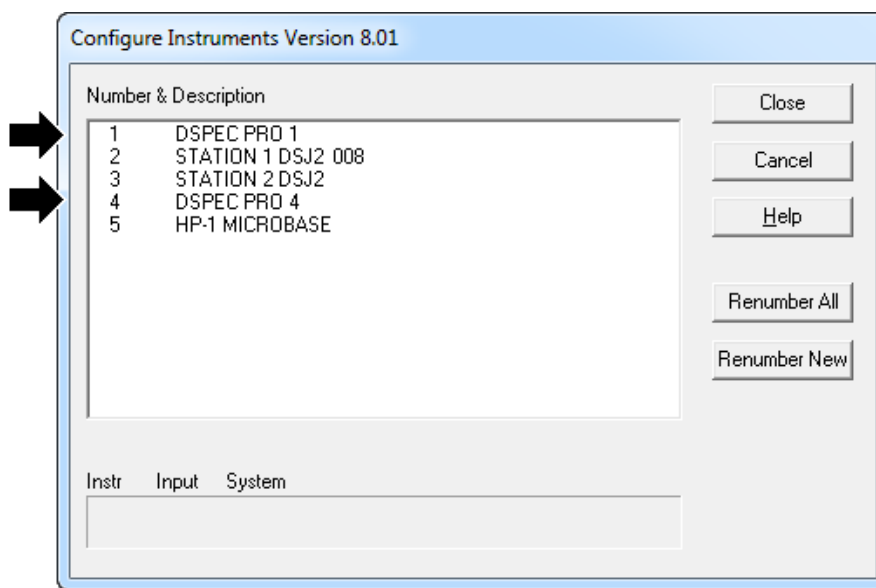


Figure 4. Original MCB Configuration Showing Our Two DSPEC Pro MCBs.

Suppose we add one new MCB to the system and remove two. We must then manually re-run MCB Configuration to add the new instrument to the Master Detector List. Suppose we then find that our two DSPEC Pro units, originally assigned IDs of **1** and **4**, have been renumbered with IDs of **2** and **3**, respectively. **Before** closing the Configure Instruments dialog, double-click the MCB entries that must be renumbered and/or renamed. This will open the Change Description or ID dialog. Restore the original instrument number in the **ID** field and click **OK**, as shown in Fig. 5.

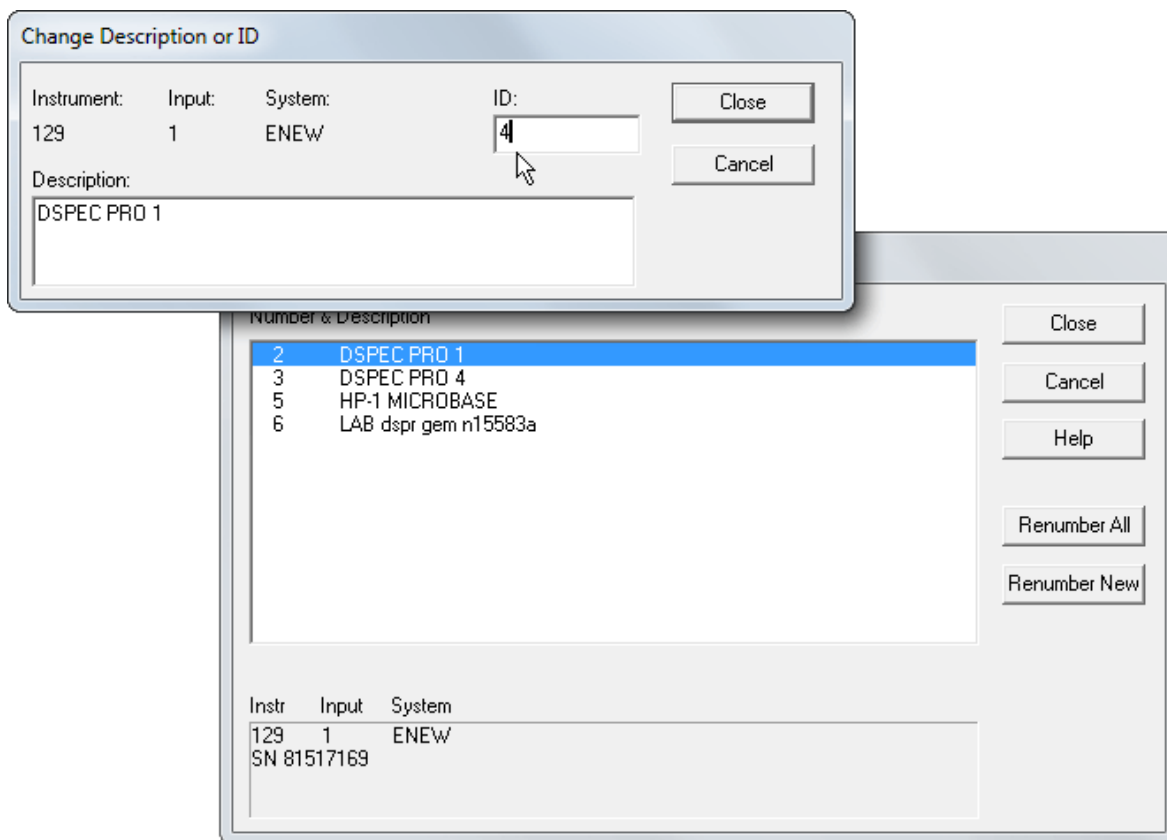


Figure 5. Manually Renumbering and/or Renaming Detectors to Maintain QA Integrity.

Repeat for all Detectors that must be renumbered and/or renamed. When you are finished, click **Close**.

2.4.2. Confirming the MCB Identification to Maintain QA Integrity

To confirm that the original QA **Settings...** are still in effect, run background and sample QA measurements and check the results dialogs to confirm that the MCBs are being properly tracked.

2.4.3. Editing the MCB Configuration Command Line

The command line for the MCB Configuration program is:⁴

`"C:\Program Files\Common Files\ORTEC Shared\UMCBI\mcbcon32.exe"`

⁴As noted earlier, 32-bit Windows uses the \Program Files folder and 64-bit Windows uses \Program Files (x86).

You can modify the way the MCB Configuration program runs by adding one or more of the following flags to the command line. You can use any combination of flags or none, and the flags are not case-sensitive.

- I Ignore duplicate IDs. MCB Configuration allows you to accept an instrument list with duplicate detector ID numbers; no renumbering is required. Useful for customers using our QA tools, JOB commands, and “Gamma Total” function; and when sharing a network with other users of ORTEC MCBs.
- L Configure only local instruments (i.e., no discovery of ORTEC instruments across a network except “attached” digiBASE-E units). This can significantly reduce the time it takes to run MCB Configuration, if you have only local MCBs.
- P Append all newly discovered instruments to the existing list (i.e., don’t clear the existing list before starting discovery). Useful when you don’t have all your instruments connected or powered-on at the same time but wish to configure new detectors.

There are two ways to modify the MCB Configuration command line:

- To retain the flags from use to use, right-click **MCB Configuration** in the Start menu, select **Properties**, then in the **Target** field, add the flags *outside* the right-hand quotation mark and click **OK**. For instance:

```
"C:\Program Files\Common Files\ORTEC Shared\UMCBI\mcbcon32.exe" -I -L
```

- To temporarily change the command line, open the Windows Start menu’s **Run...** dialog, browse to locate the MCB Configuration file, `mcbcon32.exe`, add the flags *outside* the right-hand quotation mark, and click **OK**.

2.5. Enabling Additional ORTEC Device Drivers and Adding New MCBs

You can enable other device drivers later with the Windows **Add/Remove Programs** utility on the Control Panel. Follow the instructions in the CONNECTIONS Driver Update Kit.

[Intentionally blank]

3. GETTING STARTED IN RENAISSANCE

Getting started in Renaissance requires using the Supervisor program to configure several crucial parameters for the Operator program. Supervisory configuration includes such steps as selecting which Detectors will be available to the operator, naming each Detector (for instance, assigning mnemonic names like *Chair*, *Thyroid*, *Top*, or *Bottom*), choosing to use either English or metric units of measure for subject weight and height, and deciding whether subject measurements will be corrected for chest-wall thickness. The remainder of this chapter outlines the setup steps and their corresponding commands, and highlights some key factors to consider during setup.

- 1) Decide on the MCB identification numbers and descriptions you wish to assign to the various instruments in your system. We suggest this as a time-saving first step because you will have the opportunity to customize these ID numbers and descriptions when you run the MCB Configuration program as part of installing the Renaissance software. (Otherwise, you will have to run MCB Configuration a second time and perform the customization then.) ***Be sure to read Section 2.4, which discusses the importance of maintaining instrument identification numbers and descriptions in Renaissance!***
- 2) Install the Renaissance software and run the MCB Configuration program to build the master list of MCBs as described in Chapter 2.
- 3) If using a motorized bed, run the **Motor Setup** program and set the parameters according to the instructions in Appendix B.
- 4) Figure 6 shows the Renaissance start menu. To start one of the programs, type the first few letters in the “*Search programs and files*” box on the Windows Start panel, then click the appropriate search result; or open the Windows Start menu and click **Renaissance** and the desired program. You can also start Renaissance by entering **run** in the search box and choosing the **Run** option; or (in XP) by selecting **Run** from the Start menu. The Run option allows you to start up from the command line, with or without arguments, as described in Section A.1.
- 5) The first time you start Renaissance Supervisor, only the “Buffer” selection will be available on the **Detector** droplist. To set up the germanium and sodium detectors that will be available in both the Supervisor and Operator programs:

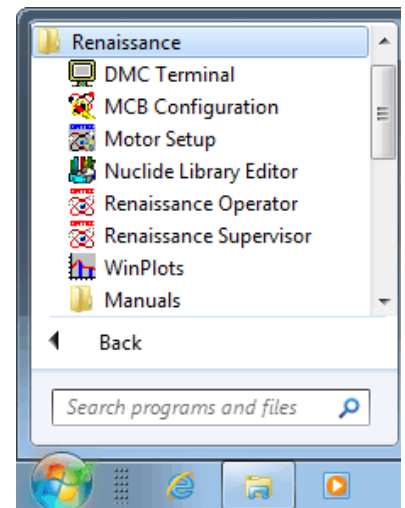


Figure 6. Renaissance Menu.

- Use **Services/Edit Detector Lists/Edit Ge Lists...** (Section 5.7.6.1) to add the germanium detectors to the Ge detector pick list.
- Use **(Services/Edit Detector Lists/Edit NaI Lists...** (Section 5.7.6.1) to add the sodium iodide detectors to the NaI detector pick list.

Germanium detectors will have a **Ge** prefix before the name and sodium iodide detectors will have an **NaI** prefix.

- 6) Assign these detectors to *detector groups* (**Services/Edit Detector Lists/Edit Groups...**; Section 5.7.6.2). Each detector must be assigned to a group (even if that group contains only the one detector), and a detector can belong to more than one group. To avoid configuration and analysis conflicts, detector groups should normally be composed of only Ge or NaI detectors.
- 7) Create libraries for the nuclides of interest. See the guidelines in Section 5.6.1, page 165.
- 8) In preparation for calibration, establish the set of spectrum *analysis options* for your Ge detectors and/or your NaI detectors, as discussed in **Analyze/Settings/Sample Type...**, beginning in Section 5.5.1. (The setup for each specific detector in a group will be determined when you create *Scan Types* in step 14.) These analysis option sets include settings such as peak search sensitivity, analysis range, analysis engine, decay correction, attenuation correction, and calibration and background overrides. You will, in most cases, save them as *analysis options files* (.SDF files for Ge spectrum analysis; .SVD files for NaI). The sample default files are used directly in the Supervisor program and indirectly in the Operator program. For NaI detectors, note the “Important Considerations When Creating NaI Analysis Options Settings” discussion on page 134.
- 9) Establish the acquisition settings for each detector in a detector group (**Acquire/Acquisition Settings...**, Section 5.2.1).
- 10) If performing peak background corrections in the analysis, create a .PBC file for each detector both for use in Supervisor and for incorporation into the scan type files you will create in step 14 (**Analyze/Settings/Peak Background Correction/Create PBC...**, Section 5.5.1.5).
- 11) Adjust the MCB voltage and amplifier gain to align the energy peaks from a known source to the appropriate channels to establish an approximation for the energy/channel relationship and the energy range for the measurement (**Acquire/MCB Properties...**, Section 5.2.9).

- 12) Calibrate detectors with the commands on the **Calibrate** menu (Section 5.3). If using a motorized bed, use the Motor Setup program to start the bed excursion at the same time you start the calibration acquisition in Supervisor. Note that if all efficiency calibrations are performed at one scan length, should the scan length be changed, the efficiency calibrations will no longer be applicable and must be redone.
- 13) Renaissance optionally allows you to create separate databases for storing results from different subject groups, such as employees, contractors, client origin, training, and testing (see **Services/Database Management/Create Database...**, Section 5.7.3.1). Each database contains its own scan types, alarm limits, and attenuation coefficient information. At this point, you might wish to create one or more separate databases.
- 14) Set up the *scan type* (.OPR) files that determine the detector group, chest-wall-thickness correction, counting presets, and analysis options file(s) to be used for measurements in the Operator program; the suite of reports and database records to be generated; and the database in which the results will be stored (**Services/Operator Scan Type**; Section 5.7.8). These parameter sets will then be available on the **Scan Type** droplist in Operator so that users can choose the appropriate parameter set for the type of measurement they are performing. Note the discussion, “General Factors to Consider in Creating Scan Type Files,” on page 181 and the discussion points for each wizard page.
- 15) Set up the *operator permissions* (**Services/Operator Permissions...**; Section 5.7.7).
- 16) Set the *alarm limits* for the Operator program (**Services/Alarm Limits...**; Section 5.7.9). Note that these alarm and warning limits are specific to the database being used to store the Operator analysis results.
- 17) Establish the parameters necessary to perform background and sample QA measurements for each detector in the Supervisor and Operator programs. For QA measurements in Supervisor, use the QA Settings dialog (Section 10.2.1) to select the analysis settings, counting presets, alarm and warning limits, and other parameters for each detector.

To run QA in Operator, you must create a scan type file that specifies the detector(s) used in the QA measurement, the counting presets, analysis settings, and other parameters for this type of acquisition. This QA **Scan Type** must be selected in the Operator program when QA is performed through the **Startup** function. See also Section 10.1.1, “Setting Up QA for Renaissance Operator.”

To maintain consistency between QA measurements in the two programs, we recommend that the .SDF/.SVD file used for a particular detector in Supervisor QA also be used in the scan type file for that detector’s Operator QA measurements.

NOTE Be sure to read the discussion in Section 2.4 on how QA data integrity can be affected by re-running the MCB Configuration program.

- 18) The Operator program allows you to create one or more categories of **Optional Comments** so operators can capture, in an organized manner, information such as subject date of birth, radiation work permit number, and contract or work ticket number. To set up this list, start Operator, go to the menu bar, and select **Services/Options Text**. Follow the instructions in the Operator user's manual to configure the list, *be sure to perform a test scan, using the appropriate scan type, to save the optional fields in the associated database*, then close the Operator program.

4. DISPLAY FEATURES

This chapter addresses the Renaissance Supervisor display features, discusses the role of the mouse and keyboard, covers the use of the Toolbar and sidebars, and shows how to change to different disk drives and folders.

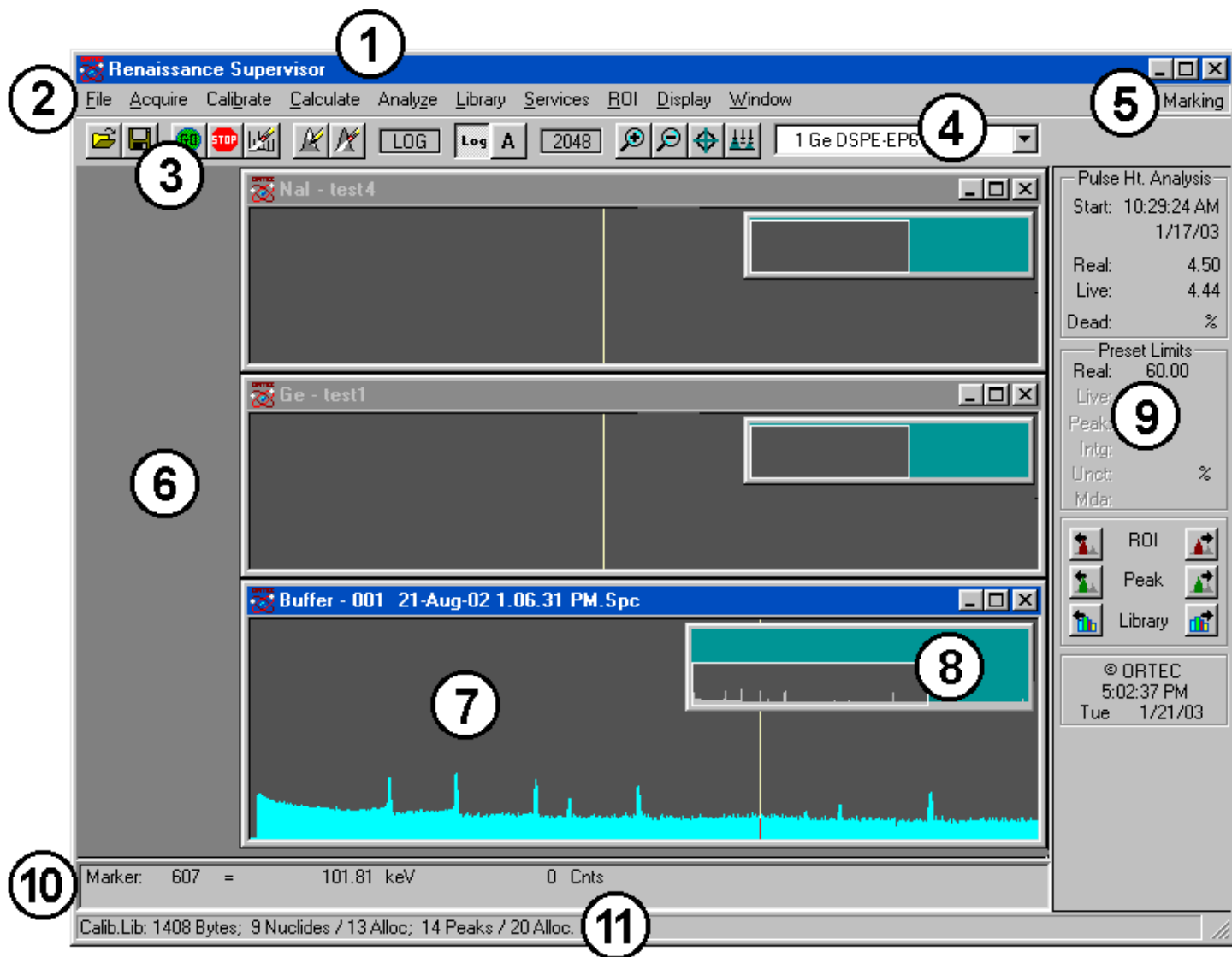


Figure 7. Main Renaissance Screen Features.

Figure 7 shows Renaissance principal screen features.

- 1) **Title bar**, showing the program name and mode selected. On the far right are the Minimize, Maximize, and Close buttons. There is also a title bar on each of the spectrum windows showing the data source, which will be either the Detector name or the word “Buffer” and the spectrum name. The title bar on the active spectrum window will normally be a brighter color than the bar on inactive windows (the color scheme will depend on the desktop colors you have selected in Windows Control Panel).

- 2) **Menu Bar**, showing the available menu commands (which can be selected with either the mouse or keyboard); these functions are discussed in detail in Chapter 5.
- 3) **Toolbar**, beneath the Menu Bar, contains icons for recalling spectra, saving them to disk, starting and stopping data acquisition, and adjusting the vertical and horizontal scales for the active spectrum.
- 4) **Detector Droplist**, on the Toolbar, displays the list of currently available Detectors (remember that, on first use, you must populate this list with the **Edit Ge Lists...** and **Edit NaI Lists** commands [Section 5.7.6.1]). Clicking this field opens a list of all Detectors currently available in Supervisor and Operator. Germanium detectors have a **Ge** prefix before the name and sodium iodide detectors have an **NaI** prefix. Selecting a Detector will open a new spectrum display and show the spectrum for this Detector.
- 5) **ROI Status Area**, on the right side of the menu bar, indicates whether the ROI marking mode is currently **Mark**, **UnMark**, or **Off**. This operates in conjunction with the **ROI** menu commands and arrow keys (see Section 5.8).
- 6) **Spectrum Area**, which can display one or more windows of data from Detectors, buffers, or spectrum files. These windows can be moved, sized, minimized, maximized, and closed with the mouse, as well as tiled horizontally or vertically from the **Window** menu. When more than one window is open, only one is active — available for data manipulation and analysis — at a time. The title bar on the active window will normally be a brighter color than those on the inactive windows (again, this will depend on your Windows desktop colors). The title bar will contain the Detector name for MCBs or for buffers into which an MCB memory has been copied, or the spectrum name and sample description for buffers containing spectra from disk. To switch windows, click on the window that you wish to activate, use the **Window** menu (see Section 5.10), or cycle between windows by pressing **<Ctrl + Tab>**.

Each spectrum window contains an **Expanded Spectrum View** and a **Full Spectrum View** (see items 7 and 8 below).

- 7) The **Expanded Spectrum View** shows all or part of the full histogram; this allows you to zoom in on a particular part of the spectrum and see it in more detail. You can change the expanded view vertical and horizontal scaling, and perform a number of analytical operations such as peak information, marking ROIs, or calibrating the spectrum. This window contains a vertical line called a marker that highlights a particular position in the spectrum. Information about that position is displayed on the Marker Information Line (see item 10 below).

- 8) The **Full Spectrum View** shows the full histogram from the file or the Detector memory. The vertical scale is always logarithmic, and the window can be moved and sized (see Section 4.3.4). The Full Spectrum View contains a rectangular window that marks the portion of spectrum now displayed in the Expanded Spectrum View. To quickly move to different part of the spectrum, just click on that area in the Full Spectrum View and the expanded display updates immediately at the new position.
- 9) **Status Sidebar**, on the right side of the screen, provides information on the current Detector presets and counting times, the time and date, and a set of buttons to move easily between peaks, ROIs, and library entries (see Section 4.4).
- 10) **Marker Information Line**, beneath the spectrum, showing the marker channel, marker energy, channel contents and in some modes, other details about the marker channel, such as the efficiency at this energy.
- 11) **Supplementary Information Line**, below the Marker Information Line, used to show library contents, the results of certain calculations, warning messages, or instructions.

4.1. Spectrum Displays

The Full and Expanded Spectrum Views show, respectively, a complete histogram of the active spectrum and an expanded view of all or part of the spectrum. These two windows are the central features of the Renaissance screen. All other windows and most functions relate to the spectrum windows. The Full Spectrum View shows the entire data memory of the Detector as defined in the configuration. In addition, it has a marker box showing which portion of the spectrum is displayed in the Expanded Spectrum View.

The Expanded Spectrum View contains a reverse-color marker line at the horizontal position of the pixel representing the marker channel. This marker can be moved with the mouse pointer, as described in Section 4.3.1, and with the <->/<-> and <PgUp>/<PgDn> keys, the peak buttons or by selections in other lists, such as the library energy list.

The spectrum display can be expanded to show more detail or contracted to show more data using the **Zoom In** and **Zoom Out** features. Zooming in and out can be performed using the Toolbar buttons, the **Display** menu commands, or the rubber rectangle (see Section 4.3.3). The rubber rectangle allows the spectrum to be expanded to any horizontal or vertical scale. The baseline or “zero level” at the bottom of the display can also be offset with this tool, allowing the greatest possible flexibility in showing the spectrum in any detail.

The Toolbar and **Display** menu zoom commands offer a quick way to change the display. These change both the horizontal and vertical scales at the same time. For **Zoom In**, the horizontal

width is reduced by about 6% of full width (ADC conversion gain) and the vertical scale is halved. The **Zoom In** button and menu item zoom to a minimum horizontal scale of 6% of the ADC conversion gain. For **Zoom Out**, the horizontal width is increased by about 6% of full width (ADC conversion gain) and the vertical scale is doubled.

The **Keypad<+>** and **Keypad<->** accelerator keys duplicate the **Zoom In** and **Zoom Out** Toolbar buttons and **Display** menu commands. The <F5>/<F6> and <↓>/<↑> keys change the vertical scale by a factor of two without changing the horizontal scale. The <F7>/<F8> and *keyboard* <->/<+> keys change the horizontal scale by a factor of two without changing the vertical scale. The <Alt + F7> key displays the whole spectrum in the expanded view.

Depending on the expansion or overall size of the spectrum, all or part of the selected spectrum can be shown in the expanded view. Therefore, the number of channels might be larger than the horizontal size of the window, as measured in pixels. In this case, where the number of channels shown exceeds the window size, all of the channels cannot be represented by exactly one pixel dot. Instead, the channels are grouped together, and the vertical displacement corresponding to the maximum channel in each group is displayed. This maintains a meaningful representation of the relative peak heights in the spectrum. For a more precise representation of the peak shapes displaying all available data (i.e., where each pixel corresponds to exactly one channel), the scale should be expanded until the number of channels is less than or equal to the size of the window.

Note that the marker can be moved by no less than one pixel or one channel (whichever is greater) at a time. In the scenario described above, where there are many more memory channels being represented on the display than there are pixels horizontally in the window, the marker will move by more than one memory channel at a time, even with the smallest possible change as performed with the <-> and <+> keys. If true single-channel motions are required, the display must be expanded as described above.







In addition to changing the scaling of the spectrum, the colors of the various spectrum features (e.g., background, spectrum, ROIs) can be changed using the **Display** menu.

4.2. The Toolbar

The row of buttons below the Menu Bar provides convenient shortcuts to some of the most common Renaissance menu functions.





The **Recall** button retrieves an existing spectrum file. This is the equivalent of selecting **File/Recall** from the menu.

-  **Save** copies the currently displayed spectrum to disk. It duplicates the menu function **File/Save As...**
-  **Start Acquisition** starts data collection in the active Detector. This duplicates **Acquire/Start** and **<Alt + 1>**.
-  **Stop Acquisition** stops data collection in the active Detector. This duplicates **Acquire/Stop** and **<Alt + 2>**.
-  **Clear Spectrum** clears the Detector or file spectrum in the active window. This duplicates **Acquire/Clear** and **<Alt + 3>**.
-  **Mark ROI** automatically marks an ROI in the active spectrum at the marker position, according to the criteria in Section 5.8.4. This duplicates **ROI/Mark Peak** and **<Insert>**.
-  **Clear ROI** removes the ROI mark from the channels of the peak currently selected with the marker. This duplicates **ROI/Clear** and **<Delete>**.

The next section of the Toolbar (Fig. 8) contains the buttons that control the spectrum vertical scale. These commands are also on the **Display** menu. In addition, vertical scale can be adjusted by zooming in with the mouse (see Fig. 14).



Figure 8. Vertical Scaling Section of Toolbar.





-  **Vertical Log/Lin Scale** switches between logarithmic and linear scaling. When switching from logarithmic to linear, it uses the previous linear scale setting. The keyboard equivalent is **Keypad</>**.
-  **Vertical Auto Scale** turns on the *autoscale* mode, a linear scale that automatically adjusts until the largest peak shown is at its maximum height without overflowing the display. The keyboard equivalent is **Keypad<*>**.

The field to the left of these two buttons displays **LOG** if the scale is logarithmic, or indicates the current vertical full-scale linear value.

The horizontal scaling section (Fig. 9) follows next. It includes a field that shows the current window width in channels, and the **Zoom In**, **Zoom Out**, **Center**, and **Baseline Zero** buttons. These commands are also on the **Display** menu. In addition, horizontal scale can be adjusted by zooming in with the mouse (see Fig. 14).



Figure 9. Horizontal Scaling Section of Toolbar.

-  **Zoom In** decreases the horizontal full scale of the Expanded Spectrum View according to the discussion in Section 4.1, so the peaks appear “magnified.” This duplicates **Display/Zoom In** and **Keypad<+>**.
-  **Zoom Out** increases the horizontal full scale of the Expanded Spectrum View according to the discussion in Section 4.1, so the peaks appear reduced in size. This duplicates **Display/Zoom Out** and **Keypad<->**.
-  **Center** moves the marker to the center of the screen by shifting the spectrum without moving the marker from its current channel. This duplicates **Display/Center** and **Keypad<5>**.
-  **Baseline Zero** switches to autoscale mode and sets the baseline of the Expanded Spectrum View to zero. Autoscale is then switched off.

NOTE In addition to the preceding commands, see the **Full View** command on the **Display** menu (duplicated by **<Alt+F7>**). This function adjusts the horizontal and vertical scaling to display the entire spectrum in the Expanded Spectrum View.

The right-most part of the Toolbar is a drop-down list of the available Detectors (Fig. 10). To select a Detector or the buffer, click in the field or on the down-arrow beside it to open the list, then click on the desired entry. The sidebar will update to the live time, real time and presets for the spectrum selected.

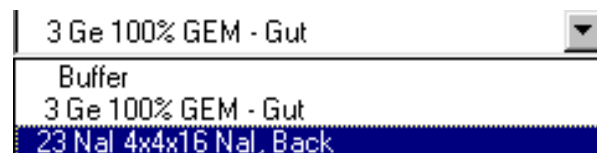


Figure 10. Detector Droplist.

Finally, when the mouse pointer is paused over the center of a Toolbar button, a roll-over *tool tip* box opens, describing the button’s function (Fig. 11).



Figure 11. Tool Tip.

4.3. Using the Mouse

The mouse can be used for every function in Renaissance except text entry. This section covers specialized mouse functions.

4.3.1. Moving the Marker with the Mouse

To position the marker with the mouse, move the pointer to the desired channel in the Expanded Spectrum View and click the left mouse button once. This will move the marker to the mouse position. Click in the Full Spectrum View to move the expanded view to that place. This is generally a much easier way to move the marker around in the spectrum than using the arrow keys and keyboard shortcuts, although mouse and keyboard commands can be mixed.

4.3.2. The Right-Mouse-Button Menu

Figure 12 shows the right-mouse-button menu. To open it, position the mouse pointer in the spectrum display, click the right mouse button, then use the left mouse button to select from the list of commands. Not all of the commands are available at all times, depending on the spectrum displayed and whether the rubber rectangle is active. Except for **Undo Zoom In**, all of these functions are on the Toolbar or in one of the Menu items. See Section 5.11 for more information on the commands.

4.3.3. Using the “Rubber Rectangle”

The rubber rectangle is used for selecting a particular area of interest within a spectrum. It can be used in conjunction with the right-mouse-button menu (see Fig. 12) for many functions. To draw a rubber rectangle:

- 1) Click and hold the left mouse button; this anchors the starting corner of the rectangle.
- 2) Drag the mouse diagonally across the area of interest. A reverse-color rectangle bisected by the marker line is drawn. Note that when drawing a rubber rectangle, the marker line combines with a horizontal line inside the rectangle to form crosshairs (Fig. 13).

They make it easy to select the center channel in the area of interest — this might be the center of an ROI to mark or unmark, a portion of the spectrum to be summed, or a peak for the **Peak Info** function.

- 3) Release the mouse button; this anchors the ending corner of the rectangle.

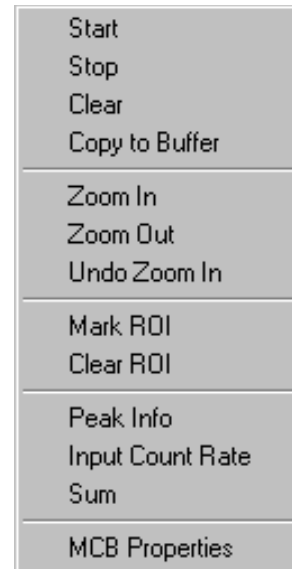


Figure 12. Right-Mouse-Button Menu for Spectra.

- 4) Click the right mouse button to open the popup menu and select one of the available commands. Once an area is selected, the commands can also be issued from the Toolbar, Menu Bar, Status Sidebar, or keyboard.

As an example, Fig. 14 illustrates the process of marking a region with a rubber rectangle and zooming in using the right-mouse-button menu.

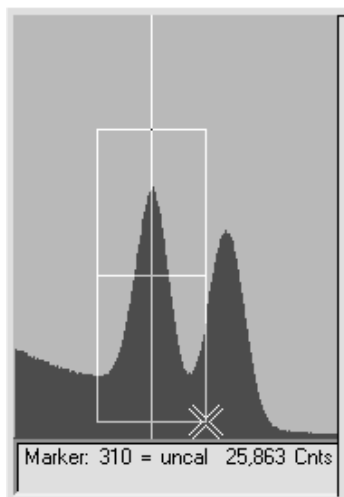


Figure 13. The Rubber Rectangle's Crosshairs.

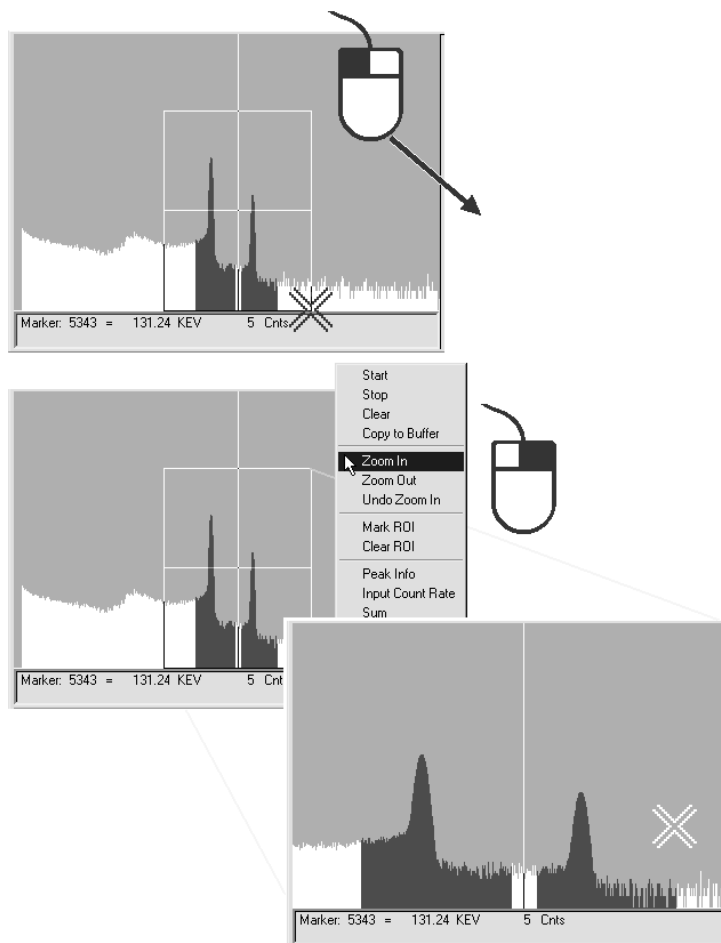


Figure 14. Zooming In Using the Rubber Rectangle and Right-Mouse-Button Menu.

The rectangle can also be moved using the arrow keys. The **<Shift + ←>** and **<Shift + →>** keys move the box left and right, while **<Shift + ↑>** and **<Shift + ↓>** move the box up and down. This enables the box to be precisely positioned.

4.3.4. Sizing and Moving the Full Spectrum View

To change the horizontal and vertical size of the Full Spectrum View, move the mouse pointer onto the side edge, bottom edge, or corner of the window until the pointer changes to a double-sided arrow (see Fig. 15). Click and hold the left mouse button, drag the edge of the window until it is the desired size, then release the mouse button.

To move the Full Spectrum View to a different part of the screen, move the mouse pointer onto the top edge of the window until the pointer changes to a four-sided arrow (see Fig. 15). Click and hold the left mouse button, drag the window to its new location, and release the mouse button.

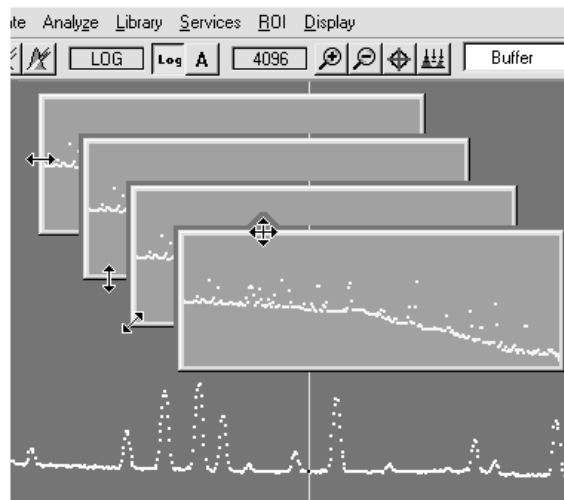


Figure 15. Two-Sided Pointer for Sizing Full Spectrum View, and Four-Sided Pointer for Moving Window.

4.4. Buttons and Boxes

This section describes the Renaissance radio buttons, indexing buttons, and checkboxes. To activate a button or box, just click on it.

Radio buttons (Fig. 16) appear on many Renaissance dialogs, and allow the selection of only one of the choices.

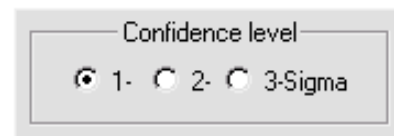


Figure 16. Radio Buttons.

Checkboxes (Fig. 17) are another common feature, allowing the selection of one or more of the options at the same time.

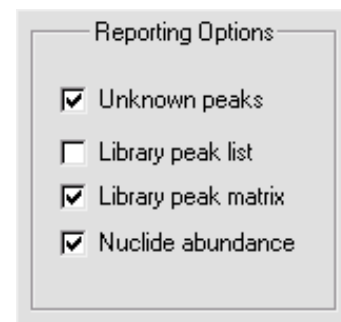
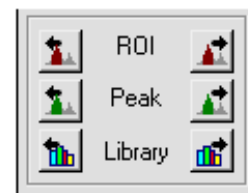


Figure 17. Checkboxes.

The **ROI**, **Peak**, and **Library** indexing buttons on the Status Sidebar are useful for rapidly locating ROIs or peaks, and for advancing between entries in the library. When the last item in either direction is reached, the computer beeps and Renaissance posts a “no more” message on the Supplementary Information Line. If a library file has not been loaded or the Detector is not calibrated, the **Library** buttons are disabled and shown in gray.

The indexing buttons are displayed in two different ways, depending on whether the active spectrum is a Detector or a buffer. This two are shown in Fig. 18.

When the active spectrum is a Detector, the buttons appear at the bottom of the Status Sidebar. If the active spectrum is a buffer, the buttons are overlaid where the **Presets** and indexing buttons are displayed in Detector mode.



The **ROI**, **Peak**, and **Library** buttons function the same for both Detector and buffer. For buffers, the additional features are the ability to insert or delete an ROI with the **Ins** and **Del** buttons, respectively (located between the **ROI** indexing buttons); and to display the peak information for an ROI with the **Info** button (located between the **Peak** indexing arrows).

The **Library** buttons are useful after a peak has been located to advance forward or backward through the library to the next closest library entry. Each button click advances to the next library entry and moves the marker to the corresponding energy.

Instead of using the **Peak** buttons to index from a previously identified peak, position the marker anywhere in the spectrum and click on the **Library** buttons to locate the entries closest in energy to that point. If a warning beep sounds, it means that all library entries have been exhausted in that direction, or that the spectrum is not calibrated. In any case, if an appropriate peak is available at the location of the marker, data on the peak activity are displayed on the Marker Information Line at the bottom of the screen.

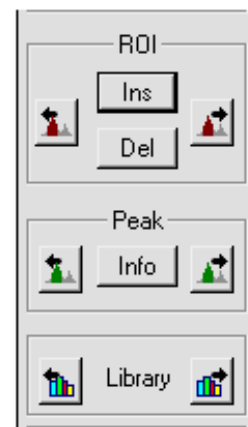


Figure 18.
Indexing Buttons
(Detector mode, top; buffer mode, bottom).

The **ROI** and **Peak** indexing buttons are duplicated by <Shift + ←>/<Shift + →> and <Ctrl + ←>/<Ctrl + →>, respectively. The **Library** buttons are duplicated by <Alt + ←>/<Alt + →>. The **Del** button function is duplicated by the <Delete> key and **Clear ROI** on the menus and Toolbar. The **Ins** button has the same function as the <Insert> key and **Mark ROI** on the menus and Toolbar. The **Info** button duplicates the **Calculate/Peak Info** and the **Peak Info** command on the right-mouse-button menu.

4.5. Drag and Drop

Several types of files can be dragged and dropped into Renaissance, including spectra (.SPC, .AN1, .CHN), calibration (.CLB), library (.LIB), analysis results (.UFO), peak background correction (.PBC), and region of interest (.ROI) files.

The drag-and-drop operation is handled the same as a read (recall) operation for that file type. For spectra, this means the file is loaded into a buffer and displayed. Library and PBC files become the working library and PBC files, respectively. The ROIs saved in an .ROI file are read and the regions set.

4.6. Associated Files

When Renaissance is installed, it registers the spectrum files in Windows so they can be opened from Windows Explorer by double-clicking the filename. The spectrum files are displayed in WinPlots. The .JOB, .EFT, and .ENT files open in Windows Notepad.

[Intentionally blank]

5. MENU COMMANDS

This chapter describes all of the Renaissance menu commands and their associated dialogs. Shortcut keys (if any) are shown to the right of the menu function they duplicate. Also, the underlined letter in the menu item indicates a key that can be used together with the <Alt> key for quick access in the menu. (So, for example, the **R**ecall... dialog under **F**ile can be reached by the following key sequence: <Alt + F>, <Alt + R>.) The ellipsis (...) following a menu selection indicates that a dialog is displayed to complete the function. Finally, a small arrow (“▶”) following a menu selection means a submenu with more selections will be shown.

There are two menu structures: a *full* menu and a *default* menu that contains the most commonly used commands (to change between them, use the **Switch to...** command on the **Services** menu). This chapter discusses the commands as they are presented on the full menus. If there are any differences between a command on the full menu and the same command on the default menu, they are noted in the text (for instance, in default mode the **File/Settings** dialog has only two tabs, but in full mode it has four). The menus and commands are:

File (page 32)

- Settings...
- R**ecall...
- Save **A**s...
- E**xport
- I**mport
- P**rint
- C**ompare...
- E**xit
- About Renaissance...

Acquire (page 43)

- Acquisition Settings...
- Start Alt+1
- Stop Alt+2
- Clear Alt+3
- Copy to **B**uffer Alt+5
- Q**A ▶
 - Settings...
 - Measure **B**ackground
 - Measure **S**ample
 - S**tatus...
 - Control **C**hart...
- Download Spectra
- Z**DT Display Select F3
- M**CB Properties...
- G**ain Adjust

Calibrate	(page 70)
Energy...	
Efficiency...	
Lower Limit...	
Description...	
Recall Calibration...	
Save Calibration...	
Print Calibration...	
Ge Calibration Wizard...	
Calculate	(page 116)
Settings...	
Peak Info	
Sum Channels	
Smooth	
Strip...	
Sum Spectra...	
Analyze	(page 122)
Settings ▶	
Sample Type...	
Reports...	
Group Sample Type...	
Peak Background Correction ▶	
Create PBC...	
Select PBC...	
Edit PBC...	
Entire Spectrum in Memory...	
Display Analysis Results...	
Interactive in Viewed Area...	
Library	(page 164)
Select Peak...	
Select File...	
Edit ▶	
GammaVision Editor...	
Nuclide Navigator...	
List...	
Services	(page 171)
Switch to Default Menu	
Job Control...	
Database Management ▶	
Create Database...	

Select Database...
Purge...
 Change Password
Lock/Unlock Detector...
Edit Detector Lists...
 Edit Ge List...
 Edit NaI List...
 Edit Groups...
Operator Permissions...
 Operator Scan Type
 Alarm Limits...

ROI (page 192)

<u>O</u> ff	F2 or Alt+O
<u>M</u> ark	F2 or Alt+M
<u>U</u> nMark	F2 or Alt+U
Mark <u>P</u> eak	Insert
<u>C</u> lear <u>D</u> elete	
Clear <u>A</u> ll	
<u>S</u> ave File...	
<u>R</u> ecall File...	

Display (page 195)

<u>L</u> ogarithmic	Keypad(/)
<u>A</u> utomatic	Keypad(*)
Baseline <u>Z</u> oom	
Zoom <u>I</u> n	Keypad(+)
Zoom <u>O</u> t	Keypad(-)
<u>C</u> enter	Keypad(5)
<u>F</u> ull View	Alt+F7
<u>P</u> references ▶	
<u>P</u> oints	
Fill <u>R</u> OI	
Fill <u>A</u> ll	
Fill <u>S</u> inglets	
Fill <u>M</u> ultiplet Peaks	
Fill <u>M</u> ultiplet Composites	
<u>S</u> pectrum Colors...	
Peak Info <u>F</u> ont/Color...	

Window (page 199)

Cascade
 Tile Horizontally
 Tile Vertically

Arrange Icons
 Close
 Close All
 [list of open spectrum windows]

Right-Mouse-Button Menu

(page 199)

Start
 Stop
 Clear
 Copy to Buffer
 Zoom In
 Zoom Out
 Undo Zoom In
 Mark ROI
 Clear ROI
 Peak Info
 Input Count Rate
 Sum
 MCB Properties

5.1. File

The **File** menu contains the spectrum file save, recall, import/export, print, and compare commands as shown in Fig. 19.

5.1.1. Settings...

The **File Settings** dialog allows you to specify how the spectrum data will be saved, imported and exported; and to set the directories for all the major file types used by Renaissance. The File Settings dialog is shown in Fig. 20. In full-menu mode, this dialog has four tabs; in default-menu mode, it has only the General and Directories tabs.

5.1.1.1. General

The entries on this tab control the file type and questions automatically asked (or the defaults for these questions) when a spectrum is saved after acquisition. When you finish setting the parameters in this dialog and click on **OK**, these settings will be used until changed.

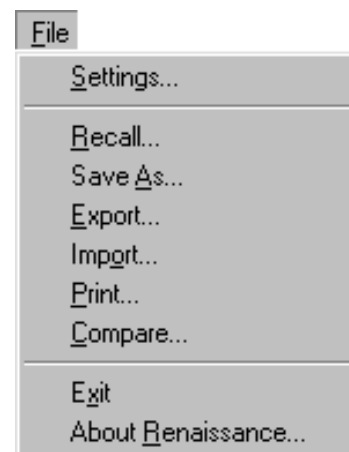


Figure 19. Full File Menu.

For other adjustable parameters, see **Acquire/Acquisition Settings...** (Section 5.2.1) and **Analyze/Settings/Sample Type...** (Section 5.5.1.1 for Ge or Section 5.5.1.2 for NaI).

Save File Format

This selection determines the file-save format in both the Supervisor and Operator programs. The formats for these and other Renaissance file types are described in the *File Structure Manual*.

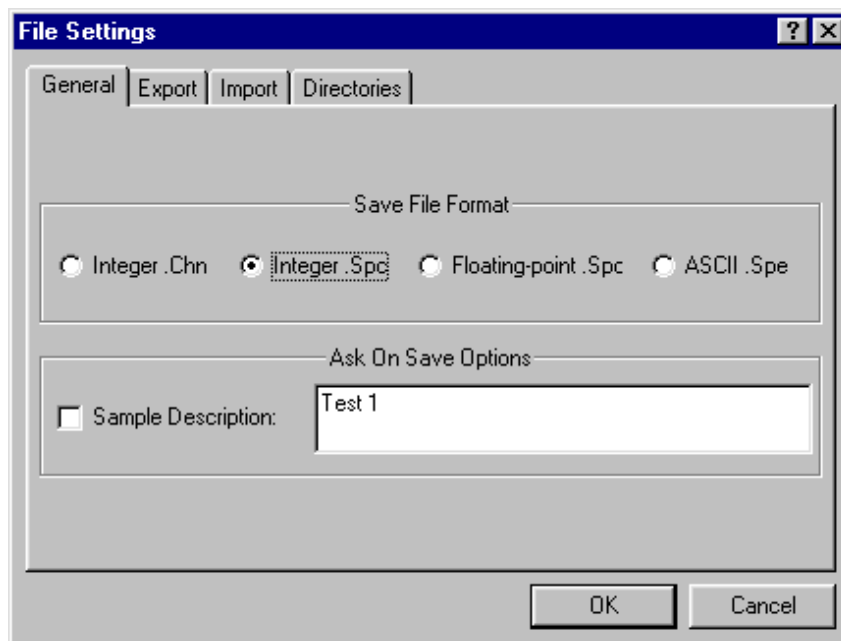


Figure 20. General Tab.

The **.CHN** file format is included for historical purposes only and *should not be used in Renaissance*. It does not contain the analysis parameter data, the complete calibration, or other data needed for the nuclide analysis.

The two **.SPC** formats, integer and floating-point, are identical except for the format of the spectrum data. The integer **.SPC** format should be used unless the files are to be used by earlier versions of ORTEC programs. The **.SPC** files contain the energy calibration data and the hardware parameters. The integer format stores the spectrum as 4-byte integers and the floating-point format uses the 4-byte exponential format used in the hardware math coprocessor and most languages for the computer. The analysis and calibration formats are defined in the *File Structure Manual*.

The ASCII **.SPE** format is used by the Comprehensive Test Ban Treaty Organization (CTBTO).

Ask On Save Options

Sample Description allows you to designate the default sample description that will be presented for acceptance or modification when the spectrum is saved. This time-saver lets you enter the common descriptors for a group of samples ahead of time, then add the unique descriptors on a sample-by-sample basis after acquisition.

5.1.1.2. Export

The Export tab (Fig. 21) is used to specify the program, arguments, and file directory to be used when the **Export...** function is selected.

Choose any program⁵ that can accept the spectrum filename as an argument on the command line. Click on **Browse...** to automatically select the complete proper path for the program.

Arguments:

The **Arguments:** to the program can be specified as user-entered character strings or the user can select from the list of “macros” shown in Fig. 22. The list is displayed by clicking on the arrow button to the right of the **Arguments:** field. Entries (macros or direct) must be separated by spaces to be read as separate arguments.

File Path Name

This will insert the complete file pathname (e.g., `c:\user\spectrum\test.chn`) into the dialog box. The filename is the name selected in the filename entry dialog.

File Base Name

This will insert the file path name *without* the extension (e.g., `c:\user\spectrum\test`) into the dialog box. The filename is the name selected in the filename entry dialog. The extension can be entered manually after the macro (e.g., `$(FullBase).CHN`) into the dialog box.

Note that the “dot” (.) must also be entered. Related filenames can also be made by adding characters before the “dot” (e.g., `$(FullBase)A.CHN`).

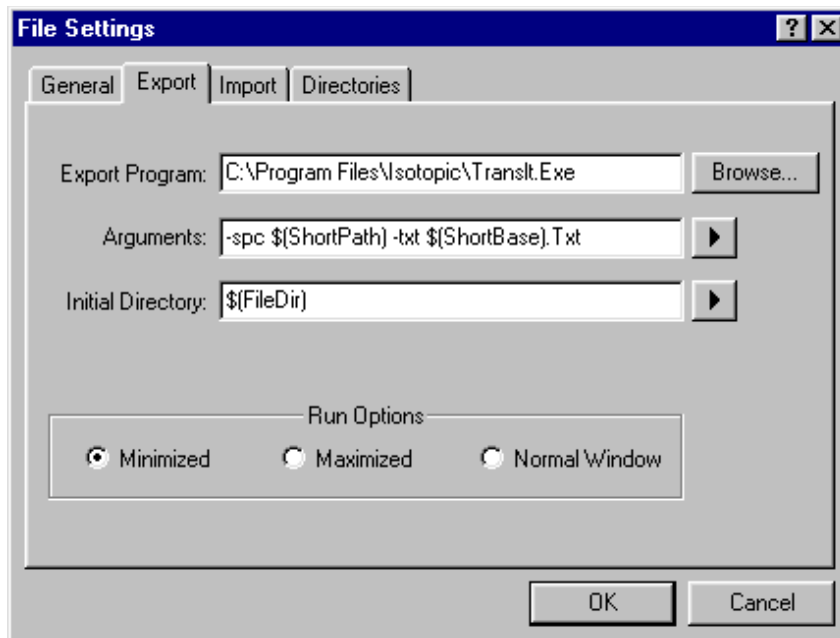


Figure 21. Export Tab.

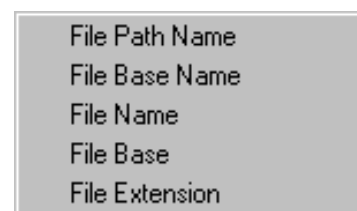


Figure 22. Export Argument Macros.

⁵Any executable program that can be executed from the Windows **Run** command can be selected, including DOS batch commands.

File Name

This will insert the filename (e.g., `test.CHN`) into the dialog box. The filename is the name selected in the filename entry dialog. **File Name** can be constructed as `[file base]. [file extension]`.

File Base

This will insert the base filename (e.g., `test`) into the dialog box. The file base name is the name selected in the filename entry dialog.

File Extension

This will insert the file extension (e.g., `CHN`) into the dialog box. The file extension is the name selected in the filename entry dialog. *Note that the “dot” is not included.*

Any manually inserted input of the macro form (`$(xxx)`) will be included in the argument list without changes.

Initial Directory

The initial directory for the program to use can be specified as directly entered character strings or the user can select from the list of macros in Fig. 23. The list is displayed by clicking on the arrow button to the right of the **Initial Directory:** field.

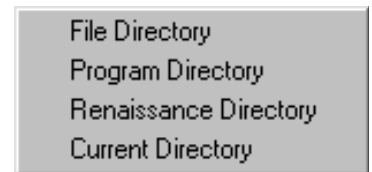


Figure 23. The Initial Directory Export Macros.

File Directory

This is the directory selected in the filename selection dialog when the export file is selected (e.g., `c:\user\spectrum\`).

Program Directory

This is the directory for the conversion program. It is shown in the first entry of this dialog.

Renaissance Directory

This is the directory where the Renaissance program is stored. The default location is `c:\Program Files\Renaissance`.

Current Directory

This is the current default directory for Windows.

Run Options

These three radio buttons (**Minimized**, **Maximized**, and **Normal Window**) are used to select the window for the program. If the program does not have any user dialogs, any option can be selected. If the program needs user inputs, **Normal Window** should be selected.

5.1.1.3. Import

Click on the Import tab to display the dialog shown in Fig. 24. The program to be executed and the default file extension when the **Import...** function is selected can then be specified. Choose any program that can accept the spectrum filename on the command line. Click on **Browse...** to automatically select the complete proper path for the program.

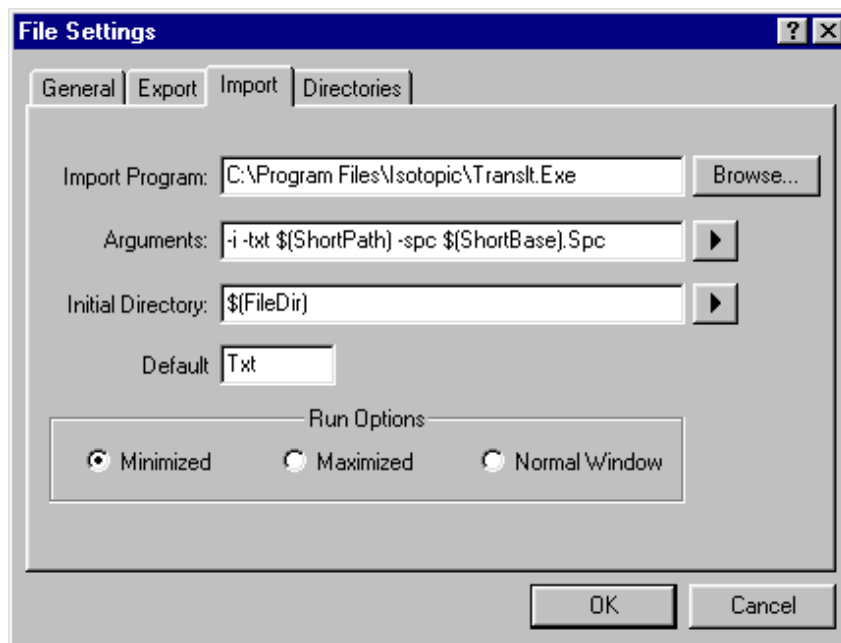


Figure 24. Import Tab.

Arguments:

The arguments to the program can be specified as directly entered character strings or you can select from the list of macros shown in Fig. 25. The list is displayed by clicking on the arrow button to the right of the **Arguments:** field. The entries (macros or direct) must be separated by spaces to be read as separate arguments.

File Path Name

This will insert the *complete* file path name (e.g., `c:\user\spectrum\test.txt`) into the dialog box. The filename is the name selected in the filename entry dialog.

File Base Name

This will insert the file path name *without* the extension (e.g., `c:\user\spectrum\test`) into the dialog box. The filename is the name selected in the file name entry dialog. The extension can be entered manually after the macro (e.g., `${FullBase}.CHN`) into the dialog box. *Note that the “dot” (.) must also be entered.* Related filenames can also be made by adding characters before the “dot” (e.g., `${FullBase}A.CHN`).

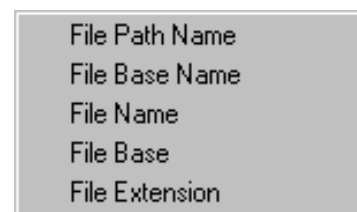


Figure 25. Import Arguments.

File Name

This will insert the filename (e.g., `test.TXT`) into the dialog box. The filename is the name selected in the filename entry dialog. **File Name** can be constructed as `[file base].[file extension]`.

File Base

This will insert the base filename (e.g., `test`) into the dialog box. The file base name is the name selected in the filename entry dialog.

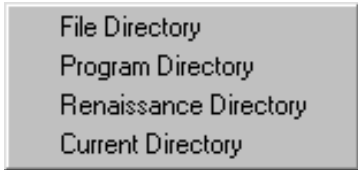
File Extension

This will insert the file extension (e.g., `TXT`) into the dialog box. The file extension is the name selected in the filename entry dialog. *Note that the “dot” is not included.*

Any manually entered input of the macro form (`$(xxx)`) will be included in the argument list without changes.

Initial Directory

Specify the initial directory for the program to use either with directly entered character strings or by selecting from the list of macros shown in Fig. 26. The list is displayed by clicking on the arrow button to the right of the **Initial Directory:** field.



File Directory
Program Directory
Renaissance Directory
Current Directory

Figure 26. Import Macros.

File Directory

This is the directory selected in the filename selection dialog when the import file is selected (e.g., `c:\user\spectrum\`).

Program Directory

This is the directory for the conversion program. It is shown in the first entry of this dialog.

Renaissance Directory

This is the directory where the Renaissance program is stored. The default location is `c:\Program Files\Renaissance`.

Current Directory

This is the current default directory for Windows.

Default

The default extension entered here is used as the extension for the filename in the filename entry dialog. For example, if **TXT** is entered, then the name list in the entry dialog will be ***.TXT**.

Run Options

These three radio buttons (**Minimized**, **Maximized**, and **Normal Window**) are used to select the window for the program. If the program does not have any user dialogs, any option can be selected. If the program needs user inputs, **Normal Window** should be selected.

5.1.1.4. Directories

Use this tab (Fig. 27) to select the default file directories for spectrum files, calibrations, **.JOB** files, Operator scan type (**.OPR**) files, libraries, and other files.⁶

To change the path (**Location**) of a particular **File Type**, click on the desired file type to highlight it, then click on **Modify...** This will open a standard file-recall dialog. Choose a new path and click **Open**.

The **All Files in Spc Directory** checkbox is a shortcut that sends all of the above file types to the location you set for **Spectra**.

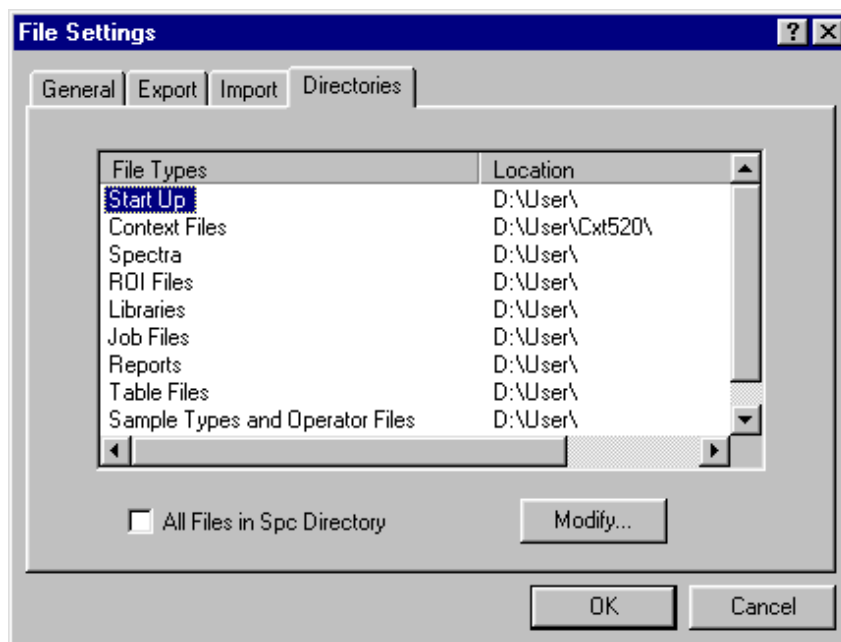


Figure 27. Directories Tab.

NOTE Scan type (**.OPR**) files are stored in the location specified for **Sample Types and Operator Files**, along with the analysis options files for Ge detectors (**.SDF** files) and NaI (**.SVD** files).

When all path changes have been completed, click on **OK** to use them or **Cancel** to retain the previous settings.

⁶Renaissance Supervisor and Operator save spectrum and analysis data to the file types and locations listed here. In addition, Operator saves spectrum and analysis data to the Renaissance database. The file types in this dialog can reside in a different location than the Renaissance databases, and different databases can have different locations.

5.1.2. Recall...

This function opens a standard file-open dialog (Fig. 28) that allows you to recall a spectrum file into a buffer window. The spectrum files are created with the **Save As...** command in both Renaissance Supervisor and Operator, and during subject scans in Renaissance Operator.⁷

NOTE To preserve the integrity of the spectrum files created when scanning subjects in the Operator program, *you must recall only spectra with the .An1 extension for modification in Supervisor, rather than the corresponding .SPC files.* The .An1 files contain all of the spectrum data and the current parameters generated from Operator.

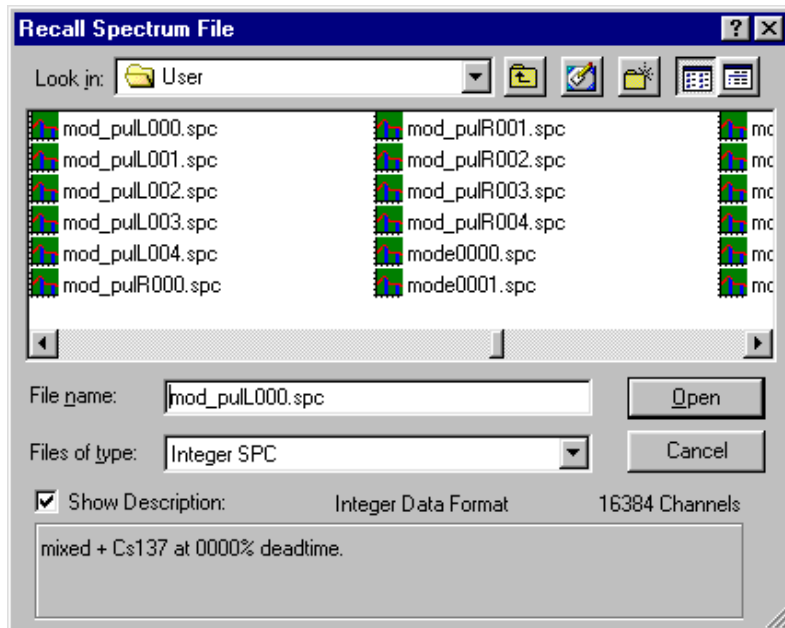


Figure 28. Recall a Spectrum File.

Note the **Show Description** checkbox on the lower left of the dialog. Mark this to display the sample description (if one was created), format, and spectrum size of each file without having to open it.

When the spectrum is successfully recalled, Renaissance loads its descriptors (start time, live time, real time, Detector and sample descriptions) and calibration information (if any), and displays the filename and sample description on the title bar of the spectrum Window.

For spectrum files containing multiple spectra (such as ZDT mode in supported digital spectrometers), both spectra are automatically recalled.

⁷In addition, you can recall spectrum files generated by other ORTEC applications, such as MAESTRO and GammaVision, that produce the .SPC, .CHN, and .SPE formats.

5.1.3. Save As...

This command opens a standard file-save dialog (Fig. 29) so the current spectrum can be saved to disk. Enter any valid filename (consisting of an optional drive and directory, a file-name, and an optional extension) in the **File name** field and click **Save**. The recommended and default extension are shown in the dialog according to the format chosen. If that file already exists, a message box opens asking you to verify the entry or cancel the operation. Clicking on **OK** will completely overwrite the existing file. After the disk file has been saved, its filename is displayed on the spectrum window title bar.

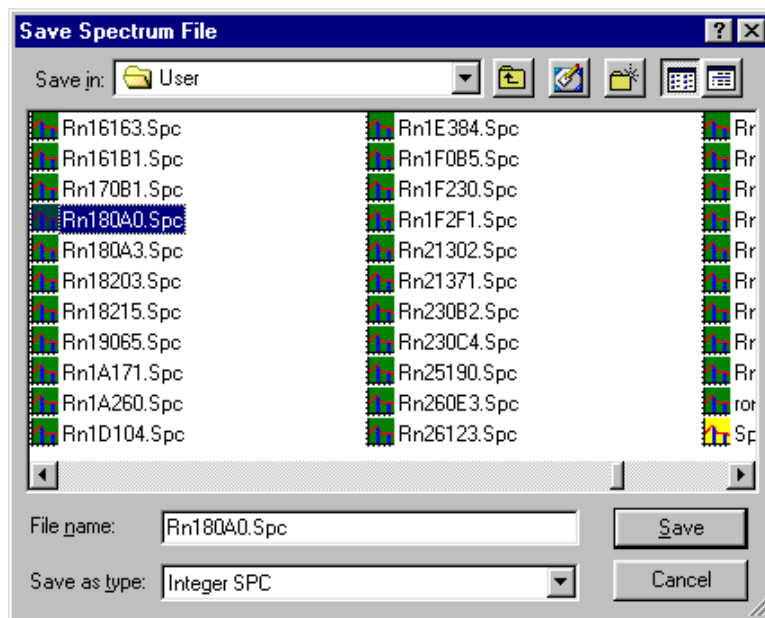


Figure 29. Save Spectrum As.

The format selected is used rather than the type specified on the General tab under **File/Settings...** (Section 4.1.1.1.) which is the default here. The file extension should be left at the default setting to avoid confusion. This is especially true if the spectra are to be used in non-ORTEC programs. For hardware with multiple spectra (such as ZDT mode in the DSPEC Pro), both spectra are saved in the file.

5.1.4. Export...

The **Export...** command is used to write spectra in formats other than the usual formats, or to perform other functions such as plotting or printing the spectrum directly. The export program is specified on the Export tab under **File/Settings...**, as discussed in Section 5.1.1.2. The program can be one of the programs supplied or can be user-supplied. When selected, the **Export Spectrum File** dialog, shown in Fig. 30, is displayed. Choose the name of the spectrum to be exported.

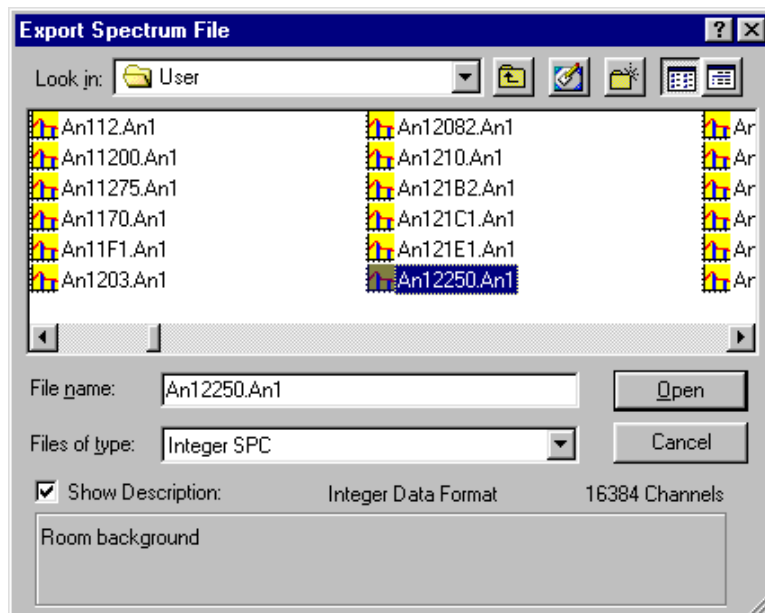


Figure 30. The Export Spectrum File Dialog.

The currently displayed spectrum must be saved to disk before it can be exported. If the currently displayed spectrum has already been stored to disk, that filename is the default. Any file can be selected. The file is then read and the output file is written by the program.

The **Export...** function is not available for a second file until the first file has been exported and the export program has stopped execution.

Export... can also be used to generate hard copy plots. To do this, select the WinPlots program (supplied with Renaissance) as the export program. When **Export...** has been selected, WinPlots will be executed. If the **-P** switch is specified on the command line (see Sections 5.1.1.2 and 13.1.3, page 380), the program will plot the spectrum and exit automatically.

5.1.5. Import...

The **Import** command opens a standard file-open dialog that allows you read spectrum files that are not in one of the usual formats (i.e., **.CHN** or **.SPC**). The import program is specified on the Import tab under **File/ Settings...**, as discussed in Section 5.1.1.3. The program can be one of the programs supplied by ORTEC or can be user-supplied. When the Import File dialog opens, select the filename and click **Open**. The file is then read and a spectrum file is written to the specified directory.

Renaissance attempts to read this file (in **.CHN** or **.SPC** format) and displays the spectrum. If the Import program does not produce a file that Renaissance can read, no spectrum is displayed.

5.1.6. Print

The **Print** function (Fig. 31) does one of the following:

- If the marker is in an ROI, the data contents of the ROI channels are printed.
- If the marker is not in an ROI, the contents of the channels in the spectrum window are printed.

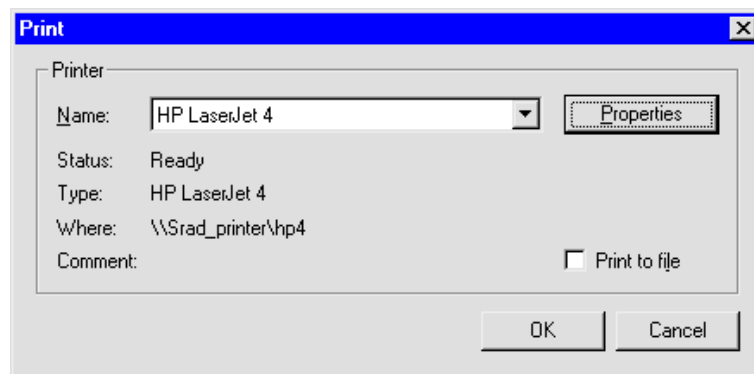


Figure 31. Print Spectrum.

Use the **Print** dialog to print the output or save it in a disk file (click on **Print to file** to mark it). Click on **Properties** to change print options such as paper orientation and resolution.

The data are formatted at seven channels per line with the channel number on the left.

5.1.7. Compare...

This function displays a spectrum from disk along with the active spectrum so the two can be visually compared. When **Compare Spectra...** is selected, a standard file-recall dialog box opens so you can choose the desired spectrum. The active spectrum window then shows both spectra, as illustrated in Fig. 32.

Note that the spectra in this illustration are displayed in **Fill All** mode, in which all of the area under the peaks is filled with a color different from the background (see **Display/Preferences/Fill All**, Section 5.9.8.1).

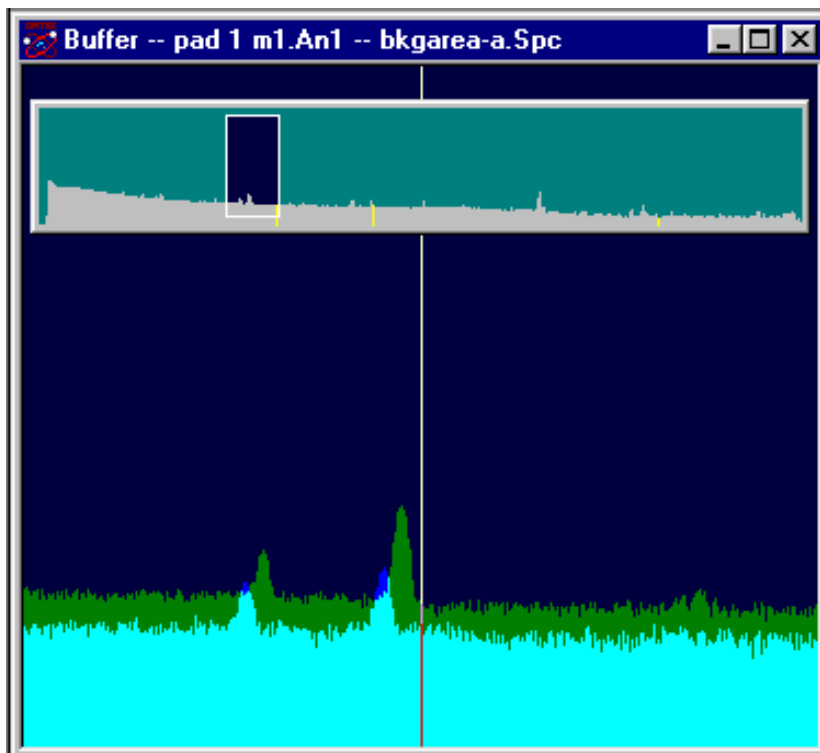


Figure 32. Compare Mode Screen.

For supported digital spectrometers, both spectra (live-time-corrected [LTC] or uncertainty [ERR] and ZDT) are compared. **Normal** refers to LTC or ERR; **Corrected** refers to ZDT. Use <F3> to switch between **Normal** and **Corrected** for both spectra, that is, to show **Normal/Normal** or **Corrected/Corrected**. To switch only the compare between **Normal** and **Corrected**, use <Shift + F3>, that is, to show **Normal/Corrected** use <Shift + F3>.

The Compare spectrum is offset from the starting spectrum and can be moved up and down incrementally with the <Shift + ↑> and <Shift + ↓> accelerators. In addition, the vertical scale of both spectra can be simultaneously changed with <↑> and <↓>.

Note that the Compare spectrum ROIs (if any were saved with the file) are not marked in this mode.

Figure 33 is a detailed view of a spectrum comparison similar to that in Fig. 32. In this illustration, the starting spectrum is displayed in color (1), the Compare spectrum is shown in color (2), the starting spectrum ROIs are marked in color (3), and the portion of the starting spectrum that exceeds the Compare spectrum is indicated by color (4). These

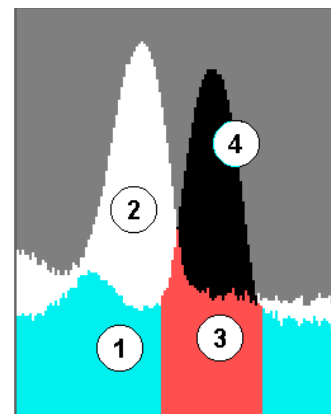


Figure 33. Spectrum Colors in Compare Mode.

colors (called **Foreground**, **Compare**, **ROI**, and **Composite**, respectively) are chosen on the **Color Preferences** dialog discussed in Section 5.9.8.3.

Press <Esc> to leave Compare mode.

5.1.8. Exit

This exits Renaissance and returns to Windows. If the buffer contains a spectrum that has not been saved, a warning message is displayed. Any JOBs are terminated. All MCBs continue to acquire data until the presets are met.

5.1.9. About Renaissance...

Figure 34 shows the About box for Renaissance. It provides software version information that will be useful should you need customer support.

Click the **Visit ORTEC OnLine** button to browse our website includes our product catalog, application notes, technical papers, information on training courses, and access to our Global Service Center.

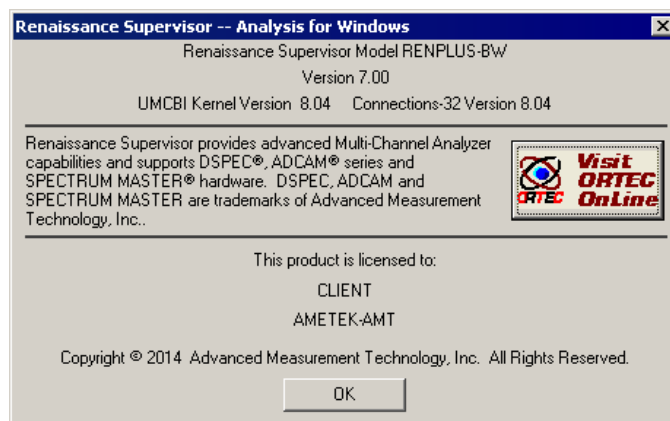


Figure 34. About Renaissance.

5.2. Acquire

The **Acquire** menu is shown in Fig. 35. Access to the various functions depends on whether the active spectrum is a Detector or buffer. **Download Spectra** is only available for the digiDART and DART. **ZDT Display Select** is enabled only for supported digital spectrometers.

NOTE In some cases, a Detector option might be inactive (gray) because it is disabled for the current Detector (while it might still be valid for some other Detector in the system, or for this Detector under different conditions).

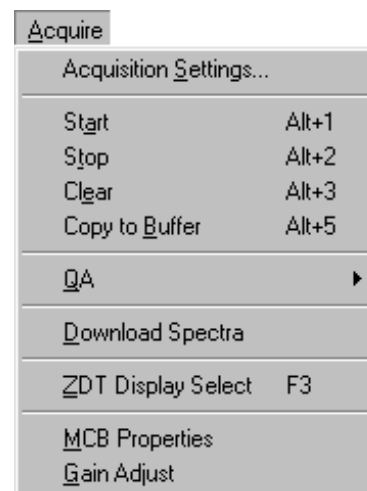


Figure 35. Full Acquire Menu.

5.2.1. Acquisition Settings...

This command opens the Acquisition Settings dialog (Fig. 36), which shows a number of questions that can be “asked on start” (when a Detector is started) and their default values.

5.2.1.1. Start Options

The **Start Options** affect *only the Supervisor program*. Click on **Clear Data** to automatically clear the spectrum each time the acquisition is started. Click on the **Ask for Presets** to display the Presets dialog at the start of the acquisition. The dialog is the same as the Preset tab in MCB Properties (see **Acquire/MCB Properties...**, Section 5.2.9).

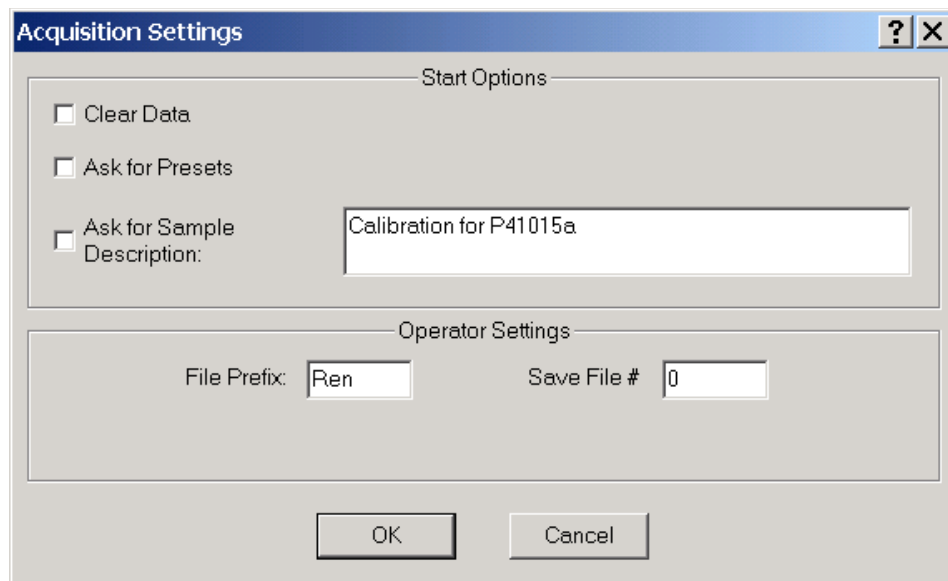


Figure 36. Acquisition Settings.

To display the Sample Description dialog at the start of the acquisition, mark the **Ask for Sample Description** box. The description entered here is the default description for the dialog. This feature is handy when processing a number of similar samples; the common part of the description can be entered here, and the unique descriptors added at the start of acquisition.

If you choose **Cancel** when responding to an ask-on-start prompt for a specific MCB, any subsequent ask-on-start prompts for that Detector will not be asked, and acquisition in that MCB will be canceled.

NOTE Because the **Sample Description** is not displayed on the Operator report, this ask-on-start feature has no application in Operator subject measurements. If you wish, the operator can capture a sample description by entering it in the **Comments** for each scan. Alternatively, you might wish to use the **Services/Options Text** command in the Operator program to create a comment category for sample descriptions.

5.2.1.2. Operator Settings

These settings are used in both the Supervisor and Operator programs, and affect the filenames assigned to sample spectra and PBC spectra (QA uses different filename settings).

In Supervisor, filenames consist of a base name (**File Prefix**) and a sequence number (**Save File #**), which is automatically incremented after each use. The **File Prefix** can be up to seven alphanumeric characters. The first one to seven characters of the filename are the file prefix. The final eight characters are the sequence digits. The sequence number for a file starts with the number entered in the **Save File #** field.

For multi-detector groups, the complete filename must be different for each detector. This is done either by making the prefix different; or by offsetting the file number by making the first detector start with **0000**, the second detector start with **0100**, and so on. (The offset must be large enough to accommodate all of the spectra to be collected.) The number increments to the number of allowed characters (e.g., **99999999**) then restarts at zero (e.g., **00000000**). The filename is expanded to eight characters with zeros. The filename will be incremented by 1 each time a spectrum is saved. For example, if 0 were entered for prefix **REN**, the first filename would be **REN00000000**, the second would be **REN00000001**, and so on.

The Operator program creates filenames based on these **File Prefix** and **Save File #** parameters, as well as the name of the subject and the detector group.

The filename is only used internally in the Operator program. The spectrum filename, all of the data collected, and analysis results are stored in the database. All review of the results and re-analysis is done using the database entries, therefore, the supervisor and operator do not have to remember the filenames. The filenames for a specific analysis can be displayed using the **Services/Database Management/Purge** command.

The **Ask for Detector Positions on Start** checkbox enables the Detector configuration dialogs to be displayed in the Operator Mode each time a measurement is started. This allows the operator to enter the exact positions of the Detector for the current measurement. If the Detector positions do not change from measurement to measurement, this option can be left unmarked.

5.2.2. Start

This initiates data collection in the active Detector. Any warnings arising from problems detected at the hardware level will appear in a message box or on the Supplemental Information Line at the bottom of the display. The Detector can also be started with the **<Alt + 1>** shortcut, the **Start Acquisition** button on the Toolbar, or the **Start** command on the right-mouse-button menu. If the Detector is already started or if a buffer is the active spectrum, this entry is grayed.

5.2.3. Stop

Stop terminates data collection in the active Detector. If the Detector is not collecting data or the active spectrum is a buffer, the entry is grayed. The Detector can also be stopped with the short-cut <Alt + 2>, the **Stop Acquisition** button on the Toolbar, and the **Stop** command on the right-mouse-button menu.

5.2.4. Clear

Clear erases the spectral data and the descriptors (e.g., real time, live time, start time) for the active spectrum. The presets are not altered. (This function might not operate on some types of Detectors when they are collecting data.) The data can also be cleared with <Alt+ 3>, the **Clear Spectrum** button on the Toolbar, or the **Clear** command on the right-mouse-button menu.

5.2.5. Copy to Buffer

The **Copy to Buffer** function opens a Buffer window (or uses an unused Buffer) then transfers the data and descriptors (e.g., live time, real time), from the active Detector to the Buffer. This function can also be performed with <Alt + 5> or the **Copy to Buffer** command on the right-mouse-button menu.

5.2.6. QA

This is explained in Chapter 10, “Quality Assurance.”

5.2.7. Download Spectra...

This is supported only by the digiDART and DART. This command downloads the spectra from the portable MCB to the computer disk. The files are stored in the directory and format defined in the File Settings dialog. The file name format is:

ssiiiiiiiddddddddtttttttt.ext

where

- | | |
|---------|---|
| sss | is the sequence number of the spectrum. This is the index number shown on the digiDART spectrum list display. |
| iiiiiii | is the ID string entered when the spectrum was collected. It is shown on the digiDART spectrum list display. |
| ddddddd | is the date the spectrum was collected, as recorded in the MCB. |

tttttttt is the time the spectrum was collected, as recorded in the MCB.

ext is the extension for the file type selected.

If any **Ask on Save** options are set in the file settings dialog, they will be asked for each spectrum individually.

NOTE This command does not erase the spectra from the Detector.

5.2.8. **ZDT Display Select**

This command is active only when the current Detector supports the zero-dead-time (ZDT) feature and is operating in one of the ZDT modes. The ZDT mode is selected on the ADC tab under **Acquire/MCB Properties...** When the MCB is in a **ZDT** mode, two spectra are collected; this selects which spectrum to display.

The spectrum is labeled in the upper-right corner of the Full Spectrum View. Either the **ZDT**, **LTC**, or **ERR** label appears in the Full Spectrum View. This function is duplicated by <F3>.

5.2.9. **MCB Properties...**

CONNECTIONS applications use a uniform dialog for data acquisition setup, accessed with the **Acquire/MCB Properties...** command. The property pages for the DSPEC-50 are described here. To see the Properties dialog for other CONNECTIONS MCBs, refer their respective hardware manuals.

Depending on the currently selected MCB, the Properties dialog displays several tabs of hardware controls including ADC setup parameters, acquisition presets, high-voltage controls, amplifier gain adjustments, gain and zero stabilizers, pole-zero and other shaping controls, and the InSight™ Virtual Oscilloscope. In addition, the Status tab for certain MCBs monitors conditions such as alpha chamber pressure, detector status, charge remaining on batteries, and the number of spectra collected in remote mode. Simply move from tab to tab and set your hardware parameters, then click **Close**. Note that as you enter characters in the data-entry fields, the characters will be underlined until you move to another field or until 5 seconds have lapsed without keyboard input. During the time the entry is underlined, no other program or computer on the network can modify this value.

If the Detector is locked (see Section 5.7.5), you must know the password before you can modify its MCB properties. To view a locked Detector's properties in read-only mode, click **Cancel** when the Unlock Password dialog opens.

5.2.9.1. DSPEC Pro

Amplifier

Figure 37 shows the Amplifier tab. This tab contains the controls for **Gain**, **Baseline Restore**, **Preamplifier Type**, **Input Polarity**, and **Optimize**.

NOTE Be sure that all of the controls on the tabs have been set *before* clicking the **Start Auto** (optimize) button. The changes you make on most property tabs *take place immediately*. There is no cancel or undo for these dialogs.

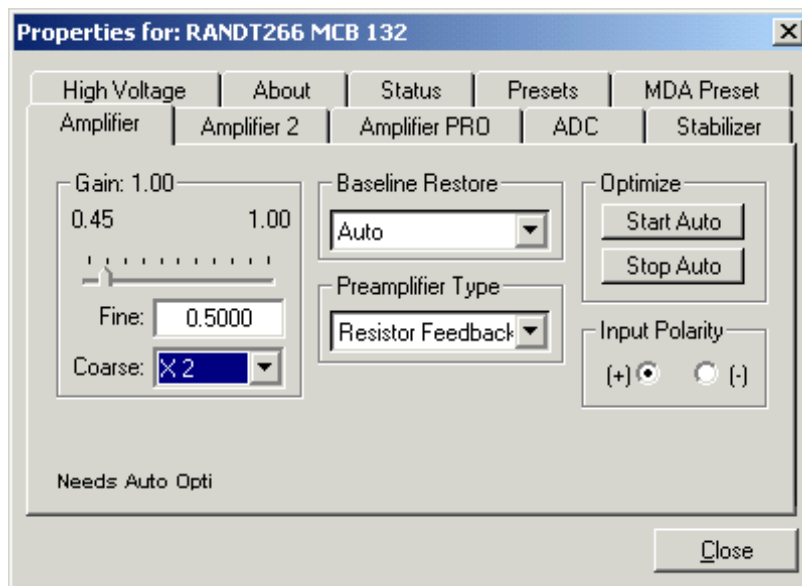


Figure 37. DSPEC Pro Amplifier Tab.

Gain — Set the amplifier coarse gain by selecting from the **Coarse** droplist, then adjust the **Fine** gain with the horizontal slider bar or the edit box, in the range of 0.45 to 1.00. The resulting effective gain is shown at the top of the **Gain** section. The two controls used together cover the entire range of amplification from 0.45 to 32.

Input Polarity — Selects the preamplifier input signal polarity for the signal from the detector. Normally, GEM (p-type) detectors have a positive signal and GMX (n-type) have a negative signal.

Baseline Restore — Returns the baseline of the pulses to the true zero between incoming pulses. This improves the resolution by removing low frequency noise from dc shifts or mains power ac pickup. The baseline settings control the time constant of the circuit that returns the baseline to zero. There are three fixed choices (**Auto**,⁸ **Fast**, and **Slow**). The fast setting is used for high count rates, the slow for low count rates. **Auto** adjusts the time constant as appropriate for the input count rate. The settings (**Auto**, **Fast**, or **Slow**) are saved in the DSPEC Pro even when the power is off. The time constant can be manually set on the InSight display (see the discussion beginning on page 65).

⁸Patent number 5,912,825.

You can view the time when the baseline restorer is active on the InSight display as a **Mark** region (see the discussion on Marks, p. 66). In the automatic mode, the current value is shown on the InSight sidebar. For a low-count-rate system, the value will remain at about 90.

Preamplifier Type — Choose **Transistor Reset** or **Resistive Feedback** preamplifier operation. Your choice will depend on the preamplifier supplied with the germanium detector being used.

Optimize — The DSPEC Pro is equipped with both automatic pole-zero logic⁹ and automatic flattop logic.¹⁰ The **Start Auto** (optimize) button uses these features to automatically choose the best pole zero and flattop tilt settings. Note that if you selected **Transistor Reset** as the **Preamplifier Type** for this DSPEC Pro, the optimize button does not perform the pole zero.

As with any system, the DSPEC Pro should be optimized any time the detector is replaced or if the flattop width is changed. For optimization to take place, the DSPEC Pro must be processing pulses. The detector should be connected in its final configuration before optimizing is started. A count rate guidance message on the lower-left of the Amplifier page will help you position a radio active source to deliver the correct count rate for optimization. The **Start Auto** optimization button will be disabled (gray) until the count rate is suitable.

Select either the **Resistive Feedback** or **Transistor Reset** option and click on **Start Auto**. The optimize command is sent to the DSPEC Pro at this time and, if the DSPEC Pro is able to start the operation, a series of short beeps sounds to indicate that optimization is in progress. When optimizing is complete, the beeping stops.

During optimization, pole zeroes are performed for several rise-time values and the DSPEC Pro is cycled through all the rise time values for the determination of the optimum tilt values. As all of the values for all the combinations are maintained in the DSPEC Pro, the optimize function does not need to be repeated for each possible rise time. The optimization can take from 1 to 10 minutes depending on count rate.

You should repeat the optimization if you change the flattop width.

The effect of optimization on the pulse can be seen in the InSight mode, on the Amplifier 2 tab. Note, however, that if the settings were close to proper adjustment before starting optimization, the pulse shape may not change enough for you to see. (In this situation, you also may not notice a change in the shape of the spectrum peaks.) The most visible effect of incorrect settings is high- or low-side peak tailing or poor resolution.

⁹Patent number 5,872,363.

¹⁰Patent number 5,821,533.

Amplifier 2

Figure 38 shows the Amplifier 2 tab, which accesses the advanced DSPEC Pro shaping controls including the InSight Virtual Oscilloscope mode.

The many choices of **Rise Time** allow you to precisely control the tradeoff between resolution and throughput (Section 5.2.9.3). This setting affects both the rise and fall times, so changing it spreads or narrows the quasi-trapezoid symmetrically.

Use the up/down arrows to set the **Rise Time** from 0.8 to 23.0 μ s.

Once the unit has been optimized (see page 49), you can use any **Rise Time** without having to re-optimize.

In the **Pole Zero** section, the **Start** button performs a pole zero at the specified rise time and other shaping values. Unlike the optimize feature, it performs a pole zero for only the one rise time. The pole-zero **Stop** button aborts the pole zero, and is normally not used.

For the more advanced user, the InSight mode lets you directly view all the parameters and adjust them interactively while collecting live data. To access the InSight mode, go to the **InSight** section on the Amplifier 2 tab and click **Start**. The InSight mode is discussed in more detail in the following section. When you are satisfied with the settings, you are ready to acquire data. Once data acquisition is underway, you may wish to return to **MCB Properties...** and click the **InSight** section's **Start** button to adjust the shaping parameters interactively with a “live” waveform showing the actual pulse shape, or just to verify that all is well.

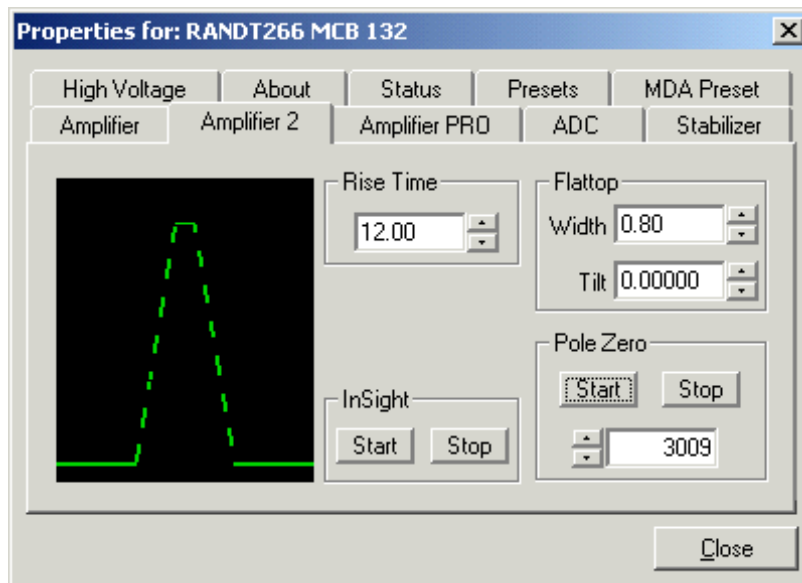


Figure 38. DSPEC Pro Amplifier 2 Tab.

Amplifier PRO

This tab (Fig. 39) contains the controls for the **Low Frequency Rejector (LFR)** filter, **Resolution Enhancer**, and **Enhanced Throughput Mode**. To enable a particular feature, mark the corresponding checkbox. Any or all of these features can be used at one time, however, the LFR and enhanced throughput modes must be set up before the resolution enhancer is configured, as discussed below.

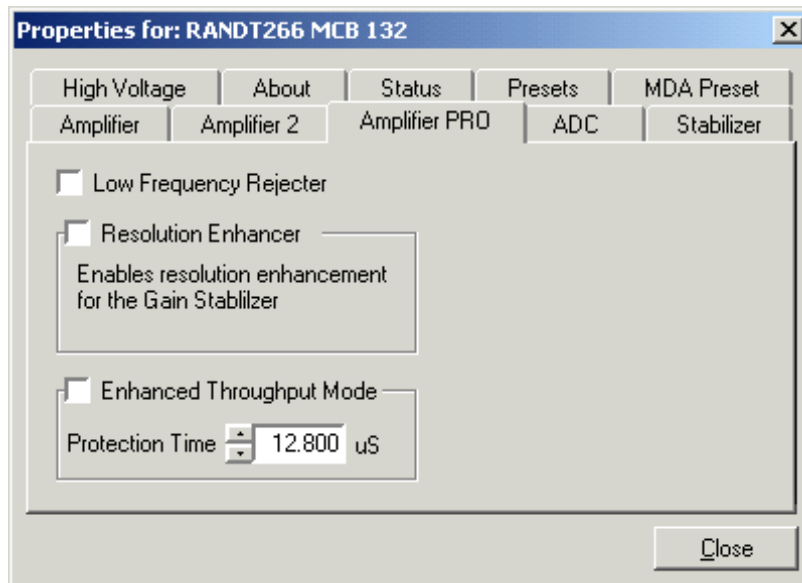


Figure 39. DSPEC Pro Amplifier PRO Tab.

Note that once an MCB is “trained” for the **Resolution Enhancer** (see the following section), it must be “retrained” if any settings are changed that can affect peak shape or position (e.g., bias, gain, rise time, flattop, PZ).

Low Frequency Rejector — This feature is discussed in detail in the hardware manual.

- *The DSPEC Pro cannot optimize or pole-zero in LFR mode.* Optimize or PZ with the filter off, then turn it back on for data collection.
- LFR mode affects the available range of protection times in **Enhanced Throughput Mode**, as discussed in the next paragraph.

Enhanced Throughput Mode — See the hardware manual for a discussion of this feature. The valid **Protection Time** settings, in 25 ns increments, range as follows:

LFR Mode	Highest Throughput (minimum Protection Time)	Lowest Throughput (maximum Protection Time)
Off	(Rise Time + flattop)	(2 × Rise Time + Flattop)
On	(3 × Rise Time + 2 × Flattop)	(6 × Rise Time + 3 × Flattop)

Turning on this feature automatically sets the minimum protection time (highest throughput rate) based on your current **Rise Time** and **Flattop** settings, however, you can adjust this value at any time. Each time you change the rise time or flattop, the DSPEC Pro will automatically set itself to the new minimum protection time.

“Training” the Resolution Enhancer

The Resolution Enhancer can help reduce the low-side peak tailing that results from increased charge trapping; see the discussion in Section ?. It operates by measuring the rise time (collection time) of the pulses and adjusting the gain based on the rise time. This is done on each pulse. The gain adjustment value for the rise time is stored in a table. The values in the table must be set by “training” the Resolution Enhancer. Training requires two to four 15-minute data acquisitions with a mixed-gamma source, for instance, mixed gamma with ^{241}Am . The source should have sufficient activity that the detector registers a count rate of 5000 cps on the endcap.

Marking the **Resolution Enhancer** checkbox enables/disables the “learning” mode. Once trained, the enhancer continues to operate until disabled as discussed on page 53.

NOTE This feature typically improves the shape of low-energy peaks more so than high-energy peaks, and does not improve poor resolution due to causes other than charge trapping.

To Enable and Train the Enhancer

Note that this procedure requires detector recalibration.

- 1) Right-click in the spectrum window and turn on the **Input Count Rate** option.
- 2) Set the desired bias and gain, position the source to deliver a count rate of 1000–5000 cps, and start the **Optimize** routine. A message at the bottom of the Amplifier tab will indicate whether the count rate is too high or low. At the optimum count rate, optimization should take less than 5 minutes.
- 2) Issue the **Clear** command, position the source on or near the endcap, set a **Real Time** preset of 1000 seconds, and acquire a spectrum.
- 3) Energy calibrate on the lowest and highest peaks (for instance, the ^{241}Am 59.54 keV and ^{60}Co 1332.51 keV gamma rays); use the **Peak Info** command to obtain the FWHM data for the ^{241}Am , ^{109}Cd , ^{137}Cs , and ^{60}Co peaks; mark the ^{137}Cs 661.62 keV peak as an ROI; and save the spectrum with a name (and optional sample description) indicating the MCB has been auto-optimized.
- 4) Position the marker in the ^{137}Cs peak, then switch to the Stabilizer tab. In the Gain Stabilizer section, click **Suggest** to capture the peak channel and width of the ^{137}Cs ROI, click the corresponding **Initialize** button, then return to the Amplifier PRO tab and mark the **Resolution Enhancer** checkbox.

- 5) Acquire the first “training” spectrum, then record the FWHM for the ^{241}Am , ^{109}Cd , ^{137}Cs , and ^{60}Co peaks. Clear the data, acquire another spectrum, and record the FWHMs for the target peaks. After 2–4 iterations, the FWHMs should no longer change appreciably, indicating the Resolution Enhancer is “trained.” Save the final spectrum with a name (and optional sample description) indicating the Resolution Enhancer was used to improve peak resolution.
- 6) The table of adjustments will be stored in the DSPEC Pro’s memory, and will continue to be used each time you mark the Resolution Enhancer checkbox, until “retrained.”

NOTE If you change any parameters that affect peak shape, you must repeat this “training” procedure.

To Turn the Enhancer Off

- 1) With the **Resolution Enhancer** checkbox still marked, switch to the Stabilizer tab and click the Gain Stabilizer section’s **Initialize** button.
- 2) Return to the Amplifier PRO tab and unmark the **Resolution Enhancer** box.
- 3) Re-optimize.

ADC

This tab (Fig. 40) contains the **Gate**, **ZDT Mode**, **Conversion Gain**, **Lower Level Discriminator**, and **Upper Level Discriminator** controls. In addition, the current real time, live time, and count rate are monitored at the bottom of the dialog..

Gate — This control allows you to select a positive TTL logic level gating function. With gating **Off**, no gating is performed (that is, all detector signals are processed); with gating in **Coincidence** mode, a gating input signal *must be* present at the proper time for the conversion of the event; in **Anticoincidence**, the gating input signal *must not be* present for the conversion of the detector signal. The gating signal must occur prior to and extend 500 ns beyond peak detect (peak maximum).

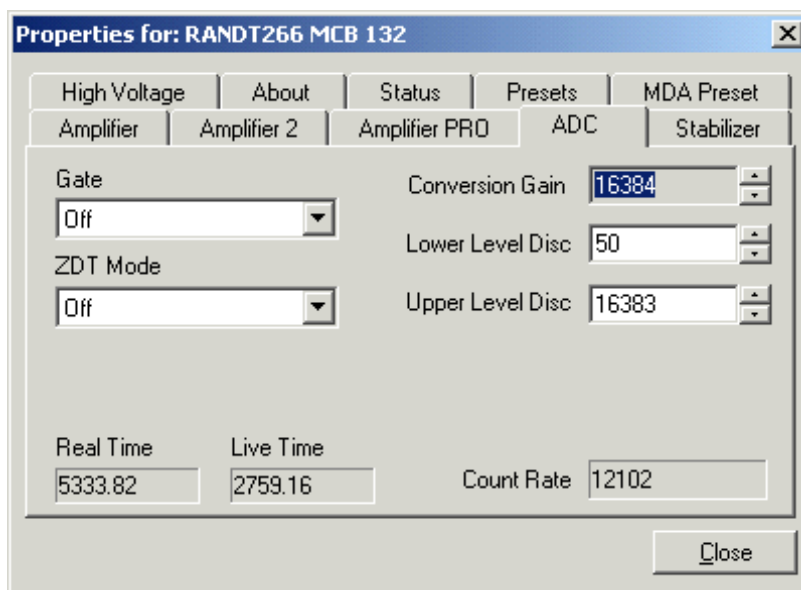


Figure 40. DSPEC Pro ADC Tab.

ZDT Mode — See the hardware manual for a detailed discussion of this feature. Use this drop-list to choose the **Off** (LTC spectrum only) or **CORR_ERR** (ERR and ZDT spectra) mode.¹¹ If a ZDT mode is selected, both spectra are stored in the same spectrum (.SPC) file. If you do not need the ZDT spectrum, you should select **Off**.

In MAESTRO, the display can show either of the two spectra. Use <F3> or **Acquire/ ZDT Display Select** to toggle the display between the two spectra. In the Compare mode, <F3> switches both spectra to the other type and <Shift+F3> switches only the compare spectrum. This allows you to make all types of comparisons.

Conversion Gain — This sets the maximum channel number in the spectrum. If set to 16384, the energy scale will be divided into 16384 channels. The conversion gain is entered in powers of 2 (e.g., 8192, 4096, 2048). The up/down arrow buttons step through the valid settings for the DSPEC Pro.

Upper- and Lower-Level Discriminators — The **Lower Level Discriminator** sets the level of the lowest amplitude pulse that will be stored. This level establishes a lower-level cutoff by channel number for ADC conversions. The **Upper Level Discriminator** sets the level of the highest amplitude pulse that will be stored. This level establishes an upper-level cutoff by channel number for storage.

Stabilizer

The DSPEC Pro has both a gain stabilizer and a zero stabilizer (see Section 5.2.9.2). The Stabilizer tab (Fig. 41) shows the current values for the stabilizers. The value in each **Adjustment** section shows how much adjustment is currently applied. The **Initialize** buttons set the adjustment to 0. If the value approaches 90% or above, the amplifier gain should be adjusted so the stabilizer can continue to function — when the adjustment value reaches 100%, the stabilizer

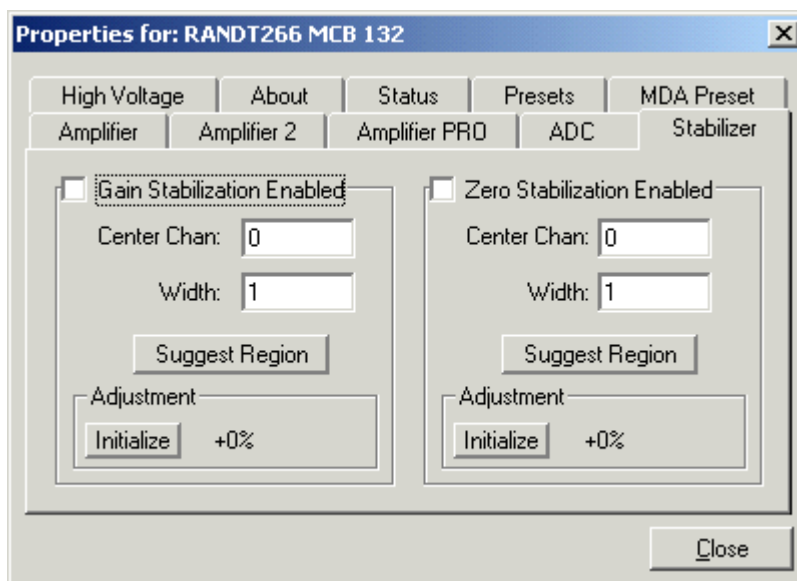


Figure 41. DSPEC Pro Stabilizer Tab.

¹¹ The NORM_CORR (LTC and ZDT) mode is typically not used; see Section ?.

cannot make further corrections in that direction. The **Center Channel** and **Width** fields show the peak currently used for stabilization.

To enable the stabilizer, enter the **Center Channel** and **Width** values manually or click on the **Suggest Region** button. **Suggest Region** reads the position of the marker and inserts values into the fields. If the marker is in an ROI, the limits of the ROI are used. If the marker is not in an ROI, the center channel is the marker channel and the width is 3 times the FWHM at this energy. Now click on the appropriate **Enabled** checkbox to turn the stabilizer on. Until changed in this dialog, the stabilizer will stay enabled even if the power is turned off. When the stabilizer is enabled, the **Center Channel** and **Width** cannot be changed.

High Voltage

Figure 42 shows the High Voltage tab, which allows you to turn the high voltage on or off; set and monitor the voltage; and choose the **Shutdown** mode.

The shutdown can be **TTL**, **ORTEC**, or **SMART**. The **ORTEC** mode is used for all ORTEC detectors except SMART-1 detectors. Use the **SMART** option for those detectors. Check with the detector manufacturer for other detectors. The **TTL** mode is used for most non-ORTEC detectors.

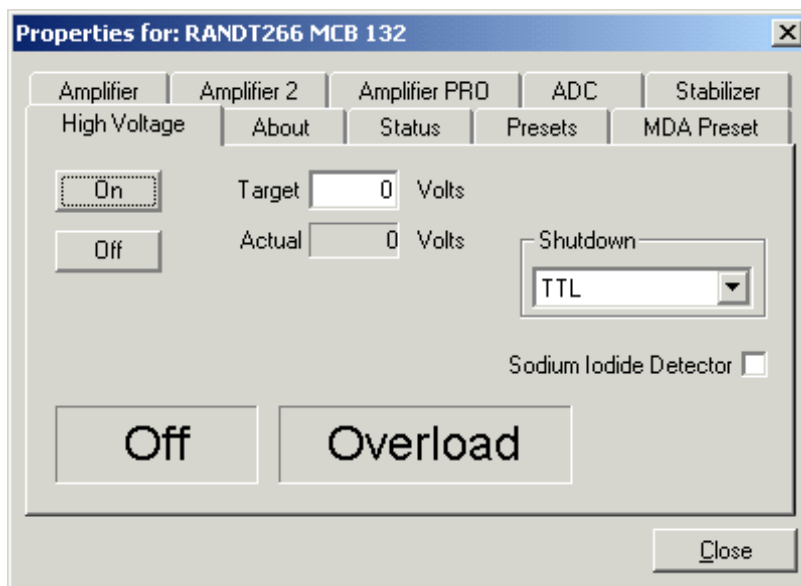


Figure 42. DSPEC Pro High Voltage Tab.

The polarity is determined by the DIM or SMART-1 module, which also supplies the bias voltage. The recommended HV for SMART-1 is displayed on the dialog. For other detectors, see the detector manual or data sheet for the recommended voltage.

Enter the detector high voltage in the **Target** field, click **On**, and monitor the voltage in the **Actual** field. Click the **Off** button to turn off the high voltage. The HV will not turn on if the detector is sending a remote shutdown or overload signal. The **Overload** indicator means there is a bad connection in your system. The **Shutdown** indicator means that either the detector is warm or you have chosen the wrong **Shutdown** or **Source** mode.

To use a **Sodium Iodide Detector**, mark the checkbox. This changes the gain and zero stabilizers to operate in a faster mode. For the DIM-296, the HV is controlled by the adjustment in the Model 296 and not here.

About

This tab (Fig. 43) displays hardware and firmware information about the currently selected DSPEC Pro as well as the data **Acquisition Start Time** and **Sample** description. In addition, the **Access** field shows whether the Detector is currently locked with a password (see Section 5.7.5). **Read/Write** indicates that the Detector is unlocked; **Read Only** means it is locked.

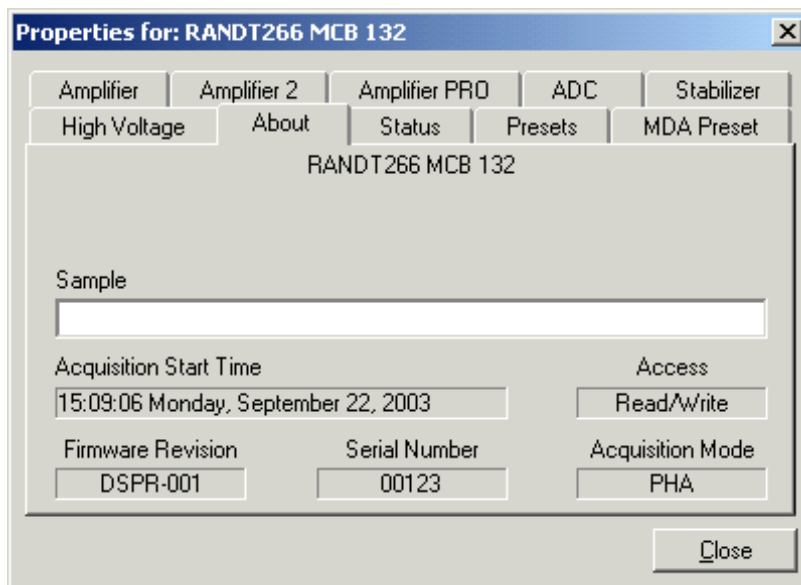


Figure 43. DSPEC Pro About Tab.

Status

Figure 44 shows the Status tab. There are 21 values monitored at all times. You can select any six of these to be displayed simultaneously on the Status tab. The parameters you choose can be changed at any time, so you can view them as needed. Two types of values are presented: **OK** or **ERR**, and numeric value. The state-of-health (SOH) parameters are all **OK** or **ERR**. If the state is **OK**, the parameter stayed within the set limits during the spectrum acquisition. If the parameter varied from the nominal value by more than the allowed limit, the **ERR** is set until cleared by the program. The numeric values are displayed in the units reported by the DSPEC Pro. **Security**, **Detector temperature**, and **Live detector temperature** are available only for SMART-1 detectors. For non-SMART-1 detectors, they show **N/A**.

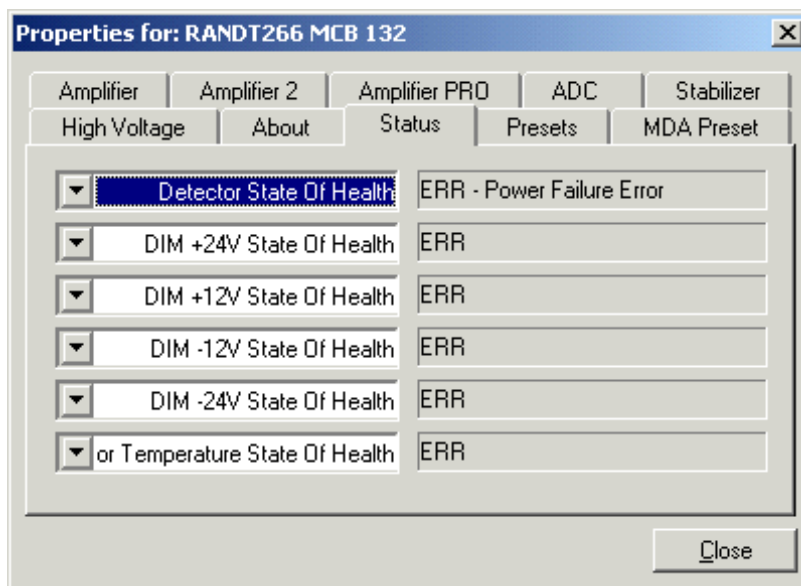


Figure 44. DSPEC Pro Status Tab.

The parameters displayed are:

Detector State of Health

This is OK if all the SOH are OK and ERR if any one is ERR.

DIM +24V State of Health

This is OK if the +24 volt supply in the DIM has stayed within 200 mV of +24 volts since the last time the SOH was cleared.

DIM +12V State of Health

This is OK if the +12 volt supply in the DIM has stayed within 200 mV of +12 volts since the last time the SOH was cleared.

DIM -12V State of Health

This is OK if the -12 volt supply in the DIM has stayed within 200 mV of -12 volts since the last time the SOH was cleared.

DIM -24V State of Health

This is OK if the -24 volt supply in the DIM has stayed within 200 mV of -24 volts since the last time the SOH was cleared.

Temperature State of Health

This is OK if the detector temperature has stayed below the high temperature limit set in the detector since the last time the SOH was cleared. This is available only for SMART-1 detectors.

High Voltage State of Health

This is OK if the HV supply in the DIM has stayed within 200 V of specified bias voltage since the last time the SOH was cleared.

Shutdown State of Health

This is OK if the detector shutdown has not activated since the last time the SOH was cleared.

Preamplifier overload State of Health

This is OK if the preamplifier overload has not activated since the last time the SOH was cleared.

Security State of Health

This is OK if the security test was passed at the end of the last spectrum acquisition. This is available only for SMART-1 detectors.

Power State of Health

This is OK if the power to the DIM was constant during the last spectrum acquisition.

+24 volts

This is the current value of the +24 volt supply in the DIM as delivered to the detector.

+12 volts

This is the current value of the +12 volt supply in the DIM as delivered to the detector.

-12 volts

This is the current value of the -12 volt supply in the DIM as delivered to the detector.

-24 volts

This is the current value of the -24 volt supply in the DIM as delivered to the detector.

High Voltage

This is the current value of the high voltage bias supply in the DIM as delivered to the detector.

Detector temperature

This is the detector temperature at the time the current spectrum acquisition stopped. This is available only for SMART-1 detectors.

Live detector temperature

This is the detector temperature at the current time. This is available only for SMART-1 detectors.

Battery voltage

This is not used in the DSPEC Pro.

Battery % full

This is not used in the DSPEC Pro.

Battery time remaining

This is not used in the DSPEC Pro.

Presets

Figure 45 shows the Presets tab. MDA presets are shown on a separate tab. The presets can only be set on a Detector that is not acquiring data (during acquisition the preset field backgrounds are gray indicating that they are inactive). You can use any or all of the presets at one time. To

disable a preset, enter a value of zero. If you disable all of the presets, data acquisition will continue until manually stopped.

When more than one preset is enabled (set to a non-zero value), the first condition met during the acquisition causes the Detector to stop. This can be useful when you are analyzing samples of widely varying activity and do not know the general activity before counting. For example, the **Live Time** preset can be set so that sufficient counts can be obtained for proper calculation of the activity in the sample with the least activity. But if the sample contains a large amount of this or another nuclide, the dead time could be high, resulting in a long counting time for the sample. If you set the **ROI Peak** preset in addition to the **Live Time** preset, the low-level samples will be counted to the desired fixed live time while the very active samples will be counted for the ROI peak count. In this circumstance, the **ROI Peak** preset can be viewed as a “safety valve.”

The values of all presets for the currently selected MCB are shown on the Status Sidebar. These values do not change as new values are entered on the Presets tab; the changes take place only when you **Close** the Properties dialog.

Enter the **Real Time** and **Live Time** presets in units of seconds and fractions of a second. These values are stored internally with a resolution of 20 milliseconds (ms) since the MCB clock increments by 20 ms. *Real time* means elapsed time or clock time. *Live time* refers to the amount of time that the MCB is available to accept another pulse (i.e., is not busy), and is equal to the real time minus the *dead time* (the time the MCB is not available).

Enter the **ROI Peak** count preset value in counts. With this preset condition, the MCB stops counting when any ROI channel reaches this value unless there are no ROIs marked in the MCB, in which case that MCB continues counting until the count is manually stopped.

Enter the **ROI Integral** preset value in counts. With this preset condition, the MCB stops counting when the sum of all counts in all channels for this MCB marked with an ROI reaches this value. This has no function if no ROIs are marked in the MCB.

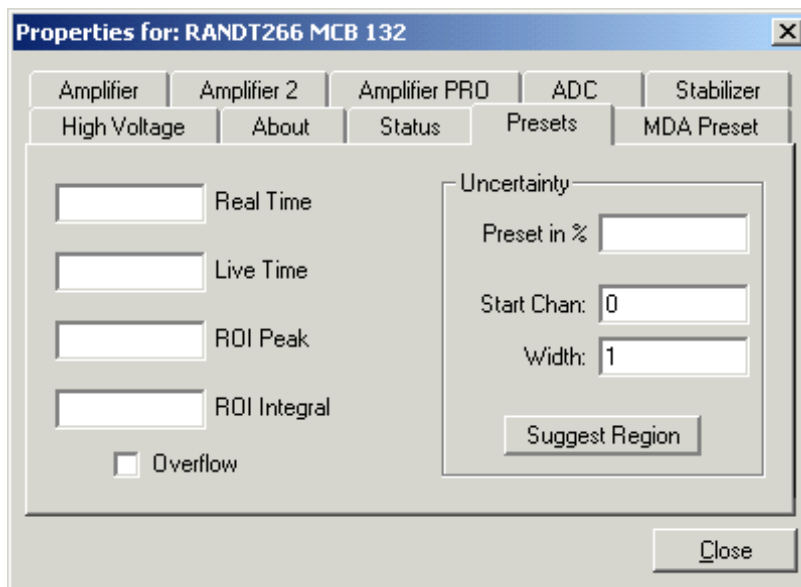


Figure 45. DSPEC Pro Presets Tab.

The **Uncertainty** preset stops acquisition when the statistical or counting uncertainty of a user-selected net peak reaches the value you have entered. Enter the **Preset in %** value as percent uncertainty at 1 sigma of the net peak area. The range is from 99% to 0.1% in 0.1% steps. You have complete control over the selected peak region. The region must be at least 7 channels wide with 3 channels of background on each side of the peak. Note that MAESTRO calculates this preset once per 40 seconds. Therefore, the software will continue data acquisition up to 40 seconds after the preset has been reached, and the uncertainty achieved for a high count-rate sample may be lower than the preset value.

Use the **Start Channel** and **Width** fields to enter the channel limits directly, or click on **Suggest Region**. If the marker is positioned in an ROI around the peak of interest, **Suggest Region** reads the limits of the ROI with the marker and display those limits in the **Start Chan** and **Width** fields. The ROI can be cleared after the preset is entered without affecting the uncertainty calculation. If the marker is not positioned in an ROI, the start channel is 1.5 times the FWHM below the marker channel and the width is 3 times the FWHM.

The net peak area and statistical uncertainty are calculated in the same manner as for the **Peak Info** command (Section 5.4.2).

Marking the **Overflow** checkbox terminates acquisition when data in any channel exceeds $2^{31} - 1$ ($>2 \times 10^9$) counts.

MDA Preset

The MDA preset (Fig. 46) can monitor up to 20 nuclides at one time, and stops data collection when the values of the minimum detectable activity (MDA) for *all* of the user-specified MDA nuclides reach the needed value. Presets are expressed in Bq, and are evaluated every 40 seconds. The detector must be calibrated for energy in all spectroscopy applications, and for efficiency in all applications but MAESTRO.

The MDA presets are implemented in the MCB (i.e., the entries you make on this screen are saved in the MCB memory), and have no direct link to MDA methods selected in the analysis options for applications such as GammaVision, ScintiVision™, ISOTOPIC, etc. The MDA preset calculation uses the following formula:

$$MDA = \frac{a + \sqrt{b + c * Counts}}{Live\ time * (CorrectionFactor)}$$

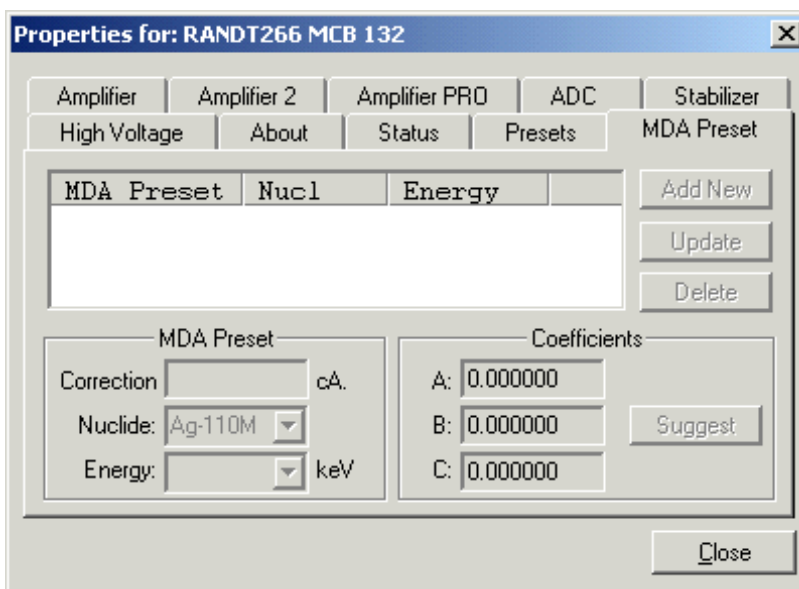


Figure 46. DSPEC Pro MDA Preset Tab.

where:

a , b , and c are determined by the MDA criteria you choose.

Counts is the gross counts in an ROI that is $2.5 \times \text{FWHM}$ around the target peak energy.

Live time is evaluated in 40 second intervals for the MDA presets.

CorrectionFactor is the product of the calibration efficiency at the specified peak energy and the peak's branching ratio (yield) as listed in the working (active) library.

NOTE MAESTRO does not support efficiency calibration. The efficiency component in the *CorrectionFactor* is set to 1.0; the preset field is labeled **Correction** instead of **MDA**; and the preset is based on counting activity (**cA**) instead of becquerels. You can enter the MDA preset either in counts; or corrected for factors such as sample volume, attenuation, or calculated efficiency. For example, if you manually calculate the efficiency for a peak, you can enter a corrected MDA target value by multiplying the desired MDA value times the calculated efficiency, and entering the product as the **Correction**.

To add an MDA preset, enter the preset value in the **MDA** or **Correction** field; select the **Nuclide** and **Energy**; enter the desired values for coefficients a , b , and c ; then click **Add New**.

To edit an existing preset, click to highlight it in the table. This will load its **Nuclide**, **Energy**, and coefficients in the lower sections of the dialog. Change as needed, then click **Update**.

To remove a preset, click to highlight it in the table, then click **Delete**.

IMPORTANT These MDA presets *are not dynamically calculated*. Each time you add an MDA preset to this table, its *CorrectionFactor* value is calculated and stored in the MCB's memory. If you then load a different library, change the efficiency calibration, or change the system geometry, the spectroscopy application *will not update* the existing *CorrectionFactors*, and your MDA presets may no longer be applicable.

When using spectrum analysis applications such as GammaVision and Scinti-Vision, you can create an analysis options file (.SDF or .SVD file) for each system geometry that you use; and include in it a set of MDA presets specific to that geometry, efficiency calibration, and nuclide library. You can then recall this tailored analysis options file as needed.

5.2.9.2. Gain and Zero Stabilization

The gain stabilizer requires a peak in the spectrum to monitor the changes in the gain of the system amplifier. The gain stabilizer controls the amplification factor of a separate amplifier so that the peak will be maintained in its original position.

The zero stabilizer enables you to control the zero-level (or offset) stabilizer. The zero-level stabilizer uses a peak in the spectrum to monitor the changes in the zero level of the system amplifier. The zero stabilizer controls the offset bias level so the peak will be maintained in its original position.

For both functions, the input pulse-height-to-channel-number relationship is:

$$\text{Channel number} = \text{Intercept} + \text{Gain} * \text{pulse height}$$

where:

Intercept = The channel number of the zero-height input pulse

Gain = The relation between pulse height and channel number (slope of the curve)

Changes in either the intercept or gain can affect the positions of all the peaks in the spectrum. When used with the zero stabilizer, both the zero intercept and the gain (slope) will be monitored to keep all the peaks in the spectrum stabilized. The zero stabilization and gain stabilization are separate functions but both will affect the position of the peaks in the spectrum.

The stabilization operates by keeping a peak centered in an ROI you have defined. The ROI should be made symmetrically about the center of a peak with reasonably good count rate in the higher channels of the spectrum. The ROI should be about twice the FWHM of the peak. If the region is too large, counts not in the peak will have an effect on the stabilization.

Before setting either stabilization peak, the coarse and fine gains should be set to the desired values, and optimization or pole-zero performed.

5.2.9.3. Setting the Rise Time in Digital MCBs

To achieve the best results for your application, when using an ORTEC digital spectrometer, we recommend that you set the rise time of the pulses being processed by the digital filter to the minimum value for the resolution needed.

The pulse rise time (and also fall time) is based on the time required for each pulse to reach its peak value. This “peaking time” is about twice that indicated by the conventional time constants displayed on the front panel of commercial analog amplifiers. For example, germanium detectors are often specified at a 6- μ s time constant; this setting is equivalent to 12- μ s peaking (rise) time in our digital spectrometers.

Up to some value of rise time, one can expect improved resolution with increasing rise time; there will, however, be a tradeoff in maximum throughput to memory. Figure 47 illustrates an example of this tradeoff. ORTEC digital spectrometers operate well above the peak of the throughput curve. Operating there allows these instruments to handle an even higher rate of incoming counts, but with less data into memory and, therefore, longer counting time to the same detection limit. It is possible to move the peak of the curve to the right (more counts to memory with higher input count rate) by reducing the pulse rise (and fall) time, thereby trading off resolution for maximum count rate.

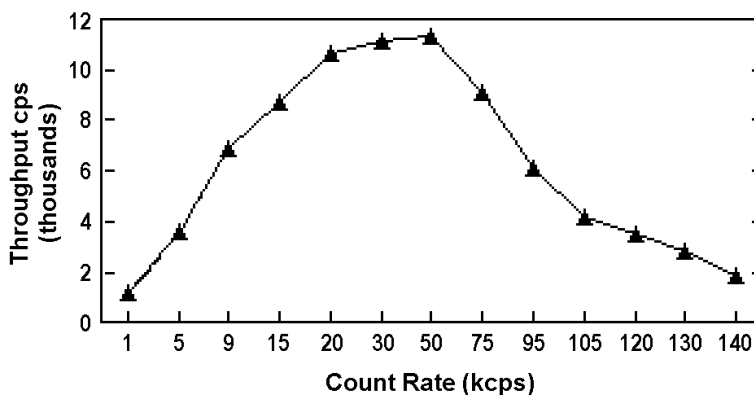


Figure 47. An Example of the Tradeoff Between Throughput and Count Rate.

Table 2 is a guide to choosing a count rate that will ensure that the most efficient operation of your digital spectrometer over the range of anticipated input count rates for your application — that is, at or below the throughput peak — while achieving the best resolution obtainable from the detector consistent with that requirement. Enter the rise time that best matches your dynamic range of count rate (note that the available rise-time settings will vary by instrument; this chart is a general guide only).

Table 2. Rise Time Selection Guide.

Input Count Rate Dynamic Range	Maximum Throughput	Rise Time (μs)
0--->20000	9000	12
0--->50000	12500	8
0--->75000	23500	4
0--->100000	37000	2.4
0--->150000	50000	1.6
0--->200k	70000	0.8
0--->220k	85000	0.6
0--->250k	100000	0.4
0--->300k	120000	0.2

The longest rise time shown in the table is 12 μ s, even though some digital instruments can be set for rise times as long as 23 μ s. If throughput is not an issue because all samples are low rate, increasing the rise time beyond 12 μ s might achieve a small improvement in resolution. For planar detectors, such as ORTEC's GLP, Si(Li), IGLET, and IGLET-X Series, operating at longer rise times frequently gives improved resolution.

5.2.9.4. InSight Mode

The **InSight** display (Fig. 48) shows the actual sampled waveform in the digital processing units on a reference graticule. The Properties dialog remains active and can be used to change settings while viewing the pulses.

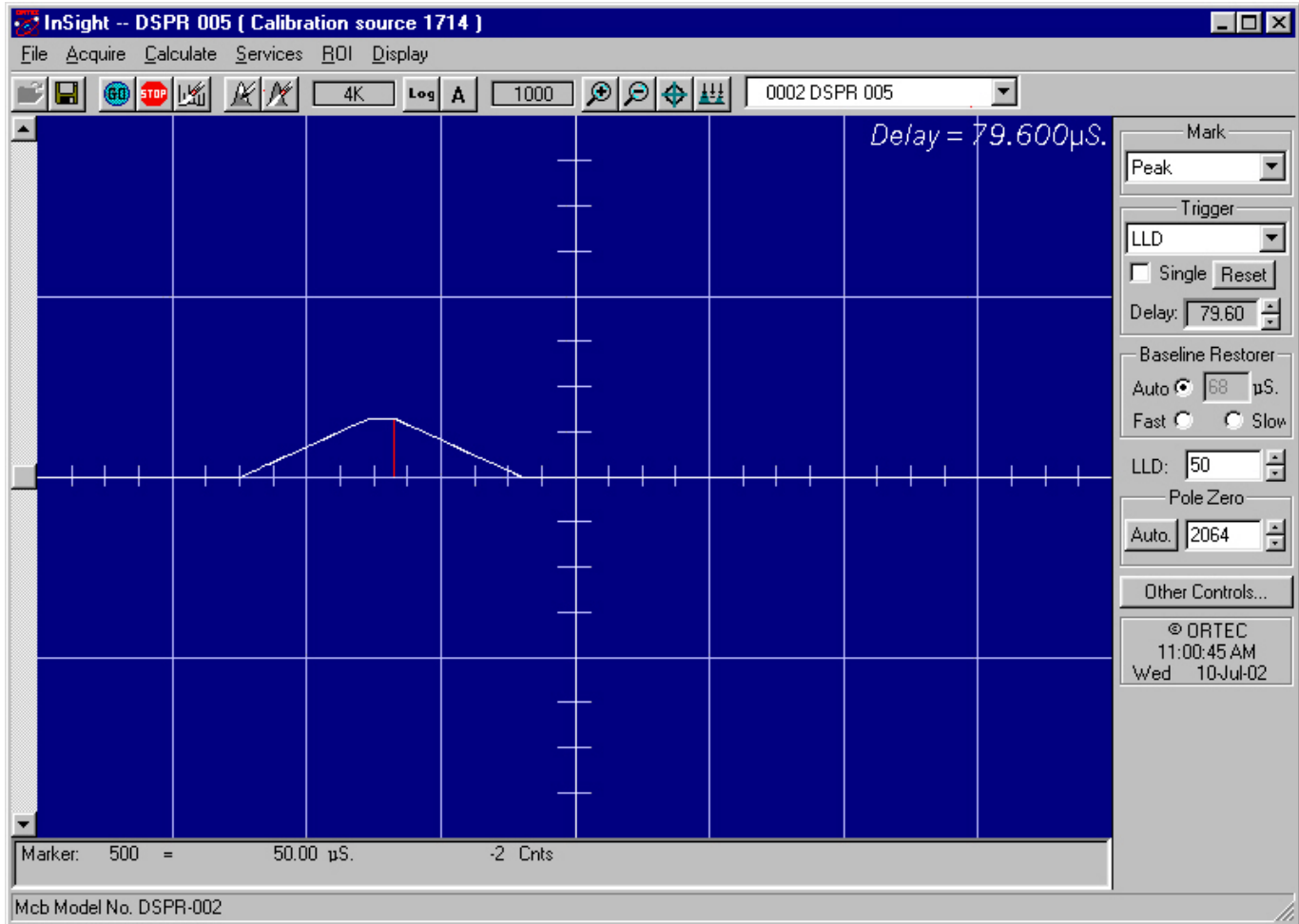


Figure 48. DSPEC Pro InSight Mode.

As none of the traditional analog signals are available in the DSPEC Pro, this mode is the only way to display the equivalent amplifier output pulse. Note that at the bottom of the window the marker channel is displayed in units of time.

To exit the InSight mode and return to the PHA display, press <Esc> or go to the **InSight** section on the Amplifier 2 tab and click **Stop**. The PHA mode is set to **STOP** when you enter the InSight mode.

The Status Sidebar changes from the PHA mode controls to the InSight controls for adjusting the peak display. On the left is a vertical scrollbar for adjusting the vertical offset of the waveform. The value of the offset is shown on the display. Double-clicking the mouse in the scrollbar will set the vertical offset to the vertical value of the channel at the marker position. This lets you conveniently zoom in on a particular part of the waveform (such as the tail for pole-zeroing).

In the **Auto** trigger mode, the display is updated every time a new pulse exceeds the trigger level. To keep a single pulse displayed, select **Single**. Click **Reset** to refresh the display to see the next pulse. There will usually be one or two pulses in the “pipeline” that will be displayed before any change entered will be seen. If the trigger is turned off, the display will be redrawn periodically, even if no pulse is there.

The **Delay** setting is the time delay between the pulse shown on the display and the trigger level crossing. The value of the time delay is shown on the display.

Just as for the PHA mode display, the vertical scale can be adjusted with the vertical adjustments. The display can be set to Log mode, but the peak shapes do not have a familiar shape in this display. The Auto mode will adjust the vertical scale for each pulse. The pulse is shown before the amplifier gain has been applied, so the relation between channel number and pulse height is not fixed.

The horizontal scale extends from 16 to 256 channels. The display is expanded around the marker position which means that in some cases the peak will disappear from the display when it is expanded.

The display can be switched from the DSPEC Pro to another detector or the buffer. In this case the other detector will be shown in the mode selected for it. The buffer will always be shown in PHA mode. The display will return to the InSight mode when you return to the first DSPEC Pro. If you exit the program with the DSPEC Pro in InSight mode, it will be in InSight mode on the next startup.

The display can include a **Mark** to indicate one of the other signals shown in Fig. 49. The Mark is a solid-color region displayed similarly to that of an ROI in the spectrum. This Mark can be used to set the timing for the gate pulse. It can also be used to set the shaping times and flattop parameters to get the best performance. For example, suppose you want to get the best resolution at the highest throughput possible. By viewing the pulses and the pileup reject marker, you can increase or decrease the rise time to obtain a minimum of pileup reject pulses.



Figure 49. Mark Display Selection.

Mark Types

For the **Mark**, choose either “points” or “filled” (to the zero line) display. This is controlled by the selection in the **Display/Preferences** menu item. That choice does not affect the PHA mode choice. The colors are the same as for the PHA mode.

None	No channels are marked in the display.
PileUpReject	The region marked indicates when the PUR circuit has detected pileup and is rejecting the marked pulses.
NegBLDisc	This shows when the negative baseline discriminator has been triggered. Typically this signal only marks the TRP reset pulse. The signal is used internally in the live-time correction, baseline restoration, and pile-up rejection circuits.
BaseLineR	This shows when the baseline restorer is actively restoring the baseline.
PosBLDisc	This shows when the positive baseline discriminator has been triggered. The signal is used internally in the live-time correction, baseline restoration, and pile-up rejection circuits.
Busy	When the DSPEC Pro busy signal is active, Busy shows in the Mark box. It represents the dead time.
Gate	This shows when the gate signal is present on the gate input connector. If the Gate mode on the ADC tab (see Fig. 40) is set to Off , then all regions are marked. If the mode is set to Coincidence , then the marked region must overlap the pulse peak (that is, must start before the beginning of the flat top and stop after the end of the flat top) for the pulse to be counted. If the mode is set to Anticoincidence , then the marked region will show the pulses that are accepted. That is, the rejected peaks will not be marked. Simply put, in all modes the accepted peaks are marked.
Peak	This is the peak detect pulse. It indicates when the peak detect circuit has detected a valid pulse. The Mark occurs about 1.5 μ s after the pulse maximum on the display.

On the lower right of the InSight display are the shaping parameter controls. The controls are split into two groups, and the **other controls...** button switches between them.

One group includes **Rise Time**, **Flattop**, **Tilt**, and the **Optimize** button. The **Rise Time** value is for both the rise and fall times; thus, changing the rise time has the effect of spreading or narrowing the quasi-trapezoid symmetrically.

The **Flattop** controls adjust the top of the quasi-trapezoid. The **Width** adjusts the extent of the flattop (from 0.3 to 2.4 μ s). The **Tilt** adjustment varies the “flatness” of this section slightly. The **Tilt** can be positive or negative. Choosing a positive value results in a flattop that slopes downward; choosing a negative value gives an upward slope. Alternatively, **Optimize** can set the tilt value automatically. This value is normally the best for resolution, but it can be changed on this dialog and in the InSight mode to accommodate particular throughput/resolution tradeoffs. The **Optimize** button also automatically adjusts the pole-zero setting.

5.2.10. Gain Adjust

The **Gain Adjust** wizard adjusts the MCB amplifier fine gain of the amplifier to center the peak in the defined ROI and at the selected center point. The change is made by acquiring spectra for a source that has the desired peak energy. You can adjust all of the MCBs in a group at one time or an individual MCB.

NOTE Each detector in the group must have a good FWHM calibration.

The first dialog for the wizard is shown in Fig. 50. Select the current detector or pick a MCB group from the droplist, then click **Next**.

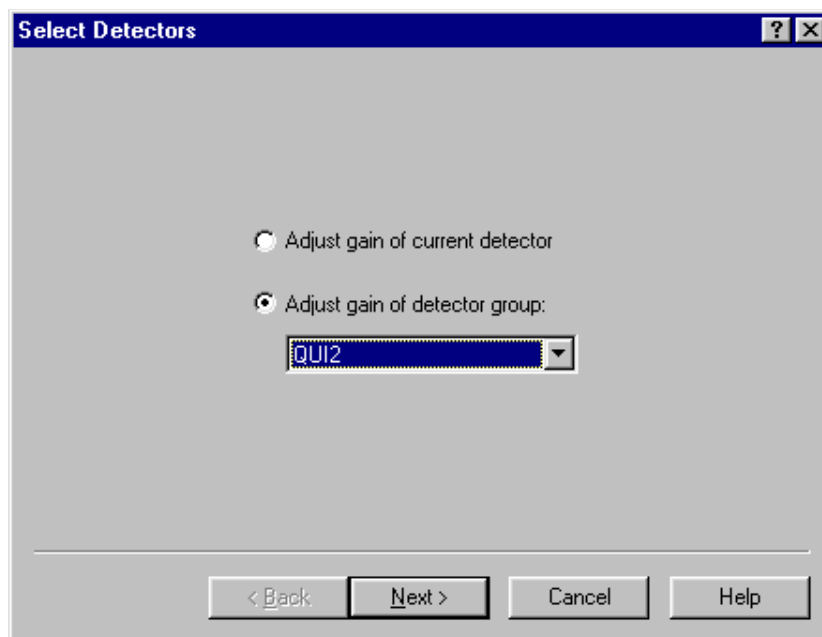
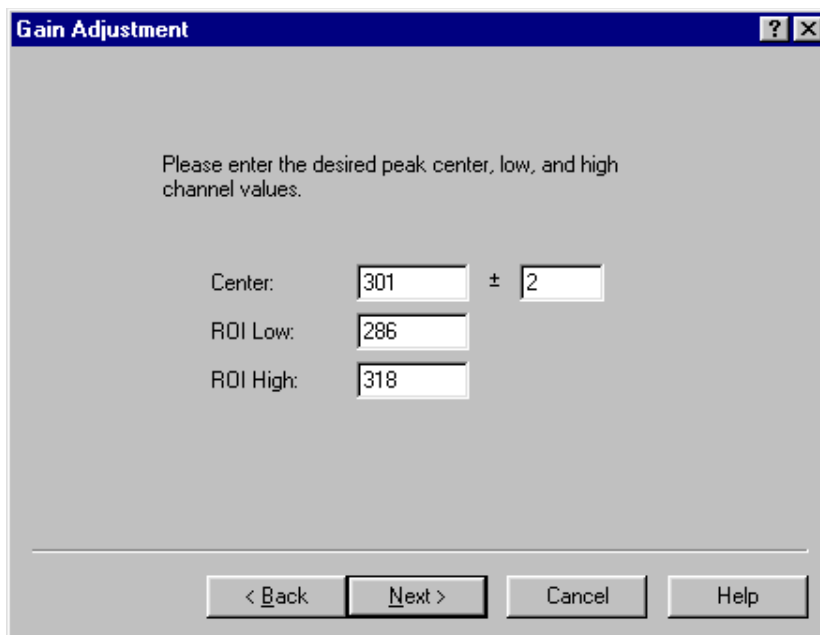


Figure 50. Set Up the Gain Adjust for the Current MCB or an MCB Group.

The next wizard screen is shown in Fig 51. In this dialog, enter the peak **Center** channel and tolerance. The peak must be within the channel limits defined in the **ROI Low** and **ROI High** values. The ROI need not be marked in the MCB. You can enter a wide range to ensure that the peak will be located. The region must contain *only one peak*.

Click on **Next**.



The dialog box titled "Gain Adjustment" contains the following text and input fields:

Please enter the desired peak center, low, and high channel values.

Center: ±

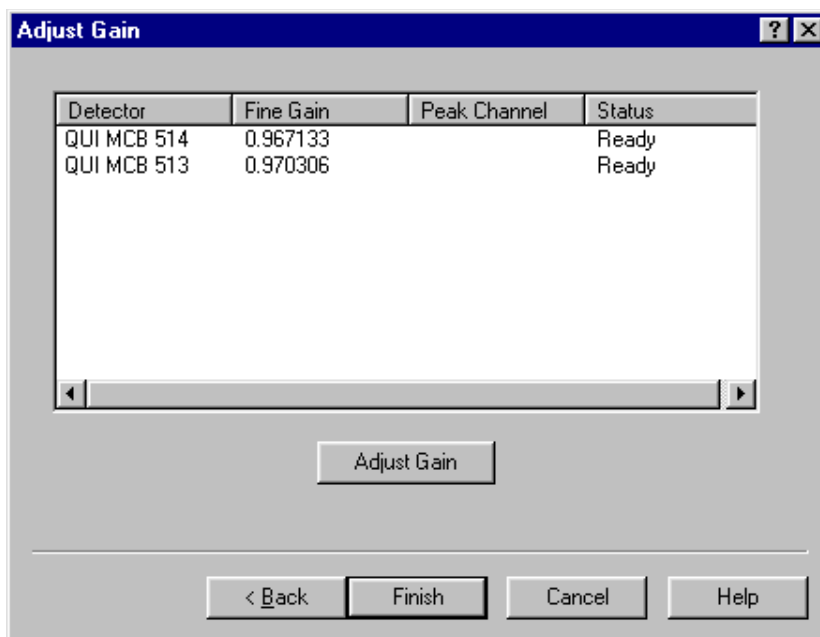
ROI Low:

ROI High:

Buttons at the bottom: < Back, Next >, Cancel, Help

Figure 51. Enter the Center Channel , Tolerance, and ROI Limits.

Figure 52 shows the next wizard dialog. This screen displays the list of MCBs to be adjusted. The current fine gain for each MCB is displayed. Now click on the **Adjust Gain** button; this will open the reminder shown in Fig. 53.



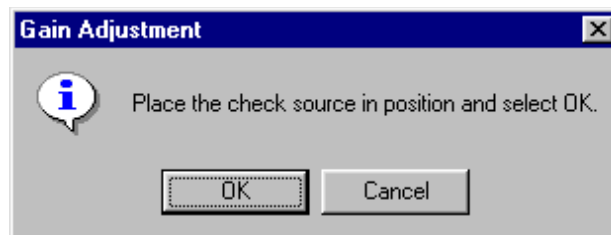
The dialog box titled "Adjust Gain" contains a table with the following data:

Detector	Fine Gain	Peak Channel	Status
QUI MCB 514	0.967133		Ready
QUI MCB 513	0.970306		Ready


Buttons at the bottom: < Back, Adjust Gain, Finish, Cancel, Help

Figure 52. MCBs to be Adjusted.

Position the source(s) and click on **OK**. Renaissance Supervisor will acquire data and periodically attempt a peak fit.



The dialog box titled "Gain Adjustment" contains the following text and buttons:

 Place the check source in position and select OK.

Buttons: OK, Cancel

Figure 53. Start Acquisition.

While the new spectrum is being acquired and the gain adjusted, the **Status** for this operation will be listed as **Acquiring**. Note that this process can take several minutes.

When the adjustment is finished, the **Status** will return to **Ready** and the new fine gain will be displayed, as shown in Fig. 54.

Click on **Finish** to complete the process.

NOTE If the gain adjustment does not succeed, (1) check the ROI to make sure the peak falls within it, then (2) check the FWHM calibration.

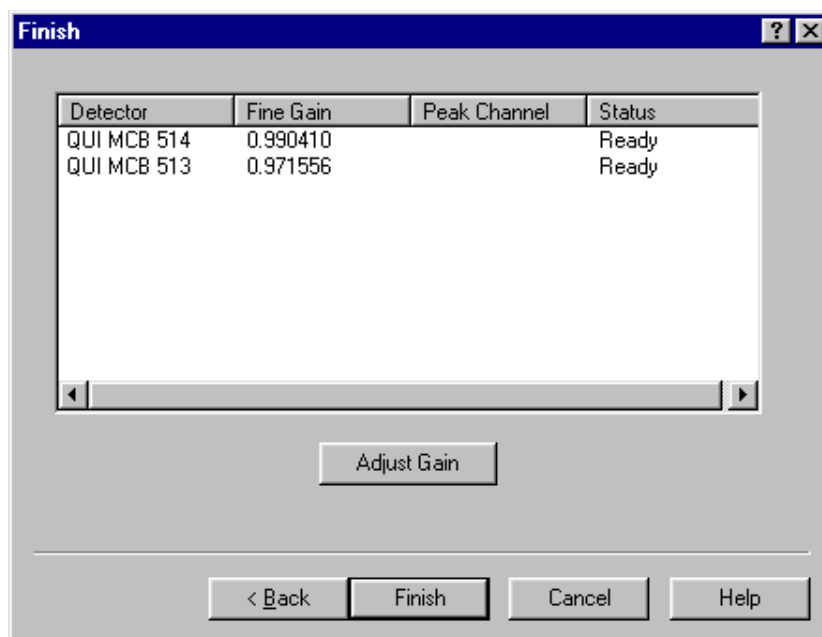


Figure 54. Gain Adjust Complete (note the new fine gain values).

5.3. Calibrate

Figure 55 shows the full **Calibrate** menu. For HPGe detectors, Renaissance includes a **Ge Calibration Wizard** to assist in performing the energy and efficiency calibrations. This menu also displays the individual commands for the energy and efficiency calibrations for cases where the wizard is not needed.

The calibration wizard and the energy and efficiency calibrations for the spectrum in the MCB are only available if the MCB is not acquiring data. If there is no energy calibration, all choices except **Energy...**, **Recall Calibration...**, and (for an HPGe detector in the active window) **Ge Calibration Wizard...** are disabled.

NOTE We recommend that you always save calibrations to a file that can be specified in the analysis options (.SDF or .SVD files) for use in the Operator program.

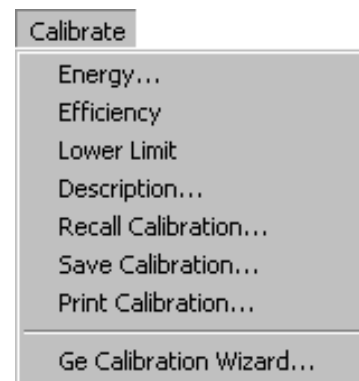


Figure 55. Full Calibration Menu.

5.3.1. General

The calibration of the system defines four relations:

- 1) Spectrum channel numbers and energy
- 2) FWHM of the peak and energy
- 3) Spectrum count rate and activity in becquerels or other units
- 4) True coincidence summing factor and energy

The data collected are in counts/unit time/channel; however, to be most useful, these data need to be converted to activities (i.e., decays/unit time at a given energy). The calibration parameters do this conversion.

These relationships are calculated from spectra, user inputs, and inputs from libraries and tables. The calibration data are merged with the spectrum when it is saved as an `.SPC` file. The information is used in the analysis section to perform the desired analysis. Spectra saved in the `.CHN` format are compatible with older software, however the `.CHN` format does not contain the efficiency calibration data.

It is important that the energy and efficiency calibrations be done correctly because the calibration results will affect all analyses employing them. The energy calibration data is used to define the energies of the peaks in the spectrum. If incorrect, the calculated energies will not correspond to the correct library entry and the peak might be incorrectly identified. The shape parameters are used to define the expected shape for a singlet peak. If incorrect, peaks will be labeled as having a bad shape when they do not, and bad peaks will not be marked. Peaks marked with poor shape might not be included in the activity calculation, resulting in loss of accuracy even for singlet peaks. For deconvolutions, these parameters define the Gaussian shape used for the components of the total peak area. Incorrect peak shapes can result in poor deconvolution results and even incorrect peak height ratios in multiplets.

An incorrect efficiency calibration can cause the nuclide activity to be incorrectly reported. The knee value, if incorrectly chosen, can cause poor results near the knee, especially below the knee.

Using many data points near the knee aids in selecting the correct knee energy. A poor choice of type of fit can result in a good fit to poor data, which will yield a poor efficiency calibration.

The energy calibration and the efficiency calibration are separated to make it easier to do these calibrations. If properly chosen sources and libraries are used, the calibration process is simple, quick and accurate. The input values can be saved so that repeated calibrations with the same source are easy and simple.

The energy calibration can be changed without affecting the efficiency calibration. By using the **Recall Calibration...** command, the previously calculated efficiency calibration can be inserted into the new calibration data.

The calibrations for the NaI and Ge detectors are performed differently. Before calibrating, use the **Services/Edit Detector Lists** commands to specify which detectors are NaI and which are Ge. If a detector is not assigned to one of these categories, it is treated as Ge.

5.3.2. A Quick Note on Calibrating Motorized Beds

If using a motorized bed, use the Motor Setup program to start the bed excursion at the same time you start the calibration acquisition in Supervisor. Alternatively, spectra can be acquired in the Operator program, where motor control is completely integrated with the **Start Count** button. To do this, you will need an .OPR file (Section 5.7.8) for the calibration acquisition. To distinguish calibration runs from subject measurements in Operator, it might be useful to assign “Calibration” as the subject name. Another option would be to create a separate database for calibrations.

Note that if all efficiency calibrations are performed at one scan length, should the scan length be changed in Motor Setup, the calibration factor used to convert peak area to activity will be wrong, so the reported activities will be wrong. The efficiency calibrations must be performed again.

5.3.3. Energy... for Ge

5.3.3.1. Introduction

The **Energy...** calibration function calculates two sets of parameters: the energy vs. channel number, and the peak shape or FWHM vs. energy. The inputs to this function are a spectrum or series of spectra with isolated peaks distributed over the energy range of interest, and either a library or table of peak energies. The library referred to here is an analysis gamma-ray library. The creation of a table of peak energies is described in this section.

The formula for energy vs. channel number is:

$$E = a_1 + a_2 C + a_3 C^2 \quad (1)$$

where:

- E = energy
- a_i = coefficients
- C = channel number

The formula for FWHM vs. channels is:

$$F = b_1 + b_2 C + b_3 C^2 \quad (2)$$

where:

- F = FWHM
- b_i = coefficients
- C = channel number

To calculate the FWHM in energy use the following:

$$F(e) = F(c) (a_2 + 2a_3 * C) \quad (3)$$

where:

- $F(e)$ = FWHM in energy
- $F(c)$ = FWHM in channels at channel C
- a_2 = energy calibration slope defined in Eq. 1
- a_3 = energy calibration quadratic coefficient defined in Eq. 1
- C = channel number

When the FWHM fit is made, the fit is automatically checked for validity. If the FWHM curve is negative at any part of the spectrum or the curve bends over (has a maximum and then goes down), a warning message, **Non-physical FWHM fit**, is displayed. Click on **OK**, then display the FWHM curve to see why the fit is incorrect. Also, if the delta between the data points and the FWHM fit is greater than 25%, a message is displayed. The curve can be accepted if the warning is due to the fit outside the energy of interest, or some of the data points should perhaps be deleted. The calibration spectrum should have good peaks with many counts, so counting longer could remedy the poor fit.

The same methods used to calculate the peak centroid and width in the **Calibrate** section are used in the **Analyze** section. This ensures consistency of results.

The energy calibration is performed using the spectrum in the buffer or the Detector. The calibration is linked to the spectrum used and is transferred with it when the spectrum is transferred (e.g., from Detector to buffer or disk file).

The first step in the calibration is to collect a spectrum of a known source with isolated peaks. The spectrum peaks must be well-defined with a small statistical uncertainty. When the Detector has finished collection (i.e., stopped), select **Calibrate** from the menu bar, then **Energy...** The Energy Calibration Sidebar (Fig. 56) will automatically open (if you wish, you can click on its title bar and drag it to another position). It is usually helpful to zoom in on the spectrum so the peaks are clearly displayed.

5.3.3.2. Auto Calibration¹²

The **Auto Calibrate** button will perform a complete energy and FWHM calibration on the displayed spectrum using the working library. There are no requirements on the spectrum or the library other than there must be at least five peaks (ten preferred) in the spectrum that are in the library. There can be a different number of peaks in the spectrum than in the library, that is, there can be peaks in the spectrum that are not in the library and peaks in the library that are not in the spectrum. The spectrum can be uncalibrated, calibrated, or even incorrectly calibrated. Spectra such as the mixed gamma standard or uranium ore can be used with the appropriate library.

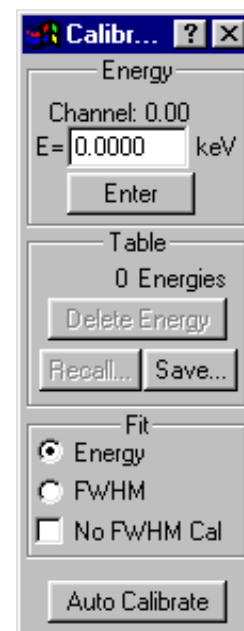


Figure 56.
Energy
Calibration
Sidebar.

The auto calibration works as follows: the spectrum is searched for all the major peaks, then this peak list is compared to the library peak list to find the calibration that gives the best match.

5.3.3.3. Manual Calibration

If there is no energy calibration, the energy of one or two known peaks must be entered. Using the Full Spectrum View, select a peak in the high energy (channel) part of the spectrum. When this part of the spectrum is visible in the expanded display, move the cursor to the known peak. At this time the centroid of the peak will be calculated and displayed in the upper part of the calibration input window as, in this example, **Channel: 8226.90**. This is the channel number of the peak centroid. Now click in the **E=** input box and enter the energy of this peak. Click on the **Enter** button or press **<Enter>**. A table and graph will appear on the screen (Fig. 57). They can be moved around and sized if they obscure the spectrum.

¹²Patent number 6,006,162.

The table shows one value (the one just entered), and the graph shows a straight line fit from (energy = 0, channel = 0) to the energy and channel just entered. This is an approximate calibration; it should be fairly accurate if the zero offset is small.

The **Energy** and **FWHM** radio buttons at the bottom of the Energy Calibration Sidebar show the table and graph for either energy vs. channel (Fig. 57) or FWHM vs. energy (Fig. 58).

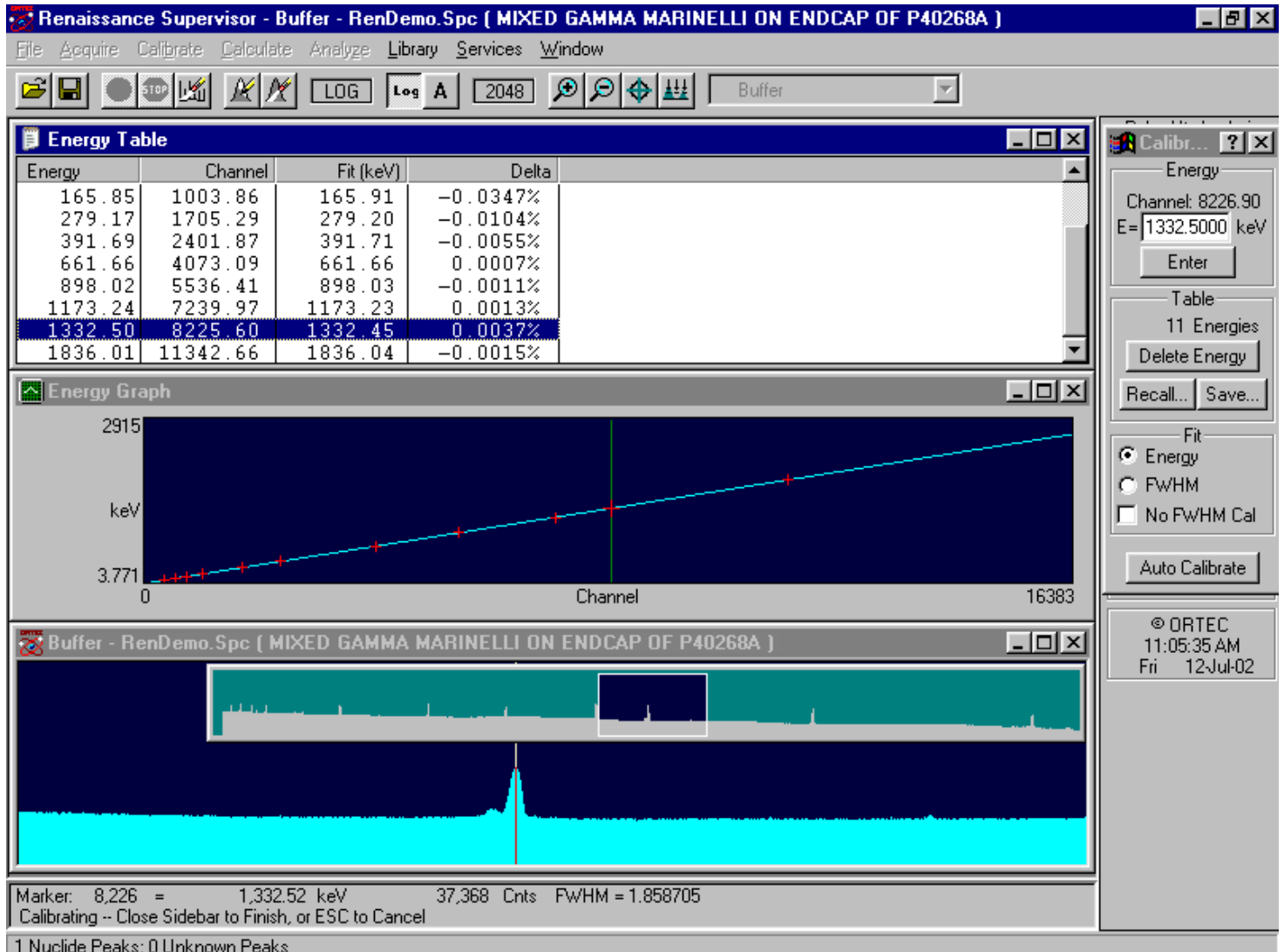


Figure 57. Energy Calibration Display.

Click on **FWHM**. The table shows the one value entered and the graph shows a horizontal line. For a single point, the FWHM is assumed to be a constant.

Using the Full Spectrum View (or the Library List window), select a peak in the low-energy part of the spectrum and move the marker to the centroid of the peak. Again click in the **E=** field at the top of the sidebar and enter the energy of this peak. Both the energy function and FWHM

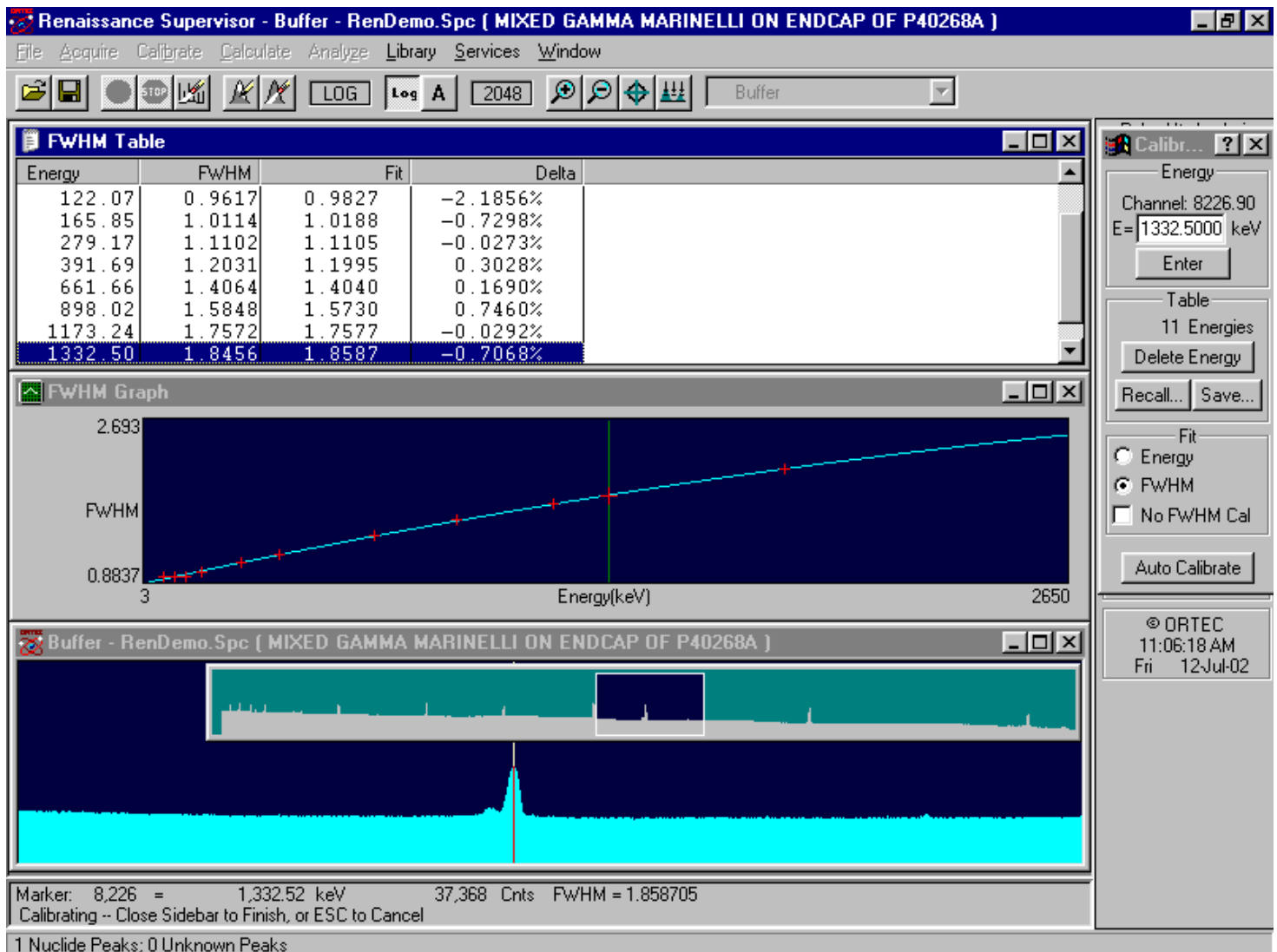


Figure 58. FWHM Calibration Display.

function, as well as their corresponding tables, will update with the new entry so progress can be monitored.

At this time, the cursor can be positioned using the calibration graphs, calibration table, Full Spectrum View, or Expanded Spectrum View. The cursor will show the energy based on the calibration up to this point.

The calibration can be refined by adding as many points as desired. Any point can be deleted by selecting that point in the table of values (**Energy** or **FWHM**) and clicking on the **Delete Energy** button on the calibration sidebar. The fit updates when a point is removed.

After the desired number of points have been entered, the energy values can be saved by clicking on the sidebar **Save...** button. This opens a standard file-save dialog (Fig. 59). Assign a filename and Renaissance will append the default energy-calibration extension, **.ENT**.

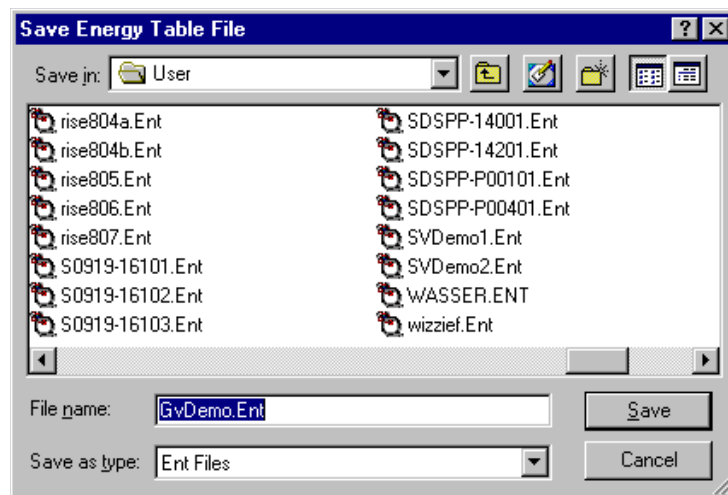


Figure 59. Save Energy Calibration Table.

The saved tables of values can be used for future calibrations using the same nuclides. The table is in ASCII format and can be changed off-line using an ASCII-compatible editor such as Windows Notepad, or from the calibration sidebar control menu.

Click on the sidebar title bar icon to open the control menu (Fig. 60).

Select **Edit File...**. Open the **.ENT** file to be edited; it will be displayed as shown in Fig. 61. Change energy values as needed and click on **Save**, or click on **Cancel** to retain the original values.



Figure 60. Calibration Sidebar Control Menu.

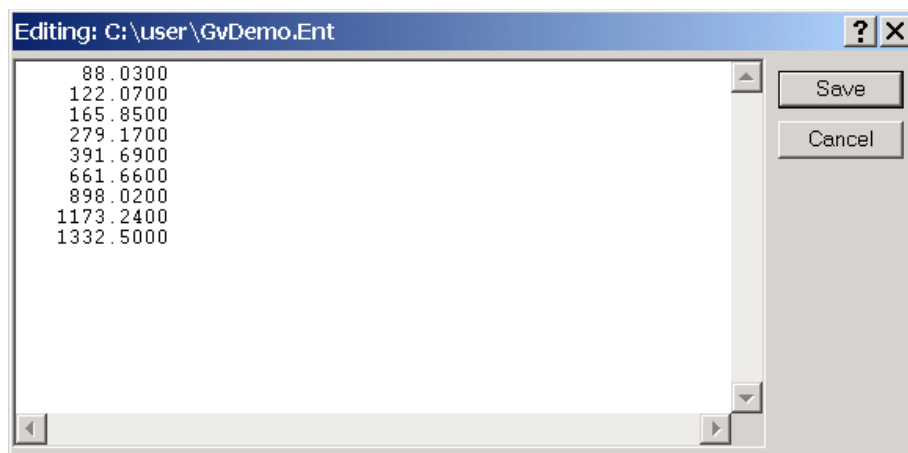


Figure 61. The Energy Calibration File (.ENT).

5.3.3.4. Easy Recalibration Using An .ENT Table

Using the table can speed up the calibration process, as follows. For an uncalibrated spectrum, enter one or two energies to establish a basic calibration. Next, click on the **Recall...** button on the Energy Calibration Sidebar to open a standard file-recall dialog (Fig. 62). Choose the .ENT file to be used. When the table is selected, the peak at each energy in the list will be evaluated for centroid energy and FWHM and added to the tables. When all the peaks have been done, the new fit and table will be displayed.

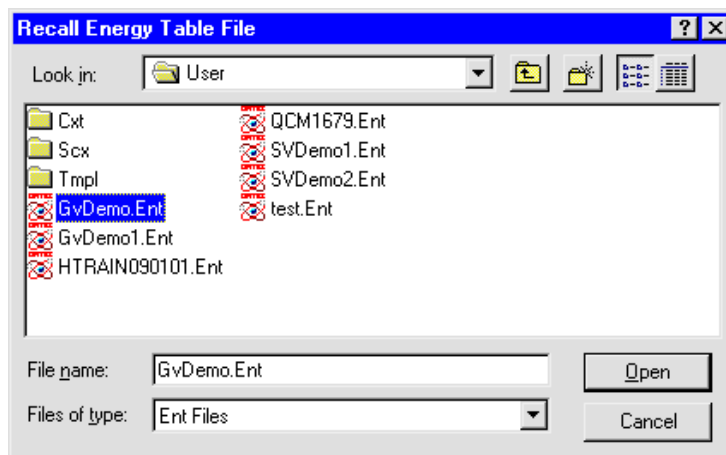


Figure 62. Recall Energy Calibration Table.

5.3.3.5. Speeding Up Calibration with a Library

A library can be used to speed up the calibration process as follows. Before entering the calibration process, choose **Library/Select File...** from the menu and open a library file that contains the nuclides in the calibration source. Next, choose **Library/Select Peak...** to show the list of peaks in the library in energy order. Now select **Calibrate/Energy...** When the table and graph appear, move the table down so the Library List is not covered (see Fig. 63). Rather than manually entering the peak energy in the Energy Calibration Sidebar **E=** field, click once on the peak energy in the Library List to automatically fill the field.

For a spectrum with an energy calibration, double-clicking on a library peak will cause the spectrum cursor to jump to the channel corresponding to that energy. If the calibration as it now stands is not sufficiently accurate, the channel which corresponds to that energy, as displayed in the Energy Calibration Sidebar, might be inaccurate. If this is not the correct peak channel, set an ROI on the peak of interest, move the cursor to the peak centroid channel, click *once* on the library peak, and click on **Enter**.

To exit the calibration function, click on the Energy Calibration Sidebar Close button. This will close the calibration function, and the new calibration will be held in memory, available for subsequent spectra gathered on this Detector. To save the calibration to disk, select **Save Calibration...** from the **Calibrate** menu.

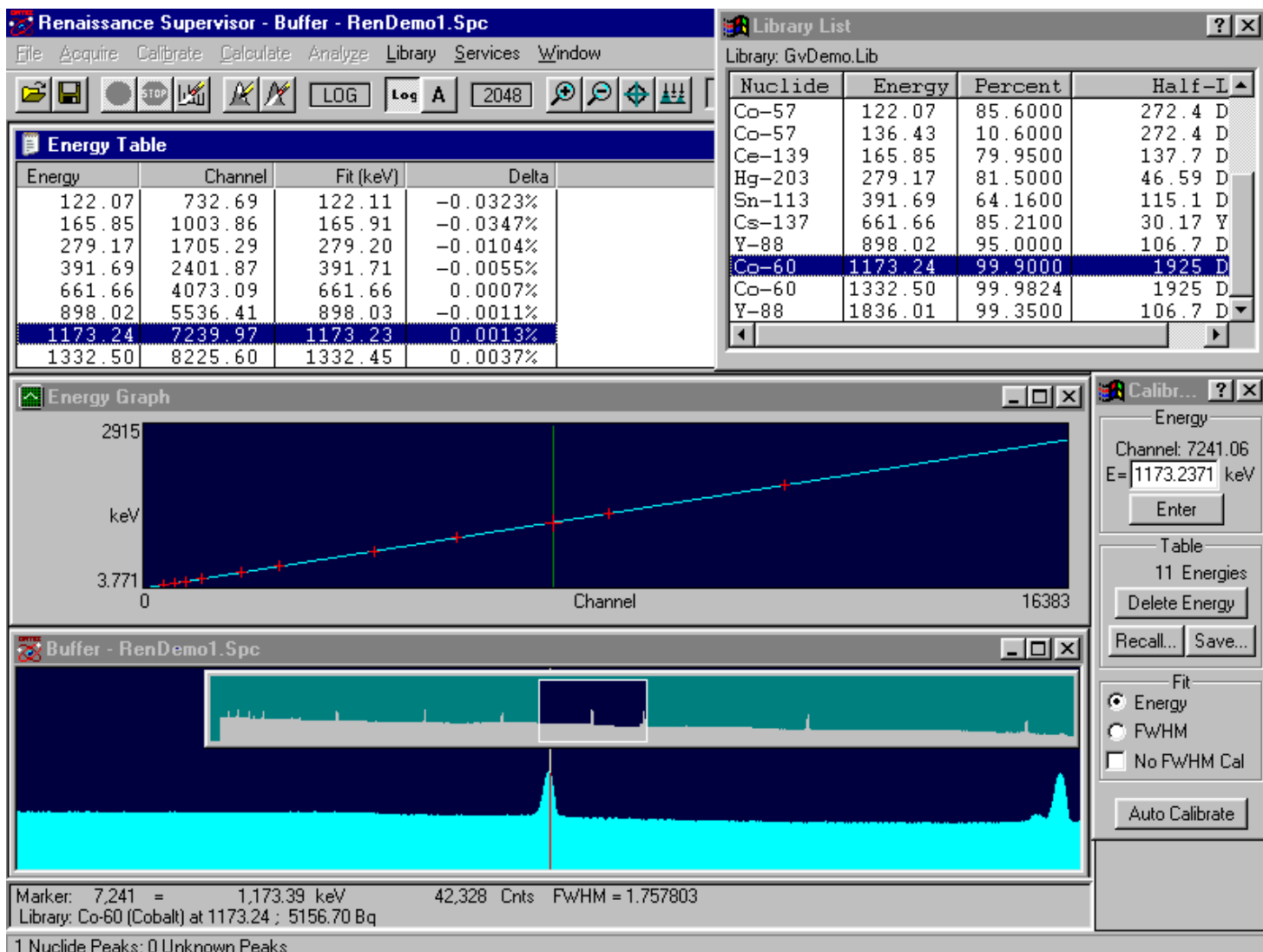


Figure 63. Speeding Up the Energy Calibration with a Library.

5.3.3.6. Other Sidebar Control Menu Functions

The remaining items on the sidebar control menu are **Move**, **Close**, **Restore**, **Clear Table**, and **Destroy**. **Destroy** clears all energy calibration values. **Restore** reinstates the internal energy calibration table to the values stored when the calibration function was entered. **Clear table** erases all the values in the table, but retains the function (energy and FWHM) to be used when the next values are entered. In this way, a recalibration can be done without manual entry of any points. **Close** exits the **Energy...** calibration function and saves the current calibration as the working calibration.

5.3.3.7. Using Multiple Spectra for a Single Calibration

To use more than one source (when simultaneous collection is not possible) to make a single calibration:

- 1) Collect a spectrum with one source or calibrate with this spectrum.
- 2) Exit the calibration function.
- 3) Clear the Detector.
- 4) Collect the spectrum of the second source.
- 5) Calibrate by adding the new lines to the existing ones (which are retained).

The process can be repeated for additional sources. When completed, the calibration should be saved on disk. The individual spectra can be saved or used in other application software. In addition, the calibrations in the spectra can be updated by recalling each spectrum in turn, recalling the complete calibration, and re-saving the spectrum.

To use more than one stored spectrum to make a single calibration:

- 1) Calibrate using one spectrum.
- 2) Exit the calibration function.
- 3) Save the calibration in a file.
- 4) Recall the second spectrum.
- 5) Recall the calibration (because recalling the spectrum has replaced the first calibration with the calibration from the spectrum).
- 6) Select **Calibrate/Energy...** and enter the peak energies for the second spectrum.

The process can be repeated for additional spectra.

5.3.4. Energy... for NaI

5.3.4.1. Introduction

The **Energy...** calibration function calculates two sets of parameters: the energy vs. channel number, and the peak shape or FWHM vs. energy. The inputs to this function are a spectrum or series of spectra with isolated peaks distributed over the energy range of interest, and either a library or table of peak energies. The library referred to here is an analysis gamma-ray library. The creation of a table of peak energies is described in this section.

The formula for energy vs. channel number is:

$$E = a_1 + (a_2 C) + (a_3 C^2) \quad (4)$$

where:

- E = energy
- a_i = coefficients
- C = channel number

The formula for FWHM vs. channels is:

$$F = b_1 + b_2C + b_3C^2 \quad (5)$$

where:

- F = FWHM
- b_i = coefficients
- C = channel number

To calculate the FWHM in energy use the following:

$$F(e) = F(c) (a_2 + 2a_3 * C) \quad (6)$$

where:

- $F(e)$ = FWHM in energy
- $F(c)$ = FWHM in channels at channel C
- a_2 = energy calibration slope defined in Eq. 4
- a_3 = energy calibration quadratic coefficient defined in Eq. 4
- C = channel number

The same methods used to calculate the peak centroid and width in the **Calibrate** section are used in the **Analyze** section. This ensures consistency of results. If fewer than four peaks are used for the calibration, the quadratic coefficient is zero.

The energy calibration is done using spectra in a Detector, buffer, or disk file window. The calibration is linked to the spectrum used and is transferred with it when the spectrum is transferred (e.g., from Detector to buffer or disk file).

5.3.4.2. Performing the Energy Calibration

The first step in the calibration is to collect a spectrum of a known source with isolated peaks. The spectrum peaks must be well-defined with a small statistical uncertainty. Ensure that the lower limit setting (**Calibrate/Lower Limit...**) is appropriate for the type of spectrum used for calibration. Refer to the discussion, **Important Considerations When Creating NaI Analysis Options Settings** (page 134), and set the lower limit to the start channel of the **Analysis Range** on the Sample tab under **Analyze/Settings/Sample Type...** (see Fig. 122, page 139). Since we are only interested in well-defined peaks, the **Peak Search Sensitivity** in the analysis options settings should be set to 5 (least sensitive). This also applies to calibrations using single nuclides.

When the Detector has finished collection (i.e., stopped), select **Calibrate** from the menu bar, then **Energy...** At this point, Renaissance will expand the active spectrum window and minimize any inactive windows.

The Energy Calibration Sidebar (Fig. 64) will open automatically (if you wish, you can click on its title bar and drag it to another position)

If there is no energy calibration or the calibration has been destroyed, mark an ROI on a single, isolated, *high-energy* peak and click on **OK**. Be sure to mark several channels on either side of the peak, to be used as background. When the FWHM has been calculated, the centroid of the peak will be displayed in the upper part of the calibration input window as, in this example, **Channel: 1495.00**. This is the channel number of the peak centroid. Now use the mouse to select the **E=** field and enter the energy of this peak. Press **<Enter>** or click on **OK**.

An **Energy Table** and **Energy Calibration Fit** graph will open on the screen (see Fig. 65). They can be moved around and sized if they obscure the spectrum.

The graph and table each have their own control menus. The table will show one value (the one just entered), and the graph will show a straight-line fit from (energy = 0, channel = 0) to the energy and channel just entered. This is an approximate calibration; it should be fairly accurate if the zero offset is small.

On the Calibration Sidebar, the **Fit** radio buttons allow you to display either the Energy-channel or FWHM-Energy table and graph. Select **FWHM Fit** now, and the table will show the one value entered, while the graph shows a horizontal line. For a single point, the FWHM is assumed to be a constant.

NOTE It is very important to the analysis of these spectra that the FWHM be correct!

In the spectrum window (or the library), select the lowest-energy peak that is well-defined (or collect another spectrum from a different source) and move the marker to the centroid of the peak. Again, position the marker at the center of the peak. Click on the **E=** field and enter the energy of this peak. Both the energy function and FWHM function will be updated with the new entry. The graphs and tables are displayed so that progress can be monitored. (The simplest way to do this is to open the library peak list [**Library/Select Peak...**] and double-click on the peak in the list; see Section 5.3.4.3).

At this time, the marker can be positioned using the calibration graphs, calibration table, or the spectrum window. The marker will show the energy based on the calibration up to this point.

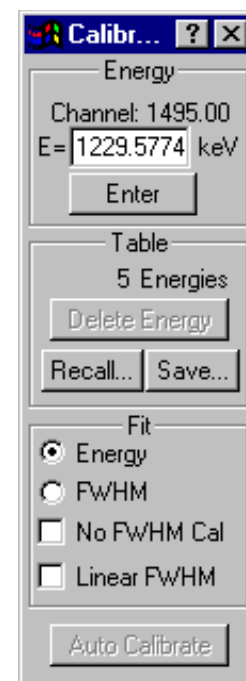


Figure 64.
Energy
Calibration
Sidebar.

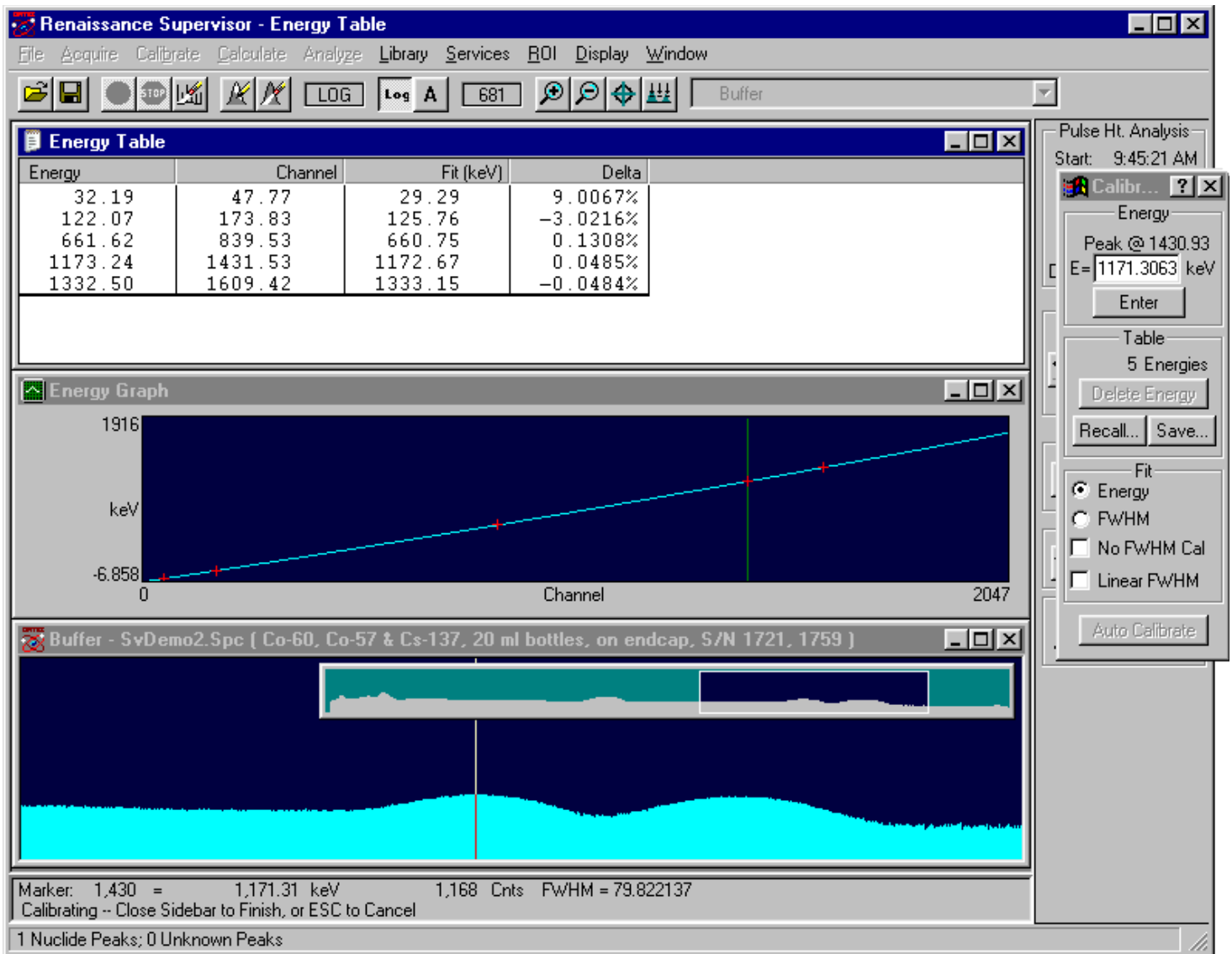


Figure 65. Energy Calibration.

Note that until >3 points are included in the calibration, the sidebar's **Linear FWHM** checkbox is marked and gray, and Renaissance automatically performs a linear fit. Generally, after 3–4 points have been added to the calibration, turning off **Linear FWHM** will provide a better fit.

The calibration can be refined by adding as many points as desired. Any point can be deleted by selecting that point in the table of values (**Energy** or **FWHM**) and clicking on the **Delete Energy** button. The fit updates when a point is removed. (Multiplet or poorly shaped peaks might not have a peak fit suitable for the calibration. These peaks will show a marked deviation from the fitted calibration curve and should in most cases be removed from the calibration.)

Other Energy Calibration Sidebar Features

Note the **Save...** and **Recall...** buttons in the Calibration Sidebar's **Table** box. The **Save...** button stores the energy (keV), the centroid channel, and the FWHM (channels) in an ASCII table file called an *energy table file*, assigned the extension **.ENT**. The saved tables of values can be used for future calibrations using the same nuclides, by clicking on the **Recall...** button. **.ENT** files can be edited with **Edit File** in the sidebar's control menu (Fig. 66; click the Title Bar icon on the Calibration Sidebar), or offline with an ASCII editor such as Windows Notepad.




Figure 66.
Calibration Sidebar Control Menu.

Other menu items in the sidebar control menu are **Move**, **Close**, **Restore**, and **Destroy**. **Destroy** clears the internal energy calibration table. **Restore** reinstates the internal energy calibration table to the values before **Destroy** was chosen, but only if done before exiting the **Energy...** calibration function. **Close** exits the **Energy...** calibration function and saves the current calibration as the working calibration.

5.3.4.3. Speeding Up Calibration with a Library

A library can be used to speed up the calibration process as follows. Before entering the calibration process, select **Library/Select File...** from the menu and choose a library with the nuclides in the calibration source. Next, select **Library/Select Peak...** to show the list of peaks in the library in energy order. Now select **Calibrate/Energy...**. When the table and graph open, move the table down so the peak list is not covered (see Fig. 67). Rather than manually entering the peak energy in the energy entry box, click *once* on the peak energy in the library list to automatically enter that library energy value in the **E=** field.

For a spectrum with an energy calibration, double-clicking on a library peak will cause the spectrum cursor to jump to the channel which corresponds to that energy. If the calibration as it now stands is not sufficiently accurate, the channel which corresponds to that energy, as displayed in the Energy Calibration Sidebar, might be inaccurate. If this is not the correct peak channel, set an ROI on the peak of interest, move the cursor to the peak centroid channel, click *once* on the library peak, and click on **Enter**.

To exit the calibration function, click on the Energy Calibration Sidebar's Close button () . This will close the calibration function, and the new calibrations will be held in memory, available for subsequent spectra gathered on this Detector. If a calibration is to be saved permanently to disk, select **Save Calibration...** from the **Calibrate** menu.

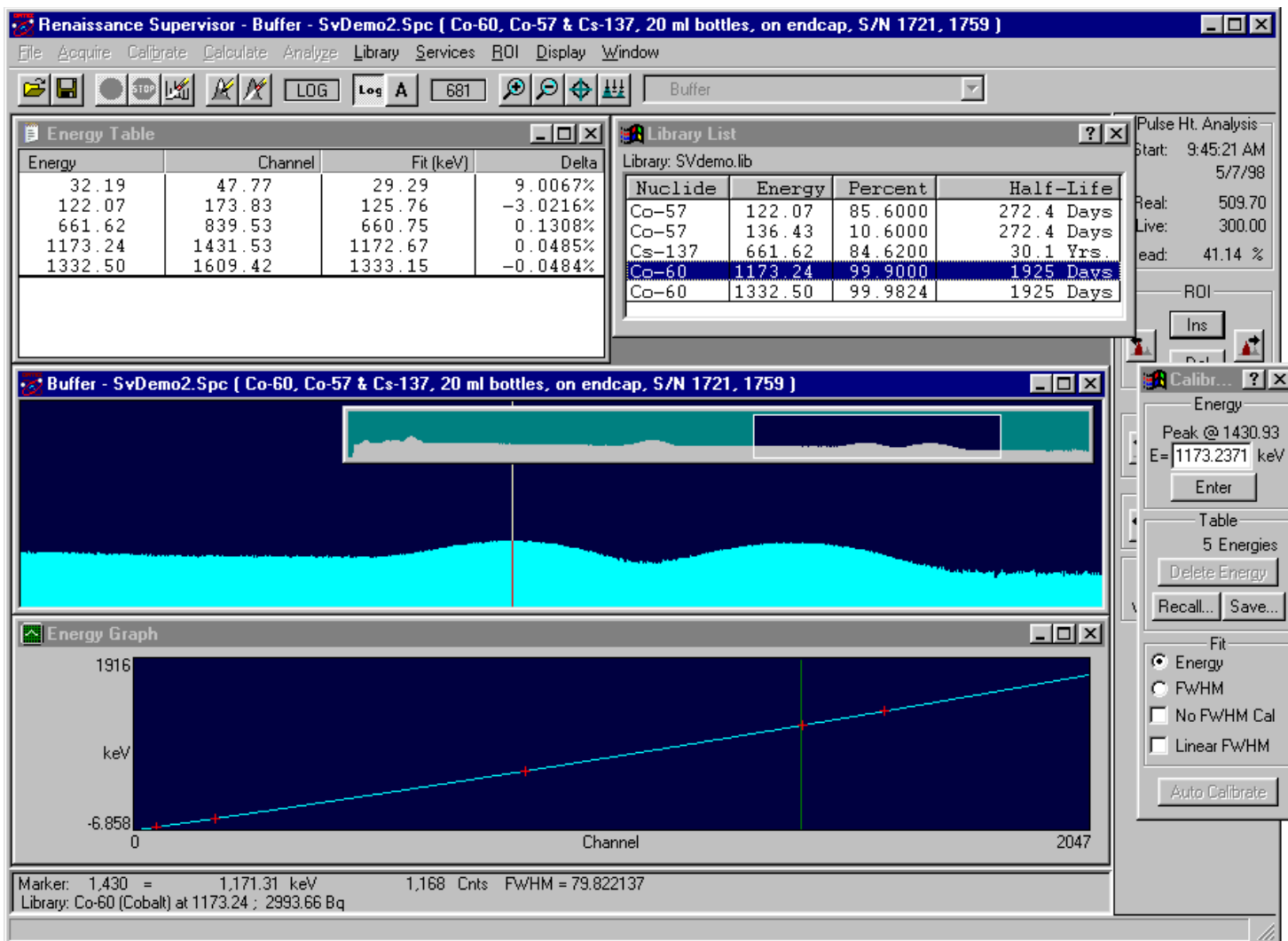


Figure 67. Speeding Up Calibration with a Library.

5.3.4.4. Using Multiple Spectra for a Single Calibration

To use more than one source (when simultaneous collection is not possible) to make a single calibration:

- 1) Collect a spectrum with one source.
- 2) Calibrate with this spectrum.
- 3) Exit the calibration function.
- 4) Clear the Detector.
- 5) Collect the spectrum of the second source.
- 6) Calibrate by adding the new lines to the existing ones (which are retained).

The process can be repeated for additional sources. When completed, the calibration should be saved on disk. The individual spectra can be saved; used in other application software; and the

calibrations in the spectra updated by recalling each in turn, recalling the complete calibration, and re-saving the spectrum.

To use more than one stored spectrum to make a single calibration:

- 1) Calibrate using one spectrum.
- 2) Exit the calibration function.
- 3) Save the calibration in a file.
- 4) Recall the second spectrum.
- 5) Recall the calibration (because recalling the spectrum has replaced the first calibration with the calibration from the spectrum).
- 6) Select **Calibrate/Energy...** and enter the peak energies for the second spectrum.

The process can be repeated for additional spectra.

5.3.5. Efficiency — Ge

The efficiency calibration can be performed here or as part of the calibration wizard. The following section describes how to perform the efficiency calibration. It can be accessed here or from the **Edit Efficiency** function at the end of the wizard.

NOTE If you are using the Motor Control feature (see Appendix B), note that if your efficiency calibrations are all performed at one scan length, changing to another scan length will require you to perform new efficiency calibrations.

5.3.5.1. Introduction

The efficiency calibration function calculates the detection efficiency of the HPGe detector system as a function of energy. The efficiency of the detector system is the relation between the number of gamma rays emitted from the source to the number of gamma rays collected in the full-energy peak.

The HPGe detector system efficiency includes effects from the detector itself, the detector-source geometry, the materials surrounding the detector, and absorption in the source material or matrix (Fig. 68).

The energy recalibration can be redone (to account for gain changes) without the need to redo the efficiency calibration.

P-type germanium detectors, such as the ORTEC GEM Series, have a maximum efficiency at about 150 keV; for n-type detectors, such as the GMX Series, it is about 100 keV. For detectors above about 50% relative efficiency, these values will be somewhat higher (Fig. 69). For both

types, these maxima, or knee values, depend on the individual detector. For p-type GEM detectors, the efficiency goes down as the energy goes down from the knee. For n-type GMX detectors, the efficiency is nearly constant at energies below the knee. For both types, the efficiency goes down at energies above the knee.

The efficiency calibration is critically important to the accuracy of the activity results from Renaissance. It is recommended that only calibrated sources traceable to a known standard be used. The time between the calibration of the radionuclide source by its manufacturer and the time the spectrum is collected is important, as this defines the decay correction needed to calculate source strength for the spectrum.

A source should be selected that contains isolated singlets over the entire energy range of interest. If the energy region near the knee is important to the analysis, several points around the knee should be used for both the two-function and polynomial type of fits. If you wish, you can perform the efficiency calibration using one or more spectra to minimize the difficulty of obtaining the required number of singlets.

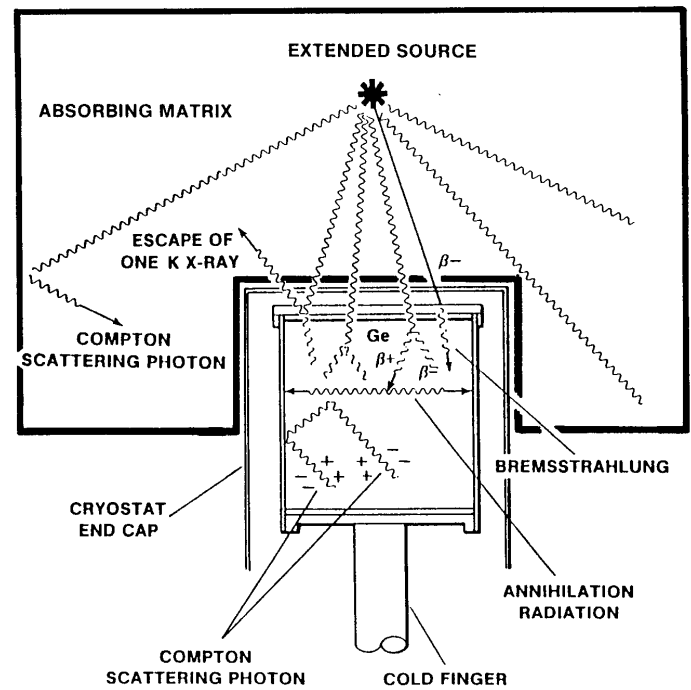


Figure 68. Detector with Extended Source.

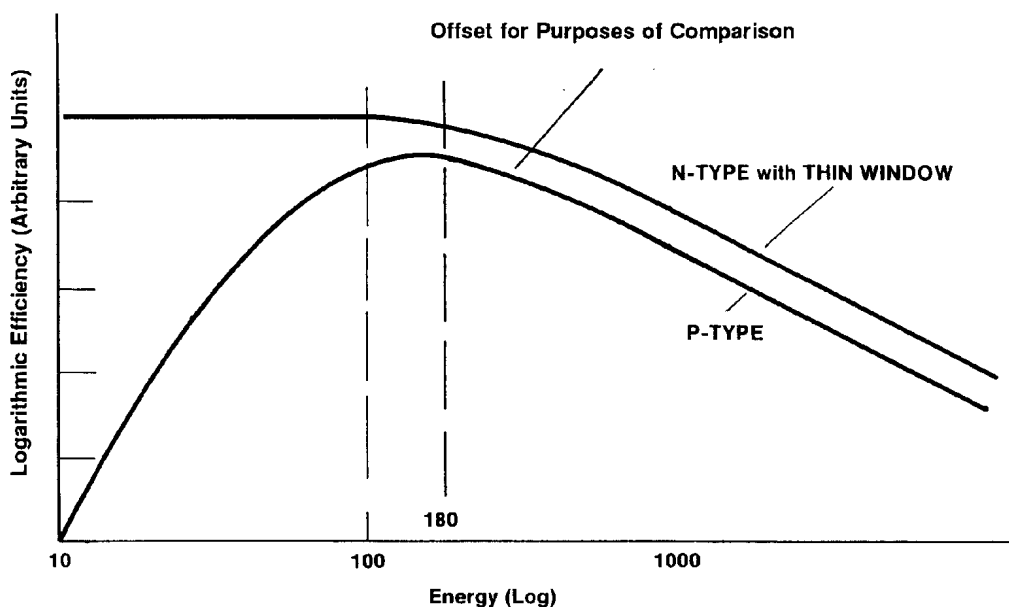


Figure 69. Detector Efficiency as a Function of Energy.

To perform the calibration, you need an energy-calibrated spectrum of the radionuclides and their source strengths and calibration dates. These data are entered into Renaissance in convenient menu-type forms, and you can review the results of each step. Questionable points can be deleted, additional points added, and the fitting process repeated until the desired result is obtained.

If there are many well-separated peaks, Renaissance can use two energy regions for separate fitting. The energy separating the two regions (called the knee) is specified by you. The best fit to the two regions is often obtained by entering a knee energy that corresponds to a region where the efficiency is slowly varying and not at the maximum point. This is usually about 400 to 500 keV. By using the calibration plotting feature, the effect of the knee energy can be seen and the best value can be easily determined.

There are several options for the type of fit used to describe the efficiency/ energy relationship (see Fig. 70). These are:

- 1) **Interpolative** fit.
- 2) **Linear** fit of the natural logarithm of the efficiency to the natural logarithm of the energy.
- 3) **Quadratic** fit of the natural logarithm of the efficiency to the natural logarithm of the energy.
- 4) Six-order **Polynomial** fit of the natural logarithm of the efficiency to the energy.¹³
- 5) **TCC Polynomial**, a different six-order polynomial fit of the natural logarithm of the efficiency to the natural logarithm of the energy.

Options 1, 2, and 3 can be selected separately for two separate energy regions. Either of the two regions can be left uncalibrated by not including any points in the region, but the analysis will report zero intensity (in the library peak output) for peaks in the uncalibrated region. If both regions are calibrated, the above-the-knee energy region is fitted first, and the calculated efficiency at the knee is included as a data point in the below-the-knee fit. This means that only one point need be below the knee, but two points are the minimum above the knee for a calibration to be done. Option 4 fits the entire energy range with one function and is best suited to p-type detectors. Option 5 fits the entire energy range with different functions over three energy regions and can be used for p- or n-type detectors.

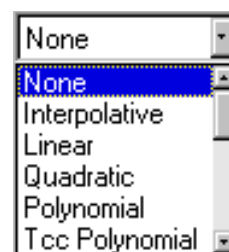


Figure 70.
Efficiency Fit
Types

¹³“Définition de Critères de Qualité Pour l’Essai des Logiciels Utilisés en Spectrométrie Gamma,” Rapport CAE-R-5347, 1986.

5.3.5.2. Interpolative Fit

The interpolative fit uses straight lines between the data points and does a linear interpolation between two points (one above and one below) to obtain the efficiency at the selected energy. For energies below the minimum energy data point or above the maximum data point, the efficiency is the straight-line projection of the last two data points at the appropriate end. The interpolative fit is used where the efficiency is recognized to be a complex function of energy that cannot be fit using the other functions.

If interpolative fit is used over the entire energy range, the knee energy should be set below the minimum energy of interest.

5.3.5.3. Linear Fit

The linear fit uses a straight-line fit to the data points. This is used when few data points are used or if the data points are all very close in energy. Also, for an n-type detector, the below-the-knee efficiency is nearly a straight-line down to approximately 10 keV, and the linear fit will produce the best result. For only two data points in the entire calibration, linear and interpolative are equivalent. If sufficient data are available, the linear fit is not as accurate as the quadratic fit because of the efficiency knee. The efficiency/energy formula is:

$$\varepsilon = e^{(a_1 + a_2 \cdot \ln(E))} \quad (7)$$

where:

ε = efficiency at energy E

a_i = fitting coefficients

E = energy

5.3.5.4. Quadratic Fit

The quadratic fit fits a quadratic function to the log (energy) vs. log (efficiency) curve. At least three data points above the knee and two below the knee are required for this fit. With only three points, the fit will be reported as exact for all data points, but the calibration might be inaccurate elsewhere.

If the input points are not well separated, the best fit to the data points might not be an accurate representation of the efficiency outside the fitted region.

The efficiency/energy formula is:

$$\varepsilon = e^{(a_1 + a_2 \cdot \ln(E) + a_3 (\ln(E))^2)} \quad (8)$$

where:

ε = efficiency at energy E

a_i = fitting coefficients

E = energy

5.3.5.5. Polynomial Fit

The polynomial fit uses a 6-term polynomial to fit the natural logarithm of efficiency to the energy. The function is optimized for p-type detectors. For n-type detectors, the low-energy region (below 60 keV) is not well modeled by this function. At least five well-separated peaks are needed for the polynomial fit. The knee value is not used in this fit and the function is disabled. The polynomial option is only on the **Above knee** list; the **Below knee** option is not used if polynomial is selected.

The polynomial efficiency/energy formula is:

$$\varepsilon = e^{\left(\sum_{i=1}^6 a_i E^{2-i} \right)} \quad (9)$$

where:

ε = efficiency at energy E

a_i = fitting coefficients

E = energy in MeV

The result of the efficiency calibration calculation is one or two sets of coefficients (one for the fit above the knee and one for below the knee, or just one for the polynomial fit), and a set of energy-efficiency pairs. The energy-efficiency pairs are used for the interpolative fit. The pairs can also be used to recalculate the efficiency and to display the efficiency plot.

5.3.5.6. TCC Polynomial Fit

The TCC polynomial fit is several polynomial fits to different energy parts of the spectrum (up to a six-order polynomial). The different energy regions are below 200 keV and above 200 keV. The details of the polynomial fit are given in the papers referenced below.^{14,15,16}

¹⁴M. Blaauw, "The use of sources emitting γ -rays for determination of absolute efficiency curves of highly efficient Ge detectors," NIM A322, 1993, pp. 483–500.

¹⁵R. Gunnink, "New method for calibrating a Ge detector by using only zero to four efficiency points," NIM A299, 1990, pp. 372–376.

¹⁶Gunnink, R., and A.L. Prindle, "Nonconventional methods for accurately calibrating germanium detectors," *J. Radioanalytical and Nuclear Chemistry*, 160(2), 1992, pp. 304–314.

5.3.5.7. Performing the Efficiency Calibration

To efficiency calibrate the system, collect an energy-calibrated spectrum of the known standard for a time sufficient to get well-formed peaks with small uncertainty. The certificate supplied with the source will have the energies, gammas/sec, nuclide names, and measurement date needed in the calibration.

The working library is used in the calculations. Load the library for the calibration source as shown in Section 5.6.3.

Expand the spectrum horizontally to show the peaks completely. Select **Calibrate** from the menu, then **Efficiency**. This will open the Efficiency Calibration Sidebar (Fig. 71). If the **Efficiency** item is gray, the system is not energy calibrated. Because there is yet no efficiency calibration, no graphs or tables are shown. Choose a spectrum peak listed in the source data sheet.

Use the Full Spectrum View (Fig. 72) to approximately locate the peak, or use the Library List and the Expanded Spectrum View to put the marker on the center of the peak. This selects the peak. The peak area and count rate are calculated in the same manner as in the analysis program.

Click on the **Calc...** button to open the Efficiency Calculation Worksheet for entering the data about the peak (Fig. 73).

In the **Assay (from Certificate)** section of the dialog, enter the calibration **Date** and **Time** from the source data sheet. Enter the **Activity** from the source and select the units from the droplist.

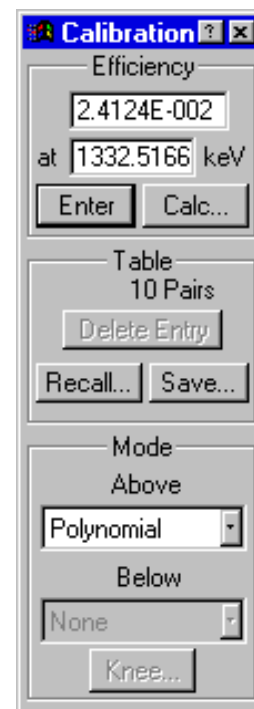


Figure 71.
Efficiency
Calibration
Sidebar.



Figure 72. Select Peak in Full Spectrum Window.

The source **Uncertainty** is entered here but can be left at 0.0. This uncertainty is used in the total uncertainty calculation.

When the values are correct, click the **Calculate Efficiency =** button at the top of the dialog and the calculated efficiency will be entered in the field beside the button. If this value is acceptable, click on **OK** to save the input and efficiency values and leave the worksheet. The graphs and tables will now be displayed.

Figure 73. Efficiency Calculation Worksheet.

Select the next peak and repeat the process. The **Date** and **Time** will default to the previously entered values, but the **Nuclide Half-Life** and **Activity** must be entered for each energy.

As each peak (above the minimum needed) is entered, the table and graph will update and new fits will be made. The fitting mode can be changed at any time to see how the various functions model the data. Note that for quadratic fit, a linear fit is made for one or two points and a quadratic fit is not done until three points are entered. For a polynomial fit, no fit is made until five points are entered. Because of the separate energy regions, the TCC polynomial fit requires more points.

Any point in the Efficiency Table can be deleted by selecting the point then clicking on the sidebar **Delete Entry** button. Any point in the table can be modified by selecting it and clicking on **Calc...** When the worksheet opens, the previously entered values will be shown. These values can be changed and a new efficiency generated by clicking on **Calculate Efficiency=**. To retain the changes, click on **OK**; to discard them, click on **Cancel**.

The knee energy is changed by clicking on the **Knee...** button in the calibration sidebar. This will open the Knee dialog box (Fig. 74) It will display the energy value for the knee. To change it, enter a new number and click on **Apply**. This will move the knee to this energy and update the fit, graph, and table. The value in the Knee dialog field will be set to the marker energy when the marker is moved and clicked in the spectrum or the Efficiency graph window. This is most easily seen in the Efficiency graph window. The knee energy is not changed until you click **Apply**.

Figure 74. Set Knee Energy.

To close the Knee dialog, click on the Close box. Renaissance will use the knee value shown the last time **Apply** was clicked.

The table of worksheet entries, including the gammas/sec, half-life, and certification date, contains all the information needed to do the calibration. It can be saved by clicking on the **Save...** button in the Table area of the sidebar. This opens a standard file-save dialog. Enter a filename and click on **Save**; Renaissance will assign a default extension of **.EFT**.

When the Efficiency graph and table are shown, the marker in the graph window can be moved to an energy by clicking the mouse on the graph, the table, the Full Spectrum View, or the Expanded Spectrum View. The **Peak**, **ROI**, and **Library** indexing buttons on the Status Sidebar can also be used to move the marker to the desired energy.

5.3.5.8. Using The Library

The library can be used to assist in the efficiency calibration in two ways:

- To direct the marker
- As input for automatic calibration

To open a library, select **Library/Select File...** To display the list of library peaks by energy, choose **Library/Select Peak...** This can be done before or during the calibration process. Arrange the Efficiency Table, graph window, and Library List so the two peak lists are not covered (see Fig. 75).

To select a peak from the Library List, double-click on the desired energy in the list. This will move the marker to that energy in the spectrum (updating the view, if necessary), and redisplay the graph and spectrum to reflect the changes.

By clicking on a library peak and then the worksheet, the worksheet is ready for the values for that peak. The half-life is copied from the library to the **Half-Life** field on the worksheet. Only the **Activity** needs to be entered.

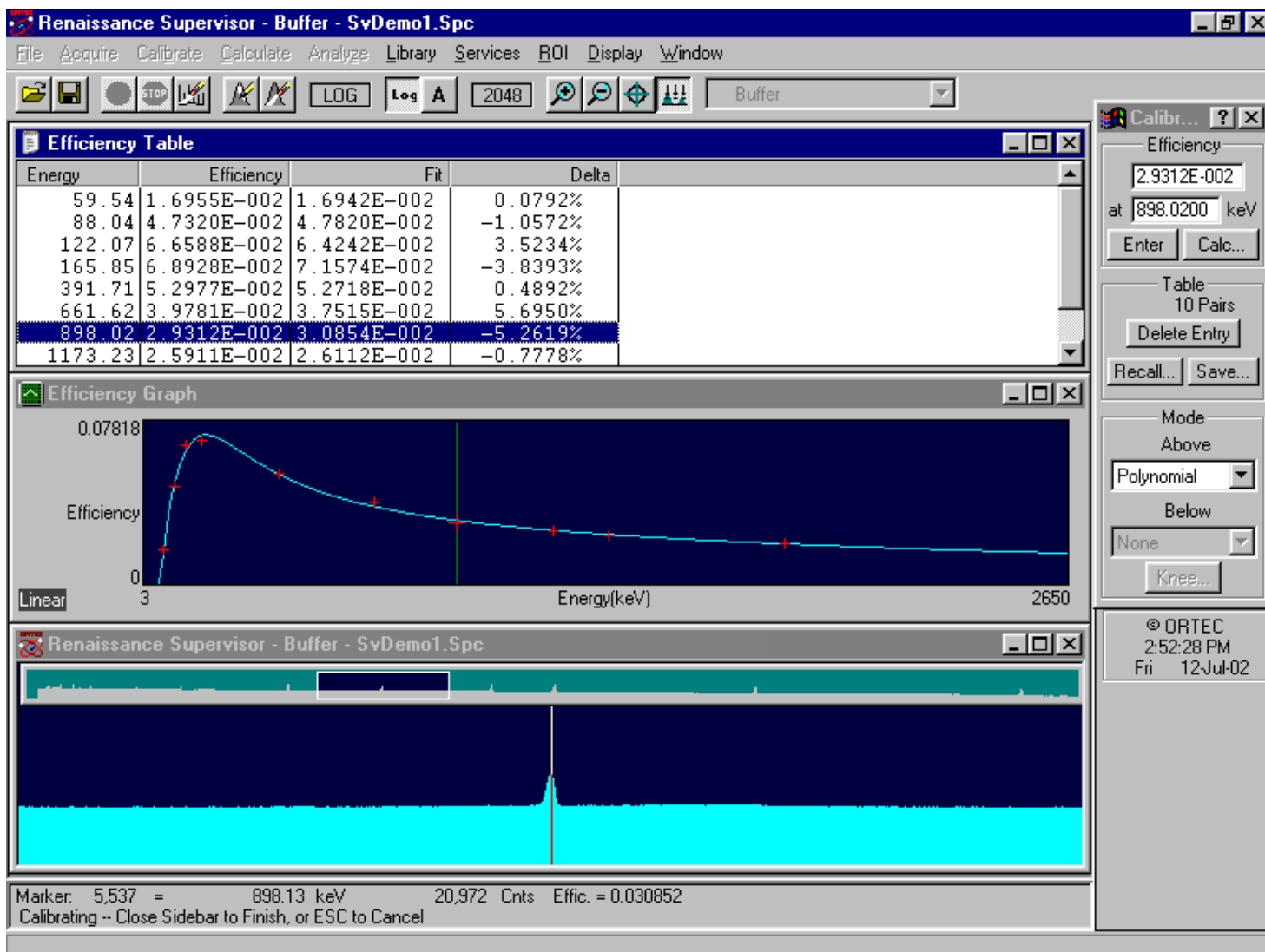


Figure 75. Using the Library in the Efficiency Calibration.

5.3.5.9. Automatic Efficiency Calibration

Renaissance can automatically perform the efficiency calibration by using the table in an existing .EFT file. Click on the calibration sidebar **Recall...** button. This will open a standard file-recall dialog (Fig. 76). Select the .EFT file to be used and click on **Open**. Renaissance will recall the table of entries and perform a calibration based on the data in the table. When the procedure is complete, the graph and table will be displayed.

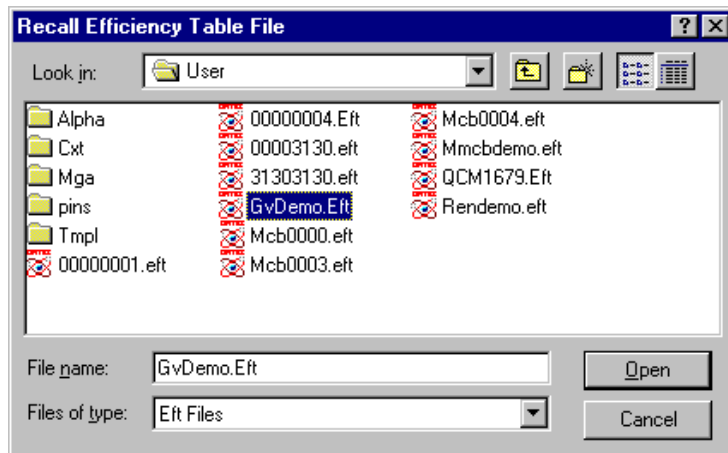


Figure 76. Recall Efficiency Table.

5.3.5.10. Manual Calibration

To perform a completely manual calibration, enter the efficiency and energy in the upper section of the Efficiency Calibration Sidebar, then click on **Enter**. The fit, graphs, and table will update after each point is entered.

If the table of values for a manually entered calibration is saved, the only values it will contain are the energy and the efficiency. Doing an automatic recalibration with this table will restore the manual calibration. If the calibration is a mixture of worksheet values and manual entries, the automatic recalibration will use recalculated values for the worksheet entries, and the manual entries will be used as entered.

5.3.5.11. Other Efficiency Sidebar Control Menu Functions

In addition to **Edit File...**, the Efficiency Calibration Sidebar control menu (Fig. 77) contains the **Move**, **Close**, **Graph**, **Table**, **Restore**, and **Destroy** functions. **Close** saves the efficiency and exits the efficiency calibration function. **Graph** and **Table** are display/hide toggles. Use **Restore** to ignore all calibration inputs made during this calibration session, and **Destroy** to clear the current working calibration and table of values.

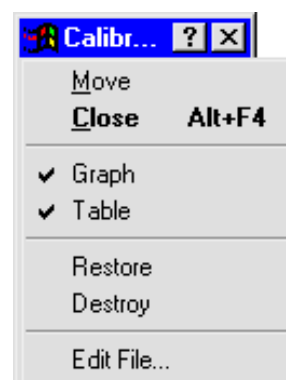


Figure 77.
Efficiency
Calibration Sidebar
Control Menu.

5.3.5.12. Editing the Standard (.EFT) Table File

An efficiency standard table file contains all the data input needed to perform a calibration using the standard. This file can be created from the Efficiency Calibration Sidebar by clicking on the **Save** button and assigning a filename, or with an ASCII text editor. The file can be modified with the **Edit File...** function on the sidebar control menu. Click on **File Edit...** to open a standard file-recall dialog. Select the **.EFT** file to be edited; it will be displayed as shown in Fig. 78.

The table contains the following information (by columns):

- 1) Isotope name (same as library).
- 2) Gamma-ray energy (keV).
- 3) Efficiency (used for manual efficiency inputs, ignored if remainder of line is valid).
- 4) Activity in Bq or μCi at the date and time specified in column 7.
- 5) Gammas/sec for this energy, at the specified date and time.
- 6) Uncertainty for this nuclide.
- 7) Calibration date and time for the gammas/sec calibration. The gammas/sec are automatically decay corrected from the date/time in column 5 to the date/time of the spectrum acquisition.

- 8) Half-life of this nuclide in days.
- 9) Branching ratio as gammas/100 disintegrations.

The screenshot shows the 'Eft File Editor -- Editing: GvDemo.Eft' window. At the top is a table with the following data:

Isotope	Energy	Efficiency	Activity	Gammas/s	Uncertainty
	59.54	1.7027101E-002		2078.00	
	88.04	4.7134101E-002		2967.00	
	122.07	6.6528901E-002		1813.00	
	165.85	6.9077797E-002		2550.00	
	391.71	5.2967198E-002		4263.00	
	661.62	3.9785799E-002		4198.00	
	898.02	2.9324301E-002		10120.00	
	1173.23	2.5913799E-002		5818.00	

Below the table are buttons: Add New, Update, Delete, Clear All, Save As... The 'Library Group' is set to 'Cd-109 @ 22.16 keV'. The 'Assay (From Certificate)' section shows: Gammas/s: 2078.00, GPS, Uncertainty: %, Date: 10/1/90, 12:00:00 PM. The 'Fit Type' section shows: Above: Polynomial, Below: None, Knee: 150.00 keV. Buttons for OK and Cancel are at the bottom.

Figure 78. Edit Efficiency Table.

The efficiency fit type is set at the bottom. If the fit type for **Above** covers the whole energy range, then the **Below** and **Knee** values are gray.

After the fit type comes the total calculated source uncertainty, the number of nuclides in the source uncertainty calculation, and the list of nuclides used in the uncertainty calculation. The total is the individual uncertainties added in quadrature.

To add an energy to the table, enter the values directly or click on **Select from Lib**, then click on **Add New**.

To delete an energy, select the energy and click on **Delete**.

To change the values for an energy, select the energy, enter the new values directly or click on **Select from Lib**, then click on **Update** to record the changes (you must click on **Update** or the changes will not be made).

When finished, click on **Save As...** to rewrite the new file to disk. To discard the changes just made, click on **Cancel**; a dialog will verify that these changes are to be discarded.

5.3.5.13. The Efficiency Graph Control Menu

Figure 79 shows the control menu for the graph of efficiency vs. energy. It contains selections to turn a **Grid** on/off and to switch from **Log/Log** to **Linear** axes. The graph can also be **Closed** (removed). If closed, it can be redisplayed with the **Graph** command from the Efficiency Calibration Sidebar's control menu.

5.3.5.14. The Efficiency Table Control Menu

Figure 80 shows the control menu for the table of efficiency vs. energy. It contains commands to **Print** and **Close** the table. If closed, it can be redisplayed with the **Table** selection from the Efficiency Calibration Sidebar's control menu.

5.3.6. Efficiency — NaI

The following section describes how to perform the efficiency calibration. It can be accessed here or from the **Edit Efficiency** function at the end of the wizard.

NOTE If you are using the Motor Control feature (see Appendix B), note that if your efficiency calibrations are all performed at one scan length, changing to another scan length will require you to perform new efficiency calibrations.

5.3.6.1. Introduction

The **Efficiency...** calibration function calculates the detection efficiency of the NaI Detector system as a function of energy. The efficiency of the Detector is the relation between the number of gamma rays emitted from the source to the number of gamma rays collected in the full-energy peak (see Fig. 81).

The NaI Detector system efficiency includes effects from the Detector itself, the Detector-source geometry, the materials surrounding the Detector, and absorption in the source material or matrix. This is shown in Fig. 82.

In general, it is not good practice to use efficiency calibrations from one Detector-source geometry for other geometries. Different calibration files can be made for all the different source-Detector combinations to compensate for the differences between the geometries. You choose

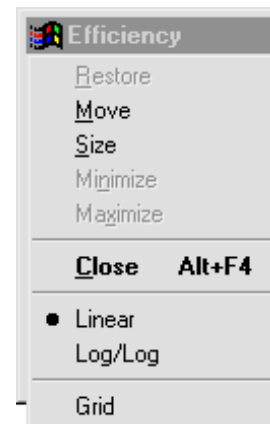


Figure 79.
Efficiency Graph Control Menu.



Figure 80.
Efficiency Table Control Menu.

the output filename for each of the different calibrations, which can subsequently be specified, for different sampling geometries, using **Recall Calibration...**

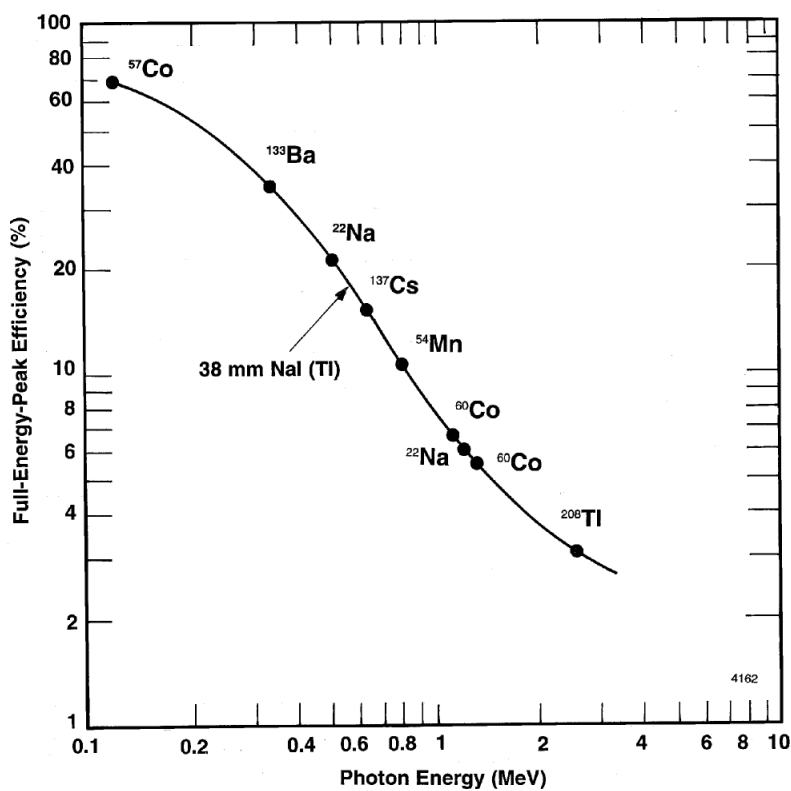


Figure 81. Detector Efficiency as a Function of Energy.

The efficiency is defined as a function of energy. Therefore, the **Energy...** calibration must be done first. The **Efficiency...** command remains grayed (disabled) until the spectrum has been energy calibrated.

NOTE The energy recalibration can be redone (to account for gain changes) without the need to redo the efficiency calibration.

The efficiency calibration is critically important to the accuracy of the activity results from Renaissance. We recommend that you use only calibrated sources traceable to a known standard. The time between the calibration of the radionuclide source by its manufacturer and the time the spectrum is collected is important, as this defines the decay correction needed to calculate source strength for the spectrum.

The selected source(s) should contain isolated singlets over the entire energy range of interest. If desired, the efficiency calibration can be performed using one or more spectra to minimize the difficulty of obtaining the required number of singlets.

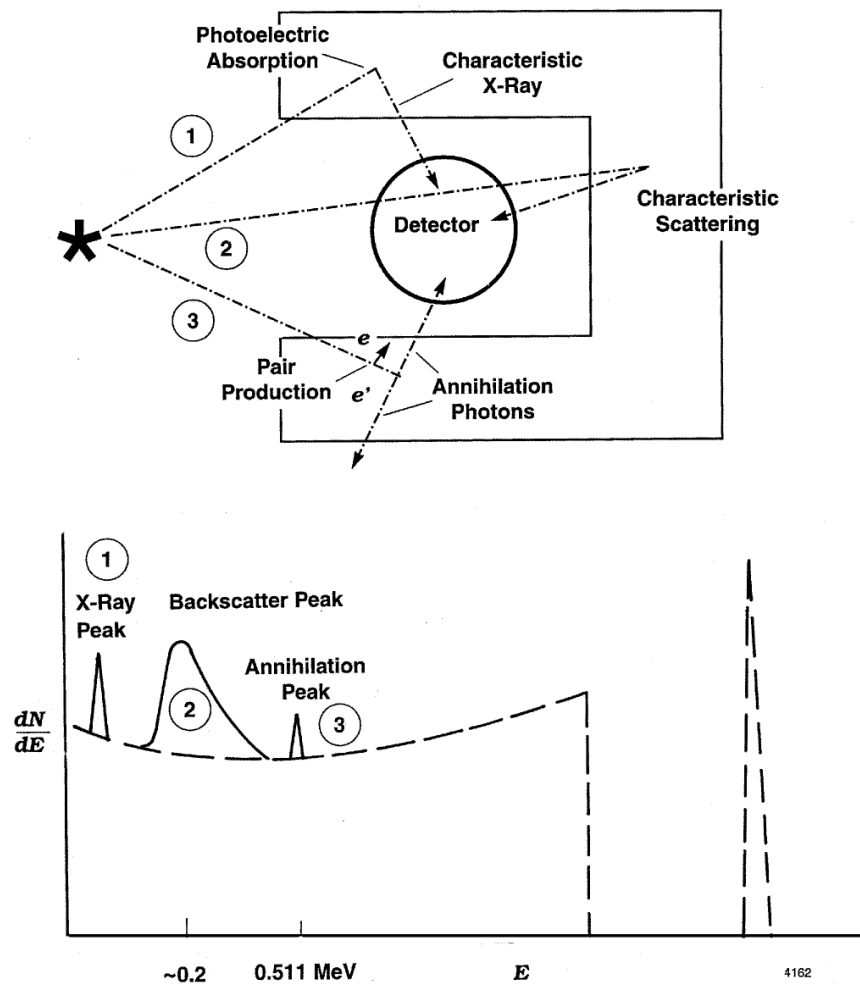


Figure 82. Detector with Extended Source.

To perform the calibration, you need an energy-calibrated spectrum of the radionuclides and their source strengths and calibration dates. These data are entered into the program in convenient menu-type forms, and you can review the results of each step. Questionable points can be deleted, additional points added, and the fitting process repeated, until you obtain the desired result.

If there are many well-separated peaks, Renaissance can use two energy regions for separate fitting. The energy separating the two regions (called the knee) is specified by you. The best fit to the two regions is often obtained by entering a knee energy that corresponds to a region where the efficiency is slowly varying and not at the maximum point. This is usually about 400 to 500 keV. By using the calibration plotting feature, the effect of the knee energy can be seen and the best value can be easily determined.

There are several options for the type of fit used to describe the efficiency/energy relationship (see Fig. 83). These are:

- 1) **Interpolative** fit.
- 2) **Linear** fit of the natural logarithm of the efficiency to the natural logarithm of the energy.
- 3) **Quadratic** fit of the natural logarithm of the efficiency to the natural logarithm of the energy.
- 4) Six-order **Polynomial** fit of the natural logarithm of the efficiency to the energy.¹⁷

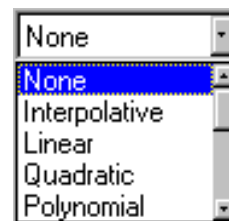


Figure 83.
Efficiency Fit
Types

Options 1, 2, and 3 can be selected separately for two separate energy regions. Either of the two regions can be left uncalibrated by not including any points in the region, but the analysis will report zero intensity (in the library peak output) for peaks in the uncalibrated region. If both regions are calibrated, the above-the-knee energy region is fitted first, and the calculated efficiency at the knee is included as a data point in the below-the-knee fit. This means that only one point need be below the knee, but two points are the minimum above the knee for a calibration to be done. Option 4 fits the entire energy range with one function and is best suited to p-type detectors. Option 5 fits the entire energy range with different functions over three energy regions and can be used for p- or n-type detectors.

5.3.6.2. Interpolative Fit

The interpolative fit uses straight lines between the data points and does a linear interpolation between two points (one above and one below) to obtain the efficiency at the selected energy. For energies below the minimum energy data point or above the maximum data point, the efficiency is the straight-line projection of the last two data points at the appropriate end. The interpolative fit is used where the efficiency is recognized to be a complex function of energy that cannot be fit using the other functions.

5.3.6.3. Linear Fit

The linear fit uses a straight-line fit to the data points. This is used when few data points are used or if the data points are all very close in energy. Also, for an n-type detector, the below-the-knee efficiency is nearly a straight-line down to approximately 10 keV, and the linear fit will produce the best result. For only two data points in the entire calibration, linear and interpolative

¹⁷“Définition de Critères de Qualité Pour l’Essai des Logiciels Utilisés en Spectrométrie Gamma,” Rapport CAE-R-5347, 1986.

are equivalent. If sufficient data are available, the linear fit is not as accurate as the quadratic fit because of the efficiency knee.

The efficiency/energy formula is:

$$\varepsilon = e^{(a_1 + a_2 \cdot \ln(E))} \quad (10)$$

where:

ε = efficiency at energy E

a_i = fitting coefficients

E = energy

5.3.6.4. Quadratic Fit

The quadratic fit fits a quadratic function to the log (energy) vs. log (efficiency) curve. At least three data points above the knee and two below the knee are required for this fit. With only three points, the fit will be reported as exact for all data points, but the calibration might be inaccurate elsewhere.

If the input points are not well separated, the best fit to the data points might not be an accurate representation of the efficiency outside the fitted region.

The efficiency/energy formula is:

$$\varepsilon = e^{(a_1 + a_2 \cdot \ln(E) + a_3 (\ln(E))^2)} \quad (11)$$

where:

ε = efficiency at energy E

a_i = fitting coefficients

E = energy

5.3.6.5. Polynomial Fit

The polynomial fit uses a 6-term polynomial to fit the natural logarithm of efficiency to the energy. The function is optimized for p-type detectors. For n-type detectors, the low-energy region (below 60 keV) is not well modeled by this function. At least five well-separated peaks are needed for the polynomial fit. The knee value is not used in this fit and the function is disabled. The polynomial option is only on the **Above knee** list; the **Below knee** option is not used if polynomial is selected.

The polynomial efficiency/energy formula is:

$$\varepsilon = e \left(\sum_{i=1}^6 a_i E^{2-i} \right) \quad (12)$$

where:

ε = efficiency at energy E

a_i = fitting coefficients

E = energy in MeV

The result of the efficiency calibration calculation is one or two sets of coefficients (one for the fit above the knee and one for below the knee, or just one for the polynomial fit), and a set of energy-efficiency pairs. The energy-efficiency pairs are used for the interpolative fit. The pairs can also be used to recalculate the efficiency and to display the efficiency plot.

The result of the efficiency calibration calculation is a set of coefficients and a set of energy-efficiency pairs. These pairs can be used to recalculate the efficiency and to display the efficiency plot.

5.3.6.6. Performing the Efficiency Calibration

To efficiency calibrate the system:

Collect an energy-calibrated spectrum of the known standard for a time sufficient to get well-formed peaks with small uncertainty. The certificate supplied with the source will have the energies, gammas/second, nuclide names, and measurement date needed in the calibration.

Expand the spectrum horizontally to show the peaks completely. Select **Calibrate/Efficiency...** from the menu. This will display the Efficiency Calibration Table and Graph, and the Efficiency Calibration Sidebar shown in Fig. 84. (As noted above, if the **Efficiency...** item is gray, the system must first be energy calibrated.)

Choose a spectrum peak listed in the source data sheet. Put the marker on the center of the peak; this selects the peak.

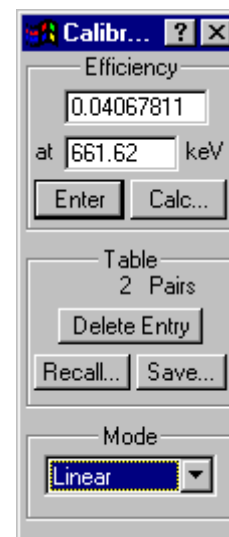


Figure 84.
Efficiency
Calibration
Sidebar.

Click on the **Calc...** button on the Efficiency Calibration Sidebar. This will open the **Efficiency Calc. Worksheet** dialog for entering the data about the peak (Fig. 85).

The peak area and count rate are calculated in the same manner as in the analysis program. In the **Assay (from Certificate)** section, select the **Date** field and enter the calibration date from the source data sheet, as well as the calibration **Time**. Enter the gammas/ second from the source in the **Activity** field, and set the units to GPS. The **Uncertainty** is the total uncertainty for the nuclide as given in the source certificate. This includes the uncertainty for the activity, the half-life, and the branching ratio.

Figure 85. Efficiency Calibration Worksheet.

Advance to the **Nuclide Half-Life** box and enter the half-life in days for this nuclide if the value from the library is not shown. The use of the **Library** checkbox is discussed in Section 5.3.6.9. Note that the peak count-rate value (**Counts/Sec.**) in the **Peak Measured (from Spectrum)** section is already filled in, based on the selected peak.

When the values are correct, click on **Calculate Efficiency=**. The efficiency will be calculated and displayed in the field at the top of the worksheet dialog. Click on **OK** to close the worksheet. If this value is acceptable, click on the **Enter** button in the Efficiency Calibration Sidebar to save the input and efficiency values.

Select the next peak and repeat the process. The date and time will default to the previously entered values, but the half-life and gammas/second must be entered for each energy unless the **Library** and **Activity...** features are used.

As each peak is entered, the table and graph will update and new fits will be made.

NOTE A linear fit is made for one or two points, a quadratic fit is made for three points, and a cubic fit is made if four or more points are entered.

Any point can be deleted by selecting the value in the **Efficiency Table** window and clicking on the **Delete Entry** button in the efficiency calibration sidebar. (**Delete Entry** is normally grayed, but becomes active when a value is selected from the table.)

Any point can be modified by selecting the value in the table dialog and clicking on **Calc...** When the worksheet opens, the previously entered values will be shown.

5.3.6.7. Saving the Efficiency Calibration Table

The table of entries, including the gammas/second, half-life, and certification date (i.e., all the information needed to do the calibration), can be saved by clicking on the **Save...** button in the **Table** section of the sidebar. This opens the **Save Efficiency Table** dialog shown in Fig. 86.

The table is saved as an ASCII file with the default extension **.EFT**. The file can be edited in Renaissance, as described in the next paragraph, or offline with an ASCII-based text editor such as Windows Notepad.

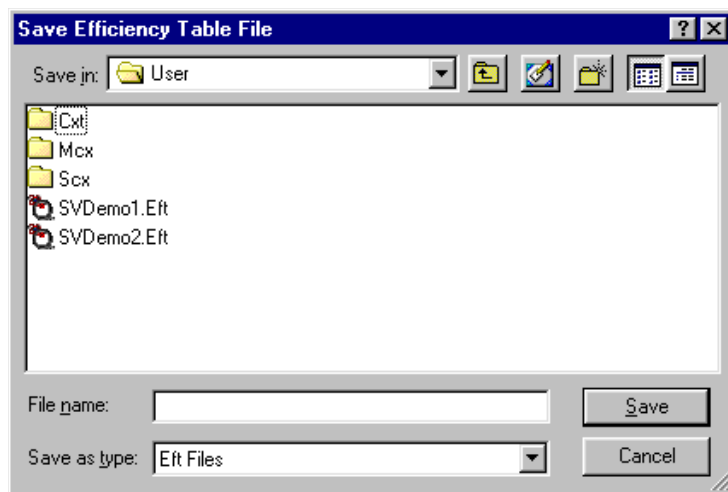


Figure 86. Save Efficiency Table.

5.3.6.8. Editing the Efficiency Calibration Table

To edit the efficiency calibration table file, open the Efficiency Calibration Sidebar's control menu and select **Edit File**. This opens the dialog shown in Fig. 87. Select the **.EFT** file to be edited; it will be displayed as shown.

The table contains the following information (by columns):

- 1) Gamma-ray energy (keV).
- 2) Efficiency (used for manual efficiency inputs, ignored if remainder of line is valid).
- 3) Gammas/sec for this energy, at the specified date and time.
- 4) Half-life of this nuclide in days.
- 5) Calibration date and time for the gammas/sec calibration. The gammas/sec are automatically decay corrected from the date/time in column 5 to the date/time of the spectrum acquisition.

After the energy list in the **.EFT** files is the following line:

FitType = <iFit>

where <iFit> is the fit type above the knee (0–3 or 6). The fit types are:

- | | |
|---|--------------------------|
| 0 | no fit and no efficiency |
| 1 | interpolative fit |
| 2 | linear fit |

- 3 quadratic fit
- 6 polynomial fit

The screenshot shows the 'Eft File Editor -- Editing: SVDemo1.Eft' window. At the top is a table with the following data:

Isotope	Energy	Efficiency	Activity	Gammas/s	Uncertainty
Co-57	122.07	2.1824780E-001		330022.19	
Cs-137	661.62	5.6180399E-002		15527.80	
Co-60	1173.24	2.4708200E-002		19640.30	
Co-60	1332.50	2.3626801E-002		19656.50	

Below the table are buttons: Add New, Update, Delete, Clear All, Save As... Below these are two main panels:

- Library Group:** A dropdown menu showing 'Co-57 @ 122.07 keV' and a 'Select from Lib' button. Below are input fields for Isotope (Co-57), Energy (122.07), Efficiency (2.1824780E-001), Halflife (Days) (2.7240E+002), and Gammas/100d.
- Assay (From Certificate):** Input fields for Gammas/s (330022.19), Uncertainty (%), Date (3/1/94), and Time (12:00:00 PM). The Date and Time fields have units 'M/d/yy' and 'h:mm:ss tt' respectively.

At the bottom is a 'Fit Type' section with dropdowns for 'Above' (Quadratic) and 'Below' (None), and a 'Knee' input field (0.00 keV). At the very bottom are 'OK' and 'Cancel' buttons.

Figure 87. Editing the Efficiency Table.

When an Efficiency Table is recalled, this line is used to select the fit type to be used.

Following the fit type are the total calculated source uncertainty, the number of nuclides in the source uncertainty calculation, and the list of nuclides used in the uncertainty calculation. The total is the individual uncertainties added in quadrature. When finished, click on **Save** to rewrite the new file to disk. To discard any changes, click on **Cancel**; a dialog will verify that you want to discard.

5.3.6.9. Using The Library in Efficiency Calibrations

The library can be used to assist in the efficiency calibration in two ways: (1) to direct the marker, and (2) as input for automatic calibration.

To open a library, select **Library/Select File...** A list of the library peaks by energy is displayed by selecting **Library/Select Peak...** Now select **Calibrate/Efficiency**. When the table and graph appear, move the table down so the peak list is not covered (see Fig. 88).

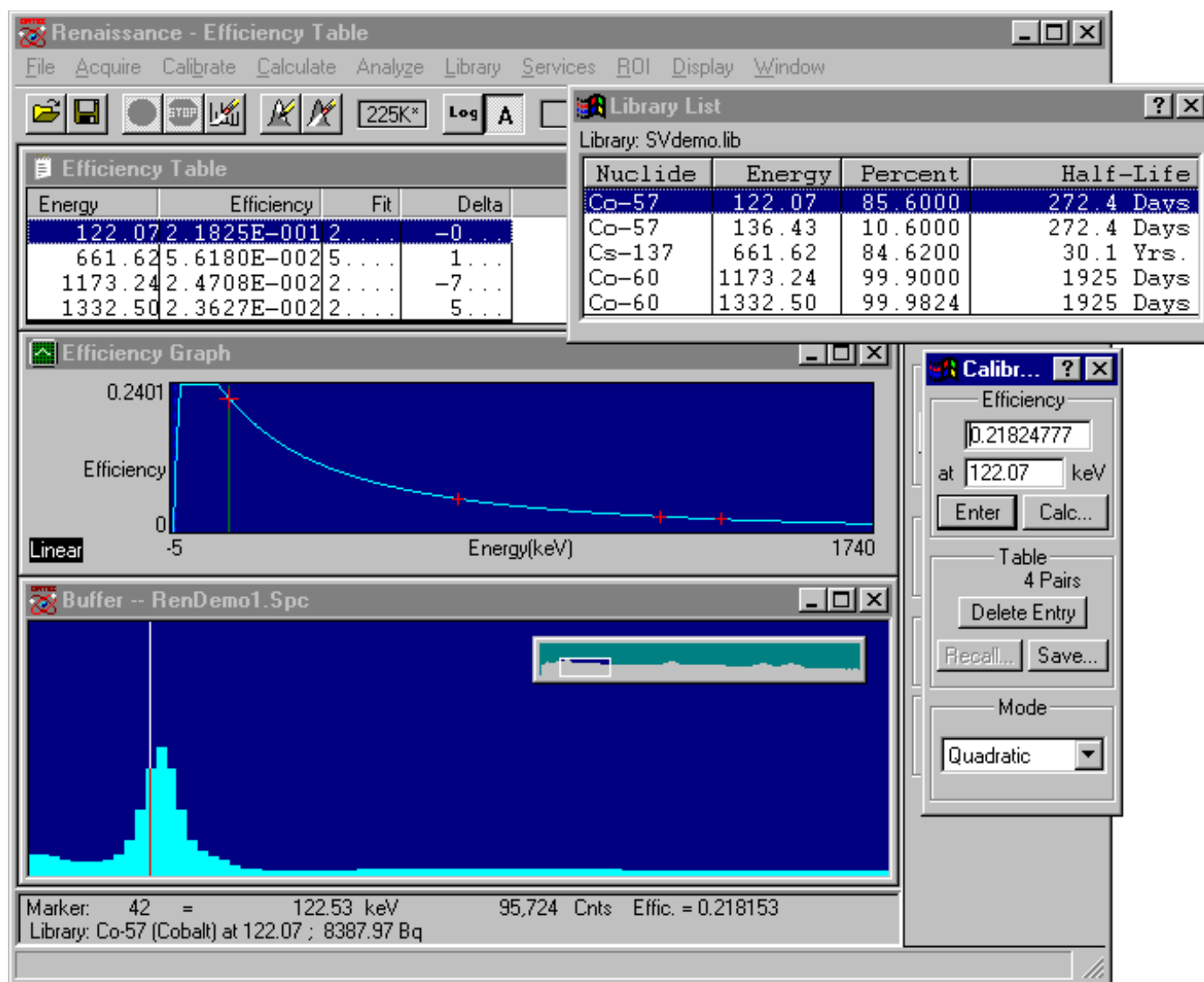


Figure 88. Using the Library in an Efficiency Calibration.

With the library peak list displayed, the peaks can be selected by double-clicking on the energy in the library list. This will move the marker to that energy in the spectrum (updating the view, if necessary), and change the graph and spectrum to reflect the changes.

By clicking on a library peak and then the worksheet, the worksheet is ready for the values for that peak. The half-life will be copied from the library peak list to the **Half-Life** field on the worksheet. You will only have to enter the **Gamma/Sec.**

5.3.7. Lower Limit...

This command opens the dialog shown in Fig. 89, which allows you to set the low-channel limit to be used during calibration of NaI detectors. It is not used for Ge detector calibrations. This is useful for nuclides such as ^{57}Co , when the low-energy edge of the peak could be very close to the LLD setting of the Detector. Refer to the discussion, **Important Considerations When Creating NaI Analysis Options Settings** (page 134), and set the **Lower Limit** to the start channel of the **Analysis Range** on the Sample tab under **Analyze/Settings/Sample Type...** (see Fig. 122, page 139).

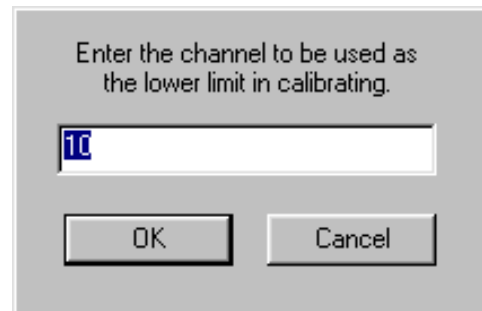


Figure 89. Lower Limit for Calibrations.

5.3.8. Recall Calibration...

This command (see Fig. 90) recalls the calibration fields from the specified file to the working calibration for the currently selected Detector. The current working calibration is lost. The calibration data can be read from any file containing the correct records. This includes .CLB, .SPC, and analysis (.UFO) files.

You can recall the energy calibration, the efficiency calibration, or both.

The **Recall Energy Calibration** and **Recall Efficiency Calibration** check-boxes at the bottom of the dialog indicate which parts of the calibration

will be retrieved. The original calibration is retained for the parts not retrieved. In all cases (even with no box marked), the calibration description is retrieved.

To change the calibration stored in a spectrum file, recall the spectrum file (its calibration is automatically loaded), recall the desired calibration, and store the spectrum back to disk.

5.3.9. Save Calibration...

Save Calibration saves the current working calibration to disk in the .CLB format. Both the energy and efficiency data are saved.

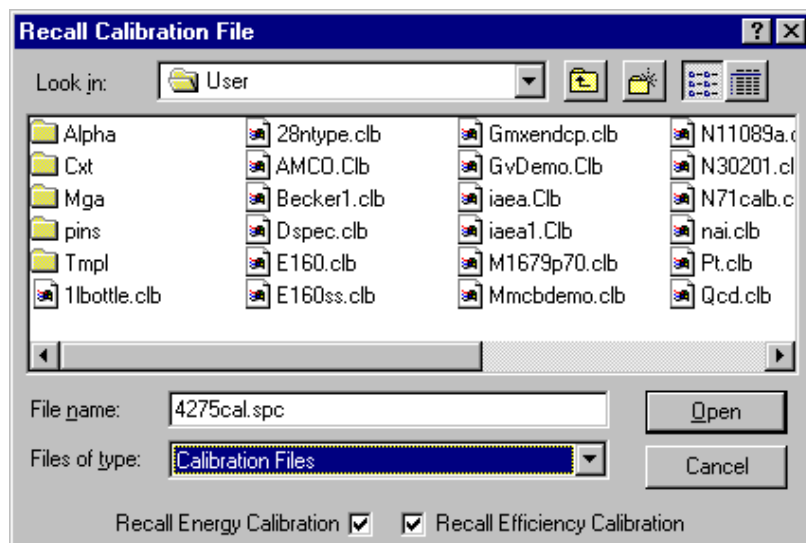


Figure 90. Recall Calibration.

5.3.10. Print Calibration...

This sends all the calibration data in the working calibration to the display, a printer, or a disk file. If the calibration tables exist, they will also be printed.

5.3.11. Ge Calibration Wizard...

The **Ge Calibration Wizard** guides you through the calibration process for one or more Ge detectors. The actual calculations are described in Sections 5.3.3 and 5.3.5.

- The calibration process is normally fully automatic and seldom requires adjustment when a good library and strong peaks are used.
- You might want to remove weak energy peaks or include additional peaks. This can be accomplished using the interactive mode available on the last page of the calibration wizard.

5.3.11.1. Select Detectors

The first dialog is shown in Fig. 91. To calibrate the active detector only, select the first (**current**) radio button. To calibrate a **group**, click on the second button, then choose a group from the **Detector Group** droplist. The **Calibrate sum** option will sum the spectra from the group of detectors and calibrate using the composite spectrum. This calibration should be used if you are going to analyze the composite spectra. (See Section 5.7.8.3).

NOTE In both cases where multiple detectors are used, *the source must be in the field of view for all detectors*. The data from all detectors is collected simultaneously.

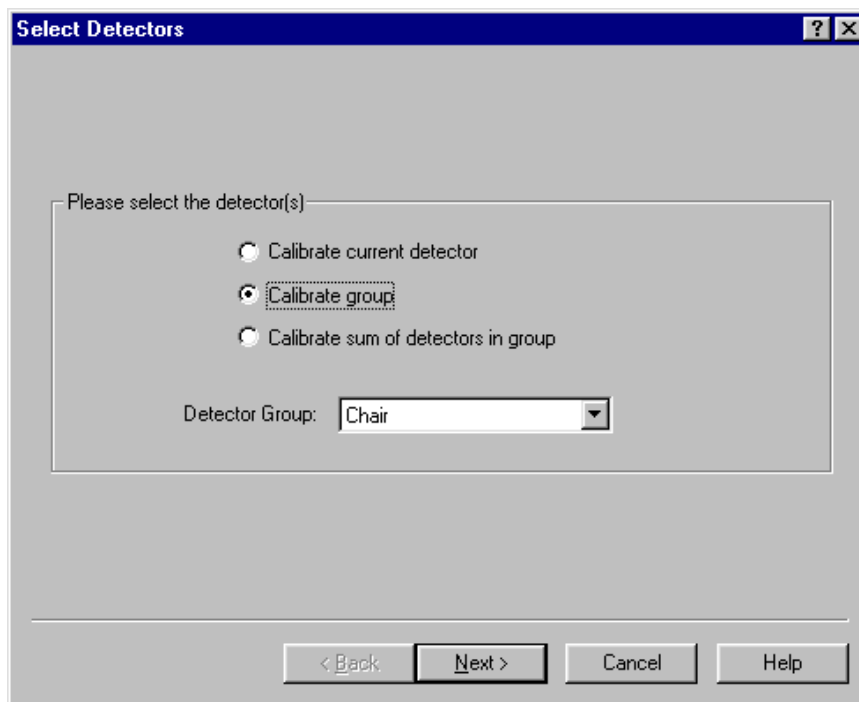


Figure 91. Select the Detectors to be Calibrated.

5.3.11.2. Choose the Calibrations to be Performed

The Renaissance calibration wizard automates the complete calibration process, including spectrum acquisition. The calibration can be performed on the data in an MCB or in a buffer window, using spectra on disk. At the end of the calibration, the complete results are presented for review. During the review, any or all of the calibration steps can be repeated with any changes necessary to improve the calibration. Figure 92 shows the next screen of the calibration wizard. The options for each type of calibration are to **Keep Current** or **Create New**.

Keep Current — This means to continue using the calibration stored in the MCB or in the spectrum (the current working calibration). The wizard will skip this calibration step. However, if review of the calibration shows a problem, you can repeat the process with new options using the **Edit** buttons on the final wizard dialog.

Create New — This choice means that the calibration selected (energy or efficiency) will be replaced by the results of the subsequent steps.

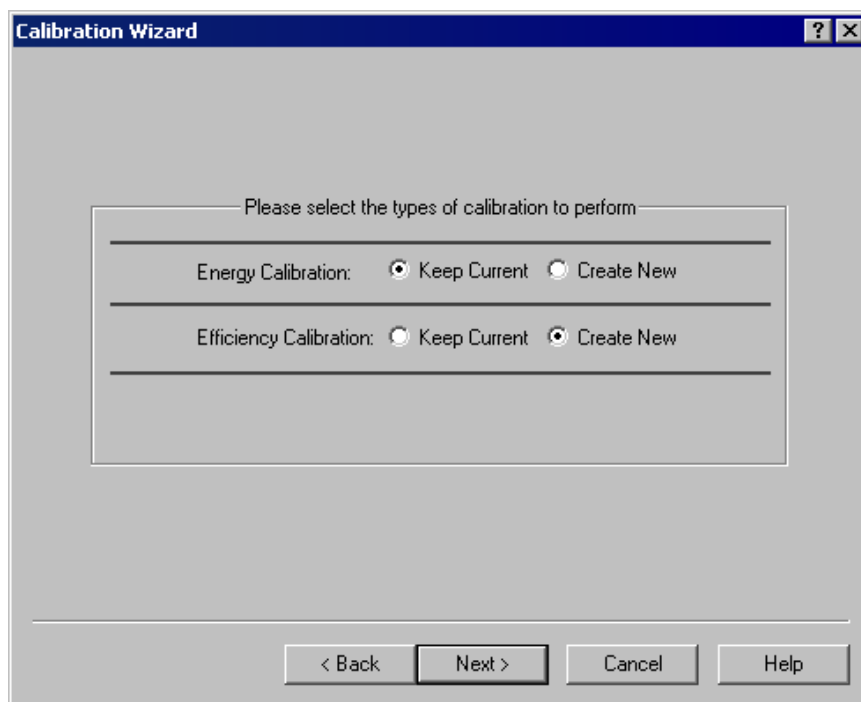


Figure 92. Choose the Calibrations to be Performed.

All of the peak calculations use the **Analyze/Settings/Sample Type...** values. This is to ensure that the calibration and analysis calculations are the same. Be sure to check the settings before starting the wizard. There are several important analysis settings. If spectrum has high dead time, there will also be a significant amount of random summing. The correction for random summing is applied in the calibration calculations. The **Random Summing** factor is discussed in Section 8.11 and entered on the Sample tab of the Analysis Options dialog. The starting channel of the **Analysis Region** should be set above the low-level cutoff. The peak-cutoff sensitivity used in the calibration is the smaller of the following: 10% or the value entered in the Analysis Options dialog. The peak-search level is the larger of the following: 4 or the value selected in the Analysis Options dialog.

When you have made your selections, click on **Next** to go to the next step in the wizard. The next step will depend on the choices made on this first screen.

5.3.11.3. Choose Calibration Files

Figure 93 shows the filename entry dialog. The **data source file** contains information about the calibration sources. The **Creation** and **Edition** dates show, respectively, when the file was created and when it was last changed. You can (1) use the **Browse** button to recall an existing **.CAL** file, the contents of which will be read and used as defaults in the remaining calibration wizard dialogs; or (2) enter a new filename then proceed through the wizard setting the parameters that will be saved in this new **.CAL** file.

Figure 93. File Selection.

Enter the library name for the energy and efficiency calculations. The same source is used for both. Click on **Browse** to find the correct library file. (The TCC library feature is not used in Renaissance).

Click **Next** to continue.

5.3.11.4. Calibration Settings

The next dialog is shown in Fig. 94. The energy can be recalculated without changing the FWHM values. If you want to change the FWHM calibration, mark the **Fit FWHM** box. This will fit a quadratic to the FWHM values. To force a linear fit, mark the **Linear FWHM** box.

Select the **Efficiency Fit Type** (see the discussion on page 88 for details). The available fit types are **None**, **Interpolative**, **Linear**,

Figure 94. Select the Fit Types.

Quadratic, and **Polynomial**. The normal selection for GEM is polynomial; the normal setting for GMX is quadratic above and below.

Enter the **Activity Units** for the sources to be used. The activities are entered for each gamma-ray energy on the Source Data Sheet dialog (Fig. 96).

Click **Next**.

5.3.11.5. Sources and Spectrum Settings

Figure 95 shows the next wizard screen. The **Number of Sources** is normally 1 for Ge detectors. The number refers to the number of different spectra (1 for each source) that are collected for a single calibration (see Section 5.3.3). If multiple sources are used together (e.g., several containers in a lung phantom), then the number of sources is 1 and the activity (entered on the Source Data Sheet) is the sum of the individual activities.

To collect a new spectrum, mark the **Clear Data Before Start** checkbox. If a spectrum is already in the MCB, it will be used if this box is not marked.

The spectra collected in the calibration phase will be saved to disk if the **Save Spectra** box is marked. The filename will be composed of the **Prefix** and a 6-digit number that increments for each spectrum. We recommend you save these spectra for QA purposes.

Click on **Next** to go to the Source Data Sheet (Fig. 96).

The screenshot shows a window titled "Calibration Wizard" with a standard Windows-style title bar (blue background, white text, and icons for help, maximize, and close). The main area is light gray. At the top, there is a label "Number of Sources:" followed by a text input field containing the number "1". Below this is a section titled "Spectrum Settings" enclosed in a thin gray border. Inside this section, there are three items: "Save Spectra" with a checked checkbox, "Spectrum File Prefix:" followed by a text input field containing "REN", and "Clear Data Before Start" with a checked checkbox. At the bottom of the window, there are four buttons: "< Back", "Next >", "Cancel", and "Help".

Figure 95. Sources and Spectrum Settings.

- 3) Activity in Bq or μCi at the date and time specified in column 6.
- 4) Gammas/sec for this energy at the specified date and time.
- 5) Uncertainty for this nuclide.
- 6) Calibration date and time for the gammas/sec calibration. The gammas/sec are automatically decay corrected from the date/time in column 4 to the date/time of the spectrum acquisition.
- 7) Half-life of this nuclide in days.
- 8) Branching ration as gammas/100 disintegrations.

To add an energy to the table, click on the droplist in the **Assay** section and select the desired nuclide and energy. Enter the **Activity** and **Uncertainty** fields, then click on **Add New**.

Figure 97 shows the addition of **Na-22 @ 1274.53 keV** to the table.

To delete an energy, click on its entry in the table, then click on **Delete**.

To change an energy entry's values, select the energy, enter the new values directly or click **Select from Lib**, then click **Update** to record the changes.

NOTE You must click **Update** or the changes will not be made.

When finished, click **Next**. A Source Data Sheet will be presented for each source. If this is the last source, a dialog will be displayed asking if you wish to save the changes. To save the changes, click **Yes**. This will open a file-save dialog so you can assign a filename. You can either a new name or overwrite an existing **.CAL** file. To discard the changes, click **No**.

At this point, the dialog shown in Fig. 98 is displayed, showing the status of the Detectors (e.g., **Ready**, **Acquiring**, **Completed**).

NOTE While the Calibration Status dialog shows status (e.g., **Acquiring**) for all of the Detectors in the group, the **Real Time** and **Live Time** are displayed only for the first Detector on the list to optimize the use of the computer's resources.

Isotope	Energy	Activity	Gammas/s	Uncert.
Cs-137	661.62	2.9437E+003	2491.00	5
Na-22	1274.53	3.4741E+003	3472.00	5

Figure 97. Adding a New Entry to the Source Data Sheet.

In addition to the status dialog, the message shown in Fig. 99 is displayed. Position the source and click **OK** to begin spectrum acquisition.

When spectrum collection is complete (or the buffer is used), the energy and FWHM calibration is performed. If successful, the wizard goes on to the next step.

If the energy calibration process detects a severe error, an error message is displayed. Click **OK** to acknowledge the error. The calibration process will stop at this point.

If the energy calibration process detects a minor error, a warning message is shown. Click **OK** to acknowledge the warning and remember that this warning was given. The calibration process will continue as normal. When the final review screen is displayed (Fig. 101), click **Edit Energy** to review the cause of the error and correct it if needed (see Section 5.3.11.8).

If the FWHM calibration fails one of the internal validity tests, a message is displayed. Click **OK** to acknowledge the message and the calibration process will continue. Remember to check the FWHM at the end of the process by clicking on **Edit Energy** on the review page.

After the energy calibration is complete, the efficiency calibration is performed.

5.3.11.7. Efficiency Calibration

If the efficiency calibration process detects a severe error, an error message is displayed. Click on **OK** to continue the calibration process. Several different errors could be displayed depending on the state of the spectrum. The “peaks too close together” error can be ignored.

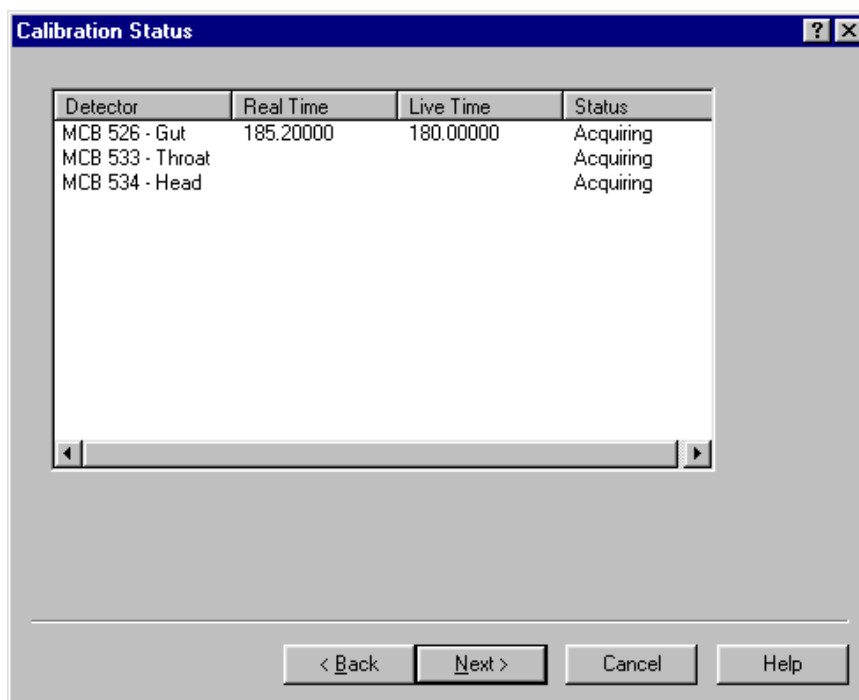


Figure 98. Detector Status.

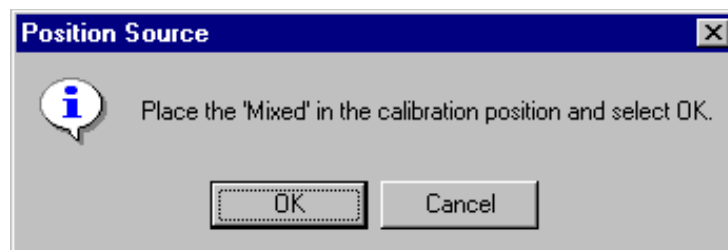


Figure 99. Position the Source for Energy Calibration.

If you chose to use multiple sources, the wizard asks for the next source to be positioned (see Fig. 100). Click on **OK** to begin spectrum acquisition.

After all the spectra have been collected, the wizard merges the results and completes the calibration.

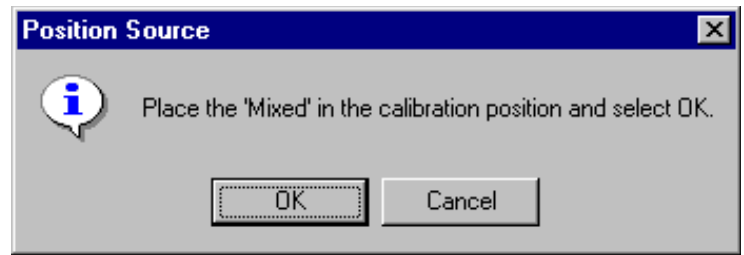


Figure 100. Position the Source for the Efficiency Calibration.

5.3.11.8. Reviewing the Calibration Wizard Results

The final screen in the calibration wizard is the review screen shown in Fig. 101. This shows the plots of the results of all the calibration steps.

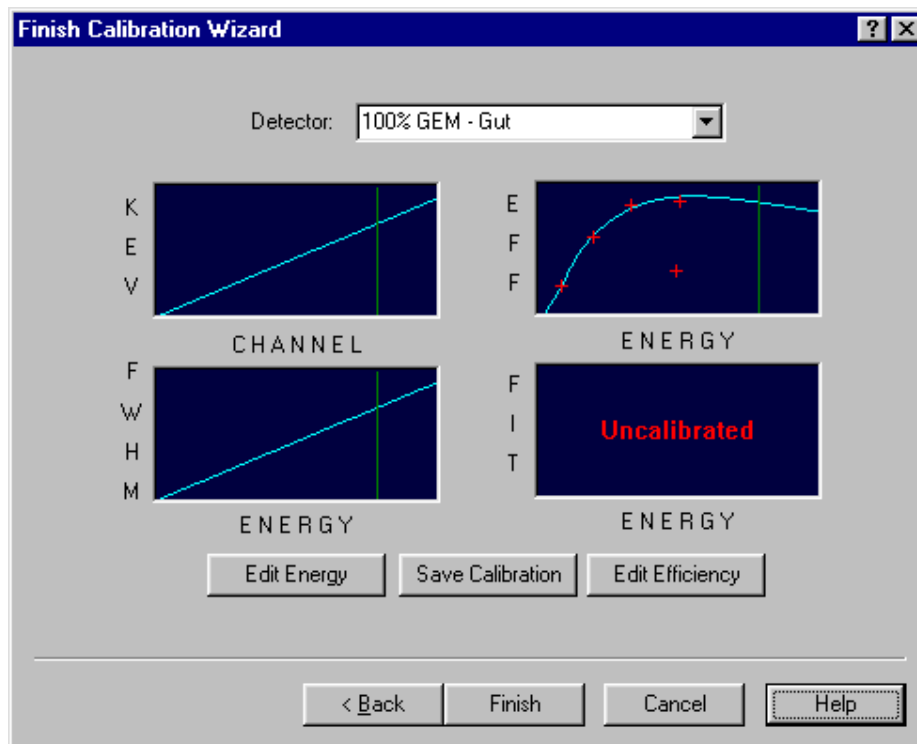


Figure 101. Review the Calibration Results.

To review or change the energy or FWHM calibration, click on **Edit Energy**. This opens the complete energy calibration dialog as explained in Section 5.3.3, page 72. If any changes are made, the efficiency calibration should be repeated (this can be redone by clicking **Edit Efficiency**. This will open up the complete efficiency calibration dialog as explained on page 86 in Section 5.3.5.

Alternatively, calibration can be changed by clicking on **Back** to return to previous wizard screens. Click on **Back** to return to the efficiency dialog, then **Back** again to return to the energy dialog.

NOTE If the spectrum currently in the MCB is the spectrum you wish to use, be sure to unmark the **Clear Data Before Start** checkbox. If multiple spectra were used, you must reacquire the spectra.

Once the calibration entries have been changed, the process will continue on as before with the spectrum collection or file recall.

The calibration is now stored with the MCB but not on disk. Use the **Save Calibration** button to save the calibration to a file. We recommend that you always save calibrations so the files can be specified in the analysis options (.SDF or .SVD files) for use in the Operator program.

To complete the calibration wizard and close the dialog, click on **Finish**. (**Cancel** operates the same as **Finish**.)

5.4. Calculate

Figure 102 shows the **Calculate** menu. These commands provide useful analytical tools for spectrum manipulation. **Smooth** and **Strip...** are only available in buffer windows.

5.4.1. Settings...

This dialog (Fig. 103) displays the “x” factor used by the **Peak Info** command to calculate full width at 1/x maximum (FW[1/x]M) for the ROI peak marked by the marker. The background is subtracted before starting the calculation (see Section 5.4.2). Enter the factor **x**, an integer from 2 to 99. This number will be retained and used until changed. (**Peak Info** always prints the FWHM, so an x of 2 is not useful.)

5.4.2. Peak Info

This command does one of the following:

If the marker is in an ROI:

- 1) If the spectrum is not calibrated, the channel centroid, FWHM, and FW(1/x)M, in channels, are displayed.

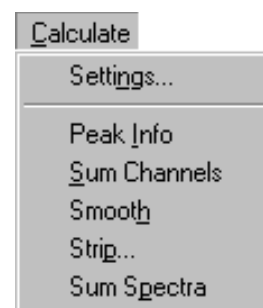


Figure 102. Full Calculate Menu.

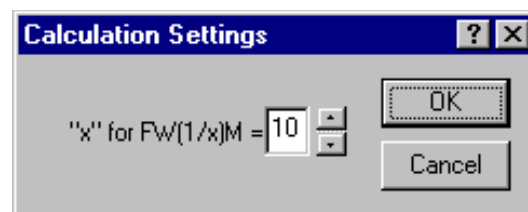


Figure 103. FW(1/x)M Dialog.

- 2) If calibrated, the channel centroid, FWHM, and FW(1/x)M, in channels and energy, the gross and net area, and the library “best match” and activity are displayed.

If the marker is not in an ROI, the peak limits used are the same as the limits for the **ROI Insert** button on the Status Sidebar, and the report is generated according to items 1 and 2 above.

The **Next Peak** and **Previous Peak** buttons on the Status Sidebar will move the Peak Info box up and down in the spectrum.

The x-factor is determined in **Calculate/ Settings...** The peak information is displayed in a pop-up box at the top of the peak (Fig. 104). It can also be displayed by double-clicking the mouse in the ROI (or on the peak) or with the right-mouse-button menu. To close the box, press <Esc> or click in the box.

This calculation is described below, and might not give results identical to the complete analysis peak results. If the Detector is acquiring data, the values displayed are continuously updated with new values based on the new data.

The background on the low-channel side of the peak is the average of the first three channels of the ROI (see Fig. 105). The channel number for this background point is the middle channel of the three points. The background on the high-channel side of the peak is the average of the last three channels of the ROI. The channel number for this background point is also the middle channel of the three points. These two points on each side of the peak form the endpoints of the straight-line background.

The background is given by:

$$B = \left(\sum_{i=l}^{l+2} C_i + \sum_{i=h-2}^h C_i \right) \frac{h-l+1}{6} \quad (13)$$

where:

- B = the background area
- l = the ROI low limit
- h = the ROI high limit

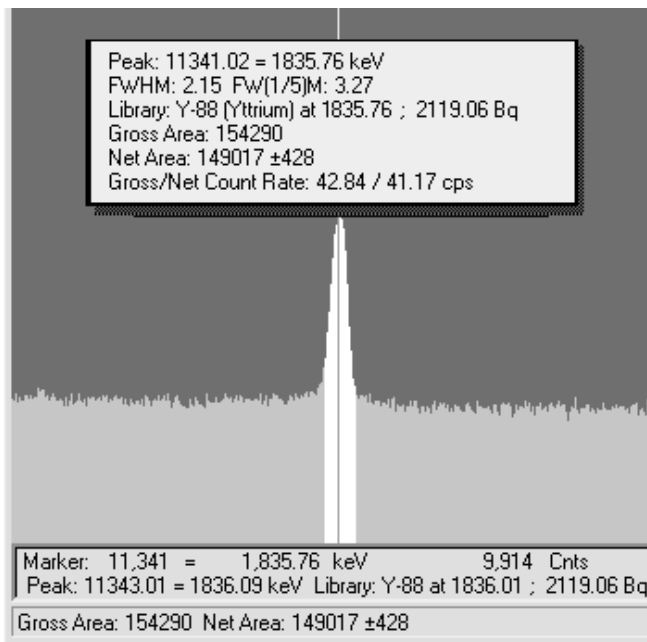


Figure 104. Peak Info Displayed at Top of Peak.

- C_i = the contents of channel i
 6 = the number of data channels used (three on each end)

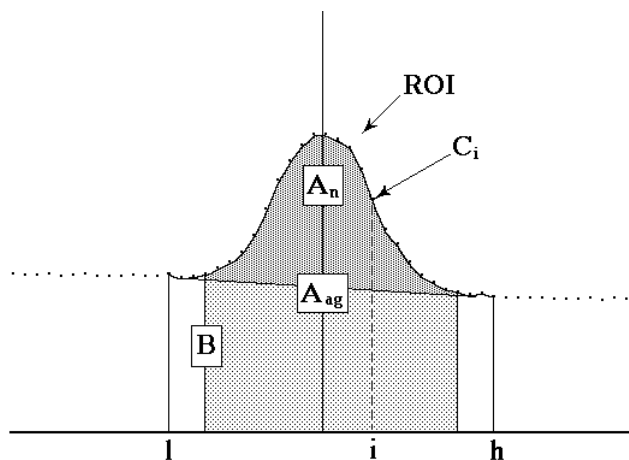


Figure 105. Background Calculation Details.

The gross area is the sum of all the channels marked by the ROI according to the following:

$$A_g = \sum_{i=l}^h C_i \quad (14)$$

where:

- A_g = the gross counts in the ROI
 l = the ROI low limit
 h = the ROI high limit
 C_i = the contents of channel i

The adjusted gross area is the sum of all the channels marked by the ROI but not used in the background, calculated as follows:

$$A_{ag} = \sum_{i=l+3}^{h-3} C_i \quad (15)$$

where:

- A_{ag} = the adjusted gross counts in the ROI
 l = the ROI low limit
 h = the ROI high limit
 C_i = the contents of channel i

The net area is the adjusted gross area minus the adjusted calculated background, as follows:

$$A_n = A_{ag} - \frac{B (h-l-5)}{(h-l+1)} \quad (16)$$

The uncertainty in the net area is the square root of the sum of the squares of the uncertainty in the adjusted gross area and the weighted error of the adjusted background. The background uncertainty is weighted by the ratio of the adjusted peak width to the number of channels used to calculate the adjusted background. Therefore, net peak-area uncertainty is given by:

$$\sigma_{A_n} = \sqrt{A_{ag} + B \left(\frac{h-l-5}{6} \right) \left(\frac{h-l-5}{h-l+1} \right)} \quad (17)$$

where:

- A_{ag} = the adjusted gross area
- A_n = the net area
- B = the background area
- l = the ROI low limit
- h = the ROI high limit

5.4.3. Sum Channels

This function performs its calculation in one of three ways, depending on the position of the marker:

- 1) If the marker is not in an ROI and a box is not defined, the sum of the data channels of the Detector is shown on the display. The complete channel width (e.g., 1 to 16384) is summed.
- 2) If the marker is not in an ROI and a box is defined, the sum of the data channels in the box is shown on the display.
- 3) If the marker is in an ROI, the sum of the data channels in the ROI is shown on the display. This is the same as the gross counts in the **Peak Info** display, but can be used on wider ROIs.

5.4.4. Smooth

The **Smooth** function transforms the data in the buffer spectrum according to a five-point, area-preserving, binomial smoothing algorithm. That is, the existing data is replaced, channel-by-channel, with the averaged or smoothed data as follows:

$$S_i = (O_{i-2} + 4O_{i-1} + 6O_i + 4O_{i+1} + O_{i+2}) / 16 \quad (18)$$

where:

S_i = the smoothed data in channel i

O_i = the original data in channel i

5.4.5. Strip...

This function strips the specified disk spectrum from the spectrum in the buffer. When **Strip...** is selected, the dialog box shown in Fig. 106 opens, prompts for a filename and **Stripping Factor**.

NOTE The file must be a valid spectrum data file containing the same number of channels as the displayed spectrum.

The **Stripping Factor** is a real number that is multiplied channel-by-channel times the disk spectrum before being subtracted from the base spectrum. If the **Use Ratio of Live Times** box is marked, the stripping factor is calculated as the ratio of the live time of the base spectrum divided by the live time of the disk spectrum. The factor can be negative, in which case the spectra are added.

NOTE The live times and real times are not altered by any strip operation. The peak uncertainty (see Chapter 8, “Analysis Methods — Ge”) will not include the stripped areas and might not represent the true uncertainty.

5.4.6. Sum Spectra...

This command allows you to add spectra to the active buffer window. The resulting spectrum can then be analyzed using the calibration created in the **Calibration sum of detectors group**. Calibration of summed Ge spectra can be performed in the **Ge Calibration Wizard**. For summed NaI spectra, define an .OPR file for “Calibration” that collects the summed spectra in the Operator program, then return to Supervisor to calibrate using that stored spectrum with the **Calibrate/Energy...** and **Efficiency...** commands.

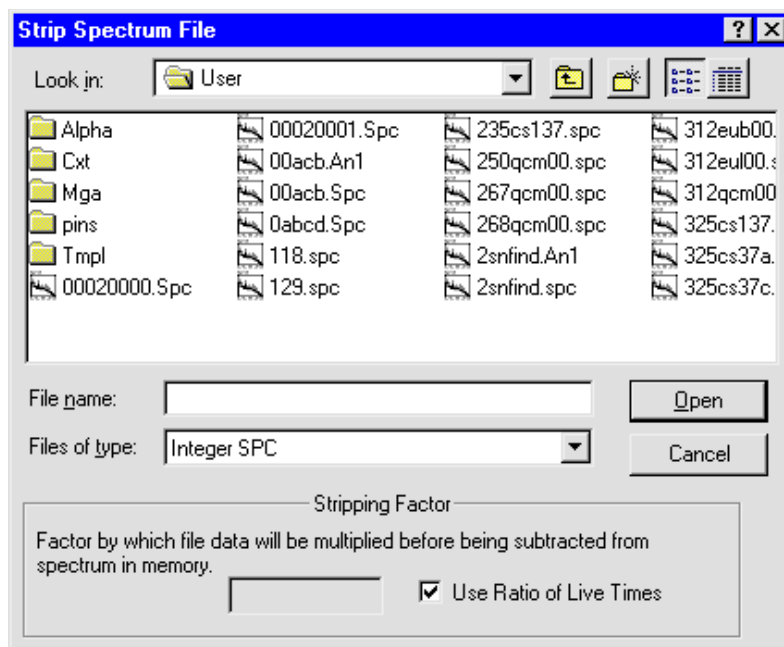


Figure 106. Strip Dialog.

Use the standard file-open dialog (Fig. 107) to recall the first spectrum into a buffer window.

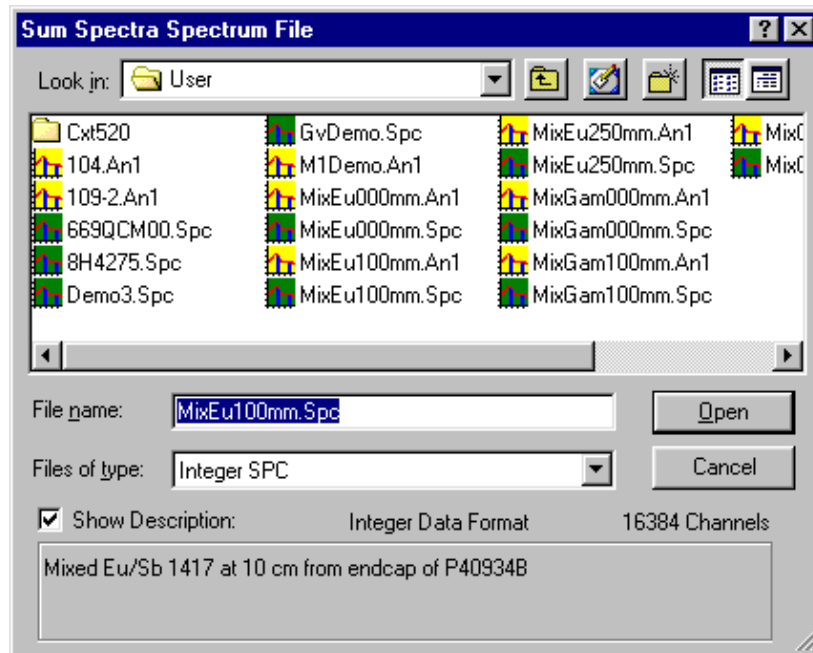


Figure 107. Select a Spectrum to Sum.

The sum function uses the live time and acquisition time of the first spectrum. Spectra are summed as follows:

$$Ch_{iSum} = \sum_{S=1}^N \left(Ch_{iS} \left(\frac{LT_1}{LT_S} \right) \right)$$

where:

- Ch_{iSum} = i^{th} channel counts for the summed spectrum
- Ch_{iS} = i^{th} channel counts for spectrum S
- LT_1 = live time for the first spectrum in the group
- LT_S = live time for spectrum S

5.5. Analyze

Figure 108 shows the **Analyze** menu containing commands for analyzing all or part of a spectrum on the screen. The results can be displayed in both graphic and text forms. In the interactive analysis mode, peaks can be added, deleted, or shifted in energy. These commands can be performed on data in the active spectrum buffer. The Detector cannot be acquiring data. **Interactive in Viewed Area...** is disabled (gray) for display widths above 4096 channels; **Display Analysis Results...** shows the results for all channels.

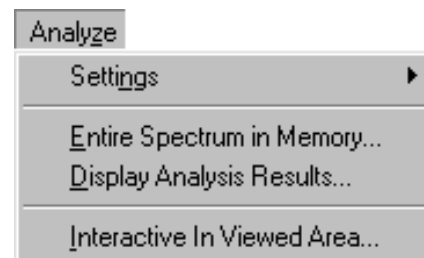


Figure 108. Full Analyze Menu.

5.5.1. Settings

Figure 109 shows the **Settings** submenu. The user-controlled factors in the analysis are defined with these commands. The **Sample Type...** setup for Ge analysis begins here; the setup for NaI analysis begins on page 133.

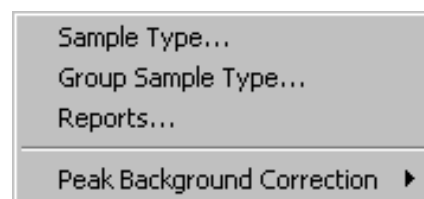


Figure 109. Full Settings Submenu.

5.5.1.1. Sample Type... (for Ge Analysis)

This opens the Ge Analysis Options dialog shown in Fig. 110. The fields in this dialog define the set of spectrum analysis parameters used in both the Supervisor and Operator analyses. Once defined, this parameter set can be saved to an *analysis options file*, which, for germanium detectors, is assigned the default extension **.SDF**. This **.SDF** file can then be used as the current working default for the currently selected Detector, in **.JOB** files, in Supervisor and Operator QA analysis, and as part of the *operator scan type (.OPR) file* that governs the analysis of subject scans in Renaissance Operator (see Section 5.7.8). You can create as many analysis options files as you wish.

In Supervisor, when you use this dialog and click on **OK**, the settings you have just saved (or retrieved from disk) are immediately applied to the currently active Detector. However, in Operator, the **.SDF** file to be used in a particular analysis is specified in the operator scan type file for that analysis. Because the calibrations and peak background corrections are unique for each detector, you must either preset the internal (working) calibration and/or PBC for each Detector in a detector group before exiting Supervisor and starting Operator, or use the **.OPR** file to specify a separate calibration file and/or **.PBC** file for each Detector.

NOTE Before creating **.SDF** files for use in the scan types in the Operator program, we recommend that you read Section 5.7.8.1, “General Factors to Consider in Creating **.OPR** Files.”

To create an **.SDF** file, complete all screens of the dialog, then return to the **Sample** tab. Click on the **Save As...** button in the upper right of the dialog; this will open a standard file-save dialog. Enter the new filename, then click on **Save** to return to the **Sample** tab. Click again on **OK** to close the Analysis Options dialog. The **Save As** button also allows you to save changes to an existing **.SDF** file or save an existing **.SDF** file to a new filename. You can then edit the new **.SDF** file while preserving the contents of the original file.

NOTE Although this dialog has multiple tabs, any changes to the current set of “working” parameters for the selected Detector will not take effect until you click on **OK**. To retain the current working parameters, click on **Cancel** instead of **OK**.

Sample Tab

Sample settings (Fig. 110) are those whose values are generally different for each sample type.

- For most analysis applications, the **Nuclide Library** and **Calibration** files should be set explicitly on this tab instead of using the **Internal** option. This is particularly important when analyzing the sum of spectra for a group of detectors to ensure that the appropriate calibration parameters are applied during analysis in the Operator program. The **Internal** option should normally only be used when a single geometry and library is used for all analyses including the instrument QA.

When internal files are specified, users of the Supervisor program must be sure that *the correct library and calibration files are the last library and calibration files loaded into memory before exiting Supervisor and starting the Operator program*. If you are running the Supervisor and Operator programs at the same time, changes to internal library and/or calibration files made in the Supervisor program do not take effect in the Operator program until you exit and restart it.

- The **Recalibrate Energy** option on the Operator program’s **Startup** dialog applies only when the **Internal** calibration option is set here as an analysis option. *Note, however, that the internal calibration is updated each time an analysis is performed using a calibration override file, so this option is useful only where the calibration will not routinely be changed.*
- When using a specified calibration file instead of the **Internal** calibration, the **Adjust Gain** option on the Operator program’s **Startup** dialog can be used to realign peaks back to the original calibration position making an energy recalibration unnecessary.

When an **.SDF** file is recalled, the date of **Creation** and last date the file was updated (**Edition**) are displayed. Whenever the file is changed, the edition date is updated when it is saved.

The **Description** is used to identify the sample-type file, and can be 64 characters long.

Clicking on the **Presets** button opens a Presets dialog corresponding to the available presets for this MCB, as discussed in **Acquire/MCB Properties...** The presets entered here will be used for sample QA analysis in both the Supervisor and Operator programs. (The background acquisition presets entered on the Quality Assurance Settings dialog [Section 10.2.1] are used for background QA measurements in both programs, and the operator scan type file contains the presets for routine subject measurements in Operator.)

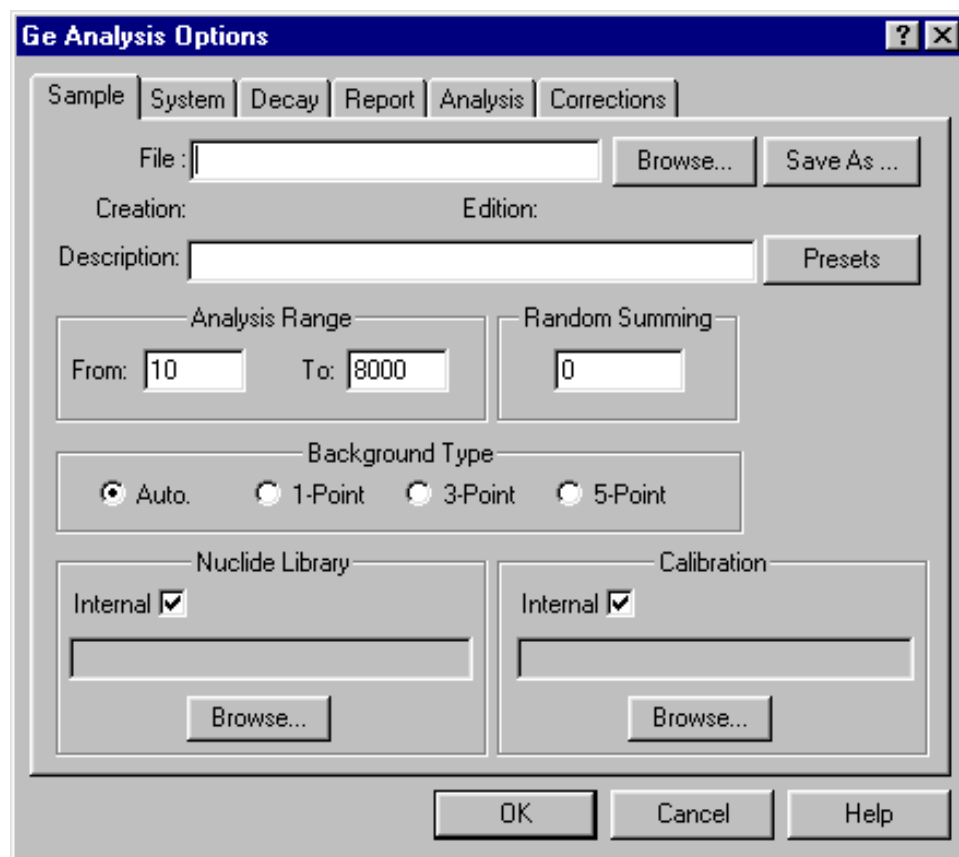


Figure 110. Sample Tab for Ge Analysis.

The **Calibration** data to be saved with the spectrum or used for interactive analysis can be the currently loaded **Internal** (working) calibration or a calibration stored on disk. The internal calibration is the calibration most recently created with the **Calibrate** menu functions (see Section 5.3.1) or the calibration most recently recalled from disk, and *is specific for the currently selected Detector*.

NOTE Keep in mind that each time you create or recall a calibration in Supervisor, if a Detector window is currently active (rather than a buffer window), *that Detector's internal calibration has just been changed*. This calibration update also takes place whenever an Operator analysis specifies an override calibration.

As noted above, a specific calibration file should normally be used here, rather than the **Internal** setting, particularly if this analysis options file will be used in a scan type (.OPR) file that uses the **Analyze sum of spectra** option.

When the .SPC file for this spectrum is saved to disk, the current calibration will be saved with it for later analysis. The interactive analysis (performed with **Analyze/Interactive in viewed**

area), uses the currently loaded (internal) calibration. Note that each Detector and buffer can have separate calibrations.

The filename of the **Nuclide Library** to be used in the spectrum analysis can be the **Internal** (working) library or a library file on disk. The internal library is the library most recently selected using **Library/Select File...** Unlike the **Calibration** file, the **Nuclide Library** file *is not Detector-specific*. It will include any modifications made during the interactive analysis mode. As noted above, a specific library file should normally be used here, rather than the **Internal** setting.

The **Background Type** can be set to **Auto, 1-pt., 3-pt., or 5-pt.** These are explained in more detail in Section 8.2.1.

Random Summing is the random summing correction factor discussed in Section 8.11. Entering zero turns this correction off.

The **Analysis Range**, in channels, is entered here. This is usually used to eliminate analysis of the ends of the spectrum that do not contain useful data. The **Analysis Range** should be as wide as possible because the automatic energy recalibration feature (see Section 8.2.6) requires separated library peaks to work properly. Also, the correlation of lines from a single nuclide done by the analysis is defeated if the energy range analyzed does not include all the lines.

System Tab

System settings are those settings that are generally the same from sample to sample. However, all of these entries except the **Laboratory** name can be different for each sample type. The dialog is shown in Fig. 111.

The **Laboratory name**, composed of any 64 characters, is printed as the second line on each page of the Supervisor report. The spectrum name is printed on the next line.

The **PEAK SEARCH SENSITIVITY** sets the sensitivity for the peak search used in the **Interactive in viewed area** (Section 5.5.4) and the full-spectrum analysis (Section 5.5.2). Before a suspected peak is accepted, the magnitude of the second difference must be greater than the weighted error of the channel counts. The **PEAK SEARCH SENSITIVITY** is a multiplicative factor used in error weighting. The sensitivity can be set at any integer value from 1 to 5, with 1 the most sensitive (that is, "1" finds the most peaks). A value of 1 will find small peaks, but will also "find" many false peaks. A value of 5 will locate all the large peaks, but might miss some of the smaller peaks. If too high, some small peaks will be missed. In the interactive mode, many regions will be deconvoluted unnecessarily if the value is too sensitive. If the sensitivity is set to 1, the parabolic background method is disabled for energies above 200 keV.

In the **Library** section, **Match Width** sets the maximum amount by which a peak centroid can deviate from the nearest library peak energy and still be associated with that library peak. The value entered is multiplied by the FWHM at the peak energy to get the width used. If the value is too small, some spectrum peaks will be misidentified due to statistical variation in the centroid, and if it is too large, some library peaks will be incorrectly identified. A value of 0.5 is the factory default. If the **Match Width** is set to a value other than 0.5, the value will be printed on the report.

Figure 111. System Tab for Ge Analysis.

The **Fraction Limit** is one of the parameters used to determine the presence or absence of a nuclide. The sum of the emission probabilities of the peaks in the spectrum identified with the nuclide is divided by the sum of the emission probabilities of all peaks of the nuclide in the energy range being analyzed. If the result is greater than the fraction limit, the nuclide is marked as being present. To turn off this test, set the limit to zero.

The **Units** section allows you to:

- Establish the units of measure and subject weight for analyses performed in Supervisor with this set of analysis options.
- Determine the units of measure that will be used for activity and subject height and weight in the Operator program.

Select the desired **Activity** units, and a **Multiplier** and **Divisor** to scale the numbers up or down to make any other units needed. The units label is printed at the top of the activity columns on the report and should reflect the values chosen; that is, if **µCi** is chosen with a multiplier of 1000, then “nanocuries” should be entered in the **Activity** field.

If you select **lb**, the **Weight** field in Operator will be displayed in pounds and the **Height** will be displayed in inches. If you select **Kg** or **None**, the **Weight** and **Height** fields will be in terms of kg and cm, respectively.

NOTE The **Weight** units will be displayed on the Supervisor analysis report if set to anything other than **None** (i.e., Bq/kg or $\mu\text{Ci/lb}$). If the scan type that uses this analysis options file *does not* specify **Divide Activity by Weight**, the **Weight** will always be set to **1** and the units set to **None** when an analysis is performed in Operator.

Enter the subject **Weight** to be used for analysis in the Supervisor program. Note that nuclide activities are always divided by **Weight** in the Supervisor analysis. In Operator, entering the subject's **Weight** overrides any existing entry (see the preceding NOTE).

Regardless of the units selected here, subject weight and height are always stored in the database in terms of kg and cm, respectively. These values are appropriately converted when read from or written to the database and when displayed on the standard Operator text reports. Operator reports generated using SAP® BusinessObjects Crystal Reports™ templates will display the height and weight in terms of kg and cm. For this reason, Chest Wall Thickness calculation coefficients established in the scan type files should always be based on weight/height expressed in terms of kg/cm.

Decay Tab

The Decay tab (Fig. 112) allows you to enable or disable decay correction **During Acquisition** and decay correction to a given **Date and Time (Collection)**. Both of these affect the report of the analysis of the total spectrum.

Only the **During Acquisition** correction is automatically applied in the Operator program. Regardless of the setting specified here, the operator determines whether or not the **Collection** correction

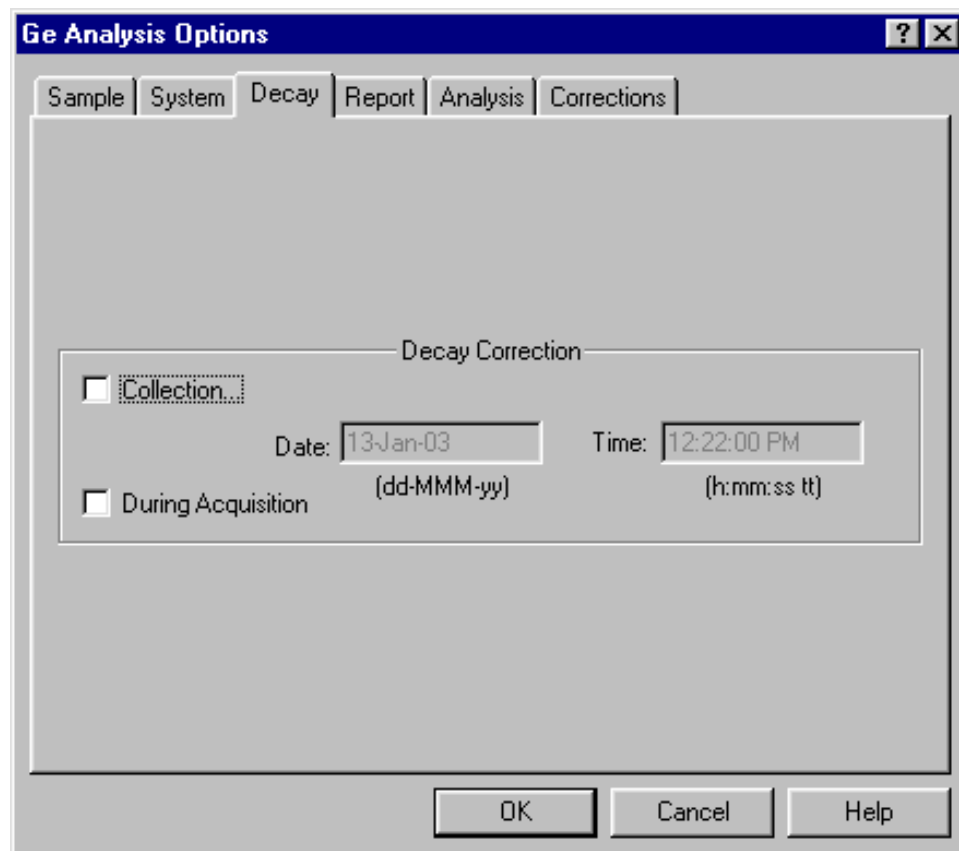


Figure 112. Decay Tab for Ge Analysis.

is applied by adding, changing, or removing the entry in the Operator program's **Decay Date** field.

NOTE In Operator, decay correction to a collection time will not be calculated if the operator does not enter a **Decay Date** for the current measurement.

Report Tab

This screen (Fig. 113) controls the contents, destination, and some details of the output report discussed in Chapter 6.

The **Reporting Options** control only the spectrum analysis report in the Supervisor mode. The **Output** options affect both the Supervisor and Operator reports, with the exception of **Report Writer**, which affects only the Operator report; and **Display Analysis Results**, which affects only the Supervisor report.

Select one or more **Reporting Options** by marking the checkboxes. If there is

not enough information for Renaissance to print all of the requested options, the program might print another option if there is enough information for it. For example, suppose a nuclide activity report is the only report option selected. If the spectrum has not been efficiency calibrated, the activities cannot be calculated. In this case, the spectrum report will instead contain the peak list because there is sufficient information to do that.

When Renaissance performs an analysis, it writes the results to a **.UFO** file and writes an ASCII-format **.RPT** file. If you are analyzing a spectrum that has not yet been saved to disk, Renaissance automatically creates a spectrum file with the extension of **.AN1**. The **.UFO**, **.RPT**, and **.AN1** files share the same filename.

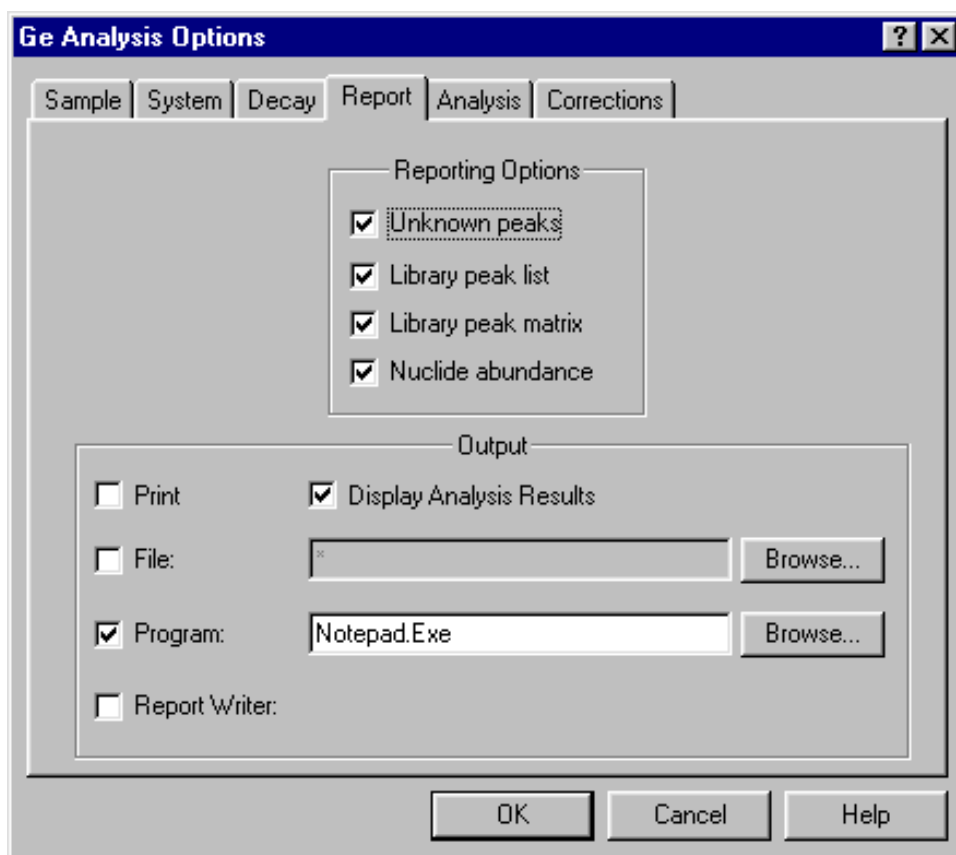


Figure 113. Report Tab for Ge Analysis.

The **Print** option sends the **.RPT** file to the default Windows printer for this computer. The full Ge report discussed in Chapter 6 is produced in Supervisor and *for sample QA measurements in Operator*. For all other measurements in Operator, a shorter subject count report is generated (see the Operator user's manual).

The **Display Analysis Results** feature applies only to the Supervisor program; interactive peak fitting is not available in Operator. If you mark the **Display Analysis Results** box, when the analysis is complete, the results will be displayed onscreen in the same format as for **Analyze/Display analysis results** (Section 5.5.3).

File lets you assign a new filename to the report or browse for an existing filename (this will overwrite the existing report file with the new analysis). The default is an asterisk (*) for the filename. In this case, the report filename will be the spectrum filename with the extension **.RPT**.

Program allows you to select any Windows program to be run with the report filename as an argument on the command line. The report filename sent to the program is the spectrum filename with the extension **.RPT**. The default program is Windows Notepad (**Notepad.exe**). In this case, when the analysis finishes, Notepad automatically starts and opens the **.RPT** file. (Notepad can be used to save the **.RPT** file to a different filename, if you wish, or to print the report.) The analysis is not complete until you close the selected program.

The **Report Writer** field affects only the Operator program. With this option selected, when analysis is complete in the Operator program, a Crystal Report is generated according to the options set with the **Analyze/Settings/Reports...** function. See the Operator user's manual for the contents and format of the ASCII text and **Report Writer** reports.

NOTE When the **Report Writer** is enabled, the weighted average and concatenated reports are not displayed in the Operator program's Crystal Report. To display and/or print these report types, you must *also* mark the **Print** and/or **Program** options to generate the standard text report.

Analysis Tab

Use this screen (Fig. 114) to select the **Analysis Method**, **Additional Error**, **Analysis**, and **Peak Stripping** options to be used. The actual analysis is done by a separate program called an *analysis engine*.

Analysis Method

The analysis engine for the normal analysis is RENWAN. Renaissance also offers the RENGAM, RENNPP, and RENENV engines.

When **RENGAM** is selected, the **Library Based Peak Stripping** and **Directed Fit** methods are turned off and the selections disabled.

When **RENNPP** is selected, the automatic **Library Based Peak Stripping** is enabled. This option should be left enabled. It can be turned off or **Manual Based** (manual, library-based) peak stripping can be enabled, but these selections will not allow **RENNPP** to function in its intended mode. To perform the analysis without any library-based peak stripping, use the **RENGAM** engine. For manual library-based peak stripping, use **RENGAM**.

When **RENENV** is selected, the automatic **Library Based Peak Stripping** is enabled. This option should be left enabled. It can be turned off or **Manual Based** peak stripping can be enabled, but these selections will not allow **RENENV** to function in its intended mode. To perform the analysis without any library-based peak stripping, use the **RENGAM** engine. For manual library-based peak stripping, use **RENGAM**.

See Chapter 8 for more information on the four Ge analysis programs.

Renaissance also accommodates user-supplied analysis programs. The program must be able to read the spectrum name from the command line. There are no other restrictions, but if the program does not produce a results file in the **.UFO** format, the display results functions and the Renaissance database will not work. All the analysis options can be taken from the **.SPC** file. The analysis program should also produce an ASCII report file so the report can be printed by the Windows print spooler.

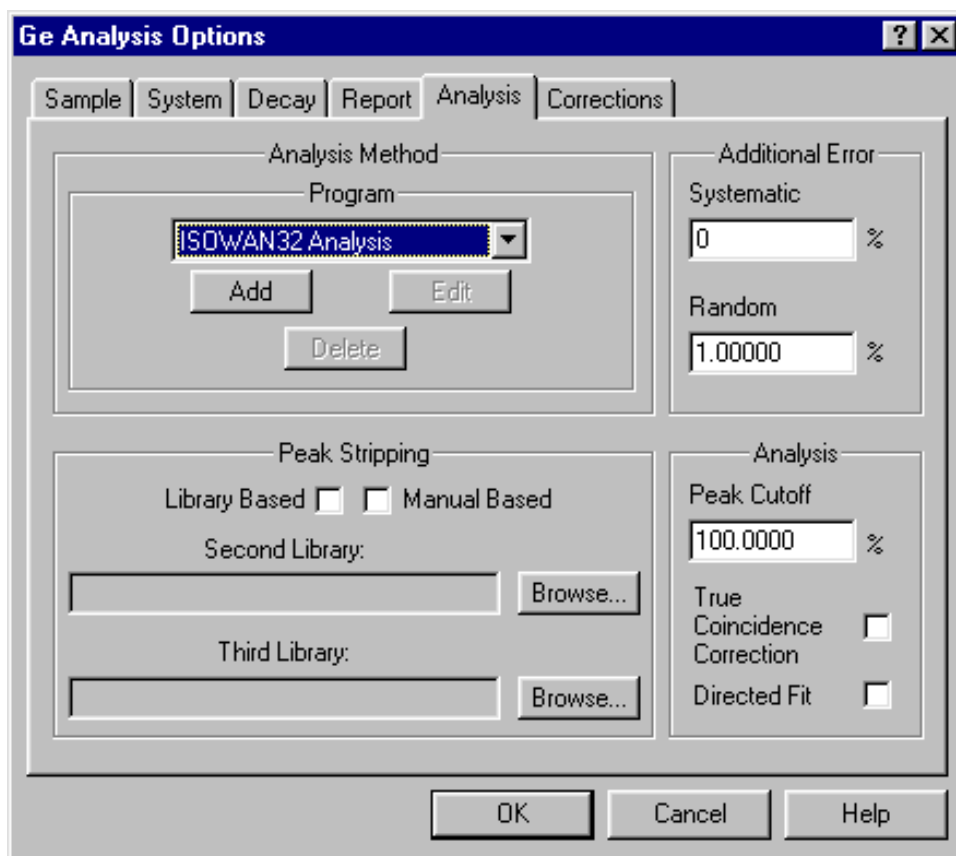


Figure 114. Analysis Tab for Ge Analysis.

Additional Error

The parameters in the **Additional Error** section are used in the calculation of the total uncertainty. Total uncertainty is composed of the systematic and random uncertainties in all of the factors involved in producing the final Renaissance concentration result. To account for other uncertainties in the system, enter two values — **Systematic** and **Random** — that will be included in the total calculation. The **Systematic** value is added to the total uncertainty as a systematic component; the **Random** is added as a random component. These are summed as explained in Section 8.12.

Peak Stripping

When **Peak Stripping** is enabled, the analysis will perform the library-based peak deconvolution or “peak interference correction” described in Section 8.4.5. Briefly, this will separate peak areas that are too close together to be accurately separated by mathematical deconvolution. Renaissance supports two types of peak stripping: **Library Based** and **Manual Based**. In **Library Based** peak stripping, the program automatically detects overlapped peaks and the associated peaks needed. The program then performs the peak stripping using these peaks. In **Manual Based** peak stripping, the overlapping peaks and the associated peaks are specified in separate libraries. The associated peaks are given in the **Second Library** and the analysis peaks are given in the **Third Library**.

Analysis

The **Peak Cutoff** limits the unknown peak list to peaks with 1-sigma uncertainty below this value. Library peaks with 1-sigma uncertainty are printed, but are not used in the activity calculation.

Click on **True Coincidence Correction** to enable this correction. If the detector has not been calibrated for TCC, the correction is automatically turned off.

Click on **Directed Fit** to allow for negative peak areas in low-level spectra. Directed fit is described in Section 8.2.2.2.

Corrections Tab

The Corrections tab is shown in Fig. 115.

Peaked Background Correction

When the **Peaked Background Correction** (Section 8.9.4) is turned **On**, you can specify a **.PBC File** on disk or use the current **Internal** (working) file. The internal file for the currently selected detector is the one most recently created with the **Create PBC...** command or loaded with the **Select PBC...** command (see Section 5.5.1.5).

If you specify a .PBC file here, that file will always be used for the analysis (in both Supervisor and Operator) regardless of any changes made to the .PBC files currently loaded in the detectors or specified for a multi-detector group.

NOTE This correction should be turned **off** for .SDF files used in the scan type for creating .PBC files.

If .PBC files will be routinely generated for a detector group or individual detectors using the Operator program **Startup** function, use the **Internal** option to allow updates from within Operator. This is because the internal files are updated each time .PBC files are updated or new files are selected in the Operator program.

NOTE When creating or recalling .PBC files in Operator, the internal .PBC files are updated (a) for each detector if **Analyze sum of spectra** is turned off in the current scan type file, or (b) for the group sum if **Analyze sum of spectra** is turned on.

Attenuation Correction

The **Attenuation** correction lets you correct the activity for attenuation by various absorbers. The selected options, attenuation material, and CWT calculation methods should be based on site protocols.

NOTE Attenuation correction is only enabled for the Operator analysis if the following conditions are met. If so, the attenuation correction is performed using the **CWT** value in Operator as the attenuation **Length**.

- The Attenuation correction must be **On**.
- An attenuation material (either **Tissue** or **Muscle**) must be selected; if **None** is selected, the correction is disabled.

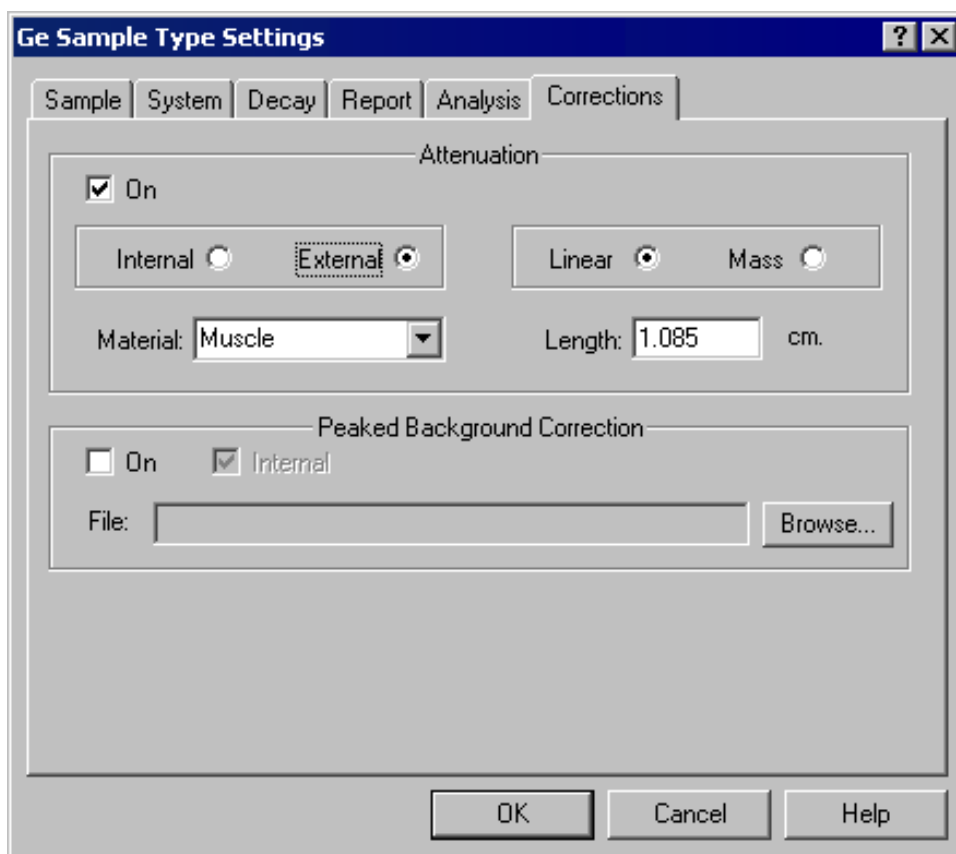


Figure 115. Corrections Tab for Ge Analysis.

- **Chest Wall Attenuation** must be enabled in the scan type file (page 183), and the **User Defined** calculation (if used) must give an answer > 0 (zero).
- The CWT manually entered or automatically calculated in the Operator program must be > 0 (zero).
- See also the Chest Wall Attenuation conditions listed in Section 5.7.8.1.

Note that if Chest Wall Attenuation is enabled in the `.OPR` file but the attenuation correction is not enabled in the `.SDF` file, Renaissance will still calculate an Internal Attenuation Correction factor and Absorption Uncertainty Estimate (both of which are included in the Total Uncertainty Estimate).

Internal absorption is for cases where the radioactive material is distributed throughout the absorber (matrix) and **External** is where the absorber is between the radioactive material and the detector.

The correction parameters are chosen from the built-in Renaissance database of stored coefficients. Enter a **Material** and **Length**, and choose between **Linear** and **Mass** according to the entry for this absorber in the database. The database values are based on an absorber **Length** of 1 cm. For larger or smaller lengths (external) and thicker or thinner materials (internal), enter the actual length or thickness. The attenuation correction is explained in detail in Section 8.9.6.

This option is normally used to correct the activity for attenuation in the chest. Assuming that the activity is deposited in the lung and not distributed throughout the chest wall, the **External** option should be selected with **Linear** attenuation. If this correction is applied to the intestines, you might wish to specify a different CWT calculation in the scan type file, and the **Internal** option might be more appropriate.

5.5.1.2. Sample Type... (for NaI Analysis)

This opens the NaI Analysis Options dialog shown in Fig. 122.

NOTE To open this dialog for NaI analysis, *you must first select an NaI detector or recall an NaI file* (otherwise, the Ge dialog opens by default).

The fields in this dialog define the set of spectrum analysis parameters used in both the Supervisor and Operator analyses. Once defined, this parameter set can be saved to an *analysis options file*, which, for sodium iodide detectors, is assigned the default extension `.SVD`. This `.SVD` file can then be used as the current working default for the currently selected Detector, in `.JOB` files, in Supervisor and Operator QA analysis, and as part of the scan type that governs the analysis of subject scans in Operator (see Section 5.7.8). You can create as many analysis options files as you wish.

In Supervisor, when you use this dialog and click on **OK**, the settings you have just saved (or retrieved from disk) are immediately applied to the currently active Detector. However, in Operator, the **.SVD** file to be used in a particular analysis is specified in the scan type (**.OPR**) file for that analysis. Because the calibrations and peak background corrections are unique for each detector, you must either preset the internal (working) calibration and/or PBC for each Detector in a detector group before exiting Supervisor and starting Operator, or use the **.OPR** file to specify a separate calibration file and/or **.PBC** file for each Detector.

NOTE Before creating **.SVD** files for use in the Operator program, we recommend that you read Section 5.7.8.1, “General Factors to Consider in Creating **.OPR** Files.”

To create an **.SVD** file, complete all screens of the dialog, then return to the **Sample** tab. Click on the **Save As...** button in the upper right of the dialog; this will open a standard file-save dialog. Enter the new filename, then click on **Save** to return to the **Sample** tab. Click again on **OK** to close the Analysis Options dialog.

The **Save As** button also allows you to save changes to an existing **.SVD** file or save an existing **.SVD** file to a new filename. You can then edit the new **.SVD** file while preserving the contents of the original file.

NOTE Although this dialog has multiple tabs, any changes to the current set of “working” parameters for the selected Detector will not take effect until you click on **OK**. To retain the current working parameters, click on **Cancel**.

Important Considerations When Creating NaI Analysis Options Settings

The following settings are critical to fitting peaks properly from NaI spectra:

- **Background Type** and **Analysis Range** on the Sample tab.
- **Peak Search Sensitivity** on the System tab.
- **Linear Background Energy** on the Analysis tab.

The **Background Type** is the number of points on each side of a singlet peak to be used to determine the background.

The **Linear Background Energy** is the energy above which the background is fit as a straight line, with a step under each peak in a multiplet. Below the linear energy, the background is fit as an exponential. We recommend an initial setting of zero (0) keV.

These parameters should be set based on the type of spectra encountered in your particular application. In general, the most complex peak fits occur in the lower energy range (<200 keV) on a

high background continuum. Fitting these peaks properly requires an optimal combination of the analysis parameters; this combination must be experimentally determined. In most cases, the optimal settings for the lower-energy peaks will also work well for fitting higher-energy peaks.

Example: Iterative Peak Fitting

As a general rule, fitting a single low-energy peak on the edge of a high background continuum gives a better fit if you use an exponential polynomial background fit. To accomplish this, set the **Linear Background Energy** to a value that is slightly higher than the elevated background continuum. This is demonstrated in Fig. 116, which shows a ^{57}Co 122 keV peak on the edge of a high background. The analysis options are set to a **5-Point** background, channel **20** as the lower limit of the **Analysis Range**, and a **Linear Background Energy** setting of 200 keV.

In contrast, Fig. 117 shows the same peak with a **Linear Background Energy** setting of zero, which forces the background into a linear fit.

As mentioned above, this is accomplished by setting the **Linear Background Energy** to a low value. (A setting of zero will force a linear background fit for all peaks. For spectra with multiple peaks in the low-energy/high-background region, a linear background setting generally results in the best peak fits.) As Figs. 118 and 120 show, the linear background fit models the spectrum peaks very well. In Figs. 119 and 121, the **Linear Background Energy** has been changed to 400 keV, which reduces the peak areas because the background curve takes in part of the peak.

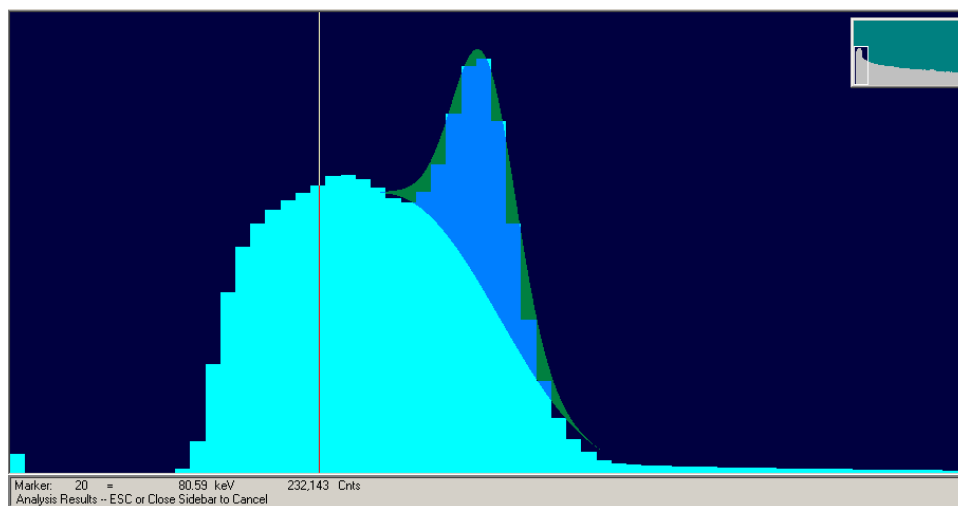


Figure 116. Linear Background Energy, 200 keV.

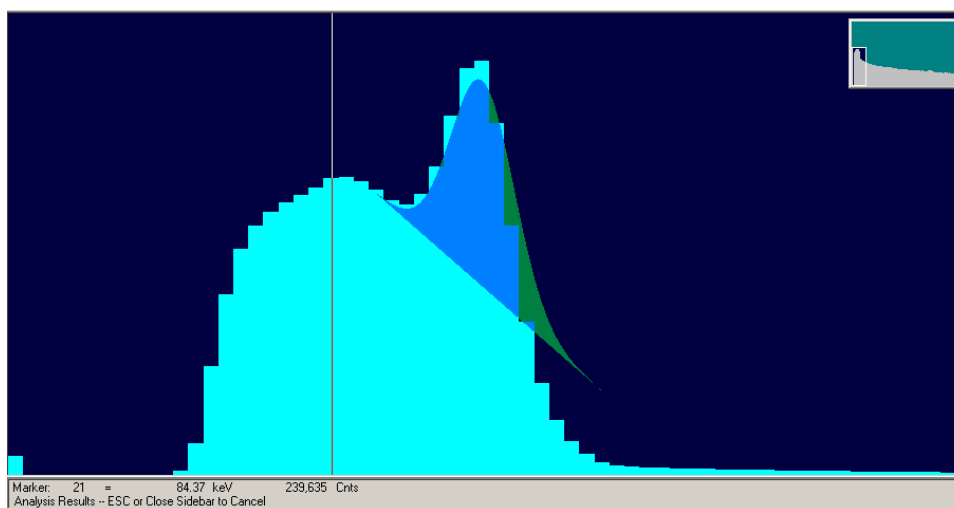


Figure 117. Linear Background Energy, 0 keV.

Note that the peak fit can be further improved by changing the number of points used to fit the background. For peaks that are very close together, as illustrated below, fewer points generally result in a better peak. Regardless of the number of points used, however, the linear background fit for this type of spectrum will typically result in the most representative peak fit.

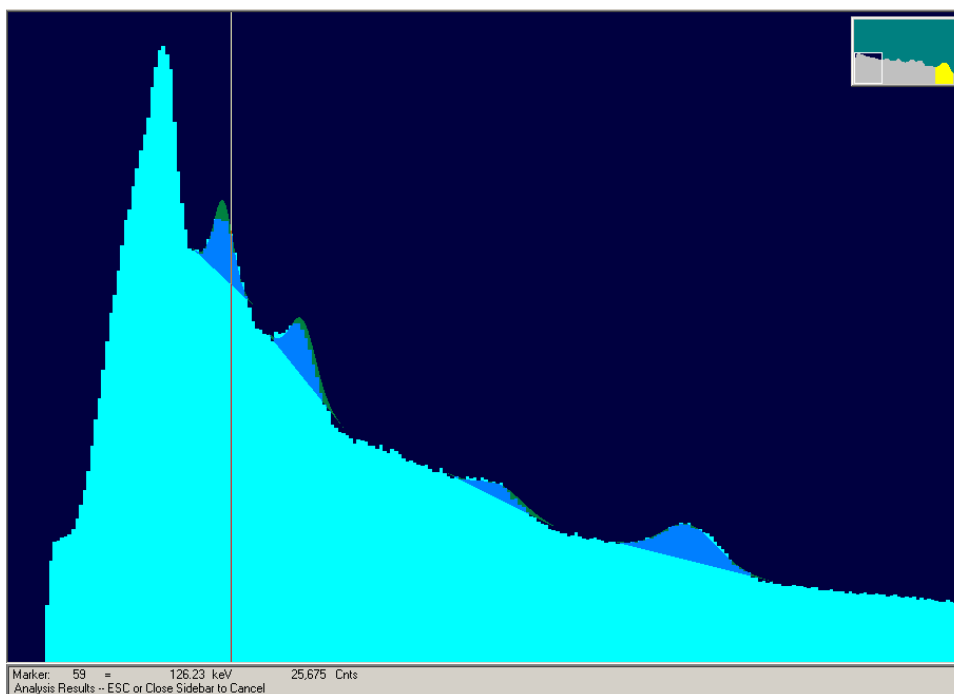


Figure 118. Linear Background Fit.

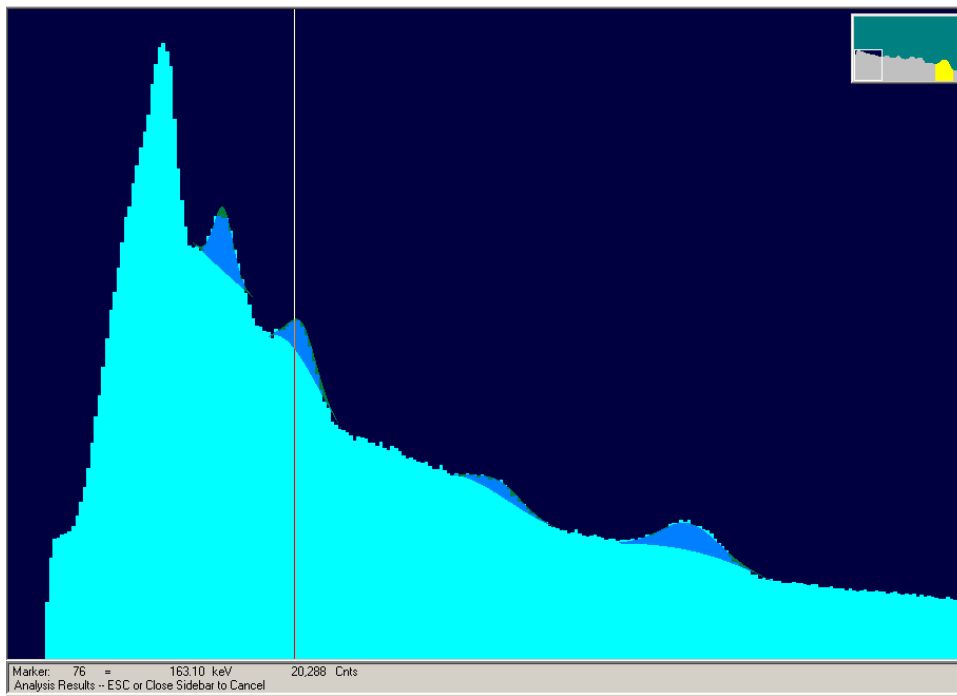


Figure 119. Exponential Polynomial Background Fit.

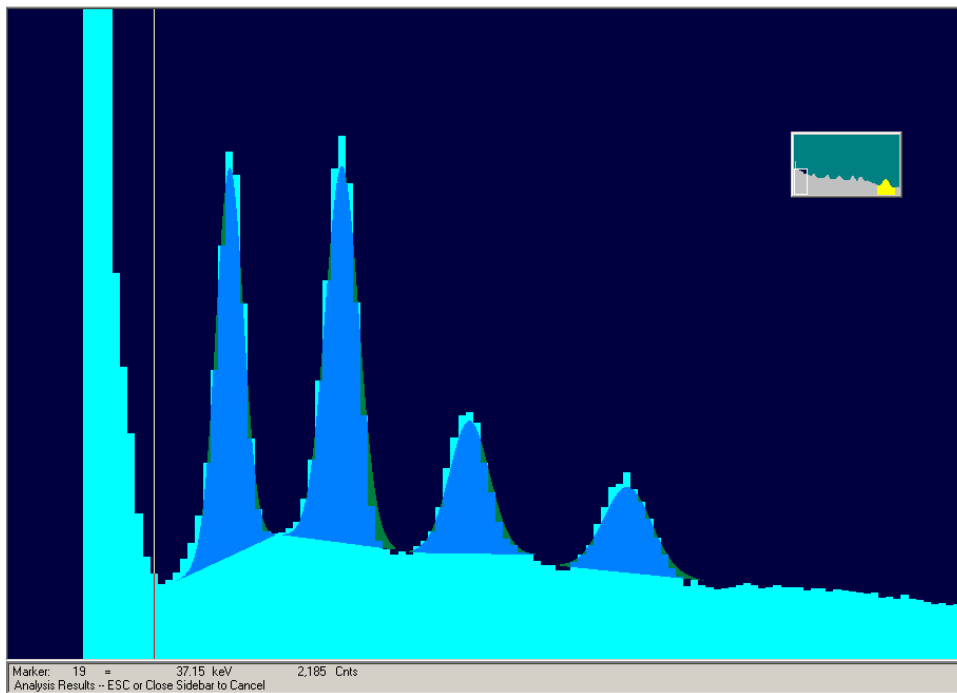


Figure 120. Linear Background Fit.

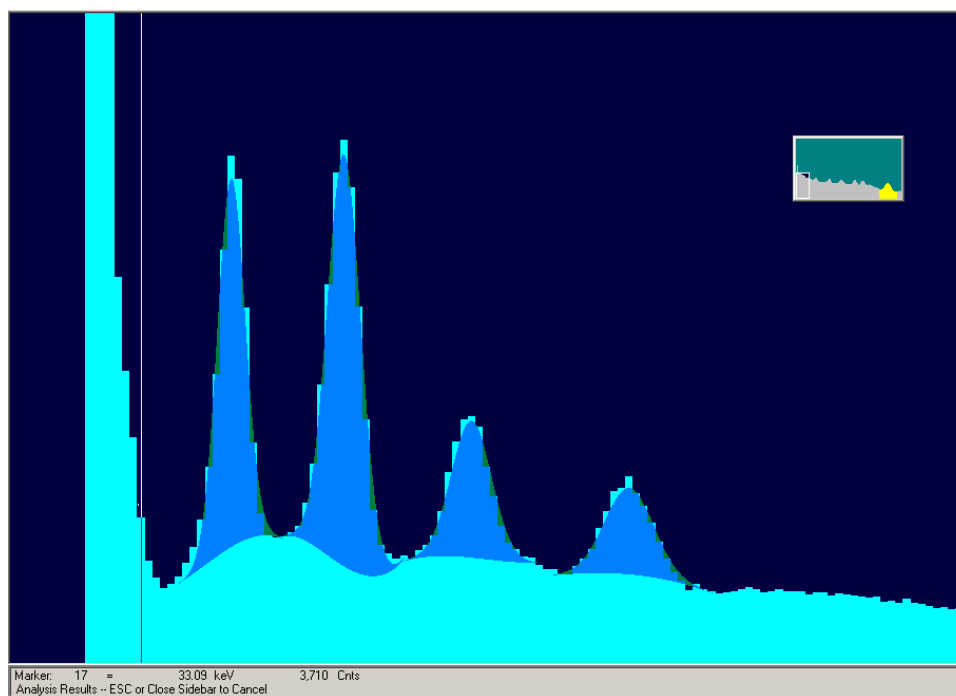


Figure 121. Exponential Polynomial Background Fit.

In Figs. 118 and 119, note that the first peak in the spectrum (88 keV) is not found by the analysis because the background falls off essentially to zero. If this peak is key in the analysis, then a lower-energy peak such as the 59.5-keV peak of ^{241}Am should be included in the source to generate a measurable background below the 88-keV peak (see Figs. 120 and 121). When a clearly definable background exists (i.e., one that is horizontal or has a valley near the low side of the lowest-energy peak of concern), the lower **Analysis Range** value should be set to this region. This setting can be crucial in properly fitting the lowest-energy peaks.

Sample Tab

Sample settings (Fig. 122) are those whose values are generally different for each sample type.

- For most analysis applications, the **Nuclide Library** and **Calibration** files should be set explicitly on this tab instead of using the **Internal** option. This is particularly important when analyzing the sum of spectra for a group of detectors to ensure that the appropriate calibration parameters are applied during analysis in the Operator program. The **Internal** option should normally only be used when a single geometry and library is used for all analyses including the instrument QA.

When internal files are specified, users of the Supervisor program must be sure that *the correct library and calibration files are the last library and calibration files loaded into memory before exiting Supervisor and starting the Operator program.* If you are running

the Supervisor and Operator programs at the same time, changes to internal library and/or calibration files made in the Supervisor program do not take effect in the Operator program until you exit and restart it.

- The **Recalibrate Energy** option on the Operator program's **Startup** dialog applies only when the **Internal** calibration option is set here as an analysis option. *Note, however, that the internal calibration is updated each time an analysis is performed using a calibration override file, so this option is useful only where the calibration will not routinely be changed.*
- When using a specified calibration file instead of the **Internal** calibration, the **Adjust Gain** option on the Operator program's **Startup** dialog can be used to realign peaks back to the original calibration position making an energy recalibration unnecessary.

When an **.SVD** file is recalled, the date of **Creation** and last date the file was updated (**Edition**) are displayed. Whenever the file is changed, the edition date is updated when it is saved.

The **Description** is used to identify the sample-type file, and can be 64 characters long.

Clicking on the **Presets** button opens a Presets dialog corresponding to the available presets for this MCB, as discussed in **Acquire/MCB Properties...**

The presets entered here will be used for sample QA analysis in both the Supervisor and Operator programs. (The background acquisition presets entered on the Quality Assurance Settings dialog [Section 10.2.1] are used for background QA measurements in both programs, and the operator scan type file contains the presets for routine subject measurements in Operator.)

Figure 122. Sample Tab for NaI Analysis.

The **Calibration** data to be saved with the spectrum or used for interactive analysis can be the currently loaded **Internal** (working) calibration or a calibration stored on disk. The internal calibration is the calibration most recently created with the **Calibrate** menu functions (see Section 5.3.1) or the calibration most recently recalled from disk, and *is specific for the currently selected Detector*.

NOTE Keep in mind that each time you create or recall a calibration in Supervisor, if a Detector window is currently active (rather than a buffer window), *that Detector's internal calibration has just been changed*. This calibration update also takes place whenever an Operator analysis specifies an override calibration.

As noted above, a specific calibration file should normally be used here, rather than the **Internal** setting, particularly if this analysis options file will be used in a scan type (.OPR) file that uses the **Analyze sum of spectra** option.

When the .SPC file for this spectrum is saved to disk, the current calibration will be saved with it for later analysis. The interactive analysis (performed with **Analyze/Interactive in viewed area**), uses the currently loaded (internal) calibration. Note that each Detector and buffer can have separate calibrations.

The filename of the **Nuclide Library** to be used in the spectrum analysis can be the **Internal** (working) library or a library file on disk. The internal library is the library most recently selected using **Library/Select File...** It is *not* detector-specific, and will include any modifications made during the interactive analysis mode. As noted above, a specific library file should normally be used here, rather than the **Internal** setting.

The **Background Type** can be set to **Auto, 1-pt., 3-pt., or 5-pt.** These are explained in more detail in Section 8.2.1.

The **Analysis Range**, in channels, is entered here. This is usually used to eliminate analysis of the ends of the spectrum that do not contain useful data. The **Analysis Range** should be as wide as possible because the automatic energy recalibration feature (see Section 8.2.6) requires separated library peaks to work properly. Also, the correlation of peaks from a single nuclide done by the analysis is defeated if the energy range analyzed does not include all the peaks.

System Tab

System settings are those settings that are generally the same from sample to sample. However, all of these entries except the **Laboratory** name can be different for each sample type. The dialog is shown in Fig. 123.

The **Laboratory name**, composed of any 64 characters, is printed as the second line on each page of the Supervisor report. The spectrum name is printed on the next line.

The **PEAK SEARCH SENSITIVITY** sets the sensitivity for the peak search used in the **Inter-**

active in viewed area (Section 5.5.4) and the full-spectrum analysis (Section 5.5.2). Before a suspected peak is accepted, the magnitude of the second difference must be greater than the weighted error of the channel counts. The **PEAK SEARCH SENSITIVITY** is a multiplicative factor used in error weighting. The sensitivity can be set at any integer value from 1 to 5, with 1 the most sensitive (that is, "1" finds the most peaks). A value of 1 will find small peaks, but will also "find" many false peaks. A value of 5 will locate all the large peaks, but might miss some of the smaller peaks. If too high, some small peaks will be missed. In the interactive mode, many regions will be deconvoluted unnecessarily if the value is too sensitive. If the sensitivity is set to 1, the parabolic background method is disabled for energies above 200 keV.

In the **Library** section, **Match Width** sets the maximum amount by which a peak centroid can deviate from the nearest library peak energy and still be associated with that library peak. The value entered is multiplied by the FWHM at the peak energy to get the width used. If the value is too small, some spectrum peaks will be misidentified due to statistical variation in the centroid, and if it is too large, some library peaks will be incorrectly identified. A value of 0.75 is the factory default. If the **Match Width** is set to a value other than 0.75, the value will be printed on the report.

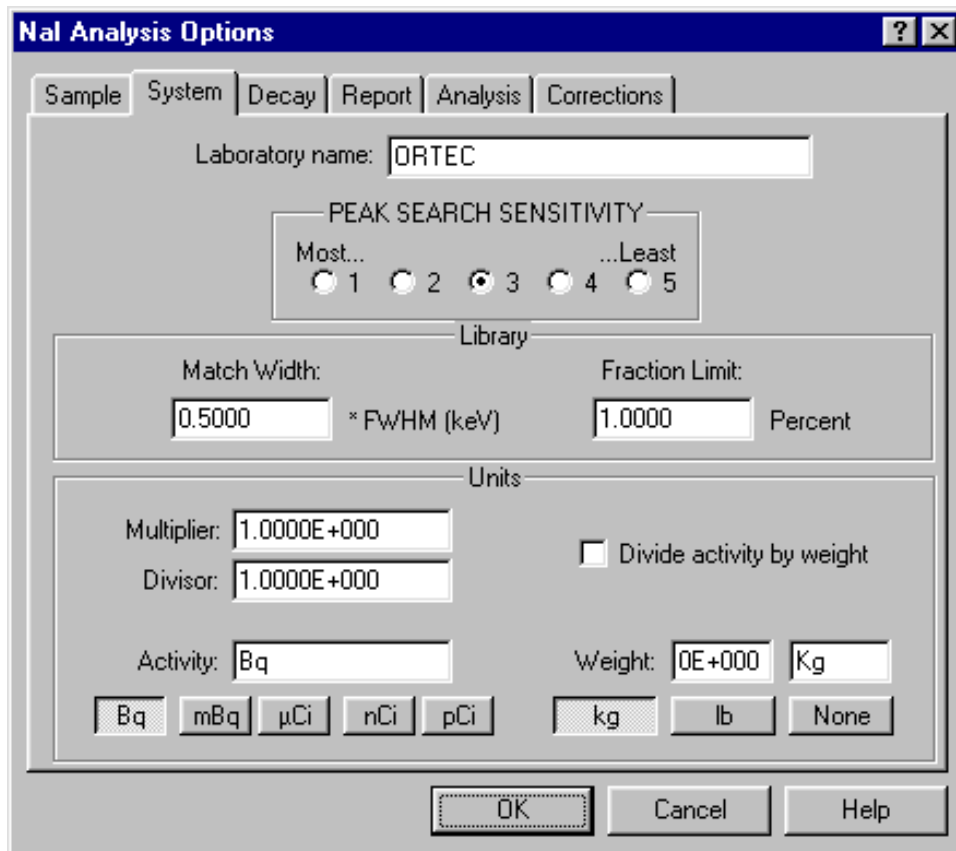


Figure 123. System Tab for NaI Analysis.

The **Fraction Limit** is one of the parameters used to determine the presence or absence of a nuclide. The sum of the emission probabilities of the peaks in the spectrum identified with the nuclide is divided by the sum of the emission probabilities of all peaks of the nuclide in the energy range being analyzed. If the result is greater than the fraction limit, the nuclide is marked as being present. To turn off this test, set the limit to zero.

The **Units** section allows you to:

- Establish the units of measure and subject weight for analyses performed in Supervisor with this set of analysis options.
- Determine the units of measure that will be used for activity and subject height and weight in the Operator program.

Select the desired **Activity** units, and a **Multiplier** and **Divisor** to scale the numbers up or down to make any other units needed. The units label is printed at the top of the activity columns on the report and should reflect the values chosen; that is, if **µCi** is chosen with a multiplier of 1000, then “nanocuries” should be entered in the **Activity** field.

If you select **lb**, the **Weight** field in Operator will be displayed in pounds and the **Height** will be displayed in inches. If you select **Kg** or **None**, the **Weight** and **Height** fields will be in terms of kg and cm, respectively.

NOTE The **Weight** units will be displayed on the Supervisor analysis report if set to anything other than **None** (i.e., Bq/kg or µCi/lb). If the scan type that uses this analysis options file *does not* specify **Divide Activity by Weight**, the **Weight** will always be set to **1** and the units set to **None** when an analysis is performed in Operator.

Enter the subject **Weight** to be used for analysis in the Supervisor program. Note that nuclide activities are always divided by **Weight** in the Supervisor analysis. In Operator, entering the subject’s **Weight** overrides any existing entry (see the preceding NOTE).

Regardless of the units selected here, subject weight and height are always stored in the database in terms of kg and cm, respectively. These values are appropriately converted when read from or written to the database and when displayed on the standard Operator text reports. Operator reports generated using Crystal Reports templates will display the height and weight in terms of kg and cm. For this reason, Chest Wall Thickness calculation coefficients established in the scan type files should always be based on weight/height expressed in terms of kg/cm.

Decay Tab

The Decay tab (Fig. 124) allows you to enable or disable decay correction **During Acquisition** and decay correction to a given **Date and Time (Collection)**. Both of these affect the report of the analysis of the total spectrum.

Only the **During Acquisition** correction is automatically applied in the Operator program. Regardless of the setting specified here, the operator determines whether the **Collection** correction is applied by adding, changing, or removing the entry in the Operator program's **Decay Date** field.

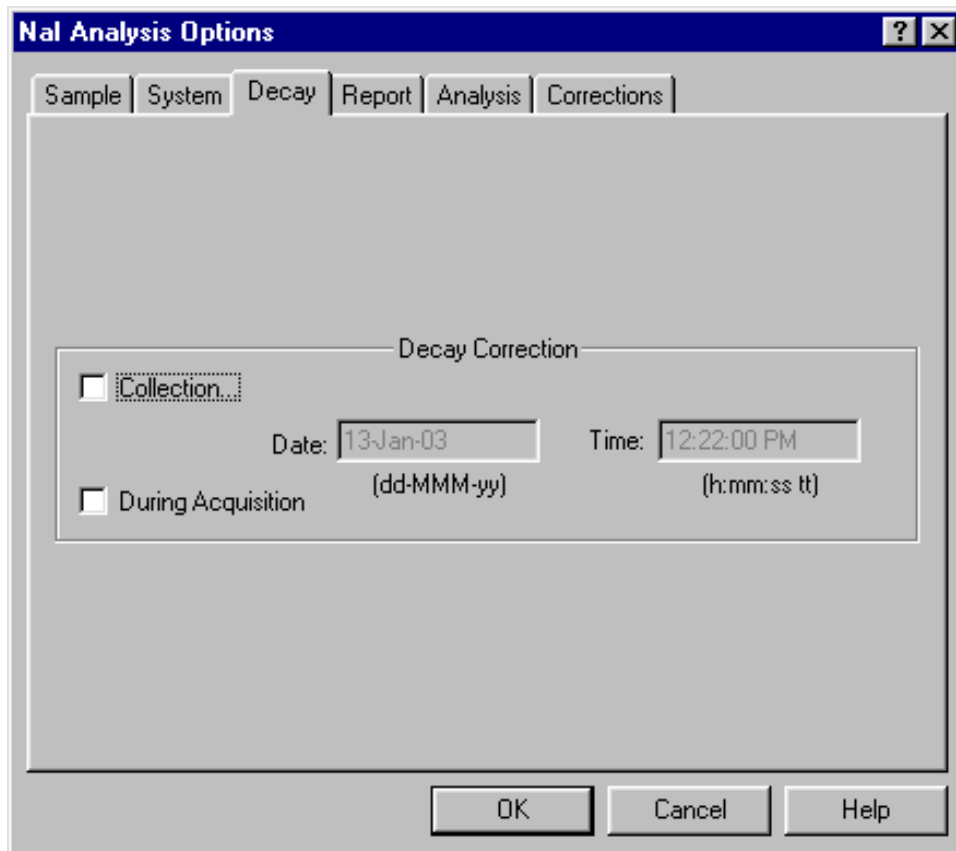


Figure 124. Decay Tab for NaI Analysis.

NOTE In Operator, decay correction to a collection time will not be calculated if the operator does not enter a **Decay Date** for a the current measurement.

Report Tab

This screen (Fig. 125) controls the contents, destination, and some details of the output report discussed in Chapter 7.

The **Reporting Options** control only the spectrum analysis report in the Supervisor mode. The **Output** options affect both the Supervisor and Operator reports, with the exception of **Report Writer**, which affects only the Operator report; and **Display Analysis Results**, which affects only the Supervisor report.

Select one or more **Reporting Options** by marking the checkboxes. If there is not enough information for Renaissance to print all of the requested options, the program might print another option if there is enough information for it. For example, suppose a nuclide activity report is

the only report option selected. If the spectrum has not been efficiency calibrated, the activities cannot be calculated. In this case, the spectrum report will instead contain the peak list because there is sufficient information to do that.

When Renaissance performs an analysis, it writes the results to a .UFO file and writes an ASCII-format .RPT file. If you are analyzing a spectrum that has not yet been saved to disk, Renaissance automatically creates a spectrum file with the extension of .AN1. The .UFO, .RPT, and .AN1 files share the same filename.

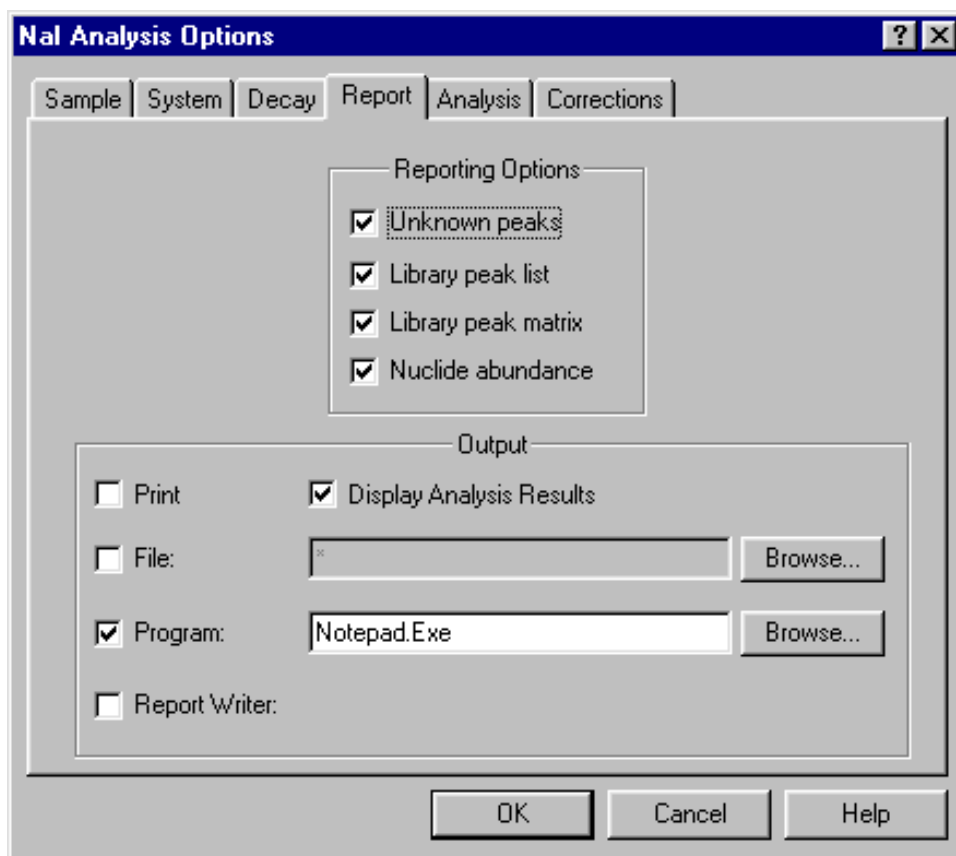


Figure 125. Report Tab for NaI Analysis.

The **Print** option sends the .RPT file to the default Windows printer for this computer. The full NaI report discussed in Chapter 7 is produced in Supervisor and *for sample QA measurements in Operator*. For all other measurements in Operator, a shorter subject count report is generated (see the Operator user's manual).

The **Display Analysis Results** feature applies only to the Supervisor program; interactive peak fitting is not available in Operator. If you mark the **Display Analysis Results** box, when the analysis is complete, the results will be displayed onscreen in the same format as for **Analyze/Display analysis results** (Section 5.5.3).

Selecting **File** lets you assign a new filename to the report or browse for an existing filename (this will overwrite the existing report file with the new analysis). The default is an asterisk (*) for the filename. In this case, the report filename will be the spectrum filename with the extension .RPT.

Program allows you to select any Windows program to be run with the report filename as an argument on the command line. The report filename sent to the program is the spectrum filename

with the extension **.RPT**. The default program is Windows Notepad (**Notepad.exe**). In this case, when the analysis finishes, Notepad automatically starts and opens the **.RPT** file. (Notepad can be used to save the **.RPT** file to a different filename, if you wish, or to print the report.) The analysis is not complete until you close the selected program (e.g., Notepad).

The **Report Writer** field affects only the Operator program. With this option selected, when analysis is complete in the Operator program, a Crystal Report is generated according to the options set with the **Analyze/Settings/Reports...** function. See the Operator user's manual for the contents and format of the ASCII text and **Report Writer** reports.

NOTE When the **Report Writer** is enabled, the weighted average and concatenated reports are not displayed in the Operator program's Crystal Report. To display and/or print these report types, you must *also* mark the **Print** and/or **Program** options to generate the standard text report.

Analysis Tab

Use this screen (Fig. 126) to select the **Analysis Method** and **Analysis** options to be used. The actual analysis is done by a separate program referred to as an analysis engine.

Analysis Method

The analysis engine for the normal analysis is REN-GSA. See Chapter 9 for more information on the analysis program.

Renaissance also accommodates user-supplied analysis programs. The program must be able to read the spectrum name from the command line.

There are no other restric-

tions, but if the program does not produce a results file in the **.UFO** format, the display results functions and the Renaissance database will not work. All the analysis options can be taken from

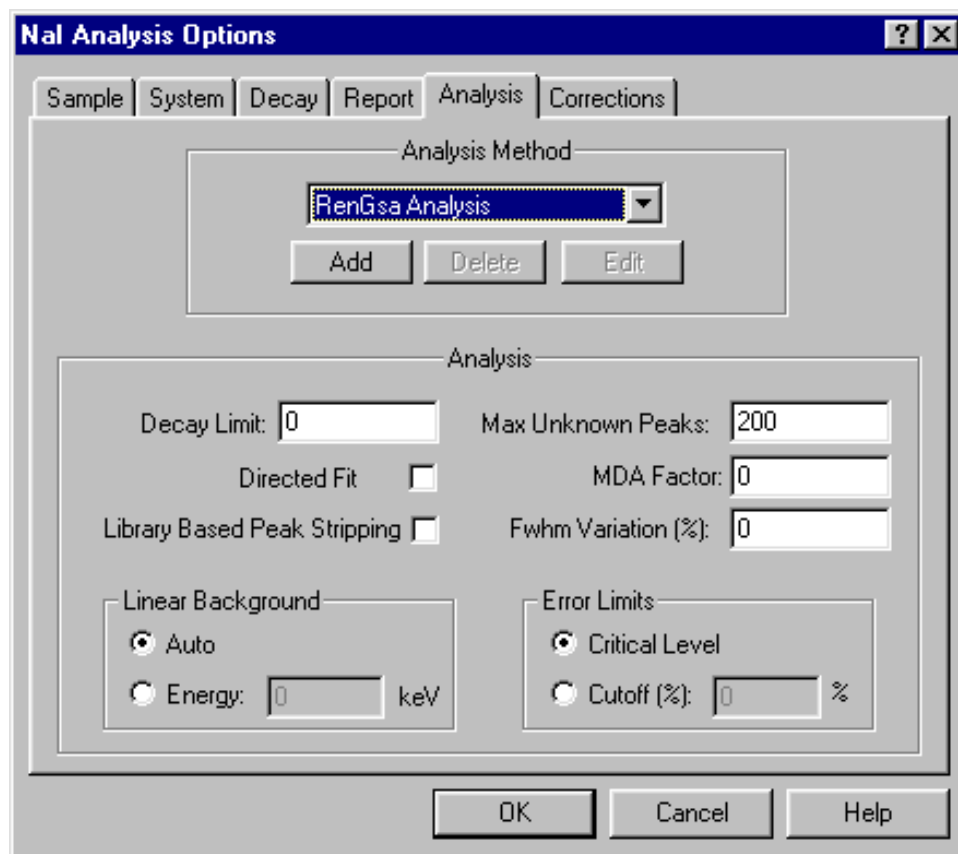


Figure 126. Analysis Tab for NaI Analysis.

the .SPC file. The analysis program should also produce an ASCII report file so the report can be printed.

Analysis

The **Decay Limit** is used to determine the presence or absence of a nuclide. If a spectrum is being analyzed with the decay correction, nuclides that have decayed more half lives than the decay limit are marked as absent, whether or not the peaks are found. On the Supervisor report the peak is listed in the Identified Peak Summary and Summary of Library Peak Usage. In the Summary of Nuclides in Sample it is listed as an MDA value with a message indicating that the cutoff has been exceeded.

Click on **Directed Fit** to allow for negative peak areas in low-level spectra. For this type of analysis of NaI spectra, we recommend that you use as small a library as possible. Directed fit is described in Section 9.2.2.2.

When **Library Based Peak Stripping** is enabled, the analysis performs the library-based peak deconvolution or “peak interference correction” described in Section 9.3. Briefly, this separates peak areas that are too close together to be accurately separated by mathematical deconvolution. The program automatically detects overlapped peaks and the associated peaks needed. It then performs the peak stripping using these peaks.

The **Max Unknown Peaks** field is usually set to 200. Larger values will increase the size of the analysis results (.UFO) file. If the program finds more unknown peaks than the maximum, then a message is printed on the report. The analysis should be repeated with a higher number. All unknown peaks are stored in the .UFO file, even if they are not reported on the output.

The **MDA Factor** determines the total width of the region to be used to calculate the background variance if the peak is not detected. The region high and low limits are $(0.5 \times MDA \text{ Factor} \times FWHM)$ above and below the peak centroid energy. The default value is 2.53.

The **FWHM Variation** is the amount (as percent of the initial FWHM) the FWHM is allowed to vary in fitting the peak region. Typically, a setting of 50% will allow the peak widths to vary enough to give a good fit. If a spectrum has been well calibrated, the FWHM variation can be set to 10%; however, if the variation is set too low, single peaks will sometimes be fitted as doublets. This should not be set above 100%; if the FWHM varies by more than a factor of 2, the calibration is not correct for the spectrum.

The best type of background to use in a fit varies with the type of spectrum. The **Linear Background** energy is the value at which the background under a peak changes from a curve to a straight line. If **Auto** is selected, the program determines the best fit for the background at all energies. In the case where a multiplet is spread over a large portion of the spectrum with the

peaks overlapping by only a few channels, the background should be fitted as a polynomial even if it is very flat. If **Energy** is selected, we recommend an initial setting of zero (0) keV. If varying this setting to improve peak-fitting, enter the energy at which the background flattens out. Above this energy, the background of a multiplet is fit as a straight line, with a step added under each peak. Below, the background of both singlets and multiplets is fitted as a polynomial. See the peak-fitting example on page 135.

Error Limits — In Renaissance, if a peak fails a statistical test, the peak is identified (labeled) in the report, but its value is not used in determining the amount of that nuclide present. You can select either the **Critical Level** or enter a **Cutoff (%)**.

For the **Critical Level**, the cutoff value is software-calculated at $2.33 \times \sqrt{\text{Background Variance}}$ and the peak area must be greater than this value in order to be included.

If using **Cutoff (%)**, enter the percent uncertainty for the cutoff. A peak with counting uncertainty greater than the cutoff will be rejected.

Corrections Tab

The Corrections tab is shown in Fig. 127.

Attenuation Correction

The **Attenuation** correction allows you to correct the activity for attenuation by various absorbers. The selected options, attenuation material, and CWT calculation methods should be based on site protocols.

NOTE Attenuation correction is only enabled for the Operator analysis if the **Chest Wall Attenuation** feature is enabled in the scan type file (see “Chest Wall

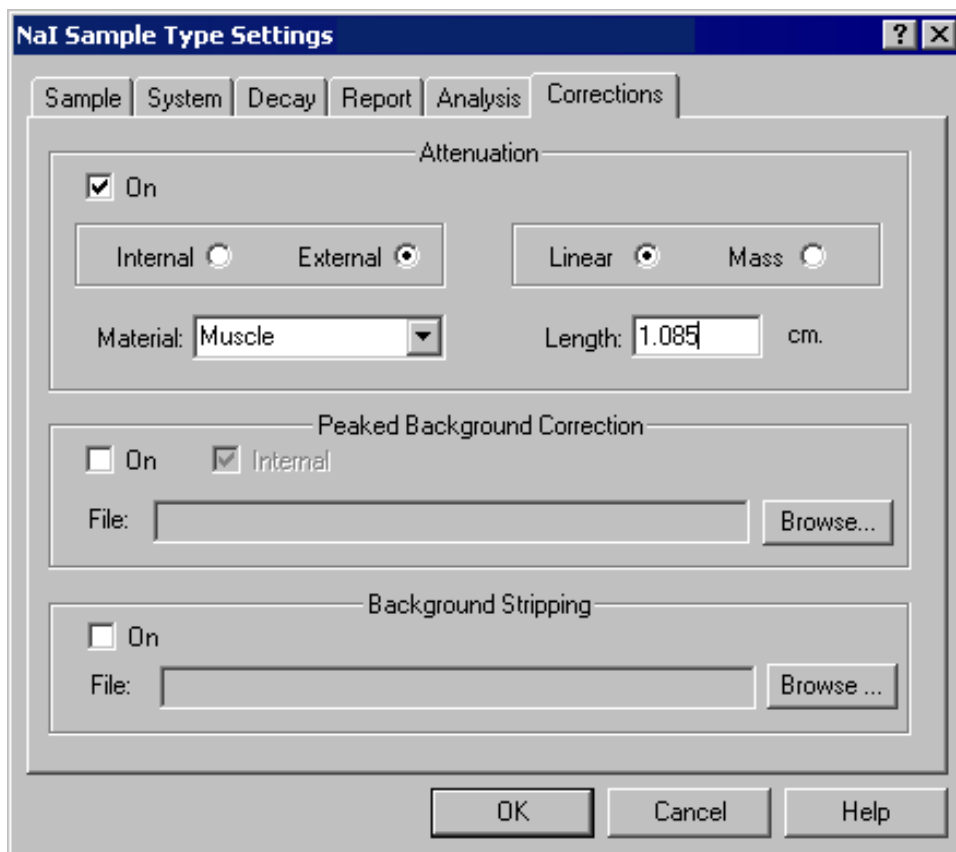


Figure 127. Corrections Tab for NaI Analysis.

Attenuation,” page 183). If the **CWT** entered in Operator is set to zero, no attenuation correction is performed in the analysis. If the operator enters a non-zero value, the correction is performed with the attenuation **Length** set to the **CWT** value entered.

Internal absorption is for cases where the radioactive material is distributed throughout the absorber (matrix) and **External** is where the absorber is between the radioactive material and the detector.

The correction parameters are chosen from the built-in Renaissance database of stored coefficients. Enter a **Material** and **Length**, and choose between **Linear** and **Mass** according to the entry for this absorber in the database. The database values are based on an absorber **Length** of 1 cm. For larger or smaller lengths (external) and thicker or thinner materials (internal), enter the actual length or thickness. The attenuation correction is explained in detail in Section 8.9.6.

This option is normally used to correct the activity for attenuation in the chest. Assuming that the activity is deposited in the lung and not distributed throughout the chest wall, the **External** option should be selected with **Linear** attenuation. If this correction is applied to the intestines, you might wish to specify a different CWT calculation in the scan type file, and the **Internal** option might be more appropriate.

Peaked Background Correction

When the **Peaked Background Correction** (Section 8.9.4) is turned **On**, you can specify a **.PBC File** on disk or use the current **Internal** (working) file. The internal file for the currently selected detector is the one most recently created with the **Create PBC...** command or loaded with the **Select PBC...** command (see Section 5.5.1.5).

If you specify a **.PBC** file here, that file will always be used for the analysis (in both Supervisor and Operator) regardless of any changes made to the **.PBC** files currently loaded in the detectors or specified for a multi-detector group.

For scan types that specify spectrum summing, note that internal **.PBC** files will be updated each time the operator uses the **Create Background File...** or **Select Background File...** commands on the **Analyze** menu, and the **Update Background Files** function in **Startup**.

NOTE This correction should be turned *off* for **.SVD** files used in the scan type for creating **.PBC** files.

If **.PBC** files will be routinely generated for a detector group or individual detectors using the Operator program **Startup** function, use the **Internal** option to allow updates from within Operator. This is because the internal files are updated each time **.PBC** files are updated or new files are selected in the Operator program.

NOTE When creating or recalling .PBC files in Operator, the internal .PBC files are updated (a) for each detector if **Analyze sum of spectra** is turned off in the current scan type file, or (b) for the group sum if **Analyze sum of spectra** is turned on.

Background Stripping

If the Detector Group contains only NaI detectors, you can choose channel-by-channel background stripping. This functions as described in Section 5.4.5 for the **Calculate/Strip...** command with the **Use ratio of Live Times** checkbox marked.

Mark the **On** checkbox and browse for the background spectrum to be used. If analyzing the summed spectrum, the **Background Correction** file must be a sum of spectra for all Detectors in the group. A background measurement can be generated at once for the entire group in Operator, or Detector-by-Detector in Supervisor with the **Calculate/Sum Spectra** command (Section 5.4.6). To use this option, *all Detectors in the group must be of the same type (Ge or NaI) and use the same conversion gain.* The stripping file is listed on the NaI report.

5.5.1.3. Reports...

This dialog (Fig. 128) controls the Crystal Reports template that will be used to format Operator program reports, as well as standard print options such as the number of copies to be printed and whether or not to collate multiple copies.

NOTE This function operates in conjunction with the **Report Writer** option on the Report tab under **Analyze/Settings/ Sample Type...** The **Report Writer** option on the Report tab must be checkmarked before the Crystal Reports template specified here will be used.

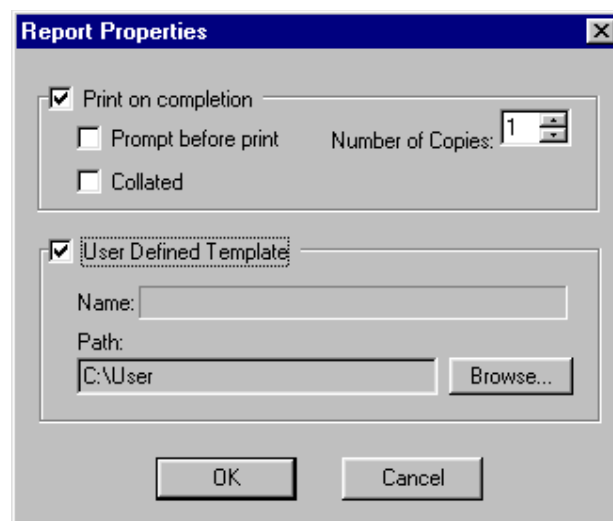


Figure 128. Operator Report Options.

When **Report Writer** has been activated:

- If the **User Defined Template** box is not marked in this dialog, the Operator program will use the default Operator Crystal Reports template.
- If the **User Defined Template** box is marked, use the **Browse** button to locate an existing Crystal Reports report template to be used for the Operator report. (The file must exist before you can use the **Browse** button to select it. Characters cannot be directly typed into the field.)

If the **Report Writer** option is not activated, Renaissance Operator will generate only the fixed-format, ASCII text report.

5.5.1.4. Group Sample Type...

The **Group Sample Type...** command opens the dialog shown in Fig. 129, which allows you to change, in batch mode, the analysis parameters (the **.SDF** or **.SVD** settings) for one or more **.SPC** files. For instance, suppose you wish to change the peak-search sensitivity for 100 **.SPC** files from 3 to 2. To do this, select the type of analysis options file that you wish to use by clicking on either **Ge** (**.SDF**) or **NaI** (**.SVD**). Next, **Browse** for the analysis options file that contains the desired peak-search sensitivity setting. Then click **Add** to locate the files you wish to adjust. You can use the mouse and the **<Ctrl>** and **<Shift>** keys to select more than one file at a time. Use the **Remove** button to delete one or more **.SPC** files from the dialog. Finally, click **Apply**.

NOTE Every parameter in the analysis options file will be applied to each spectrum in the list.

*To preserve the integrity of the original **.SPC** file(s), **we recommend that you make copies of the files before performing this operation.***

Click on **Clear** to remove all entries from the spectrum file table. You can repeat this operation as many times as you wish on as many files as you wish to change. Only files with the same **Detector Type** (Ge or NaI) can be adjusted at one time.

To close the dialog, click the Close (×) button.

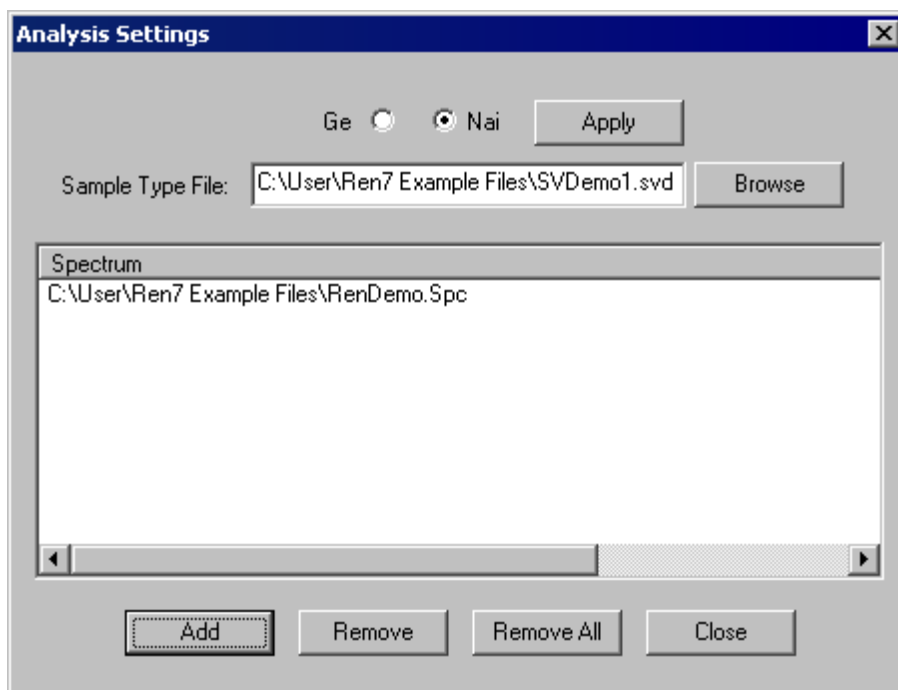


Figure 129. Group Sample Type.

5.5.1.5. Peak Background Correction

The **Peak Background Correction** submenu is shown in Fig. 130. Use these commands to load a new internal (working) .PBC file, and to create or edit .PBC files. The .PBC files are organized by nuclide, then by peaks, for each nuclide.

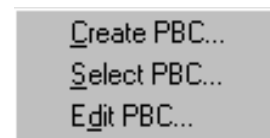


Figure 130. PBC Menu.

The PBC table file is used with the peak background correction in the spectrum analysis. Note that the PBC correction is related to the detector and the shield, but not to the geometry of the sample. Any of the correction table nuclide data include the nuclide name, which can be any combination of eight characters, but must be consistent throughout all files.

Create PBC...

This will start the PBC wizard, which will collect the background spectrum, analyze the spectrum and create the PBC file automatically. The wizard will run in either a buffer or Detector window. The dialog is shown in Fig. 131. Enter the library for the analysis of the spectrum. This will normally be a library of background nuclides. Enter the **Real Time** or **Live Time** preset. The count rate in background situations is normally low, so either preset can be used.

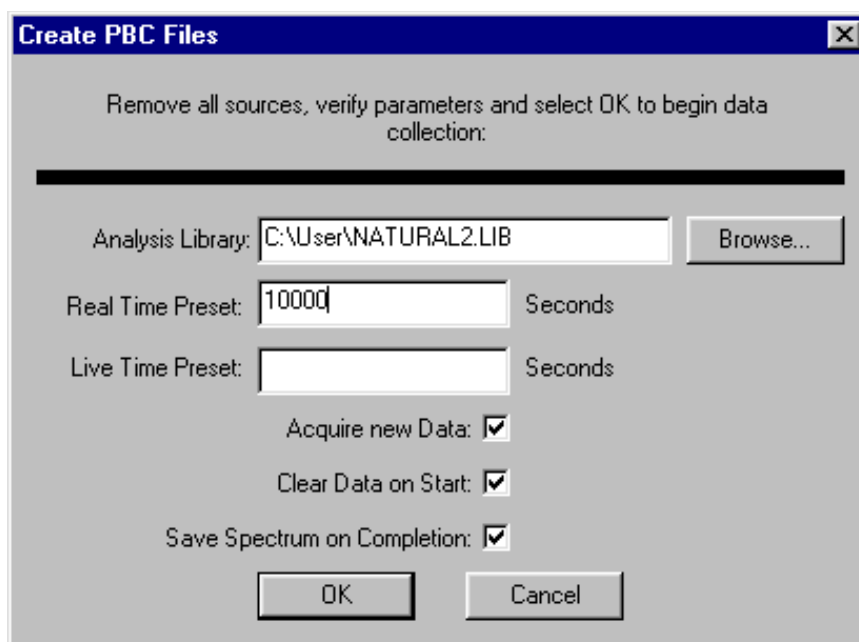


Figure 131. PBC Wizard.

The **Acquire new Data** and **Clear Data on Start** are used to control the data acquisition in the Detector. Both are disabled when analyzing a buffer. If the Detector contains a good spectrum and no more data is needed, unmark the **Acquire new Data** box. This will ignore the **Preset** fields above and read the spectrum in the Detector.

To collect more data for the **Preset** time entered above, mark the **Acquire new Data** box. To clear the Detector before collecting data for the preset time, mark the **Clear Data on Start** box. To use the existing data in the Detector and add more data to it, unmark the **Clear** box. *Note that the preset above is the **total data collection time** (not just the additional time). If the preset is less than the actual time, no new data will be added.*

Mark the **Save Spectrum on Completion** box to save the spectrum after the analysis. The file name will be determined by the settings in the **Acquire/Settings** menu.

Prepare the detector, remove all sources and press **OK** to continue. The data will be collected as specified, analyzed and the PBC table created. A pop-up “All PBC Files Have Been Created!” message will be displayed. The PBC filename will be the same as the spectrum filename. Click **OK**.

At startup, Renaissance automatically attempts to load the PBC table last loaded. Thereafter, it can be replaced at any time using **Select PBC....** It stays resident in memory after it have been loaded.

Select PBC...

Use this command to open a standard file-open dialog and select a new working .PBC file. If a .PBC file is already loaded, its name will be displayed in the **File name:** field; otherwise, the default, *.PBC, will be shown. Select the desired file and click on **Open**.

Edit PBC...

This function is used to manually create a new .PBC file from a spectrum previously analyzed or to change the contents of an existing .PBC file. To create a .PBC file, click on **Edit PBC...** to open the **Editing:** dialog shown in Fig. 132.

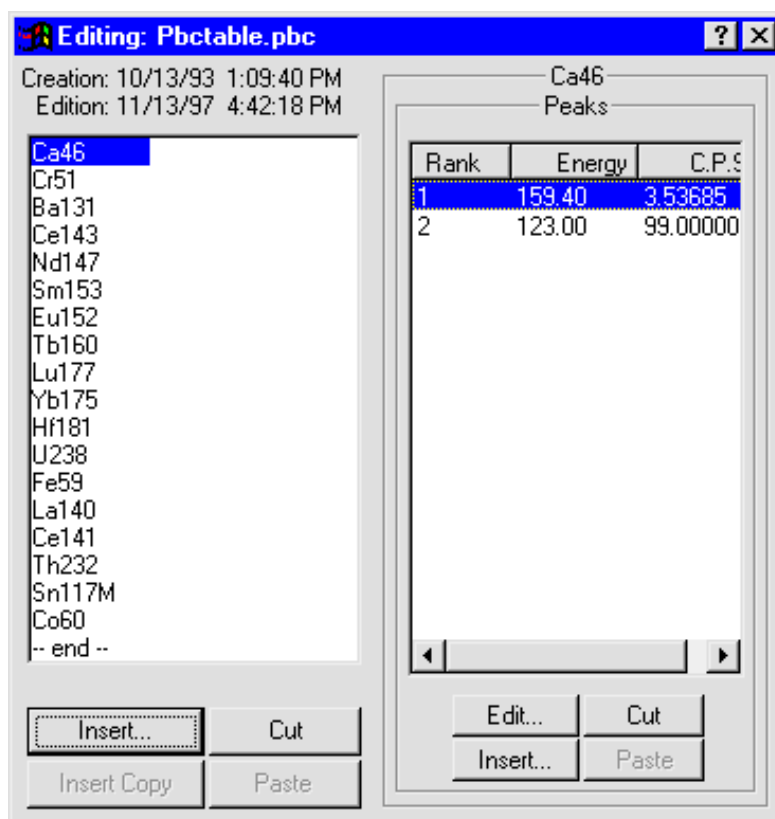


Figure 132. PBC Table Editing Dialog.

Figure 133 shows the dialog control menu (click on the Title Bar icon to open it). It contains several of the commands necessary to create and edit .PBC files.

Manually Creating a New PBC Table

Open the control menu and click on **New**. This will clear the **Edit** window so nuclides can be entered manually.

Click on the **Insert...** button to open the dialog shown in Fig. 134. Enter the nuclide name exactly as it appears in the library. Click on **OK** to add the nuclide.

Now, in the (right-hand) peak portion of the dialog, click on **Insert...** to open the dialog in Fig. 135. Enter the energy of the gamma ray and the counts per second of the background peak. The energy must be the same as the library value. Peak energies in the PBC Table and not in the library for this nuclide will not be corrected, and peak energies in the library and not in the PBC Table for this nuclide will not be corrected. Click on **OK** to add the nuclide.

Automatically Creating a PBC Table

A .PBC file can be made from the background spectrum analysis results (.UFO) file. In this process, the background count rates are extracted from the analysis results file and inserted in a .PBC file. To do this, open the control menu and click on **Show Background Analysis...** This will open a standard file-open dialog. Select the correct .UFO file and click on **Open**. The list of nuclides in the analysis will be displayed to the left of the PBC Table (see Fig. 136). If no peaks are shown, none were in the analysis file, possibly because they were all outside the energy analysis range.

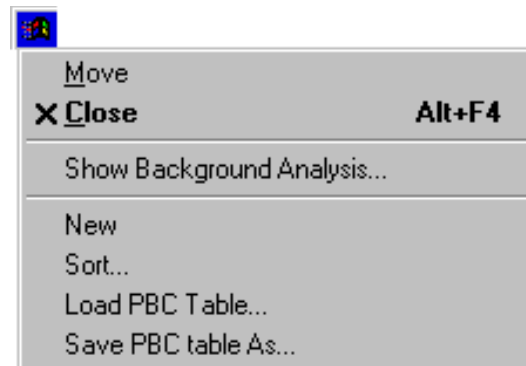


Figure 133. Edit PBC Dialog Control Menu.

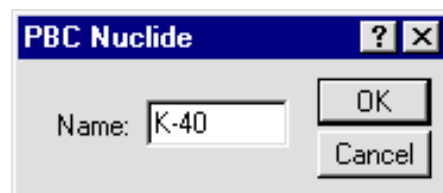


Figure 134. Edit or Manually Add Nuclide Name.

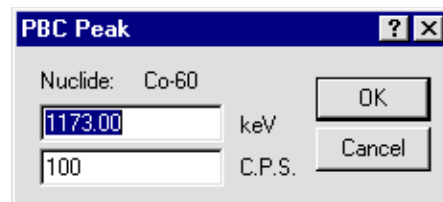


Figure 135. Edit PBC Peak Values.

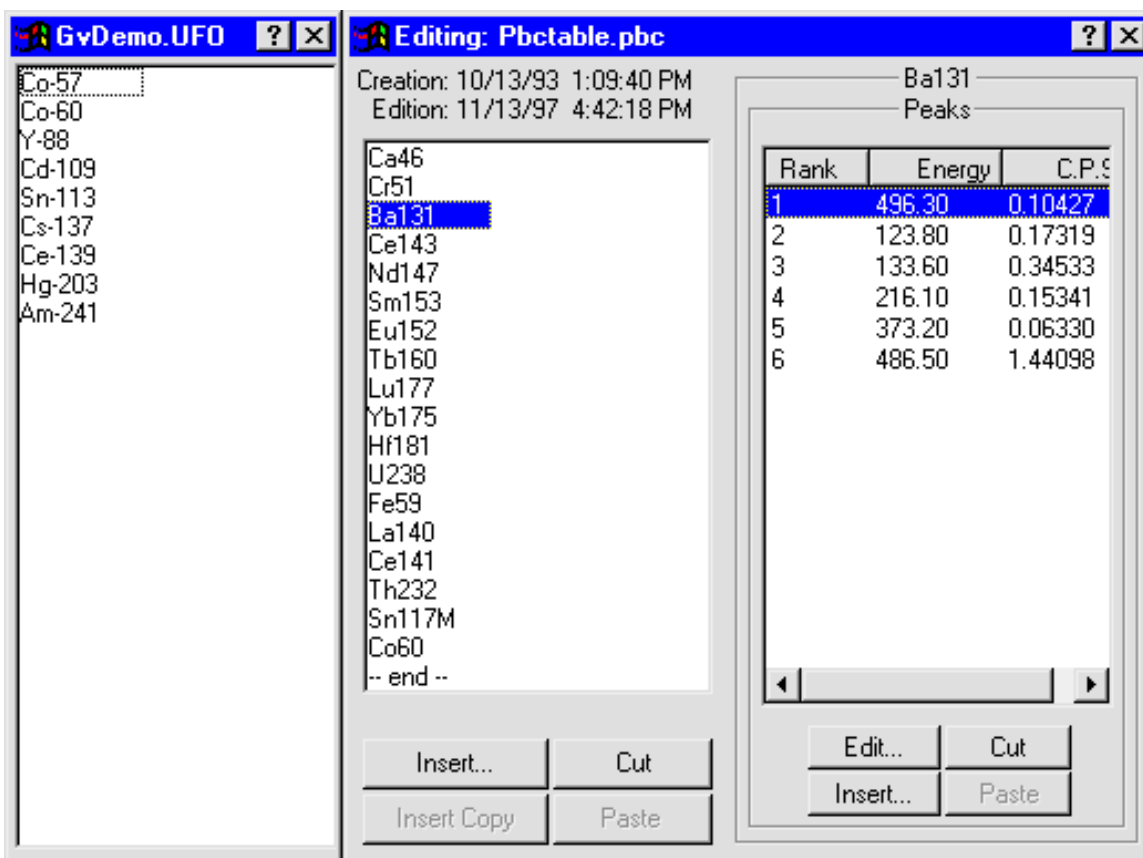


Figure 136. The List of Analysis Nuclides (left) and the PBC Table (right).

Adding Nuclides

There are two **Insert** buttons at the bottom of the PBC nuclide list: **Insert...**, which is for manually specifying the nuclide; and the button below it, which will be labeled with the name of the nuclide selected in the analysis results list (when no nuclide is selected, this button is labeled **Insert Copy**).

To automatically add an analysis nuclide to the PBC list: Go to the analysis results list and click once on the nuclide of interest. This will activate the gray **Insert Copy** button at the bottom of the PBC list, and change its label to **Insert** plus the name of the nuclide. Now, in the PBC list, click on the nuclide immediately below the desired insertion position, then click on **Insert [nuclide name]**. This will insert the nuclide, and display the energies and backgrounds for its peaks in the analysis.

Double-clicking a nuclide in the analysis results list will insert it into the PBC list immediately above the highlighted PBC-list nuclide.

To manually add a nuclide to the PBC list, locate the nuclide immediately below the desired insertion position, and click once to highlight it. Next, click on the manual **Insert...** button to open the dialog shown in Fig. 134, then follow the manual nuclide and peak insertion instructions that begin on page 153.

The entire analysis nuclide list can be copied to the PBC list by opening the analysis list control menu (Fig. 137) and selecting **Copy All to PBC**.

To change the name of a nuclide on the PBC list, double-click it to open the PBC Nuclide dialog (Fig. 134).

To remove a nuclide from the PBC list, click on the nuclide, then on **Cut**. This will remove the nuclide from the list. In addition, it will activate the gray **Paste** button at the bottom of the PBC list, and change its label to include the name of the cut nuclide. This is illustrated for ^{152}Eu in Fig. 138.

Rearranging a PBC List

Nuclides can be rearranged in the .PBC file list by cutting and pasting them into a different location. To move a nuclide to a new position in the list, highlight the nuclide to be moved; **Cut** it from the list; locate the nuclide immediately *below* the desired new position and click once on that nuclide to highlight it; then click on the **Paste** button (which will be labeled with the name of the **Cut** nuclide). The **Cut** nuclide will be inserted in the space above the highlighted nuclide.

Several nuclides can be cut at one time from the list, then pasted back into the list into a different order. Cut nuclides remain queued up for pasting, last one first, according to the nuclide name on the **Paste** button.

To move a nuclide to the end of the PBC list, **Cut** the nuclide from the list, highlight the **--end--** entry, and click on the **Paste** button.

Peak Editing

When a nuclide is selected in the working .PBC file, the right half of the Edit PBC dialog shows the peak list. Note the column headers, **Rank**, **Energy**, and **C.P.S.**. To sort the peak list by a particular parameter in the list, click on the appropriate header.

To edit a peak, either double-click on the peak in the right-hand list, or click once on it, then click on the **Edit** button. This will open the PBC Peak dialog (Fig. 135).

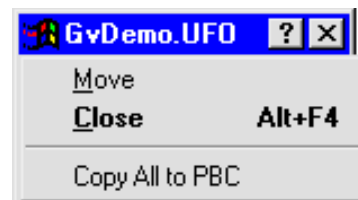


Figure 137. Analysis Results List Control Menu.



Figure 138. Cut Nuclide is Ready to Paste.

Use the same PBC Peak dialog to add a peak: click on the peak *just below* the desired insertion point in the peak list, then click on **Insert...** This will open the PBC Peak dialog. Enter the energy and counts for the peak and click on **OK**.

Peaks can be deleted with **Cut** and moved with **Cut/Paste**. The order of the peaks is not important and has no effect on the correction.

Several peaks can be cut at one time from the list, then pasted back into the list into a different order. Cut peaks remain queued up for pasting, last one first. Each relocated peak will be assigned a **Rank** number according to its new position. Click on the peak *just below* the desired insertion point in the peak list, then click on **Paste**.

Saving or Canceling Changes and Closing the Edit Session

To save this modified .PBC file and use it as the working file, click on the control menu, then **Save PBC Table As...** Either use the current filename (which will overwrite the previous values) or assign a new filename, then click on **Save**. (Renaissance will assign the default .PBC extension.) To exit the edit session, click on the control menu, then **Close**.

To abandon any changes and restore the .PBC file to its condition before editing, click on the control menu, then **Close**. A dialog will open to confirm the deletion of the changes; select **No**.

5.5.2. Entire Spectrum in Memory...

This initiates an analysis of the entire spectrum in the active buffer or Detector window (if the Detector is not acquiring data), generating .RPT, .UFO, and .AN1 files. The analysis is performed in the background and the display is available for continued interactive use. The spectrum is moved to disk for the analysis so the spectrum in the Detector or buffer can be changed if needed. When the analysis is completed, you are notified and the report is generated. If any errors occur, the error number is displayed along with the spectrum name. The errors corresponding to the error numbers are explained in Appendix D.

If the **Program** radio button on the Report tab of **Analyze/Settings/Sample Type...** has been selected, with **Notepad.exe** designated as the output program, Renaissance will open Windows Notepad and display the analysis report. The software will not accept inputs while the report display is shown. When you exit Notepad, control returns to Renaissance. At this point, if you select **Analyze/Display Analysis Results**, the .UFO file for the spectrum just analyzed will automatically be displayed.

5.5.3. Display Analysis Results...

This command displays the results of an analysis of the complete spectrum by reading the analysis results stored in a .UFO file. This differs from the interactive analysis results in that the analysis considers all of the spectrum and all of the library entries. The .UFO files are created by **Analyze/Entire Spectrum in Memory**. Select the .UFO file from the file-open dialog.

Figure 139 shows the display for a typical .UFO file, along with its spectrum file. Figure 140 shows the Analysis Results Sidebar. The buttons move the marker up and down through the results list, library, and spectrum simultaneously.

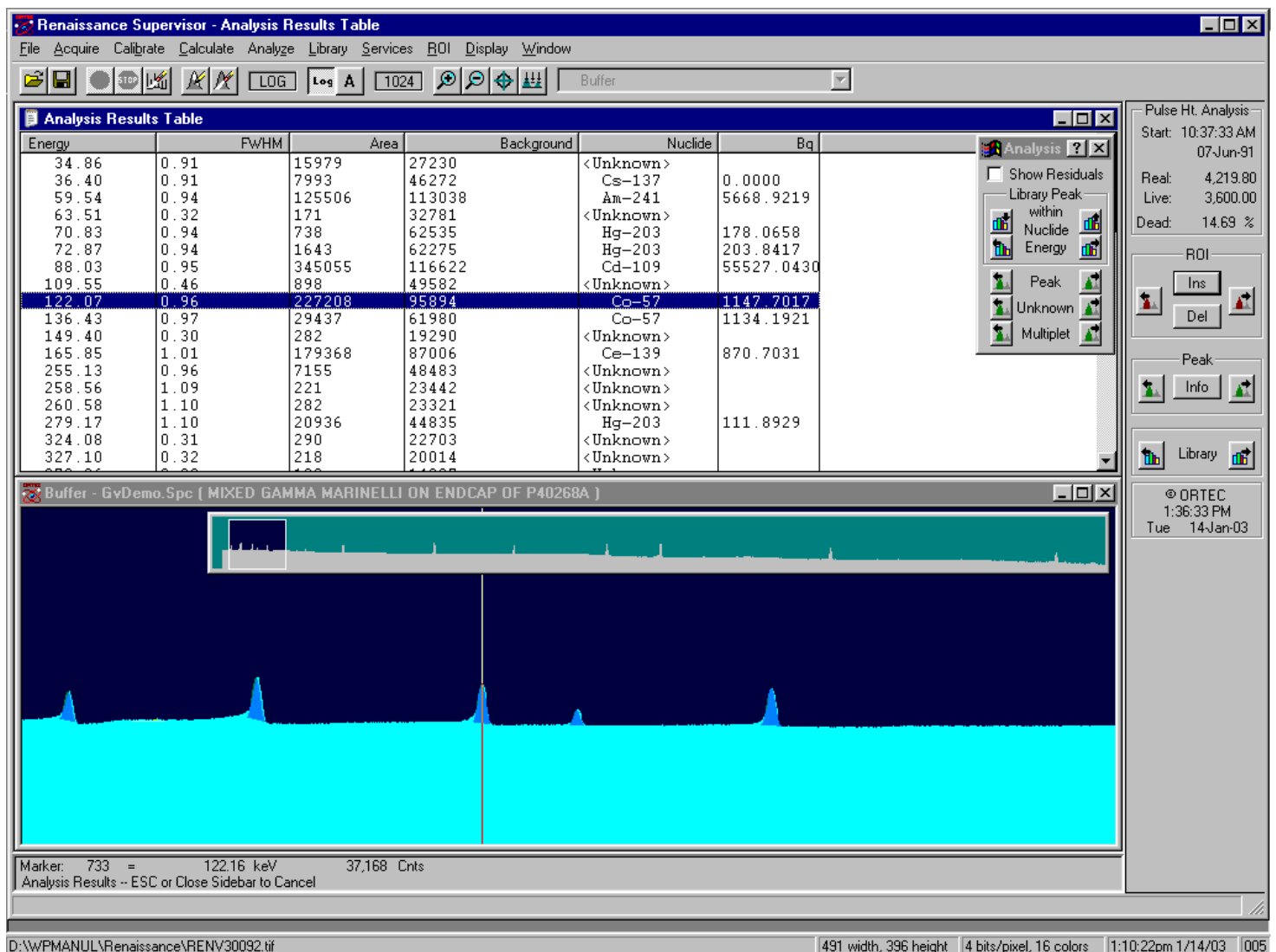
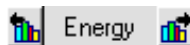


Figure 139. Display from .UFO File.



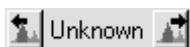
The **within Nuclide** buttons move up/down the library list for the selected nuclide, in the order the energies are stored in the library. Since the library energies are not usually stored in increasing energy order, this will cause the marker to jump about the spectrum. This is useful in deciding if a nuclide is present or not, by looking for all the lines associated with the nuclide. If the selected peak has a zero area, it is not displayed.



The **Energy** buttons move the cursor up/down through the library peak list in energy order. Only non-zero-area peaks are shown. Since the library used for the analysis may not be the same as the working library, this may be a different set of peaks than found with the **Library** buttons on the Status Sidebar.



The **Peak** buttons move the marker up/down through all the peaks in the spectrum. This includes non-zero-area library peaks and unknown peaks above the peak-search sensitivity cutoff.



The **Unknown** buttons move the marker up/down through the unknown peaks that satisfy the sensitivity cutoff, in energy order, skipping over any library peaks.



The **Multiplet** buttons move up/down through the multiplet or deconvoluted regions in the spectrum. The multiplet up button goes to the first (lowest-energy) peak of the next higher multiplet. Similarly, the multiplet down button goes to the last (highest-energy) peak of the next lower multiplet.

To look at individual peaks in the multiplet, use the **Peak**, **Energy**, or **Unknown** buttons.

The **ROI**, **Peak**, and **Library** buttons on the Status Sidebar are also active.



Figure 140.
Analysis Results
Sidebar.

Marking the **Show Residuals** check box adds a line beneath the spectrum that displays the difference between the actual spectrum and the calculated spectrum based on the analysis and the calibration peak shape. An example is shown in Fig. 141.

Figure 139 shows the Analysis Results Table window. The table records can be sorted by any parameter (e.g., energy, area, nuclide, FWHM) by clicking on the desired column header.

The Analysis Sidebar control menu is shown in Fig. 142 (click the title bar icon to open the menu). Mark or unmark **Table** to show or hide the Analysis Results Table; use **Print** on the results window's control menu to print the table as displayed (note that this is not the same as the complete report described in Chapters 6 [Ge] and 7 [NaI]).

When the Analysis Results Table is displayed and Renaissance is in interactive-analysis mode, more details can be displayed for any peak by double-clicking on that peak in the table. This opens a **Details** window, as shown in Fig. 143. Use the **Peak** buttons to step to the next-highest-energy and next-lowest-energy peaks. Click on **Close** or press <Esc> to exit.

The **Details** window shows the following peak information, derived from the .UFO file structure (see the *File Structure Manual*):

Energy	The library peak energy in keV, or the centroid energy for unknown peaks.
Centroid	The peak centroid energy from the spectrum.
Center	The peak centroid channel from the spectrum.
mlo, mhi	The low and high channel numbers for the peak region. These are the beginning and end channel numbers for the background region around a single peak. See also multilo, hi .

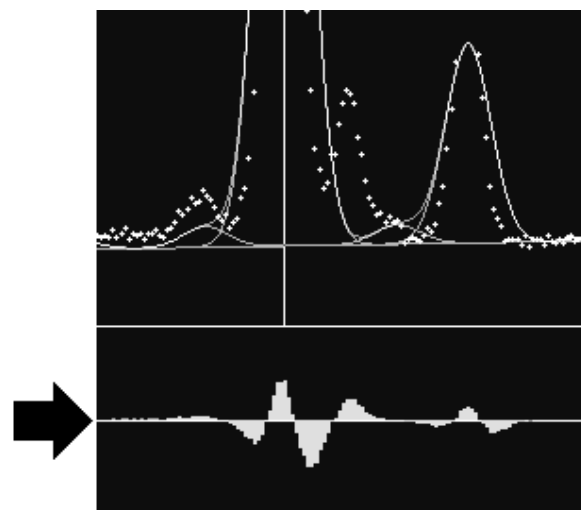


Figure 141. Spectrum Residuals Display (arrow).



Figure 142. Analysis Sidebar Control Menu.

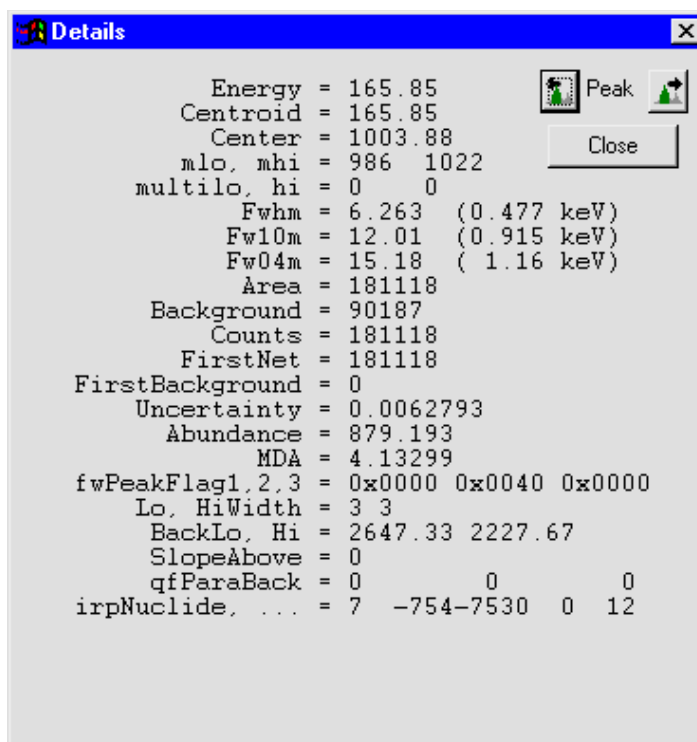


Figure 143. UFO Peak Record Description.

- multilo, hi** The low and high channel numbers for the multiplet region. These are the beginning and end channel numbers for the background region around the entire multiplet. All peaks in the multiplet will have the same **multilo, hi** values.
- Fwhm** The full width at half maximum of the peak. It is a measured value for single peaks and a calculated value for peaks in a multiplet region.
- Fw10m** The full width at tenth maximum of the peak. It is a measured value for single peaks and a calculated value for peaks in a multiplet region.
- Fw04m** The full width at twenty-fifth maximum of the peak. It is a measured value for single peaks and a calculated value for peaks in a multiplet region.
- Area** The corrected net area of the peak. For example, the PBC correction could be applied to this number.
- Background** The corrected peak background calculated by the program.
- Counts** The uncorrected net area of the peak.

FirstNet	The net area of the peak calculated on the first pass through the spectrum.
FirstBackground	The peak background calculated by the program on the first pass through the spectrum.
Uncertainty	The 1-sigma counting uncertainty in the peak net area, as a fraction.
Abundance	The activity for this nuclide based on this peak only. It is zero for unknown peaks or if there is no efficiency calibration.
MDA	The minimum detectable activity for this nuclide based on this peak only. It is zero for unknown peaks or if there is no efficiency calibration.
fwpeakflag1,2,3	The peak flags described in the <i>File Structures Manual</i> as hexadecimal numbers.
Lo, HiWidth	The number of channels used in the calculation of the background below and above the peak. If the background selection is set to a given number, then these will both be the same. For auto background, these can be different.
BackLo, Hi	The calculated background values used to calculate the background.
SlopeAbove	The slope of the background above the peak.
qfParaBack	The parabolic factors for calculating the background. If the parabolic background has not been used, these are 0.
irpNuclide, ...	The pointers to other records in the .UFO file as described in the <i>File Structures Manual</i> . They are only used in debugging.

To step to the next peak higher or lower in energy, click on the **Peak** buttons. When finished viewing, click on **Close**.

5.5.4. Interactive in Viewed Area...

This selection starts an interactive analysis session for analyzing the spectrum now displayed, and functions only for display widths ≤ 4096 channels. The working library selected with **Library/Select File...** is used. The analysis parameters have been set in the **Analyze/Settings/Sample Type...** dialogs.

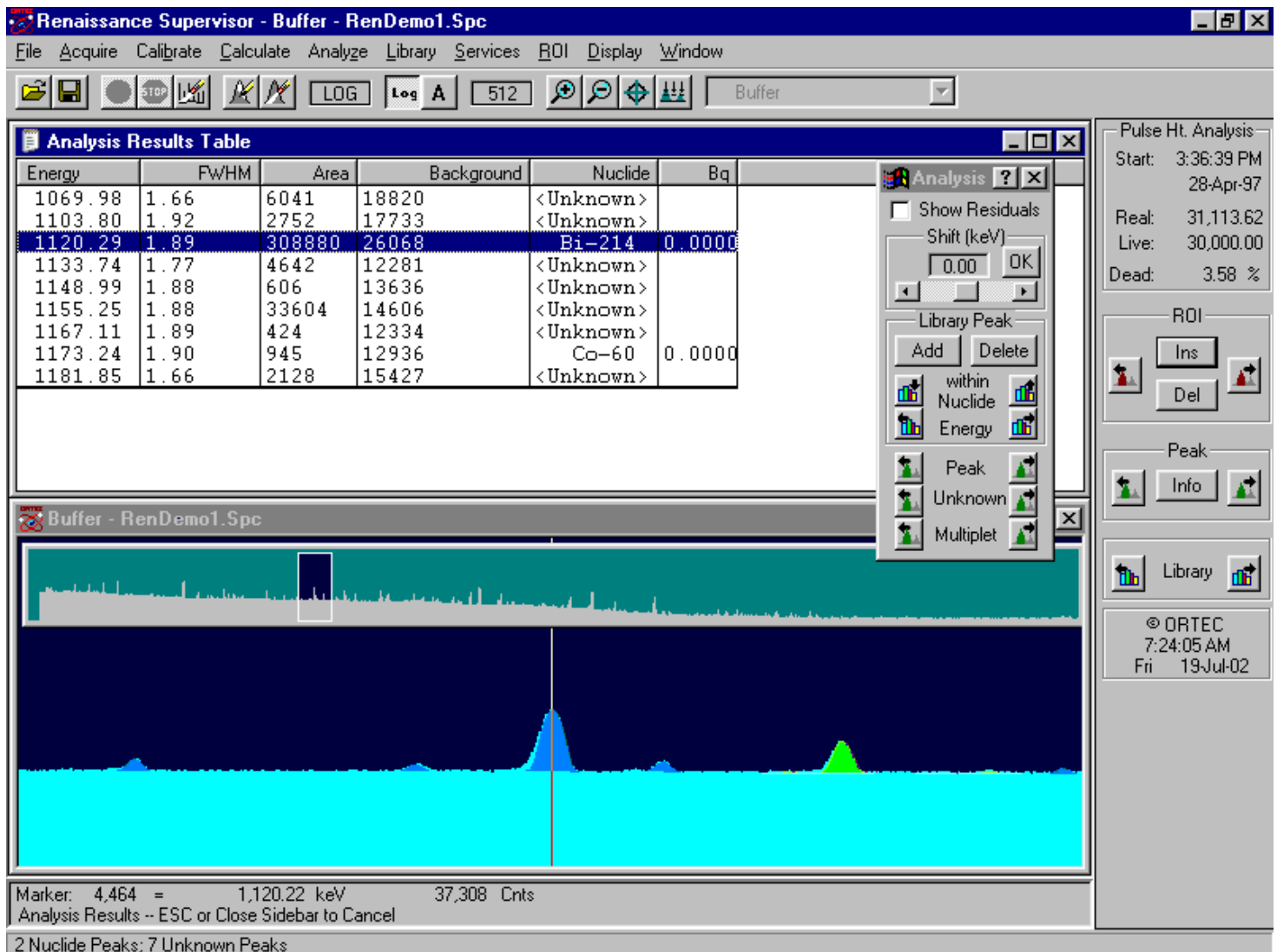


Figure 144. Results Interactive in Viewed Area.

When the analysis is complete, the graphical results and peak area table are displayed as illustrated in Fig. 144. The table records can be sorted by such parameters as energy, area, FWHM, and background by clicking on the desired column header.

Figure 145 shows the interactive Analysis Sidebar. The buttons move the marker up and down through the results lists, library, and spectrum simultaneously.

The buttons in the **Library Peak** section pertain to the results from the analysis; the other buttons pertain to the spectrum. The peak-found buttons

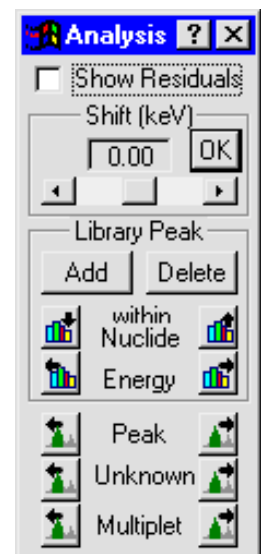
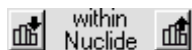
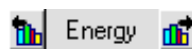


Figure 145.

move to the next higher or lower peak in the analysis results list. This includes non-zero-area library and unknown peaks above the cutoff. See **Peak** button below.



The **within Nuclide** buttons move up and down the library list for the selected nuclide, in the order the energies are stored in the library. Since the library energies are not usually stored in increasing energy order, this will jump the marker around in the spectrum. This is useful in deciding if a nuclide is present or not, by looking for all the lines associated with the nuclide. Only non-zero-area peaks are displayed.



The **Energy** buttons move the marker up and down through the library peak list in energy order. Only non-zero-area peaks are shown. Since the library used for the analysis may not be the same as the working library, this may be a different set of peaks than found with the **Peak** buttons.



The **Peak** buttons move up and down through the peaks found by the on-line peak search. (The sensitivity is set in the system settings.) This may select more peaks than the analysis peaks above because of the difference in the cut-off. If the sensitivity for analysis is low, e.g., 5%, many peaks will not be reported because their uncertainty is too high. They will have been found by the analysis, but not reported.



The **Unknown** buttons move the marker up and down through the unknown peaks in energy order, skipping over any library peaks. Only peaks that satisfy the sensitivity cutoff are shown. Note that the **Library Peak** and **Unknown** buttons select different groups of peaks.



The **Multiplet** buttons move up and down through the multiplet or deconvoluted regions in the spectrum. The next time the multiplet up button is clicked, the marker goes to the first (lowest-energy) peak of the next-higher multiplet. The next down button goes to the last (highest-energy) peak of the next-lower multiplet. To look at individual peaks in the multiplet, use the **Peak**, **Energy**, or **Unknown** buttons.

To add a peak to the analysis library, position the marker at the desired location and click on **Add**. This adds a temporary nuclide to the library (assigned the name “**Analyze**” in the results table) with a peak at this energy. A new analysis is performed and the new results are displayed. More peaks can be added as needed.

To delete a peak, click on the peak energy in the Analysis Results List. The marker will jump to this channel in the spectrum. Click on **Delete**. A new analysis is performed and the new results are displayed.

The energy calibration for all the peaks in the spectrum can be shifted with the **Shift (keV)** field and slide bar (Fig. 146). Select the amount of shift and click on **OK**. The shift increments in energy equivalent to 0.1 channel. Renaissance will perform the new analysis and display the results.

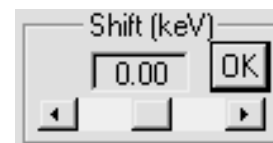


Figure 146. Shift keV.

The residuals are the differences between the calculated spectrum (based on peak shape, peak area, and background) and the actual raw data. These can be displayed in the spectrum window by marking the **Show Residuals** checkbox (refer to Fig. 141). The scaling factor for the residual display is the same as for the data display. In log mode, the scale of the residuals display is somewhat exaggerated and the residuals might appear more significant than they actually are.

The results of this analysis are stored in memory and can be stored as a **.UFO** file on disk by selecting **Store Results As...** from the Analysis Sidebar control menu (see Fig. 140). Mark/unmark the **Table** item to show/hide the Analysis Results Table. Use the **Print** command in the results window control menu to print the results table.

5.6. Library

The **Library** menu is shown in Figure 147. The **Library** commands select, display, create, edit, or print the library files used in the **Analyze** and **Calibrate** sections, with either the GammaVision library editor discussed here or the NuclideNavigator III library editor, if NuclideNavigator is installed. Library files are organized by nuclide, then by the nuclide peaks.

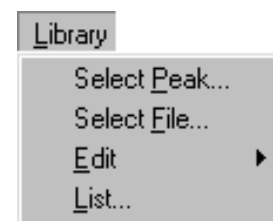


Figure 147. Full Library Menu.

The nuclide library is used with reference to the peak-search or report functions for quantitative identification of and activity calculations for spectral components according to calibrated peak energy. The nuclide library data include the nuclide name, half-life, and half-life uncertainty. The nuclide names can be any combination of eight characters, but must be consistent throughout all files. The library peak data include the energies and branching ratio or gammas/disintegration for each energy. The default file extension is **.LIB**.

At startup, Renaissance automatically attempts to load the library last loaded. Thereafter, this *internal* (or *working*) library can be replaced at any time with **Library/Select File...** The library stays resident in memory after it has been loaded.

In the analysis report, the nuclides are listed according to their order in the library file.

5.6.1. General Guidelines for Renaissance Libraries

- For NaI analysis, the libraries should be as uncomplicated as possible with few interferences. Calibration libraries for NaI should normally include only the primary nuclide peaks.
- All libraries (Ge or NaI analysis) should normally contain energy peaks within the range of calibration. Peaks outside the calibration range might not generate accurate results because of calibration error at that energy. Erroneous results could place the entire analysis report in question due to possible peak shifting error, interference corrections, etc.

5.6.2. Select Peak...

This opens a window containing a list of the library peaks in energy order (Fig. 148). This list shows the nuclide name, energy, gammas/100 disintegrations, and half life. Clicking any field moves the marker line to that energy in the spectrum.

The Library List can be sorted by nuclide, energy, percent, or half life by clicking the desired column header.

5.6.3. Select File...

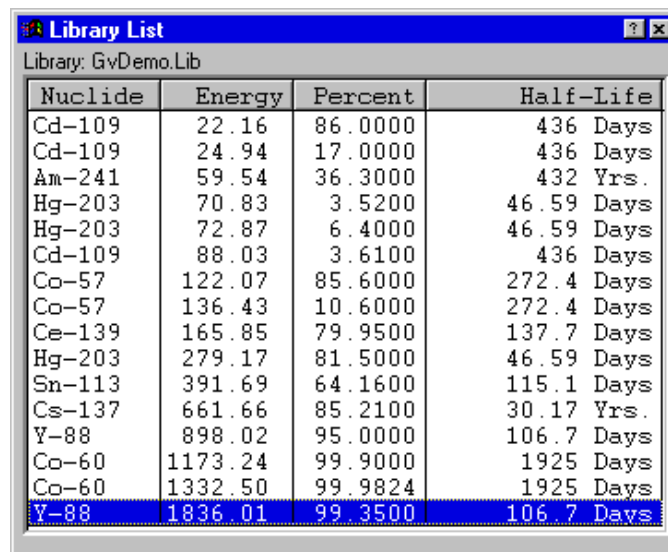
This opens the **Load Library File** dialog.

If a library has already been selected, it is

shown in the **File name:** field. Select the desired disk and filename and click on **Open**. This library becomes the working library. The Renaissance analysis requires the .LIB format.

5.6.4. Edit...

Use this command to create a new library file or change the contents of an existing library file. Select the **GammaVision Editor...** or **Nuclide Navigator...** (if NuclideNavigator III is installed). The GammaVision library editor is discussed here; the Nuclide-Navigator editor is described in the NuclideNavigator III user manual.



Nuclide	Energy	Percent	Half-Life
Cd-109	22.16	86.0000	436 Days
Cd-109	24.94	17.0000	436 Days
Am-241	59.54	36.3000	432 Yrs.
Hg-203	70.83	3.5200	46.59 Days
Hg-203	72.87	6.4000	46.59 Days
Cd-109	88.03	3.6100	436 Days
Co-57	122.07	85.6000	272.4 Days
Co-57	136.43	10.6000	272.4 Days
Ce-139	165.85	79.9500	137.7 Days
Hg-203	279.17	81.5000	46.59 Days
Sn-113	391.69	64.1600	115.1 Days
Cs-137	661.66	85.2100	30.17 Yrs.
Y-88	898.02	95.0000	106.7 Days
Co-60	1173.24	99.9000	1925 Days
Co-60	1332.50	99.9824	1925 Days
Y-88	1836.01	99.3500	106.7 Days

Figure 148. Library List Dialog.

Figure 149 shows the GammaVision library Editing dialog. The control menu is shown in Fig. 150 (click on the title bar icon to open it); it contains several of the commands necessary to create and edit the .LIB files.

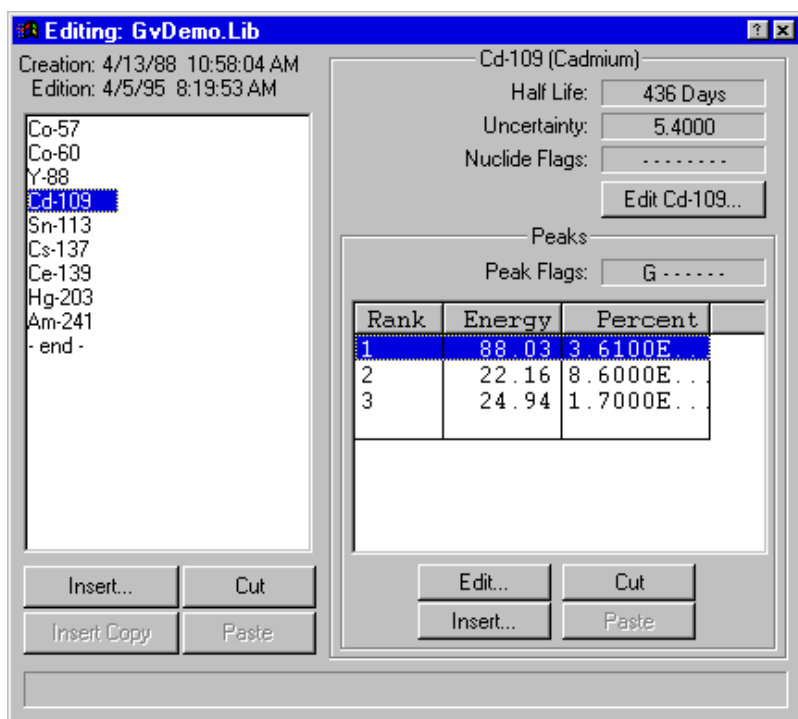


Figure 149. Editing Library Dialog.



Figure 150. Library Edit Dialog Control Menu.

5.6.4.1. Copying Nuclides From Library to Library

To copy nuclides from one library to another library — for example, to make a working library from a master library — click on the **Edit** window control menu and select **Show Master Library**. This will open a file selection dialog. Choose the desired disk and file and click on **Open**. Both libraries will be displayed side by side, as illustrated in Fig. 151.

To copy a nuclide from the master library to the working library: Go to the master library list and click once on the nuclide of interest. This will activate the gray **Insert Copy** button at the bottom of the Editing dialog's nuclide list, and change its label to **Insert** plus the name of the nuclide. Now, in the Editing dialog, locate the nuclide immediately below the desired insertion position, click on it once, then click on **Insert [nuclide name]**. This will insert the nuclide and display its peak list on the right.

Double-clicking on a nuclide in the master library will add it to the working library, inserting it immediately above the currently highlighted nuclide in the list.

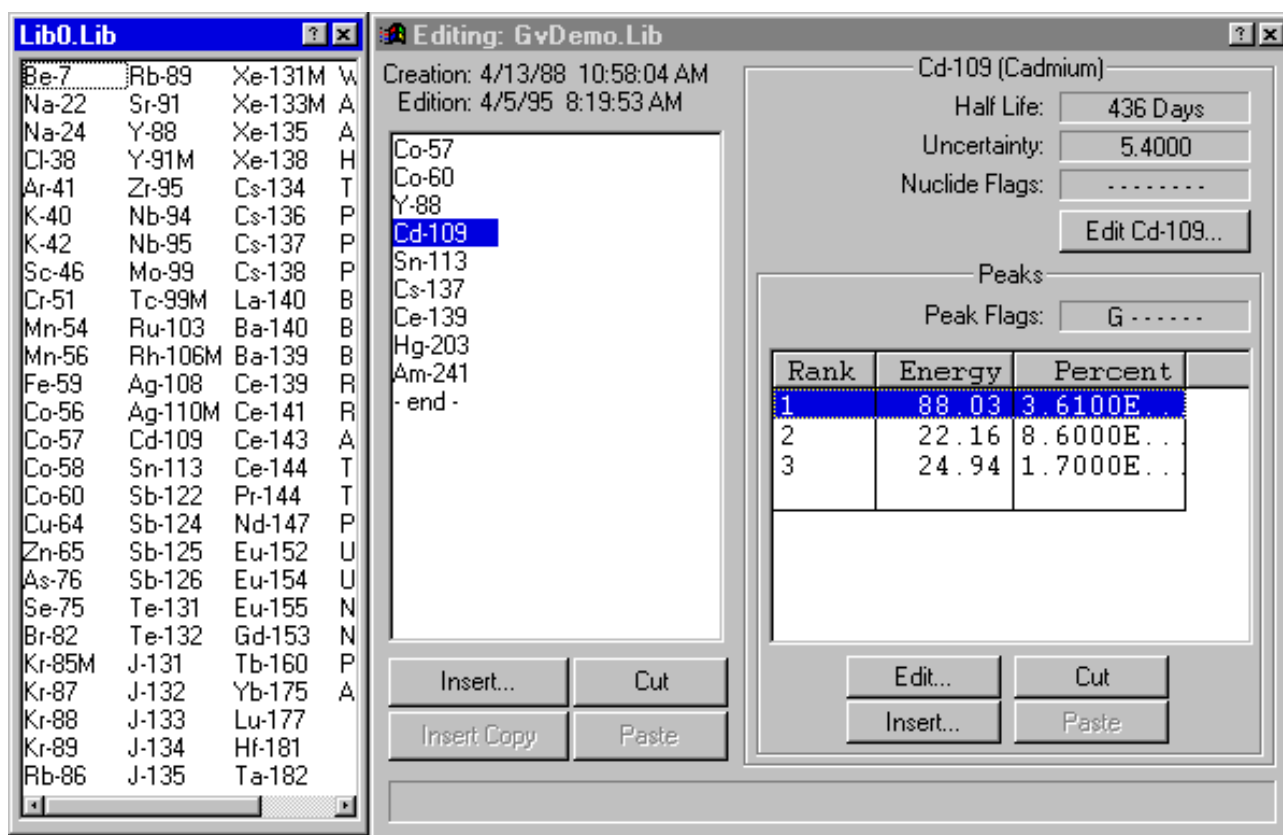


Figure 151. The Master Library (left) and Library Editing Dialog (right).

5.6.4.2. Creating a New Library Manually

Open the control menu and click on **New**. This will clear the Editing dialog so nuclides can be entered manually. Click on the **Insert...** button to open the Insert Library Nuclide dialog, shown in Fig. 152. Enter the **Nuclide Name** and **Half Life** and click on **OK**.

Now, at the bottom of the (right-hand) peak list, click on **Insert...** to open the Edit Library Peak dialog (Fig. 156). Enter the energy of the gamma ray and the branching ratio of the peak.

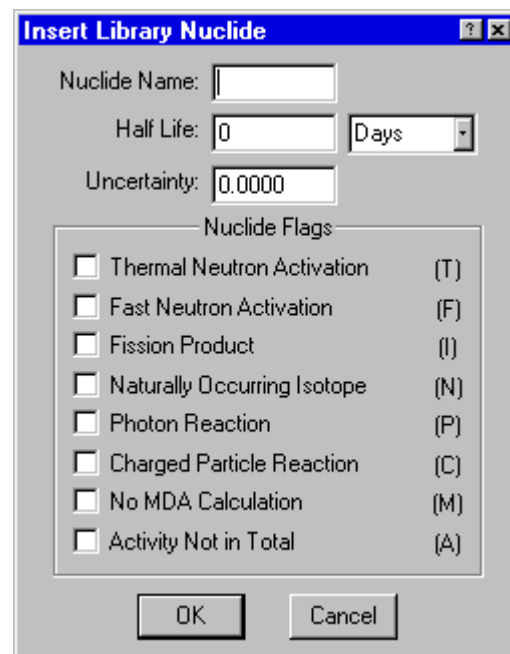


Figure 152. Insert a Nuclide into a Library.

5.6.4.3. Editing Library List Nuclides

To edit the information about a nuclide in the working library:

Click on the nuclide to highlight it. The **Edit...** button (in the upper right of Fig. 149) will change to **Edit** plus the name of the nuclide, as shown in Figure 153.



Figure 153. Ready to Edit this Nuclide.

Click on **Edit [nuclide]...** This will open the Edit Library Nuclide dialog (Fig. 154). The **Nuclide Name**, **Half Life**, **Uncertainty**, and **Nuclide Flags** will already be listed.

The **Uncertainty** is a single number that represents the uncertainty (2 sigma or 95% confidence level) in the values entered for this nuclide. It is added in quadrature to form the total uncertainty on the final report. The **Uncertainty** value should be taken from the nuclear data sheet for this nuclide. The default is zero, but 2% is a realistic number.

The first six **Nuclide Flags** are used to show how the nuclide was produced. For example, **Thermal Neutron Activation (T)** indicates that this nuclide is produced when the parent nuclide absorbs a slow neutron. This can be helpful in organizing reports by nuclide category. More than one flag can be marked. Libraries produced with NuclideNavigator II or later versions will already have these flags set. For other libraries, it will be necessary to consult a reference for the proper settings.

Figure 154. Edit or Manually Add Nuclide Name.

The **No MDA Calculation** flag indicates that the nuclide will not be reported unless present in the spectrum. If this is not marked, the MDA value will be printed if the nuclide is not present in the spectrum.

The **Activity Not in Total** flag indicates that the activity for this nuclide will not be included in the total activity for this sample.

These flags are listed on the report and saved in the .UFO file.

Manually Adding Nuclides

To manually add a nuclide to the library list, locate the nuclide immediately *below* the desired insertion position, and click once to highlight it. Next, click on the manual **Insert...** button to open the Edit Library Nuclide dialog. The dialog will be blank. Fill in the name and half life as well as any other inputs and click on **OK**.

Deleting Nuclides from the Library

To remove a nuclide from the library, click on the nuclide, then on **Cut**. This will remove the nuclide from the list. In addition, it will activate the gray **Paste** button at the bottom of the nuclide list, and change its label to include the name of the cut nuclide. This is illustrated for ^{152}Eu in Fig. 155.



Figure 155. Cut Nuclide is Ready to Paste.

Rearranging the Library List

The order of the nuclides in the library is the order in which they are listed on the report. Nuclides can be rearranged in the `.LIB` file list by cutting and pasting them into a different location. To move a nuclide to a new position in the list, highlight the nuclide to be moved; **Cut** it from the list; locate the nuclide immediately below the desired new position and click once on that nuclide to highlight it; then click on the **Paste** button (which will be labeled with the name of the **Cut** nuclide). The **Cut** nuclide will be inserted in the space above the highlighted nuclide.

Several nuclides can be cut at one time from the list, then pasted back into the list into a different order. Cut nuclides remain queued up for pasting, last one first, according to the nuclide name on the **Paste** button.

To move a nuclide to the end of the library list, **Cut** the nuclide from the list, highlight the `--end--` entry, and click on the **Paste** button.

Editing Nuclide Peaks

When a nuclide is selected in the working `.LIB` file, the right half of the Editing dialog shows the peak list. Note the column headers, **Rank**, **Energy**, and **Percent**. To sort the peak list by a particular parameter in the list, click on the appropriate header.

To edit a peak, either double-click on the peak in the right-hand list, or click once on it, then click on the **Edit** button. This will open the Edit Library Peak dialog (Fig. 156). The **Energy (keV)**, **Gammas per 100 Disintegrations**, **Photon Flags**, and **Peak Flags** will already be listed.

The **Photon Flags** are used to show the origin of the peak. Only one can be selected at a time.

Gamma Ray (G) and **X-Ray (X)** mean the peak energy is due to a nuclear or atomic transition, respectively. **Positron Decay (P)** is used for the 511-keV peak. **Single-Escape (S)** peaks are peaks for which a single 511-keV photon has escaped the detector. This can only occur for full-energy peaks above 1.022 MeV. **Double-Escape (D)** peaks are peaks for which two 511-keV photons have escaped the detector. Both single- and double-escape peaks are broader than gamma-ray peaks. Neither can be used for activity calculations because the intensity of the peak is not related directly to the intensity of the full-energy peak. Nonetheless, these can be included in the library to account for the peak in the spectrum.

The **Not In Average (A)** flag in the **Peak Flags** section of the dialog should be set for these peaks. All the peaks marked as **Key Line (K)** must be present before the nuclide will be listed as present on the report. If no lines are marked as key lines, the nuclide will be listed as present if the first line is in the spectrum.¹⁸

Some old libraries could have these flags set in an unwanted manner. These libraries should be checked before use.

Adding Nuclide Peaks

To add a peak: Click on the peak just below the desired insertion point in the peak list, then click on **Insert...** This will open the Edit Library Peak dialog; all the fields will be blank. Enter the necessary information for the peak and click **OK**.

Rearranging the Peak List

The entries in the peak list can be rearranged with the **Cut** and **Paste** buttons. Several peaks can be cut at one time from the list, then pasted back into the list into a different order. Cut peaks remain queued up for pasting, last one first. Each relocated nuclide will retain its energy and counts/sec values, but will be assigned a **Rank** number according to its new position. Click on the peak just below the desired insertion point in the peak list, then click **Paste**.

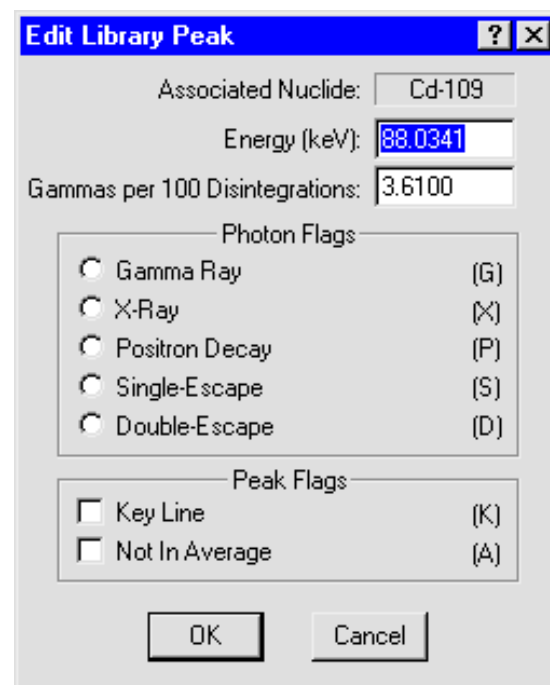


Figure 156. Edit or Manually Add Library Peak Values.

¹⁸To duplicate the operation of older versions of Renaissance, mark either no lines or only the first line as a key line.

5.6.4.4. Saving or Canceling Changes and Closing

To save this modified .LIB file and use it as the working file, click on the control menu, then **Save Library As...** Either use the current filename (which will overwrite the previous values) or assign a new filename, then click on **Save**. (Renaissance will assign the default .LIB extension.) To exit the edit session, click on the control menu, then **Close**.

To abandon any changes and restore the .LIB file to its condition before editing, click on the control menu, then **Close**. A dialog will open asking if the changes should be saved; select **No**.

5.6.5. List...

The **List...** function (Fig. 157) will print a list of the library, ordered either by **Nuclide** or **Energy**, to either the printer or a disk file.

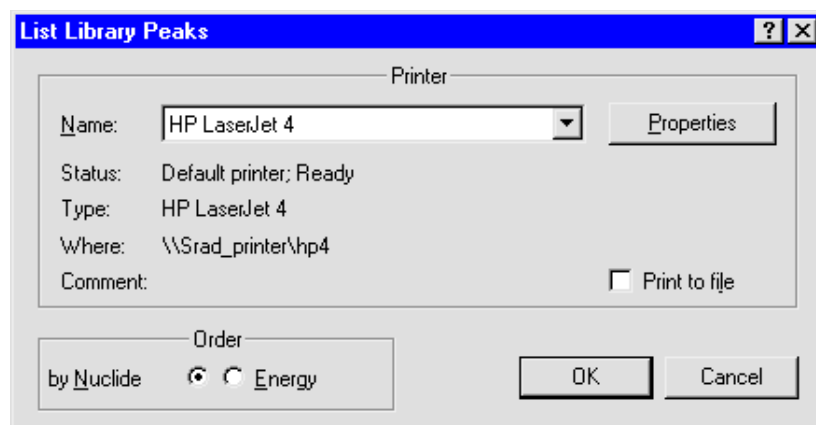


Figure 157. Print Library to Printer or File.

5.7. Services

The **Services** menu contains several functions and utilities is shown in Fig. 158.

5.7.1 Switch to Default Menu

This switches the menus to the default menu system. The default menus contain the most commonly used functions. In the default menu, this command changes to **Switch to Full Menu**.



Figure 158. Full Services Menu.

5.7.2. JOB Control...

Most of the functions under the various Renaissance menus can be automated by writing a JOB, which consists of one or more commands written in ASCII text (see Chapter 12 for an in-depth discussion). JOBS can easily perform repetitive tasks and/or define initial conditions at Detector startup. These files are given a file-name extension of .JOB. To start a JOB or edit a .JOB file, select **Services/Job Control...** to display the dialog shown in Fig. 159.

To run a JOB, select a .JOB filename and click on **Open**. The contents of the selected file can be displayed at the bottom of the dialog by using the mouse to mark the **Show Contents** checkbox.

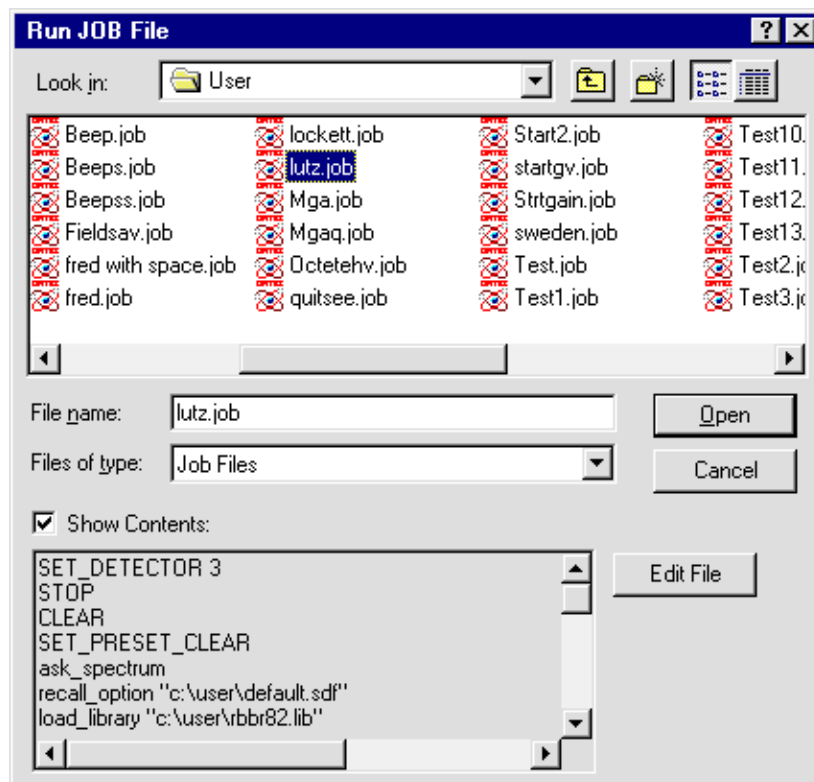


Figure 159. Run or Edit Job File.

Once a JOB is started, most menu functions will be disabled (grayed) to prevent interference with the running JOB. The .JOB file name will be displayed in the window title. Only one JOB can be active at a time. A single JOB can operate with more than one Detector. To run more than one JOB at a time, run multiple copies of Renaissance.

If you try to start another JOB while a JOB is already running, the dialog shown in Fig. 160 will be displayed, showing the name of the current JOB. In this case, the only options available are to terminate execution of the running JOB (click on **Terminate Job**) or allow the JOB to continue (click on **Close** or press <Esc>).

To edit a .JOB file from this dialog (whether or not **Show Contents** is activated), select a file from the list and click on the **Edit File** button. This will open the Windows Notepad text editor with the .JOB file loaded.

NOTE When editing is complete, save the file in Notepad (select **Save** or **Save As** under Notepad **File** menu) or any changes made will be lost. When Notepad is closed (**File/Exit**), the newly edited file will be shown in the **Show Contents** list box.

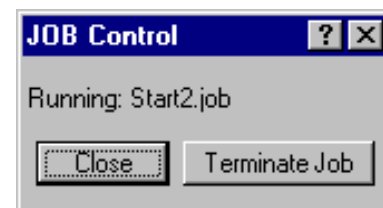


Figure 160. Terminate Job?

If a JOB terminates prematurely because of some error condition, a message box briefly explaining the cause of the error will be displayed. More details on the error can be found by cross-referencing with the error message directory in Appendix D.

5.7.3. Database Management

Figure 161 shows the **Database Management** submenu. These commands allow you to select the database to be used for the results, create a new database for use in either the Supervisor or Operator program, or purge (permanently delete) records from the selected database.

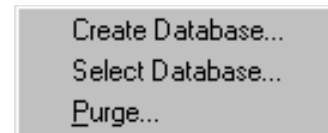


Figure 161. Database Management Submenu.

Each Renaissance database holds analysis results as well as alarm limits and attenuation coefficients. The library, calibration, and PBC file paths are stored in the spectrum files, not in the database. If the files referenced in a particular spectrum file — that is, the files used for the original analysis — are changed, different results might be generated if the spectrum is reanalyzed. In most cases, the library and calibration should not be adversely changed, but the PBC might be undesirably affected. For this reason, we generally recommend that the analysis options be set to use the **Internal** PBC file but specific library and calibration file overrides.

5.7.3.1. Create Database...

This command allows you to establish separate databases for different subject groups, such as employees, contractors, client origin, training, and testing.

Renaissance databases can only be created with this command, which opens the dialog shown in Fig. 162. All tables and item names are automatically set up, and the basic attenuation entries added. Any special additions, such as new attenuation materials and alarm limits, must be added manually to the new database.

To create a new database, simply browse to the folder in which the new database will be located, assign a new filename, and click on **Save**.

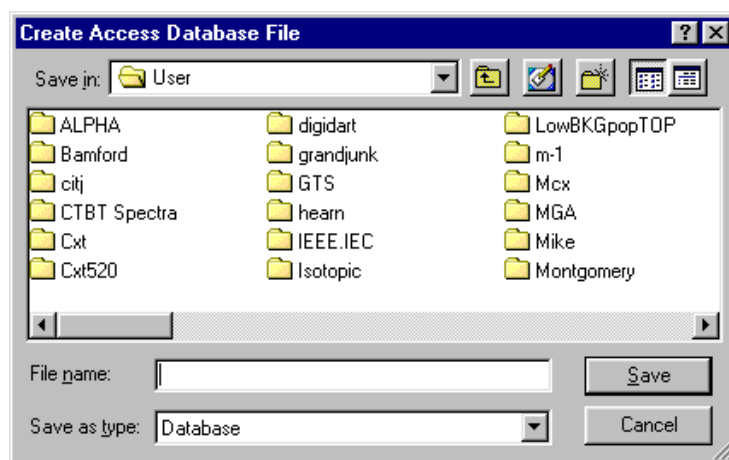


Figure 162. Create a New Database.

NOTE When you create a new database, it is automatically selected as the target database for the Supervisor program. To choose another database, use the **Select Database...** command below.

5.7.3.2. Select Database...

This function (Fig. 163) lets you select a new database for use in the Supervisor program. (The target database for Operator is determined by the .OPR file [Scan Type] the operator is using.) Note that attenuation materials and alarm limits are included in the database, and can be different for each database.

5.7.3.3. Purge...

This function displays the contents of the Renaissance database as shown in Fig. 164. All of the scans in the database are displayed by Scan ID. Also shown is the spectrum filename(s) for each scan.

This is one way to determine the spectrum filenames for a scan if the printed report is not available. Unwanted scans can be removed by selecting the scan and clicking on **Delete**. This will delete the data, but the disk space will not be recovered unless you mark the **Compress the database when the Supervisor program is closed** checkbox. The database will then be compacted to recover the space from deleted scans when you exit Renaissance Supervisor.

NOTE *There is no undo for a deletion. Before deleting any scans from the database, we strongly recommend that you make a backup copy of your database!*

Scans are listed in ascending order (oldest scan first) according to ID. To reverse the sort, mark the **Most recent scan first** checkbox. By default, only the short spectrum filenames are listed. To display the complete path and filename for each scan, unmark the **Short file name** box.

To remove a scan from the database, click on the scan to highlight it, then click on **Delete**. To remove more than scan at a time, use **<Shift + Left-click>** to highlight a contiguous block of scans or **<Ctrl + Left-click>** to highlight several different scans, then click on **Delete**.

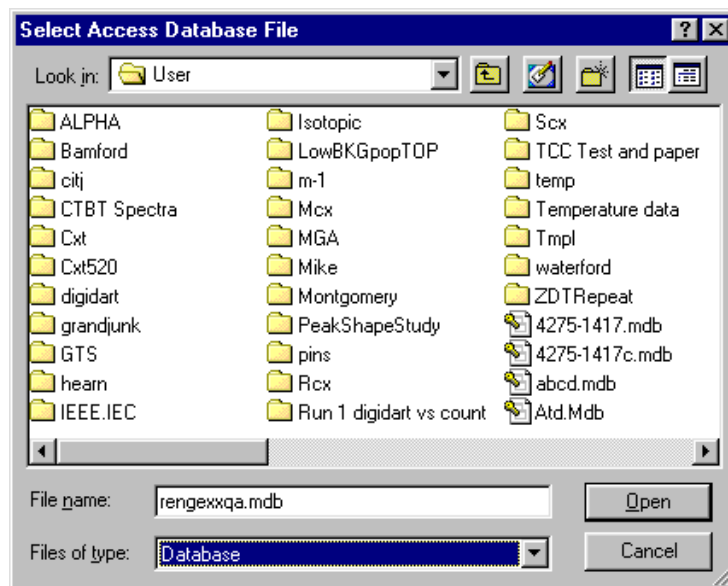


Figure 163. Select a Database.

ID	Subject	Date	Spectra
1	Able, A	7/2/03 3:26:42 PM	Able, A BAMBAM2 MCB 512 Ren00002.An1
2	Baker, B	7/2/03 3:27:21 PM	Baker, B QUI MCB 514 Ren00003.An1
3	Cain, C	7/2/03 3:27:50 PM	Cain, C QUI MCB 513 Ren00003.An1
4	Able, A	7/2/03 3:37:35 PM	Able, A QUI MCB 514 Ren00004.An1
5	Able, A	7/2/03 3:38:59 PM	Baker, B QUI MCB 513 Ren00004.An1 Able, A QUI MCB 514 Ren00005.An1
6	Able, A	7/2/03 3:38:59 PM	Baker, B QUI MCB 513 Ren00004.An1 Able, A QUI MCB 514 Ren00005.An1
7	Cain, C	7/2/03 3:39:07 PM	Cain, C BAMBAM2 MCB 512 Ren00003.An1
8	Able, A	7/2/03 5:25:24 PM	Able, A BAMBAM2 MCB 512 Ren00004.An1
9	Able, A	7/2/03 5:26:18 PM	Able, A BAMBAM2 MCB 512 Ren00005.An1
10	Baker, B	7/2/03 5:44:16 PM	Baker, B BAMBAM2 MCB 512 Ren00005.An1
11	Baker, B	7/2/03 5:45:02 PM	Baker, B BAMBAM2 MCB 512 Ren00006.An1
12	Baker, B	7/2/03 6:07:13 PM	Baker, B QUI MCB 514 Ren00006.An1 Baker, B BAMBAM2 MCB 512 Ren00007.An1...
13	Cain, C	7/2/03 6:16:39 PM	Cain, C QUI MCB 514 Ren00007.An1 Cain, C BAMBAM2 MCB 512 Ren00008.An1 C...
14	Able, A	7/2/03 6:20:14 PM	Able, A QUI MCB 514 Ren00008.An1 Able, A BAMBAM2 MCB 512 Ren00009.An1 A...
15	Able, A	7/2/03 6:22:43 PM	Able, A QUI MCB 514 Ren00009.An1 Able, A BAMBAM2 MCB 512 Ren00010.An1 A...
16	Baker, B	7/2/03 6:27:51 PM	Baker, B QUI MCB 514 Ren00010.An1 Baker, B QUI MCB 513 Ren00008.An1
17	Able, A	7/3/03 2:47:09 AM	Able, A Sum Ren00112.An1 Able, A QUI MCB 514 Ren00000.An1 Able, A QUI MCB...
18	Baker, B	7/3/03 2:47:49 AM	Baker, B Sum Ren00113.An1 Baker, B BAMBAM2 MCB 512 Ren00011.An1 Baker, B...
19	Baker, B	7/3/03 2:52:00 AM	Baker, B Sum Ren00114.An1 Baker, B QUI MCB 514 Ren00001.An1 Baker, B QUI ...
20	Baker, B	7/3/03 2:55:11 AM	Baker, B Sum Ren00115.An1 Baker, B BAMBAM2 MCB 512 Ren00012.An1 Baker, B...
21	Baker, B	7/3/03 2:59:39 AM	Baker, B Sum Ren00116.An1 Baker, B BAMBAM2 MCB 512 Ren00013.An1 Baker, B...
22	Fox, P F	7/3/03 9:10:18 AM	Fox, P F QUI MCB 514 Ren00006.An1 Fox, P F QUI MCB 513 Ren00004.An1
23	Fox, P F	7/3/03 9:25:55 AM	Fox, P F QUI MCB 514 Ren00007.An1 Fox, P F QUI MCB 513 Ren00005.An1
24	Fox, P F	7/3/03 9:27:48 AM	Fox, P F Sum Ren00117.An1 Fox, P F QUI MCB 514 Ren00008.An1 Fox, P F QUI MCB ...
25	Fox, P F	7/3/03 9:30:39 AM	Fox, P F QUI MCB 514 Ren00009.An1 Fox, P F QUI MCB 513 Ren00007.An1
26	Fox, P F	7/3/03 9:32:07 AM	Fox, P F Sum Ren00118.An1 Fox, P F QUI MCB 514 Ren00010.An1 Fox, P F QUI MCB ...

Options: Most recent scan first Short file name

Buttons: Delete, Exit

Figure 164. The List of Scans in the Database.

To close the dialog, click **Exit**.

5.7.4. Change Password...

This command allows you to protect the Supervisor program with a password so that it will only operate when the correct password is entered on startup. If no password is set, the Password dialog will not be displayed on startup.

To set a password, enter the **Password** (see Fig. 165) and confirm the entry in the **Verification** field (the two entries must agree). Click on **OK**. The password is not case-sensitive (that is, uppercase and lowercase letters are treated the same).

The dialog box is titled "Password for 'Renaissance Supervisor'". It contains two text input fields: "Password:" and "Verification:". To the right of the "Password:" field is an "OK" button, and to the right of the "Verification:" field is a "Cancel" button.

Figure 165. Create a Supervisor Password.

To remove the password, select this command and make *no entry* in the two fields (do not enter blanks), then click on **OK**.

NOTE *There is no master password.* If the password is lost, contact ORTEC Customer Service for assistance in accessing the system.

5.7.5. Lock/Unlock Detectors...

This facility will protect a Detector from destructive access (e.g., **Start, Stop, Clear**) by any program on the computer or network. While any program can view the data and read the contents on any Detector in the system — locked or unlocked — the contents of a locked Detector cannot be changed without knowing the password.

NOTE *There is no master password.* If the password is lost, contact ORTEC Customer Service for assistance in unlocking the detector.

If the Detector is unlocked, selecting **Lock/Unlock** will open the dialog shown in Fig. 166. Enter the **Owner** name. Then enter a password in the Password field, and re-enter it in the **Verify** field (the two entries must agree). Click **OK**. The password is not case-sensitive (that is, uppercase and lowercase letters are treated the same).

If the Detector is currently locked, selecting **Lock/Unlock** will display the dialog in Fig. 167. Enter the correct password to unlock the Detector.

Each time destructive access to a Detector is attempted while it is locked, the **Locked Detector** dialog (see Fig. 168) will ask for the password.

In addition, the owner of the Detector will be displayed on the Supplemental Information Line (see Fig. 169).

If the incorrect password is entered in either the **Unlock** or **Locked Detector** dialog, the dialog will reappear, waiting for the correct password. If you do not know the password, click on **Cancel** to abort the access attempt.



Figure 166. Entering Name/Password to Lock a Detector.



Figure 167. Unlocking a Detector.

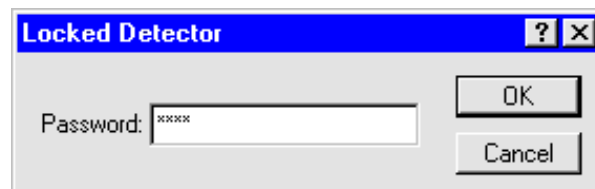


Figure 168. Password for Accessing Locked Detector.

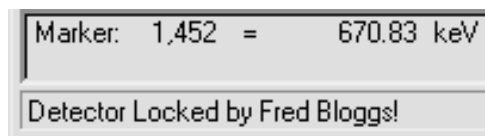


Figure 169. Name of Person Who Locked Detector.

5.7.6. Edit Detector Lists

The **Edit Detector Lists** submenu is shown in Fig. 170. These commands are used to select the MCBs on the system that will be used by Renaissance on this computer. Other applications (e.g., GammaVision, AlphaVision®, MAESTRO) on the same computer can have their own lists. In this way, the different Detectors on the network can be segregated by function or type.

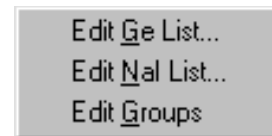


Figure 170. Edit Detector Lists Submenu.

Edit Ge List... and **Edit NaI List...** are used to define which Detectors will be considered as HPGe and which will be considered as NaI. The assignment of a Detector to one type or the other determines how the spectrum is analyzed. This affects not only the analysis engine, but the analysis parameters and aspects of some menu commands. When you select a command, the active Detector is checked for type and the appropriate dialogs are displayed. If the Detector is not assigned to a type, it is assumed to be Ge.

Edit Groups allows you to group Detectors to be used as a single function, such as three detectors in a chair or two detectors in a StandFast II®. Any number of groups can be defined.

NOTE Detector groups must be defined even if only one Detector is used because the group names are used in other dialogs for Detector selection.

5.7.6.1. Edit Ge List... and Edit NaI List...

Figure 171 shows the Detector List Editor dialog. Note that the **RGE Pick List** label above the right-hand column identifies this as the HPGe Detector List Editor dialog. The analogous dialog for NaI detectors has an **RNAI Pick List** label instead.

On the left is the **Master Detector List** of all Detectors on the system (both local and connected via network). This is created by the MCB Configuration program (see Section 2.3). The default descriptions are derived from the hardware and can be changed by running the configuration program manually. The **Master Detector List**, including the Detector descriptions, are the same for all ORTEC programs (e.g., Renaissance, MAESTRO, GammaVision) running on all computers connected to the workgroup.

To add a Detector to the Renaissance **RGE** [or **RNAI**] **Pick List** for this computer, click on the name in the Master list, then click on **Add**. To remove a Detector from this local pick list, click on the name in the **Pick List** and click on **Remove**. To remove all the Detectors, click on **New**.

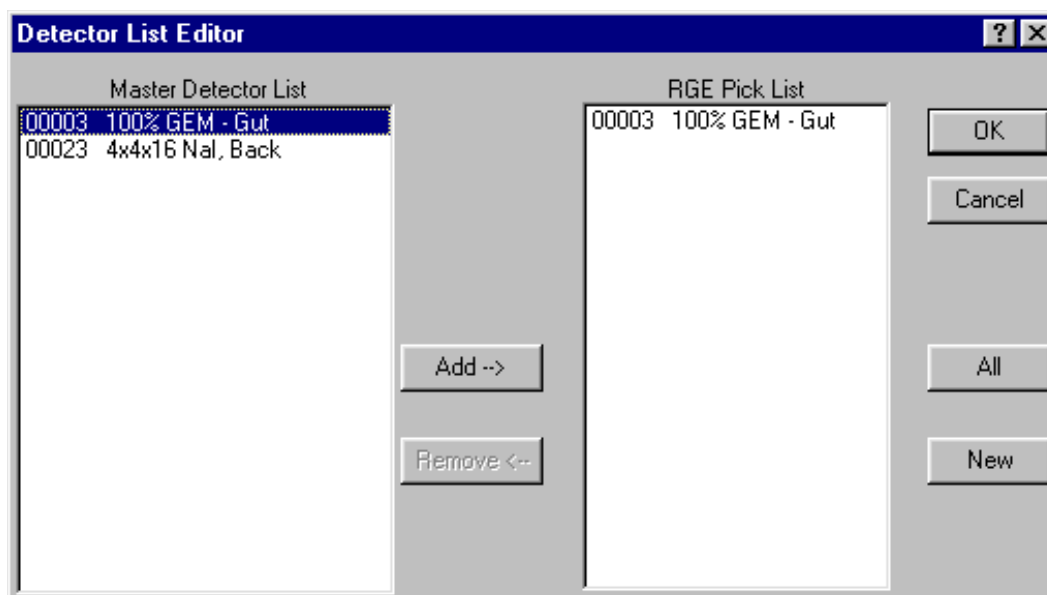


Figure 171. Detector List Editor Dialog for HPGe Detectors.

When Detector selection is complete, click on **OK**. These selections will be saved to disk and used by Renaissance until changed on this screen or until the entire network is reconfigured.

5.7.6.2. Edit Groups...

Figure 172 shows the Detector Groups dialog, which allows you to create, edit, and remove groups of Detectors, for example, a set of Detectors in a WB chair. Each detector must be assigned to a group (even if that group contains only the one detector), and a detector can belong to more than one group. To avoid configuration and analysis conflicts, detector groups should normally be composed of only Ge or NaI detectors. For summed spectra and stripping, all detectors *must* be of the same type (Ge or NaI) and must use the same conversion gain.

To create a detector group, click on **New**. This opens a dialog that allows you to define the new group name. Click on **OK** to return to the Detector Groups dialog. The new group name will be added to the **Detector Groups** droplist on upper right section of the dialog and will be displayed in the list field to indicate that this group is now active. You can now add Detectors to the group.

To add a Detector to a group, click on the Detector name in the Master list, then click on **Add**.

To add more than one Detector at a time, highlight them using the mouse and the **<Shift>** or **<Ctrl>** key, then click on **Add**. To add all the Detectors on the **Master Detector List**, click on **All**.

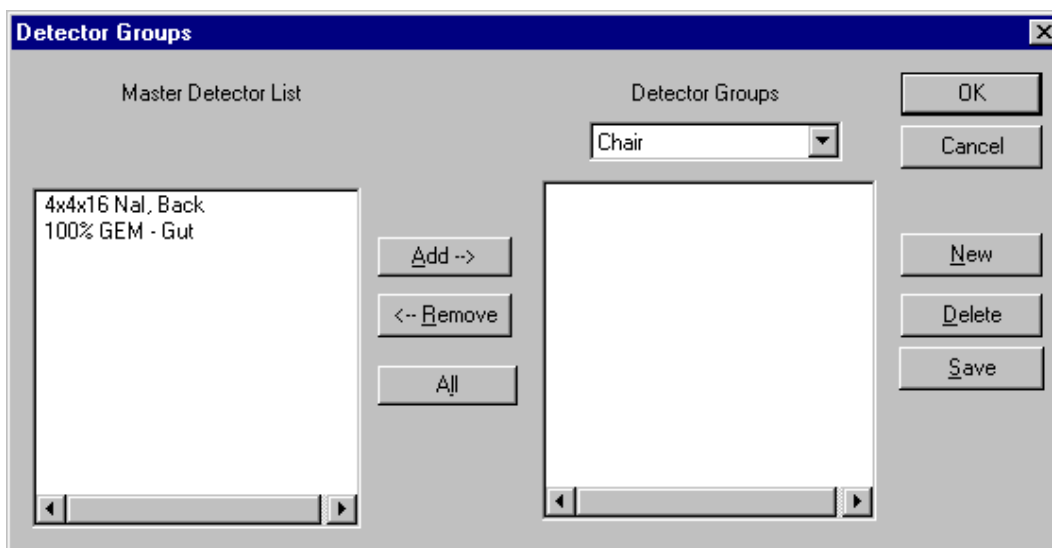


Figure 172. Create, Modify, or Remove Detector Groups.

To remove a Detector from a group, click on the name in the right-hand column then click on **Remove**.

When you have finished adding Detectors to the new group, click on **Save**.

To edit the list of Detectors in a particular group, select the group from the **Detector Groups** list, add or remove Detectors as needed, then click on **Save**.

To delete a detector group, select it from the list and click on **Delete**.

Click on **OK** to close the Detector Groups dialog. Your selections will be saved to disk and used by Renaissance until changed on this screen or until a new Master Instrument List is generated with the MCB Configuration program.

NOTE QA integrity and the ability to access your detector groups can be adversely affected by running the MCB Configuration program if, during reconfiguration, the detectors are assigned new **Instrument ID** numbers. We strongly recommend that you read the discussion in Section 2.4 on preventing these problems.

5.7.7. Operator Permissions...

The list of operator permissions is shown in Fig. 173. The upper section lists the options the operator is allowed to change for a specific analysis. If you do not want the operator to be able to perform a particular function on this dialog, unmark the corresponding checkbox. One reason for not granting a permission might be to ensure the data are collected and analyzed according to a set procedure each time.

If you unmark a checkbox here, the menu command for that function will be inactive (gray) or hidden in the Operator program.

Allow Energy Recalibration refers to the manual selection of the energy calibration (see Section 8.2.6) and not the automatic energy recalibration in the analysis program. Note that this step will generate and apply a new energy calibration to each Detector in the group that the operator is recalibrating. However, this new calibration will only be used for the analysis of subject or sample QA measurements (those begun with the Operator **Start Count** button) if the **.SDF** or **.SVD** file(s) in the associated **.OPR** file are set to use the **Internal** calibration. If the **.SDF/.SVD** file(s) call instead for a specific calibration file, the calibration in that file will be used in the analysis.

The **Allow MCB Settings Modifications** permission allows the operator to use the MCB Properties dialogs to make changes to the MCB. Under normal circumstances, this is not needed. The operator still has control over the high voltage (detector bias) even if this box is not marked.

When you enable **Require Operator Password** and assign a password, a password field is added to the login dialog in the Operator program. To remove the password, simply return to this dialog and unmark the checkbox. The password is case-sensitive.

Enable Dead Time Alarm allows you to set an alarm limit for detector dead time, in percent. If the dead time exceeds this limit when the **Allow Continue on Alarm** box is marked, a warning popup is displayed but the scan continues. When the **Allow Continue** box is unmarked, a warning popup is displayed and the scan is automatically terminated.

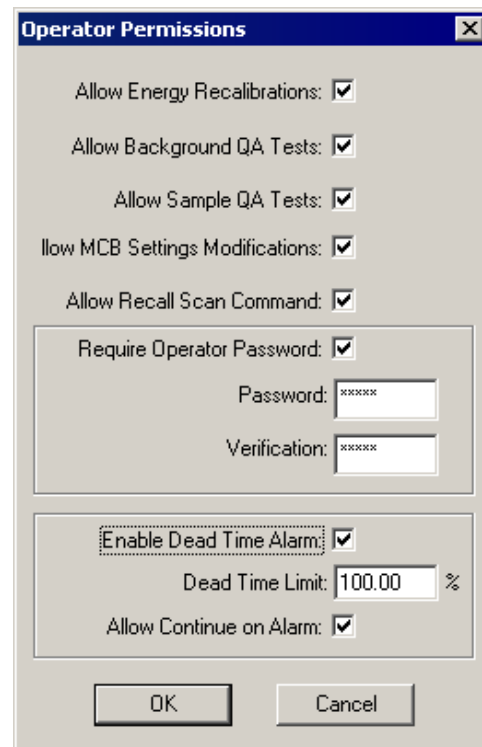


Figure 173. Set Permissions for the Operator Program.

5.7.8. Operator Scan Type...

This command starts the Scan Type wizard, in which you define how a scan will be performed in Renaissance Operator and save the scan settings as a *scan type file*, which is assigned the extension `.OPR`. The operator selects one of these defined **Scan Types** to set the proper scan parameters. Any number of scan settings can be defined. Scan type files are stored in the same directory specified for the analysis options files on the Directories tab under **File/Settings...** (Section 5.1.1.4).

5.7.8.1. General Factors to Consider in Creating Scan Type Files

- In Renaissance, almost all aspects of data analysis are controlled by the analysis options (`.SDF` or `.SVD`) files created with **Analyze/Settings/Sample Type...** (see Sections 5.5.1.1 [Ge] and 5.5.1.2 [NaI]). Consequently, a principal task in creating an `.OPR` file is to select the proper analysis options file(s) for the scan type being created.

One of the first steps is to select an `.SDF/.SVD` file that will determine the analysis parameters for all Detectors in the group; this is done on the first page of the wizard. On a later wizard page, you can choose to override that `.SDF/.SVD` file for one or more Detectors in the group. The Detector-specific analysis options files can be used to override a calibration or peak background correction, use a different attenuation material, specify a different analysis start channel for a particular Detector, and so forth.

- To perform QA measurements in Operator, you must create a scan type (`.OPR`) file for the appropriate Detector group. This file must contain the `.SDF` or `.SVD` file to be used for sample QA analysis, and the `.SDF/.SVD` file must specify the counting presets for the sample QA measurement. Typically, the same analysis options file entered on the Quality Assurance Settings dialog (Section 10.2.1) are used in the `.OPR` file so that QA is the same in both programs. The same `.OPR` file can be used for both sample and background QA, however, background QA uses the counting presets in the Quality Assurance Settings dialog for each Detector.

NOTE Operators *should not* use the **MCB Properties...** command to adjust the presets for routine subject measurements or QA acquisitions.

- If the composition of a Detector group is changed, you must open all `.OPR` files using that Detector group, reselect the group from the **Detector Group** field, and then save the `.OPR` file with either the **Save As...** button or by finishing the wizard and answering **Yes** to the “do you want to save” question. Otherwise, Operator will not register the changes to the Detector group.

- Individual and summed spectra can be analyzed in the Operator program by establishing two **Scan Types** that are identical except that one has the **Analyze sum of spectra** checkbox marked on the Analysis Options page of the wizard (see Section 5.7.8.3, page 183). After spectra have been acquired using one of these Scan Types, a user can select the other Scan Type, then reanalyze with the **Analyze\Configuration in Memory** command in Operator. This avoids the need to acquire another set of data for the detector group. Note that this method cannot be employed after the detector spectra have been modified (i.e. cleared, count extended, or another scan performed).

5.7.8.2. Scan Settings

The first dialog of the Parameters Wizard is shown in Fig. 174. The **Operator files** list allows you to select an existing **.OPR** file and load its settings into the wizard fields. Use the **Save As...** button to save the settings from the specified **.OPR** file to a new filename. The **Creation** and **Edition** fields respectively indicate when this **.OPR** file was created and when it was last changed.

Click on **New** to reset (remove the entries from) all fields in the Operator Scan Type wizard.

To remove an operator file that is no longer needed, select it from the **Operator files** list and click on **Delete**.

(You can also use Windows Explorer to delete or move **.OPR** files from the directory specified in **File/Settings**, or to mask the file by renaming the **.OPR** file extension.)

Enter a useful description of the **Scan Type**; this will be displayed for the Operator in the droplist of available scan types. Choose the **Detector Group** to be used in the scan (see Section 5.7.6.2).

Use the **Sample Default Files** fields to choose the default analysis options (**.SVD** and/or **.SDF**) files that will be used for analysis of the **NaI** and/or **Ge** detector spectra. All Detectors of the same type use the same **.SVD** or **.SDF** file unless one or more Detectors are assigned an analysis options file override, as discussed in Section 5.7.8.6. If you will be analyzing summed spectra

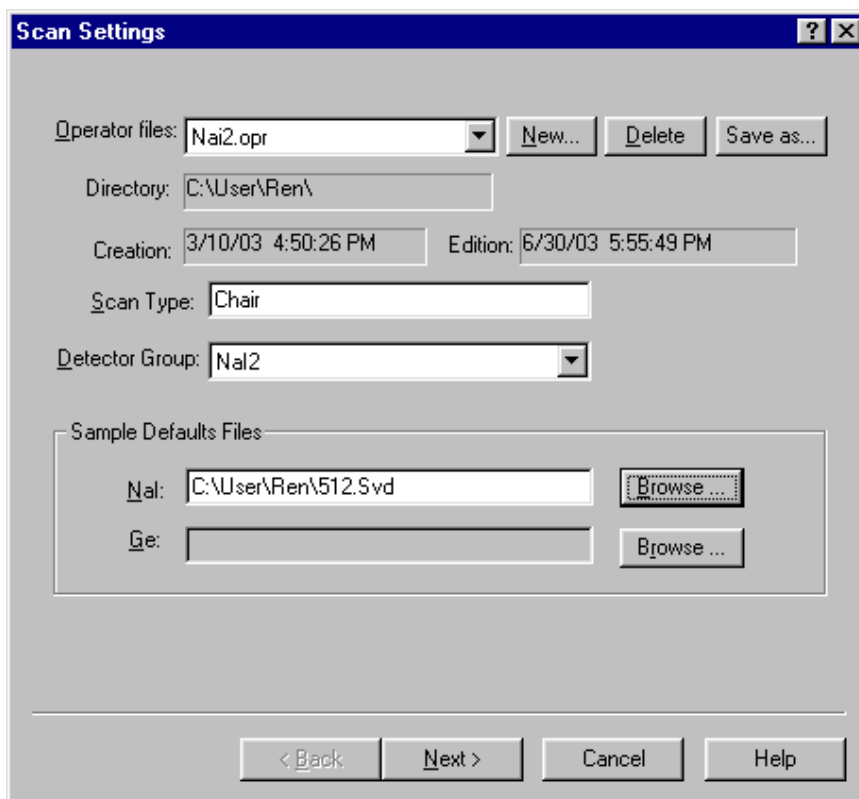


Figure 174. Scan Settings.

for a group of detectors, *they must all be of the same type*, and will be analyzed according to the analysis options file entered here; no override is allowed.

Click **Next** to go to the Analysis Options page.

5.7.8.3. Analysis Options

Use this dialog (Fig. 175) to set up the analysis options not specified in the sample default files. These settings apply to the group of detectors and the total scan.

Key

The **Key** determines whether the scans made using this operator settings file will be indexed in the database by **Name**, **Badge** number, or Social Security Number (**SSN**). The **Key** determines the first entry the operator will make for this scan type, and will force that first entry to be unique.

NOTE *To avoid the potential for duplicate entries, the **Key** field should be consistent for all scan types that use the same database.*

Figure 175. Analysis Options.

Chest Wall Attenuation

This correction is used to correct for gamma-ray absorption by the scan subject's chest, based on the subject height and weight entered in the Operator program. It is normally used only in lung counting. Mark the checkbox to turn on the correction in Operator, and select the correction formula from the droplist (Fig. 176). This will load the default constants for the selected formula into the **CWT=** fields (the formulas are explained in Section 8.10). If you wish to use a different correction, select **User Defined** and enter the values.

Figure 176. The Chest Wall Attenuation List.

- All CWT formulas calculate CWT in terms of cm since the attenuation tables are based on thickness values in cm. This is true even when **Height** and **Weight** are entered in

respective terms of pounds and inches. The standard Hanford and LANL formulas use lb/in.

- If the **Chest Wall Attenuation** *is not enabled here*, no attenuation correction will be applied in Operator, whether or not an attenuation correction is specified in the applicable .SDF or .SVD file for each detector. The **CWT** field in Operator will be set to zero and disabled.
- If **Chest Wall Attenuation** is enabled here, the attenuation correction in Operator will be performed using the attenuation parameters specified on the Corrections tab for the .SDF or .SVD file. To ensure that the proper attenuation factors are applied whenever the scan type calls for CWT correction, **Attenuation** should be turned on and appropriate parameters selected within the analysis options file(s).

When this correction is enabled, the **CWT** will automatically be calculated on the Operator interface when the operator changes the subject height or weight entries. The operator can also manually enter the **CWT** value.

- For a **User Defined** correction, be sure the CWT calculation coefficients are based on weight and height in terms of kg and cm, respectively, even if the **Weight** units in the analysis options file are set to **lb**. This is because Renaissance always converts and stores weight and height as kg and cm, even when these parameters are displayed in pounds and inches on the Operator program interface.

Spectra

The Operator Scan Type wizard gives you flexibility in saving spectra and reports for measurements made in the Operator program. Spectra can be analyzed individually or as the sum of all the spectra from the Detector group. The save options for reports and database records are on the next wizard page, Results Options.

Analyzing Individual Spectra

To analyze spectra individually and save the results to the specified target database, unmark the **Analyze sum of spectra** checkbox. The spectrum filename format will be:

[Scan Type][Subject Name] [Detector Desc] [File Prefix] [Seq No]

where:

- | | | |
|--------------|---|--|
| Scan Type | = | defined on the Scan Settings page of the Scan Type Wizard. |
| Subject Name | = | the full subject name from the Operator program. |

Detector Desc	= the Detector Description as defined in the MCB Configuration program.
File Prefix	= defined in the Acquisition Settings dialog (Section 5.2.1).
Seq No	= the Save File # defined in the Acquisition Settings dialog.

Analyzing Summed Spectra

The **Analyze sum of spectra** option generates one spectrum by summing all of the detector spectra channel by channel. The spectrum filename format is:

RenSum [Subject Name] [Detector Group] [File Prefix] [Seq No]

where:

Subject Name	= the full subject name from the Operator program.
Detector Group	= defined on the Scan Settings page of the Scan Type Wizard.
File Prefix	= defined in the Acquisition Settings dialog (Section 5.2.1).
Seq No	= the Save File # defined in the Acquisition Settings dialog.

- All detectors in the group must use the same conversion gain.
- Renaissance will not sum Ge and NaI spectra, therefore, all detectors in this group must be of the same type.
- The **Gain Adjust** option on the Operator program's **Startup** dialog can be used periodically to align all detectors to a common reference peak to keep the peak resolution for the summed spectrum from degrading.
- In addition to the summed spectrum for the group, the spectra from the individual detectors are saved and the path to those spectra reported on the Operator analysis report. When recalling a scan data set in Operator, however, only the summed spectrum will be reloaded and analyzed. The individual spectra can be analyzed using the Supervisor program, if desired.
- When analyzing the summed spectrum, the governing **.SDF** or **.SVD** file must specify a valid calibration for the sum. Calibration of summed Ge spectra can be performed in the **Ge Calibration Wizard**. For summed NaI spectra, define an **.OPR** file for "Calibration" that collects the summed spectra in the Operator program, then return to Supervisor to calibrate using that stored spectrum with the **Calibrate/Energy...** and **Efficiency...** commands.

Print Spectra prints either the summed spectrum or the individual spectra as a standard Win-Plots report. **Print MCS Plots** automatically prints the MCS plot(s) upon the completion of

analysis. These plots are automatically printed upon completion of a subject scan analysis, or analysis of a configuration in memory (whether analyzing detector data or a recalled scan data set). Click on **Next** to go to the Results Options screen.

5.7.8.4. Results Options

Reports

Renaissance generates results for each detector and for the total scan. The Results Options dialog (Fig. 177) lets you choose how the results will be reported and saved in the database. Note that only individual results are saved in the database (regardless of any analysis options or scan type settings), and these individual results are the only data used in generating the Operator program's Crystal Reports/Report Writer output.

You must choose at least one of the **Save individual reports**, **Save average report**, or **Concatenate individual reports** options. See the "Spectra" discussion beginning on page 184.

The **Reports** options use the reporting specifications in the .SDF or .SVD file (see the Report tab under **Analyze/Settings/Sample Type...**). **Save individual reports** creates an ASCII text .RPT file for each spectrum. The results are also stored in the specified **Database**, and can be viewed and printed in the Operator program with the **File/Recall Report** command. The individual spectrum files can be analyzed in Supervisor.

If you are analyzing the individual spectra from a Detector group (rather than analyzing the summed spectra), you can use the **Save average reports** option

to create an ASCII text .RPT file for the average (or weighted average) results from all of the individual Detectors in this group. (A weighting factor for each detector's nuclide activity can be set on the Spectrum Settings wizard page.) No corresponding record is saved in the **Database**. The average activity report file is assigned the name of the first detector's spectrum filename with the letter "A" appended.

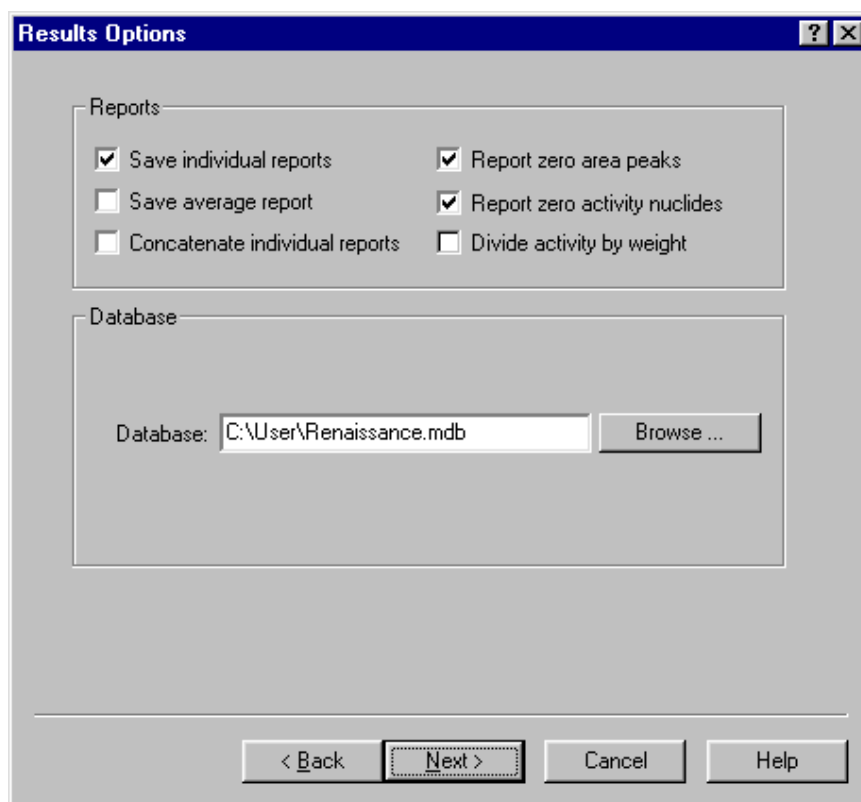


Figure 177. Report and Database Options.

The Weighted Average report displays information for each detector in the report header, including the spectrum, calibration, PBC, and spectrum stripping filenames, as well as the weighting assigned to each detector. This information is consistent with that displayed on the individual analysis reports.

Concatenate reports saves all individual reports in one ASCII text `.RPT` file that simplifies file management and reporting. This is particularly useful if you are using a large number of detectors. This report contains the same analysis results as the individual reports, but the subject information is displayed only in the header on the first page of the report. No corresponding concatenated record is saved in the **Database** (only the individual data sets). The concatenated report file is assigned the name of the first detector's spectrum filename with the letter "C" appended. In most cases, it is not necessary to save both the individual and concatenated reports.

In all cases, the `.SDF` or `.SVD` file associated with this scan type file determines which report format will be generated (the ASCII text Operator report only or both the Crystal Reports and ASCII reports), and whether the ASCII report will be printed and/or displayed in Notepad or another program. Printed reports will be sent to the default printer for this computer. If you have chosen not to save the reports, the ASCII text report file will be displayed and printed according to the `.SDF` or `.SVD` file, then deleted. The full Ge or NaI report discussed in Chapters 6 and 7 will be printed for background and sample QA measurements. For all other measurements, the routine count report discussed in the Operator user's manual will be generated.

Report zero area peaks and **Report zero activity nuclides** force all library peaks and nuclides, respectively, to be displayed on the Operator analysis report even if the peaks or nuclides were not found or were rejected because they failed the Critical Level or Peak Cutoff tests. These options affect the standard text report only and do not apply to the Report Writer report.

To set these display options for the Supervisor program analysis reports, flags must be set in the `B30Winds.ini` (Ge) or `G30Winds.ini` (NaI) files; see Sections A.2.2 and A.2.3, respectively.

Divide activity by weight — To report total activity, leave this checkbox *unmarked*. In this configuration, the **Weight** entered in the Operator program is only used to calculate the CWT (if enabled in this scan type file) which will be used to adjust activity for attenuation. A value of "1" for the weight and units of "**None**" will be saved with the spectrum so that analysis from the Supervisor program will generate comparable results.

Mark this box if you want the Operator program to report the subject's specific activity in terms of activity/weight based on the weight entered in the Operator interface. The **Weight** entered in Operator will also be stored with the spectrum so that analysis from the Supervisor program will generate comparable results. Be sure the analysis options file specifies weight units of **Kg** or **Lb** instead of **None**, otherwise, activity will appear to be displayed as total activity (i.e. no weight

units displayed) even though the nuclide activities have actually been divided by the weight value.

Database

The **Database** entered here specifies where the analysis results will be stored when this scan type is selected in Operator. This database becomes the working database for the Operator program, determining which results can be retrieved with the **Recall Reports** and **Recall a Scan Data Set** commands, as well as which subjects are available for selection in the Operator interface.

As discussed in Section 5.7.3.1, you can create separate databases to store results for different subject groups (e.g., employees, contractors, client origin, training, testing). To avoid having to create the same subject entry in multiple databases and to eliminate the possibility of duplicate entries, the **Key** field should be consistent for all scan types that use the same database.

If you plan to measure a subject multiple times using different detector configurations (for example, to perform an additional measurement using a larger detector group), you will have to create a scan type file for each type of measurement. If these related scan types specify the same results **Database**, the subject fields on the Operator program interface will not change between scans *unless the scan type specifies a different **Key** field*. This will save time and needless repetition as well as minimize the introduction of keyboarding errors.

Click **Next** to go to the Detector Settings screen.

5.7.8.5. Detector Settings

This dialog (Fig. 178) is used to enter the counting presets, to turn the Motor Control feature on/off, and to set the number of steps used for scans using a motorized bed. For subject scans, the counting presets entered here override those in the **.SDF** or **.SVD** file. This preset time is not used for QA or PBC updates. In most WBC counts, the dead time is low, so the **Real** and **Live** times are equivalent. Enter the minimum scan time.

Detector Settings

Count Time

Real: 1000 sec Extend: 0.00 sec

Live: 1100 sec

Mcs Mode (scanning with motor control)

Off Total Spectrum Counts ROI Counts

Steps: 0

< Back Next > Cancel Help

Figure 178. Detector Settings.

NOTE If using a motor, only the **Real** time preset can be used because the motor speed is calculated based on the real-time preset and the scan length.

The **Extend** time is the counting time that will be added if the operator selects the **Extend** button at the end of the count. This allows operators to collect more data to improve scan results. When extending a count, the motor speed is recalculated based on the time entered here, and a new MCS plot, similar to the original scan, is generated.

If you are using a motor (for instance, for a scanning bed), the **MCS Mode** settings allow the operator to collect, for each detector, an additional plot that is a histogram of the counts vs. time or counts vs. position. When using the **Analyze sum of spectra** option in conjunction with **MCS Mode**, a plot showing the count rate per detector will also be displayed.

The count rate recorded can be the integral of all the counts in the spectrum (**Total Spectrum Counts**) or just the part of the spectrum marked by the ROI (**ROI Counts**). For **ROI Counts**, you must have an **.ROI** file containing the ROI channels (all ROIs in the file are used) to be included in the MCS plot, which you will enter on the next wizard screen. The counts per second will be calculated based only on the counts in all channels of all ROIs.

The number of steps (**# Steps**) determines the interval at which the count rate for the specified ROI or spectrum (as applicable) is plotted, e.g., **Real Time / # Steps**.

For detailed information on Motor Control setup, see Appendix B.

Click on **Next** to go to the Spectrum Settings screen.

5.7.8.6. Spectrum Settings

Figure 179 shows the Spectrum Settings dialog. A separate dialog is displayed for each Detector in the group; or, if you marked **Analyze sum of spectra** on the Analysis Options page, a single dialog for the summed spectrum is displayed. In this case, the default analysis options are always used and cannot be overridden.

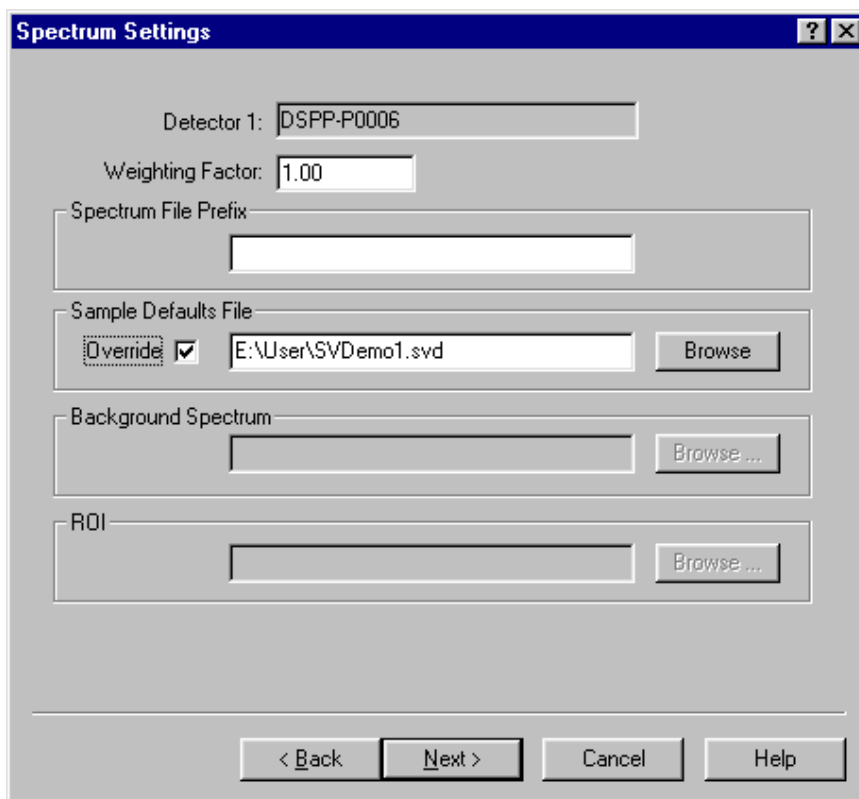


Figure 179. Spectrum Settings.

For multi-detector groups, you can average the results and report the averaged values by turning the **Save average report** feature on and **Analyze sum of spectra** off on the Results Options page. The nuclide activities, uncertainties, peak areas, and MDAs will be averaged using the **Weighting Factor** entered for each Detector in the group.

If you wish, you can enter a **Spectrum File Prefix** to be used when the spectra from this detector are saved. This character string is added to the beginning of the spectrum filename, preceding any prefix(es) specified in the Acquisition Settings.

In this case, the spectrum filename format becomes:

[Spectrum File Prefix] [Subject Name] [Detector description][File Prefix] [Seq No]

where **File Prefix** and **Seq No** are the **File Prefix** and **Save File #**, respectively, from the Acquisition Settings dialog (Section 5.2.1.2). Note that this **Spectrum File Prefix** is ignored for .PBC, calibration, and QA files.

As noted above, when you use the **Analyze sum of spectra** option, only one Spectrum Settings screen is displayed for the summed spectrum. However, you might find it useful to assign a **Spectrum File Prefix** to individual detectors in the group so that the spectrum files for each detector contributing to the sum can easily be told from one another. To do this, use the **Back** button to return to the Analysis Options screen, unmark **Analyze sum of spectra**, then return to this screen. For the first detector presented, *enter the **Spectrum File Prefix** that you wish to be assigned to the summed spectrum*. Then set the file prefix for each subsequent detector. When all detectors have been assigned a file prefix, go back to the Analysis Options screen and mark **Analyze sum of spectra**, then return to this point and continue through the remainder of the wizard.

The **Sample Defaults File Override** allows you to assign one or more Detectors in the group a different analysis options file than the one entered on the first page of the wizard. This overriding .SDF or .SVD file can specify different analysis options such as calibration, PBC, attenuation or decay correction, analysis range, or peak-search sensitivity. Enter the filename or **Browse** for the file to be used.

The **Background Spectrum** override is only available if **Strip Spectra** was selected on the Analysis Options page. Enter the filename or **Browse** for the file to be used. This stripping spectrum must have the same conversion gain as the analysis spectrum.

The **ROI** override is only available if **ROI Counts** was selected as the **MCS Mode** on the Detector Settings screen. The ROIs marked in the MCB (if any) will be used unless you specify this override. Enter the .ROI filename or **Browse** for the file to be used. Click **Next**.

5.7.8.7. Save Scan

The last dialog in the Operator Scan Type wizard is shown in Fig. 180. This screen displays the **Operator Settings File** and **Scan Type** description entered on the Scan Settings dialog (Fig. 174). Click on **Finish** to complete the Operator Scan Type wizard. If you have made any changes, you will be prompted to save or cancel them.

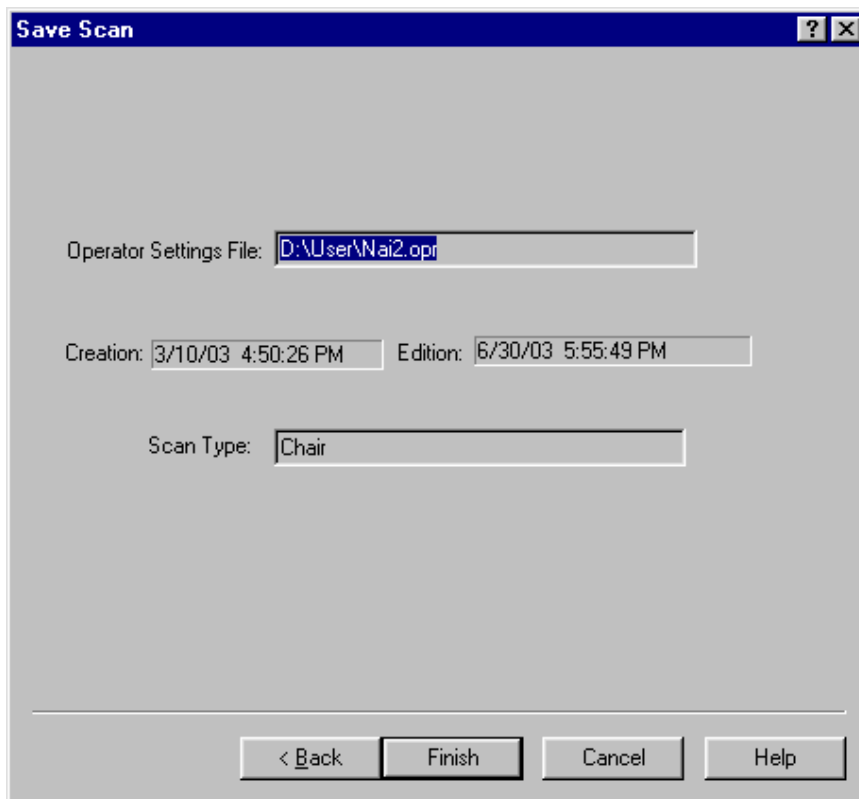


Figure 180. Save Scan.

5.7.9. Alarm Limits...

The Alarm Limits table (Fig. 181) is used in the Operator program to warn the operator if the analysis shows activities that exceed the values entered here. *These alarm and warning limits are specific to the database being used to store the analysis results.* The limits displayed are from the database currently in use in Supervisor.

When establishing alarm and warning limits, the library peaks and energies available in the dialog are drawn from the current internal (working) library. For best results, we recommend that you use the routine subject analysis library as your internal library. However, regardless of the library you use, its nuclide peaks should be consistent with the entries in the libraries used for analyzing a subject. This will ensure that the alarm and warning limit parameters match the identified nuclides and peak energies.

NOTE For each nuclide that you wish to assign limits, be sure to assign limits to the *first peak for that nuclide as it appears in the library file, not in the Peak droplist in this dialog.* Otherwise, the **Default** limits will be used in reporting. Use **Library/Edit...** to view the library contents (see Section 5.6.4). You can also set limits for any subsequent peak for that nuclide.

NOTE Alarm and warning limits are expressed in units of Bq. These limits are converted to the activity units specified for the Operator analysis and compared to the reported nuclide and peak activities, which might be scaled by the subject weight, depending on the analysis parameters. If **Divide activity by weight** is turned on in the scan type file,

the reported limits will be converted to specific activity units, as is done for subject activity. Alarm and warning limits displayed on the Operator report are converted from the total Bq per nuclide entered in this dialog to the units displayed on the analysis report. This correction takes into account conversion of activity units and any weight corrections. For example, if your report is configured to report specific activity in to convert from Bq to $\mu\text{Ci/lb}$, Renaissance will divide the total Bq per nuclide for the limit by 37000, then divide the result by the subject weight displayed on the analysis report.

The **Peak** droplist contains the list of library peaks in the current internal (working) library.

To add an entry to the table, select from the list the nuclide and energy to be monitored, enter the **Warning Limit** and **Alarm Limit** values, then click on **Add New**. The table (the upper section of the dialog) will update. A **Default** peak is always available on the list so limits can be set for any nuclides or peaks for which limits are not explicitly set.

Nuclide	Energy (keV)	Warning (Bq)	Alarm (Bq)
Default	0.0000	300.0000	600.0000
Cs-137	661.659973	300	600

Buttons: Add New, Update, Delete, Clear All

Peak: Cs-137 @ 661.66 keV

Warning Limit: 300 Bq Alarm Limit: 600 Bq

Close

Figure 181. Set the Operator Alarm Limits.

To edit an existing entry, click on it in the table, modify the peak and values, then click on **Update**.

To remove an entry from the table, select it then click on **Delete**. **Clear All** erases all entries from the table.

To exit the dialog and save all the values to the database, click on **Close**.

5.8. ROI

An ROI — *region of interest* — is a way to denote channels or groups of channels in the spectrum as having special meaning. An ROI can be used to mark peak areas for the printout or to mark a peak to stop acquisition when that peak reaches a preset value. Channels marked as ROI channels are displayed in a different color than the unmarked channels.

The commands on the **ROI** menu (Fig. 182) are available for both the buffer and Detector(s). See Section 4.3.3 for ROI operations performed with the mouse.

5.8.1. Off

This sets the ROI status to Off. In this state, the ROI bit for the channels will not change as the cursor is moved by the arrow keys. This function is duplicated by <Alt + O> and by <F2> (which toggles between **Off**, **Mark**, and **UnMark**).

The usual ROI status is Off so the marker can be moved on the display without changing any of the ROI bits.

5.8.2. Mark

This sets the ROI status to the Mark or set condition. In this state, the cursor channels are marked with the ROI bit as the cursor is moved with <-> or <+> into the channel. Moving the marker with the mouse does not change the ROI in this mode. This function is duplicated <Alt + M> and by <F2> (which toggles between **Off**, **Mark**, and **UnMark**).

ROIs can also be marked with the rubber rectangle (see Section 4.3.3) and right-mouse-button menu as described in Section 5.11.

5.8.3. UnMark

This sets the ROI status to the unmark condition. In this state, the channels are unmarked with the ROI bit as the cursor is moved with <-> or <+> into the channel. Moving the marker with the mouse does not alter the ROI in this mode. This function is duplicated by <Alt + U> and by <F2> (which toggles between **Off**, **Mark**, and **UnMark**).

5.8.4. Mark Peak

This function marks an ROI in the spectrum, at the marker position, in one of two ways.

- If the spectrum is calibrated, the region is centered on the marker with a width of three times the calibrated FWHM. There does not need to be a peak at the marker position.
- If the spectrum is not calibrated, the region is centered on the peak located within two channels of the marker and as wide as the peak. If the peak search fails, or if the peak is not well-formed, no ROI is marked. There is no limit on the size of a peak or ROI; therefore, in some uncalibrated spectra, large ROIs might be marked.

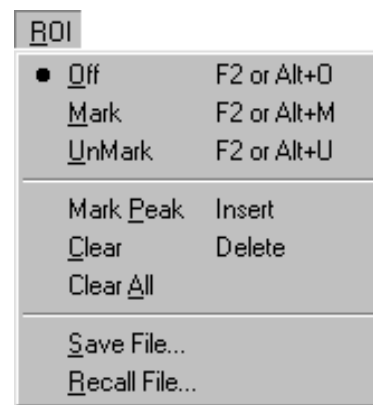


Figure 182. ROI Menu.

ROIs can also be marked this way with the **ROI Ins** button on the Status Sidebar, the **Mark ROI** button on the Toolbar, **Keypad<Ins>**, and **<Insert>**.

See also **Mark ROI** on the right-mouse-button menu, Section 5.11.8.

5.8.5. Clear

This clears the ROI bits of all ROI channels contiguous to the channel containing the marker. This is duplicated by the **ROI Del** button on the Status Sidebar, **Keypad**, the **<Delete>** key, and the **Clear ROI** Toolbar button.

See also **Clear ROI** on the right-mouse-button menu, Section 5.11.9.

5.8.6. Clear All

This resets all the ROI bits in the displayed spectrum (i.e., removes all ROI markings from the spectrum). However, it does not affect the ROI status of **Mark/Unmark/Off**.

5.8.7. Save File...

This will save the current ROI table of the channel numbers in the active spectrum, to a disk file. The contents of the spectrum are not changed.

Selecting **Save File...** displays the dialog in Fig. 183. Enter the **File name**. The **.ROI** file extension is recommended, and is used by default. An invalid or null filename will abort the **Save** operation.

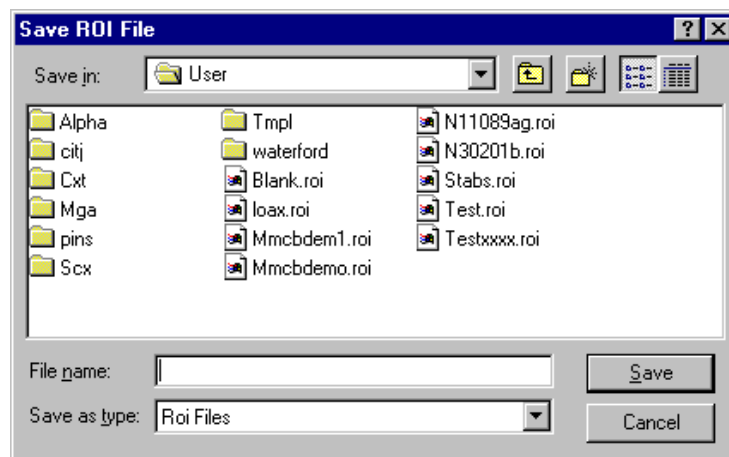


Figure 183. Save ROI File Dialog.

If the file already exists, the system will display a warning message asking if the file is to be overwritten with the new data or cancel the save. Click on **OK** to overwrite the file.

5.8.8. Recall File...

Recall File... sets the ROIs in the buffer or active Detector to the table in the disk file created by **ROI/Save File...** (Section 5.8.7), from the table stored in an **.SPC** file, from the analysis limits in a **.UFO** file, or from the energies in a library. This command opens the dialog shown in Fig. 184, prompting for a filename. When a file is selected, the ROIs in the buffer or active Detector are set to conform to the table in the file. The previous ROIs are cleared. The data contents of the buffer or Detector are not altered by this operation, only the ROI bits in the buffer or Detector.

In .ROI, spectrum, and .UFO files, the ROIs are saved by channel number. Therefore, if the spectrum peaks have shifted in position, the ROIs in the file will not correspond exactly to the spectrum data. For library files, the ROIs are generated using the library energies, and the energy and FWHM calibrations.

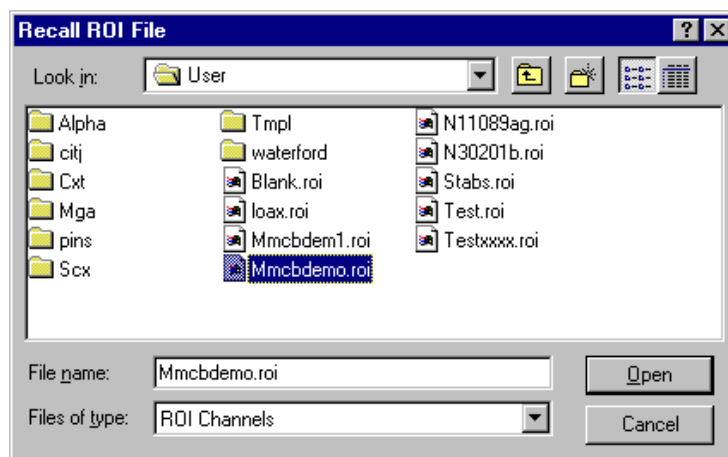


Figure 184. ROI File Recall Dialog.

5.9. Display

The **Display** menu commands (Fig. 185) control the color, fill, and scaling in the spectrum windows. These functions are duplicated by indicated hot keys, as well as commands on the toolbar and right-mouse-button menu (see Section 5.11).

5.9.1. Logarithmic

Logarithmic toggles the vertical scale of the Expanded Spectrum Window between the logarithmic and linear modes. This function is duplicated by **Keypad**</> and the **Log/Linear Display** button on the Toolbar.

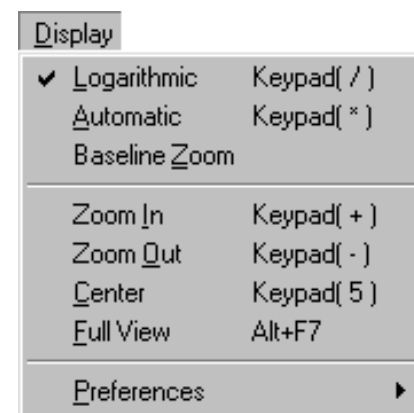


Figure 185. Display Menu.

5.9.2. Automatic

Automatic switches the Expanded Spectrum Window to a linear scale that is automatically adjusted until the largest peak shown is at its maximum height without overflowing the display. It also toggles the vertical scale of the spectrum display between the automatic and manual modes. If the logarithmic scale was enabled, the display is switched to linear. This function is duplicated by **Keypad**<*> and the **Vertical Auto Scale** Toolbar button.

5.9.3. Baseline Zoom

Baseline Zero switches to autoscale mode, then sets and keeps the baseline of the expanded display at zero counts. Autoscale is then switched off. This function is duplicated by the **Baseline Zoom** Toolbar button.

5.9.4. Zoom In

Zoom In adjusts the horizontal and vertical scales in the Expanded Spectrum Window to view a smaller portion of the spectrum. The vertical scale is divided by two and the horizontal scale is reduced by about 6% of the full horizontal scale. The current horizontal and vertical full-scale values are shown on the Toolbar (see Fig. 186).

This command is duplicated by **Keypad<+>**, the Toolbar **Zoom In** button, and **Zoom In** on the right-mouse-button menu.



Figure 186. Vertical and Horizontal Full-Scale Setting on the Toolbar.

5.9.5. Zoom Out

Zoom Out adjusts the horizontal and vertical scales in the Expanded Spectrum Window to view a larger portion of the spectrum. The vertical scale is doubled and the horizontal scale is increased by about 6% of the full horizontal scale.

This command is duplicated by **Keypad<->**, the Toolbar's **Zoom Out** button, and **Zoom Out** on the right-mouse-button menu.

5.9.6. Center

This function forces the marker to the center of the screen by shifting the spectrum without moving the marker from its current channel. This function is only required when moving the marker with the mouse; the keyboard functions for moving the marker automatically shift the spectrum to center the marker when the marker travels past the end of the current expanded display. **Center** is duplicated by **Keypad<5>** and the **Center** button on the Toolbar.

5.9.7. Full View

Full View adjusts the horizontal and vertical scaling to display the entire spectrum in the Expanded Spectrum Window. This command is duplicated by **<Alt + F7>**.

5.9.8. Preferences...

This displays the options available for selecting the screen colors and spectrum display options (Fig. 187). This selection is for the active spectrum display only.

NOTE The preferences selected here will also apply to the Operator program.

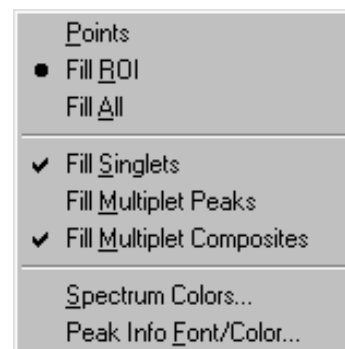


Figure 187. Display Preferences Submenu.

5.9.8.1. Points/Fill ROI/Fill All

Use these functions to select the histogram display mode for both spectrum windows.

In **Points** mode, the data are displayed as points or pixels on the screen, in the colors chosen for **Foreground** and **ROI** under **Display/Preferences/Spectrum Colors...** (see Section 5.9.8.3).

In **Fill ROI** mode, the unmarked regions of the spectrum are displayed as points, while the ROIs are filled from the baseline to the data point with the **ROI** spectrum color.

In **Fill All** mode, all the data points are filled from the baseline to the data point with the **Foreground** and **ROI** spectrum colors.

Figure 188 shows a comparison of the three display modes. Note that the point/pixel size in the **Point-** and **Fill ROI**-mode illustrations has been exaggerated to make them easier to see.

5.9.8.2. Fill Singlets/Fill Multiplet Peaks/Fill Multiplet Composites

The peaks detected during analysis can be displayed as contrasting, solid lines superimposed on the spectrum, or can be filled to background height with a contrasting color.

Choose whether to fill singlets, multiplets, and/or multiplet composites by clicking on the menu item(s) to mark them with a checkmark. Click again to remove a checkmark. The fill color for these peaks can be selected on the **Spectrum Colors...** dialog, discussed in the next section.

5.9.8.3. Spectrum Colors...

Use this dialog (see Fig. 189) to select colors for various features in the two spectrum windows. Each scroll bar controls the color of a different feature. The vertical colored stripes behind the scroll bars show the available colors.

The **Background** scroll bar controls the background color of the spectrum window, **Foreground** determines the color of the spectrum points or fill, **ROI** governs the color of the ROI points or fill.

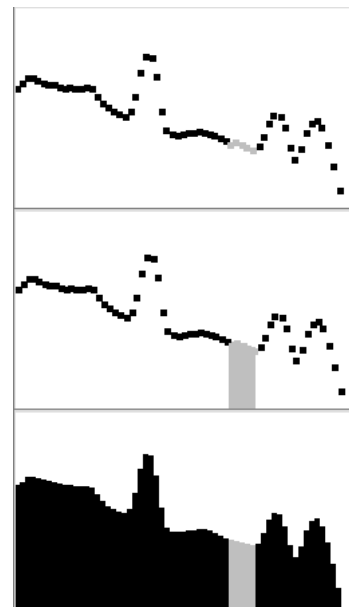


Figure 188. Comparison of the Points, Fill ROI, and Fill All Display Modes.

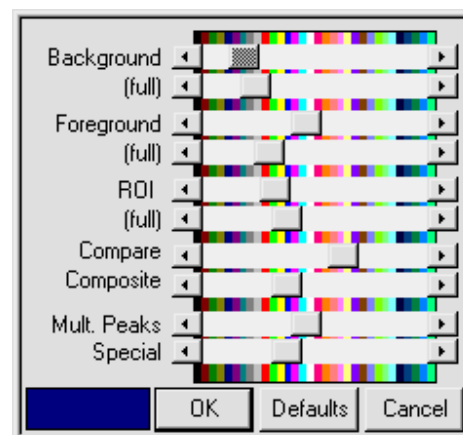


Figure 189. Display Color Selections.

The points/fill of a compared spectrum (**File/Compare...**) use the **Compare** color, unless they overlap with the original spectrum, in which case the **Composite** color is used.

To change a color, click and hold the left mouse button on the scroll bar button and drag it slowly across the different colors. When the desired color is displayed in the box beside the **OK** button, release the mouse button. The spectrum window will immediately change color.

To cancel a color change, return the slider button to its starting color, or close the **Spectrum Colors...** palette by clicking on **Cancel** or pressing <Esc>.

To reset the color values to the default colors, click on **Defaults**.

To accept the color changes, click on **OK**. These color changes will be recalled the next time Renaissance is started.

NOTE The **Spectrum Colors...** affect only the spectrum windows. The colors of the remaining features on the screen must be changed using the Windows Control Panel (which will also, of course, affect the appearance of all other Windows applications on this PC).

5.9.8.4. Peak Info Font/Color

This function opens the **Font** dialog (see Fig. 190). It allows you to select the font type, size, and color used to display **Peak Info** data in the text box in the spectrum windows (see Section 5.4.2).

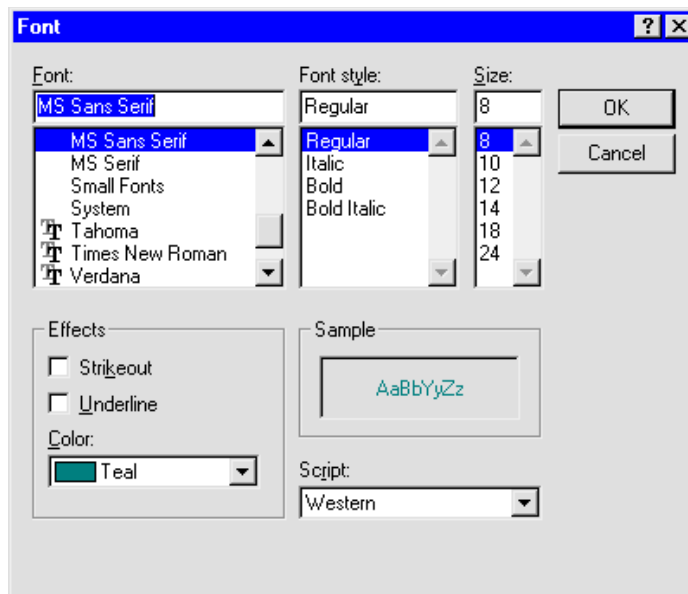


Figure 190. Peak Info Font Selection.

5.10. Window

This menu contains standard Windows commands for controlling the display of the spectrum windows (Fig. 191). In addition to the spectrum window display mode (**Cascade**, **Tile Horizontal**, **Tile Vertical**, etc.), the list of currently open buffer and Detector windows is shown. The currently active spectrum is checkmarked. To make a different window the active window, click on its entry in the list. This is especially useful if the spectrum has been expanded and not all the spectra are visible.

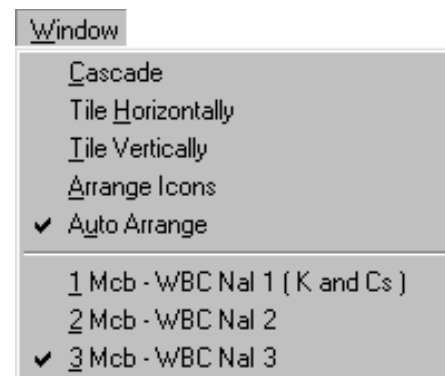


Figure 191. Windows Menu.

5.11. Right-Mouse-Button Menu

Figure 192 shows the right-mouse-button menu. To open it, position the mouse pointer in the spectrum display, click the right mouse button, then use the left mouse button to select from its list of commands.

5.11.1. Start

This initiates data collection in the selected Detector. Any warnings arising from problems detected at the hardware level will appear in a message box or on the Supplemental Information Line at the bottom of the display. The Detector can also be started with the <Alt + 1> accelerator, the **Start Acquisition** button on the Toolbar, or the **Start** command on the **Acquire** menu. If the Detector is already started or if Renaissance is in buffer mode, this entry is grayed.

5.11.2. Stop

Stop terminates data collection in the selected Detector. The display must be in Detector mode. If the Detector is not active, the entry is grayed. The Detector can also be stopped with the accelerator <Alt+ 2>, the **Stop Acquisition** button on the Toolbar, and the **Stop** command on the **Acquire** menu.

5.11.3. Clear

Clear erases the Detector spectral data and the descriptors (e.g., real time, live time, start time) for the selected Detector. The presets are not altered. (This function might not operate on some

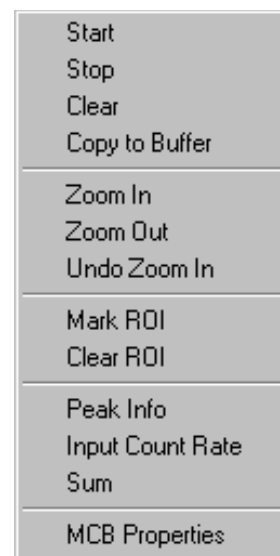


Figure 192. Right-Mouse-Button Menu.

types of Detectors when they are collecting data.) The data can also be cleared with **<Alt+ 3>**, the **Clear Spectrum** button on the Toolbar, or the **Clear** command on the **Acquire** menu.

5.11.4. Copy to Buffer

The **Copy to Buffer** function transfers the data and descriptors (e.g., live time, real time), from the selected Detector to the buffer. This function can also be performed with **<Alt + 5>** or the **Copy to Buffer** command on the **Acquire** menu.

5.11.5. Zoom In

Zoom In adjusts the horizontal and vertical scales in the Expanded Spectrum Window to view a smaller portion of the spectrum. If the rubber rectangle is not being used, the vertical scale is divided by two and the horizontal scale is reduced by about 6% of the full horizontal scale. If the rubber rectangle is being used, the display shows only the contents of the rectangle. The minimum display is 6% of the horizontal full scale. The current horizontal and vertical full-scale values are shown on the Toolbar.

This command (not using the rubber rectangle) is duplicated by **Keypad<+>**, the Toolbar's **Zoom In** button, and **Zoom In** on the **Display** menu.

5.11.6. Zoom Out

Zoom Out adjusts the horizontal and vertical scales in the Expanded Spectrum Window to view a larger portion of the spectrum. The vertical scale is doubled and the horizontal scale is increased by about 6% of the full horizontal scale.

This command is duplicated by **Keypad<->**, the Toolbar's **Zoom Out** button, and **Zoom Out** on the **Display** menu.

5.11.7. Undo Zoom In

This will undo or reverse the last **Zoom In** operation done with the rubber rectangle. It restores the display to the horizontal and vertical expansion before the **Zoom In**. It is not the same as **Zoom Out**.

5.11.8. Mark ROI

This function marks an ROI in the spectrum for the total width of the rubber rectangle. All channels are marked. See also Sections 4.3.3 and 5.8.4.

5.11.9. Clear ROI

This clears the ROI bits of all channels in the rubber rectangle or all ROI channels contiguous to the channel containing the marker. See also Section 5.8.5.

5.11.10. Peak Info

See Section 5.4.2 for peak calculation details.

5.11.11. Input Count Rate

The input count rate feature is supported by most ORTEC digital spectrometers. For these units, the input count rate can be shown in the upper left corner of the spectrum window. This is input count rate and not the number of processed pulses.

The buffer shows the input count rate when the spectrum was (1) transferred to the buffer from the MCB or (2) saved to disk. If the MCB is stopped, the value displayed is the current input count rate value and not the value when the MCB was stopped.

5.11.12. Sum

The **Sum** function performs its calculation in one of three ways, depending on the position of the marker:

- 1) If the marker is not in an ROI and a box is not defined, the sum of the data channels of the Detector is shown on the display. The complete channel width (e.g., 1 to 16384) is summed.
- 2) If the marker is not in an ROI and a box is defined, the sum of the data channels in the box is shown on the display.
- 3) If the marker is in an ROI, the sum of the data channels in the ROI is shown on the display. This is the same as the gross counts in the **Peak Info** display, but can be used on wider ROIs.

5.11.13. MCB Properties...

This command accesses the MCB setup dialogs discussed in Section 5.2.9.

[Intentionally blank]

6. THE GE REPORT

This chapter covers the contents of the Renaissance germanium analysis report, which is based on the entries in the Sample Type Settings dialog under **Analyze/Settings/Sample Type...** (Section 5.5.1). The report details depend on the analysis engine and setting, spectrum, calibration, and library content, as described below.

6.1. Report Header

The two-line report header (Fig. 193) is repeated on every page.

```
ORTEC g v - i ( 63) ROI32 G70W0.37 8/14/2013 4:36:45 PM Page 1  
AMETEK Spectrum name: GvDemo.An1
```

Figure 193.

The first line contains the program name, analysis code in parenthesis (63 in this example), analysis Engine name and version code (ROI32 G70W0.37 in this example), analysis date/time, and page number. The second line contains the Laboratory Name and Spectrum filename.

The analysis code is an integer that defines various conditions applied or encountered during the analysis. The number is decoded into binary with the following bit usage:

Bit 1	True if the spectrum is energy calibrated
Bit 2	True if the spectrum is efficiency calibrated
Bit 3	True if the library is a valid gamma-ray library
Bit 4	True if the isotopic abundance will be reported
Bit 5	True if the isotopic matrix will be reported
Bit 6	True if the Unidentified Peak Summary, Identified Peak Summary, or Summary of Library Usage table is reported
Bit 7	True if DAC/MPC is enabled
Bit 8	True if the PBC has been used
Bit 9	True if absorption correction is enabled
Bit 10	True if geometry correction is enabled
Bit 11	True is peak stripping (library or manual based) is enabled
Bit 12	True if the directed fit has been enabled

For example, an analysis code of 63 (which is binary 0000 0011 1111, digit numbers read from right to left) means that the spectrum is (1) energy calibrated, (2) efficiency calibrated, (3) valid library found, (4) isotopic abundance is reported, (5) isotope matrix is reported, (6) peak/energy matrix is reported, (8) PBC not used, and (12) Directed Fit not used.

Normally, this code just confirms that the proper analysis was performed, but it can be useful when troubleshooting a particular analysis when the reported results are not as expected.

6.2. Sample, Detector, and Acquisition Parameters

The first four sections of the report (Fig. 194) contain the sample description; the full path to the spectrum; acquisition information including the start date/time, live time, real time, and dead time.

The Sample Description may include two lines of text as entered in the Sample Description field before analyzing the spectrum. The Detector Description is displayed under the Detector System heading.

```
Sample description
  MIXED GAMMA MARINELLI ON ENDCAP OF P40268A

Spectrum Filename: C:\User\Gammavision V7 Examples\GvDemo.An1

Acquisition information
  Start time:           6/7/1991 10:37:33 AM
  Live time:           3600
  Real time:           4220
  Dead time:           14.69 %
  Detector ID:         12592

Detector system
  122%
```

Figure 194.

6.3. Calibration Parameters

This section (Fig. 195) includes the calibration filename, internal description from the calibration file, efficiency calibration uncertainty, and the energy and efficiency calibration date/time and formula coefficients. The particular coefficients displayed for the efficiency calibration depend on the calibration type and knee settings (where applicable). Refer to Section ? for details about efficiency calibration formulas and respective coefficients.


```

Calibration
  Filename:          GvDemo.An1
  1L Marinelli on Detector 12592

  Energy Calibration
    Created:         4/5/1995 8:44:58 AM
    Zero offset:     3.771 keV
    Gain:            0.162 keV/channel
    Quadratic:       2.447E-09 keV/channel^2

  Efficiency Calibration
    Created:         6/7/1991 10:37:33 AM
    Type:            Polynomial
    Uncertainty:     2.112 %
    Coefficients:   -0.217759  -3.814522  0.571410
                   -0.090628  0.005708  -0.000142

```

Figure 195.

6.4. Library Parameters

This section (Fig. 196) displays the libraries used for analysis and the Library Match Width setting.

If **Manual Based Peak Stripping** is enabled on the Analysis tab, the **Second Library** specified on the Analysis tab is identified on the report as the “Stripping library,” and the **Third Library** specified on the Analysis tab is identified as the “Second analysis library.” The primary purpose of the stripping library is to define the interference while the second analysis library defines which nuclides are assigned the remaining peak area after peak stripping is applied. The stripping and second analysis libraries are omitted from the report if **Manual Based Peak Stripping** is not enabled. Refer to Section 8.4.5.2 for more information on peak stripping.

```

Library Files
  Main analysis library:  Lib01.Lib
  Library Match width:   0.500
  Stripping library:     Lib02.Lib
  Second analysis library: Lib03.Lib

```

Figure 196.

6.5. Analysis Parameters

This section (Fig. 197) displays various analysis parameters used for the analysis, with the clarifications below.

```

Analysis parameters
Analysis engine:          wan32   G701w040
Start channel:           200 (    36.07kev )
Stop channel:            16000 (  2588.55kev )
Peak rejection level:    50.000%
Peak search sensitivity: 3
Sample size:              1.0000E+00
Activity scaling factor:  1.0000E+00/( 1.0000E+00* 1.0000E+00) =
                          1.0000E+00
Detection limit method:  Traditional ORTEC method

Random error:            1.0000000E+00
Systematic error:        1.0000000E+00
Uncertainty 1:           1.0000000E+00
Uncertainty 2:           2.0000000E+00
Uncertainty 3:           3.0000000E+00
Uncertainty 4:           4.0000000E+00
Uncertainty 5:           5.0000000E+00
Uncertainty 6:           6.0000000E+00
Uncertainty 7:           7.0000000E+00
Uncertainty 8:           8.0000000E+00
Uncertainty 9:           9.0000000E+00
Fraction Limit:          0.000%
Background width:        best method (based on spectrum).
Half lives decay limit:  12.000
Activity range factor:    2.000
Min. step backg. energy  0.000
Multiplet shift channel  2.000
alpha, beta, gamma:      5.000E-02    5.000E-02    5.000E-02
Max. ISO MDA ratio:      3.000E+00

```

Figure 197.

- “Peak rejection level” is the same value as the **Peak Cutoff** on the Analysis tab. Peaks with 1-sigma counting uncertainty greater than this value are not used in the analysis except in the special case when **Directed Fit** is enabled, which will generate an activity result for every nuclide in the library even if no peaks for that nuclide pass the **Peak Cutoff** criteria.
- The “Activity scaling factor” is the multiplier applied to the total sample activity to calculate the specific activity. This parameter includes the **Multiplier**, **Divisor**, and **Sample Size** from the System tab.
- The additional uncertainty parameters, “Uncertainty 1” through “Uncertainty 9” in Fig. 197, reflect the respective entries on the Uncertainties tab. These fields are reported only if a non-zero uncertainty is entered. If no label or non-zero uncertainty value is specified, the respective field is omitted from the report.
- The “Background width” is a description of the **Background Type** specified on the Sample tab. (In this example, “best method [based on spectrum]” refers to the **Auto** background type.)

- All parameters from “Half lives decay limit” to end of the list are specified in the `b30winds.ini` file (Section A.2.2).
- The “alpha, beta, gamma” and “Max ISO MDA ratio” fields are only displayed if the **ISO NORM** section of the report is enabled on the Report tab.

6.6. Correction Parameters

This section (Fig. 198) displays the corrections applied during the analysis for decay, coincidence and random summing, geometry and attenuation/absorption, peak background, and automatic energy recalibration (if enabled). The Status column displays a “YES” when a correction is enabled, followed by additional information related to the correction in the “Comments” column. The Status is listed as “NO” for disabled corrections.

Corrections	Status	Comments
Decay correct to date:	YES	6/8/2013 11:11:11 AM
Decay during acquisition:	YES	
Decay during collection:	YES	6/1/2013 10:37:33 AM 6/8/2013 11:11:11 AM
True coincidence correction:	YES	
Peaked background correction:	YES	1_2013-05-21_0236.PBC 5/21/2013 2:36:26 AM
Absorption (External):	YES	Cu Density g/cm3 8.9200E+00 Scaling factor 5.0000E-01 20ml-100mlBottle.Geo 8/15/2013 11:30:04 AM
Geometry correction:	YES	1_2013-03-24_001.ufo 1_2013-03-24_003.ufo Slope 3.0000E-01 Net factor 1.0000E+00
Random summing:	YES	
Iodine equivalence file:		IeqTable.Ieq 8/25/2000 1:57:23 PM
Average energy file:		EBARTable.ebr 8/25/2000 2:21:21 PM
Energy Calibration		
Normalized diff:	0.0106	Changed to fit the spectrum.
Zero offset:	3.703 keV	
Gain:	0.162 keV/channel	
Quadratic:	7.089E-10 keV/channel ²	

Figure 198.

- “Decay correct to date” should normally be set to the “Decay during collection” end time if both are enabled on the Decay tab.
- “Decay during collection” displays the collection start and stop date/time.

- “Peaked background correction” displays the PBC file name entered on the Corrections tab and the date/time the file was created.
- Absorption displays either database information as shown in Fig. 198 (material, density or mass, internal or external, and scaling factor [the latter is the **Length** value entered on the Corrections tab]) or the file information (file name, date/time created, .UFO file name used to generate the attenuation table, and the scaling factor [again, the **Length** value entered on the Corrections tab]).
- “Random summing” displays the slope value entered in the **Random Summing** field on the Sample tab; and the Net factor, which is the Random Summing Factor calculated per Section 8.11.
- The “Iodine equivalence” and “Average energy” fields are only displayed if these options are enabled on the Isotopes tab.
- The “Energy Calibration” section displays the “Normalized difference,” a measure of how well the spectrum peak energies match those in the library (see Section 8.2.6). This can range from 0.0 to 1.0, with 0.0 being the best and 1.0 the worst. High values may be due to a poor calibration or to analyzing very small peaks that do not have statistically good shape. If the automatic energy recalibration is enabled and the criteria specified in Section 8.2.6 are satisfied, a message indicates that the energy calibration was changed to fit the spectrum, and the new energy calibration coefficients used for the analysis are displayed.

6.7. Peak and Nuclide Tables

This section covers the various peak and nuclide tables GammaVision can report, based on the analysis engine used; see the following table. The content of a particular table may vary depending on the settings in the Sample Type Settings dialog or (.SDF) file, and in the `b30winds.ini` analysis parameters file, which is discussed in detail in Section A.2.2.

Section / Peak or Nuclide Table	Analysis Engine				
	ENV	NPP	WAN	ROI	GAM
6.7.1 ROI Peak Summary				✓	
6.7.2 Summary of ROI Peak Usage				✓	
6.7.3 Summary of ROI Nuclides				✓	
6.7.4 Summary of Peaks in Range	✓	✓			
6.7.5 Unidentified Peak Summary	✓	✓	✓	✓	✓
6.7.6 Identified Peak Summary	✓	✓	✓	✓	✓

Section / Peak or Nuclide Table	Analysis Engine				
	ENV	NPP	WAN	ROI	GAM
6.7.7 Summary of Library Peak Usage	✓	✓	✓	✓	✓
6.7.8 Discarded Isotope Peaks	✓	✓	✓	✓	
6.7.9 Summary of Discarded Peaks	✓	✓	✓	✓	✓
6.7.10 Summary of Nuclides in Sample	✓	✓	✓	✓	✓

6.7.1. ROI Peak Summary (RENROI Engine Only)

This table (Fig. 199) displays information for ROIs marked in the spectrum, with the clarifications below.

```

***** ROI PEAK SUMMARY *****
Nuclide  Peak      Centroid  Background  Net Area   Intensity  Uncert  FWHM
          Channel Energy    Counts      Counts     Cts/sec   1 sigma %  kev
-----
Cs-137   4073.06   661.64    41890.     609977.   169.438  0.17   1.407 s
Co-60    8225.61  1332.46   11935.     460983.   128.051  0.17   1.846
s - Peak fails shape tests.
D - Peak area deconvoluted.

```

Figure 199.

- ROI parameters are calculated per Section 8.1.1.5.
- Peaks in this table are arranged in ascending energy order based on ROIs marked in the spectrum when the analysis is run.
- Only ROIs with calculated uncertainty lower than the peak cutoff are included in the table.
- If the peak centroid cannot be calculated, then the peak channel is set to 0 (zero).
- The peak centroid energy is listed in units of keV.
- Peak flags are displayed to the right of the FWHM column. The designators for Deconvolution, Shape, and Multiplets (as applicable) can be modified in the [b30winds.ini](#) file.

6.7.2. Summary of ROI Peak Usage (RENROI Engine Only)

The content of this table (Fig. 200) is similar to the Summary of Library Peak Usage table described in Section 6.7.7, except that the analysis data are related only to peaks identified by ROIs marked in the spectrum. See Section 6.7.7 for a complete explanation of this table content.

```

***** SUMMARY OF ROI PEAK USAGE *****
- Nuclide - Average ----- Peak -----
Name Code Activity Energy Activity Code MDA Value
      Becquerels      keV      Becquerels Becquerels      Comments
-----
Cs-137      5.1919E+03      661.62 5.081E+03 ( 2.453E+01 1.10E+04 8.46E+01 G
Co-60      6.1689E+03      1332.51 6.037E+03 ( 2.090E+01 1.93E+03 1.00E+02 G

```

Figure 200.

6.7.3. Summary of ROI Nuclides (RENROI Engine Only)

The content of this table (Fig. 201) is similar to the Summary of Nuclides in Sample table described in Section 6.7.10, except that the analysis data are related only to nuclides with peaks identified by ROIs marked in the spectrum. See Section 6.7.10 for a complete explanation of this table content.

```

***** SUMMARY OF ROI NUCLIDES *****
Nuclide      Time of Count      Time Corrected      Uncertainty      2 sigma
              Activity          Activity            Counting          Total
              µCi/kg            µCi/kg            µCi/kg           µCi/kg
-----
Cs-137      1.4035E-01      1.4037E-01      4.7470E-04      4.8878E-02      6.777E-04
Co-60      8.2099E-02      8.2158E-02      5.8238E-04      2.8534E-02      2.559E-03
K-40      < 4.9064E-03      4.9064E-03
< - MDA value printed.
A - Activity printed, but activity < MDA.
B - Activity < MDA and failed test.
C - Area < Critical level.
F - Failed fraction or key line test.
H - Halflife limit exceeded
-----
SUMMARY
Total Activity ( 36.0 to 2588.5 keV)      2.225E-01 µCi/kg
Total Decayed Activity ( 36.0 to 2588.5 keV) 2.2252792E-01 µCi/kg

```

Figure 201.

6.7.4. Summary of Peaks in Range (RENENV and RENPP Only)

This table (Fig. 202) displays all of the peaks that were found during the analysis process with the clarifications below.

- The **Library peak list** option must be enabled on the Report tab for this table to be displayed.

***** S U M M A R Y O F P E A K S I N R A N G E *****									
Peak Energy	Area	Uncert	FWHM	Corrctn Factor	Nuclide Energy	Brnch. Ratio	Act. Bq/Kg	Nuc	
72.84	1583.	26.51	0.60	7.156E-02					
122.05	230464.	0.40	0.96	1.120E-01	122.07	85.735	3.431E+03	Co57	
					122.37	64.000	6.423E+03	Mo90	
136.50	29437.	1.69	0.97	1.144E-01	136.43	10.700	3.440E+03	Co57	
661.70	595119.	0.14	1.40	3.941E-02	661.62	85.235	2.514E+04	Cs137	
1173.23	495675.	0.23	1.76	2.374E-02	1173.23	97.727	3.032E+04	Co60	
1332.46	459455.	0.16	1.85	2.122E-02	1332.51	97.575	3.150E+04	Co60	
1460.90	840.	17.69	1.69	1.953E-02	1460.75	10.700	5.706E+02	K40	

Figure 202.

- The peak data and nuclide activity are based a peak search run with no library peaks (i.e., a Mariscotti peak search) and no peak stripping (interference correction) applied. Any peaks identified using the Library Directed Peak Search that do not overlap those found using the Mariscotti search are also included in this table.
- The “Uncert” (uncertainty) value is 1-sigma counting uncertainty, which is directly comparable to the **Peak Cutoff** acceptance criterion. Only peaks with 1-sigma counting uncertainty below the **Peak Cutoff** value are reported.
- The “Corrctn Factor” (correction factor) is the effective efficiency at the specified energy and takes into account any geometry or attenuation corrections enabled.
- The nuclide names (“Nuc”) have all non-alphanumeric characters removed for table formatting.
- All nuclides that have a photon energy within the Match Width \times Calibration FWHM of a listed peak are listed as a possible source candidate along with the peak energy, branching ratio, calculated activity, and nuclide name. The specific activity for each potential nuclide candidate is calculated under the assumption that the full peak area was generated entirely by that nuclide such that all applicable correction factors (decay, efficiency, branching ratio, sample size, etc.) are applied except for any potential peak interferences. The nuclide activity values from this table may be substituted for nuclide activity reported in the Summary of Nuclides in Sample if it is determined that the peak was misidentified or misinterpreted due to peak interferences. This type of correction may be desired in some cases for manual interference calculations, reporting of conservative activity results, or to correct for inaccurate nuclide identification. The data from this table can also be used to compare the results of the Mariscotti vs Library Directed Peak Search and fitting to help identify where library or analysis option changes may be needed.

6.7.5. Unidentified Peak Summary

This table (Fig. 203) displays peaks found in the spectrum that were not associated with a library nuclide, with the clarifications below.

***** UNIDENTIFIED PEAK SUMMARY *****							
Peak Channel	Centroid Energy	Background Counts	Net Area Counts	Efficiency * Area	Uncert 1 Sigma %	FWHM keV	Suspected Nuclide
345.33	59.48	115404.	127237.	4.333E+06	0.67	0.943	Am-241 s
522.03	88.02	119409.	347067.	3.761E+06	0.28	0.947	Cd-109
1705.66	279.16	31186.	21028.	2.469E+05	1.37	1.106	Hg-203 D
8179.28	1324.98	8173.	2780.	1.304E+05	7.30	2.499	- S
11342.96	1836.03	3829.	150120.	9.517E+06	0.26	2.150	Y-88 D
15486.83	2505.55	763.	19868.	1.740E+06	0.74	2.468	- D

s - Peak fails shape tests.
D - Peak area deconvoluted.
L - Peak written from unknown list.
C - Area < Critical level.
M - Peak is close to a library peak.

Figure 203.

- The **Unknown peaks** option must be enabled on the Report tab for this table to be displayed.
- Only peaks with 1-sigma counting uncertainty below the Peak Cutoff value are reported.
- The uncertainty displayed is based on the **Confidence level** selected on the Report tab.
- The “Suspected Nuclide” is determined by selecting the nuclide from the suspect library that has the closest peak energy to the unidentified peak energy and is within the `b30winds.ini` file “Range Multiplier” parameter multiplied by the peak FWHM. The Range Multiplier is normally set to 2.0 but you can modify this. If there are no nuclides with peak energies in the specified range, the “Unknown Suspect” text from the `b30winds.ini` file is displayed in this column (“-“ by default).
- If the `b30winds.ini` parameter “Unidentified Peak Summary and Library Peak Usage Format flag” is set to “T” (true), then the fifth column is labeled “Efficiency * Area” and displays the Net Area divided by the effective efficiency (which includes any Geometry or Attenuation corrections). If this parameter is set to “F”, then the fifth column is labeled “Intensity Cts/Sec” and displays the net count rate as shown in Fig. 204.


```

***** U N I D E N T I F I E D   P E A K   S U M M A R Y *****
Peak Centroid Background Net Area   Intensity   Uncert   FWHM   Suspected
Channel Energy   Counts   Counts   Cts/Sec   3 Sigma %   kev   Nuclide
-----
8179.28 1324.98   8173.   2780.   0.772   21.90   2.499   -   SM
15486.83 2505.55   763.   19868.   5.519   2.21   2.468   -   D
    
```

Figure 204.

- The designators for peaks flags (Deconvolution, Shape, and Multiplets as applicable) can be modified in the `b30winds.ini` file.
- The L, C, and M flags are applicable only to the RENNPP and RENENV analysis engines.

6.7.6. Identified Peak Summary

This table (Fig. 205) displays peaks that were found in the spectrum and associated with a library nuclide, with the clarifications below.

```

***** I D E N T I F I E D   P E A K   S U M M A R Y *****
Nuclide Peak Centroid Background Net Area Intensity Uncert FWHM
Channel Energy Counts Counts Counts Cts/Sec 2 Sigma % kev
-----
Co-57    732.81  122.07   52140.  213398.  59.277   0.58   0.977D
Mo-90    734.66  122.37  237520.  39718.   11.033   3.62   0.977D
Co-57    822.16  136.50   37910.  28373.   7.881    2.82   0.971
Cs-137  4072.92  661.62  38686.  577307.  160.363  0.30   1.402D
Co-60    7239.96 1173.23  25353.  475933.  132.204  0.33   1.757
Co-60    8225.91 1332.51  11804.  453528.  125.980  0.34   1.859D

s - Peak fails shape tests.
D - Peak area deconvoluted.
A - Derived peak area.
    
```

Figure 205.

- The **Library peak list** option must be enabled on the Report tab for this table to be displayed.
- If the library is not found or the spectrum is not calibrated, this table is suppressed.
- If **Manual Library Based Peak Stripping** is enabled on the Analysis tab (RENWAN only), a separate table for peak data associated with each library is reported with the library name displayed at the beginning of the table.

- The designators for Deconvolution, Shape, and Derived Area (as applicable) can be modified in the `b30winds.ini` file.
- If the `b30winds.ini` parameter “Zero Area Identified Peak flag” is set to “F” (false), then only peaks with 1-sigma counting uncertainty below the **Peak Cutoff** and those resulting from **Directed Fit** (when enabled on the Analysis tab) are included in this table. If this parameter is set to “T” (true), additional peaks that did not pass the **Peak Cutoff** may be included in the list based on the analysis engine as follows:
 - **RENWAN and RENROI:** Peak data are displayed for all peaks in the library.
 - **RENGAM:** Peak data are displayed for all peaks reported, but all library peaks may not be reported depending on peak quality, library content, and analysis settings.
 - **RENNPP:** Deconvoluted peaks that are rejected may not be included in the peak list. Only the peak background and FWHM are displayed for peaks that do not meet the peak cutoff criteria.
 - **RENENV:** Some rejected peaks may be included in the list, but peak data are not available.

6.7.7. Summary of Library Peak Usage

This table (Fig. 206) displays peaks that were found in the spectrum and associated with a library nuclide with the clarifications below.

***** S U M M A R Y O F L I B R A R Y P E A K U S A G E *****							
- Nuclide - Name	Average Code Activity µCi/Kg	Energy keV	Peak Activity µCi/Kg	Code	MDA	Value	COMMENTS
Cs-137	1.3575E-01	661.62	1.329E-01	(6.517E-04	1.50E-01	1.10E+04 8.46E+01 G
Co-60	7.7973E-02	1332.51 1173.23	7.631E-02 1.541E-01	(P +	2.582E-03 3.258E-03	3.55E-01 1.65E-01	1.93E+03 1.00E+02 G 9.99E+01 G

Figure 206.

- The **Library peak matrix** option must be enabled on the Report tab for this table to be displayed.
- If the library is not found or the spectrum is not calibrated, this table is suppressed.

- If **Manual Library Based Peak Stripping** is enabled on the Analysis tab, a separate table for data associated with each library is reported with the library name displayed at the beginning of the table.
- The table format and content are based on the analysis engine as follows:

— **RENNPP and RENENV:**

- Average Nuclide Activity and Peak Activity values have corrections applied including the activity scaling factor (based on the **Multiplier**, **Divisor**, and sample **Size** entered on the System tab) and decay.
- The column to the right of the Peak MDA is the peak 1-sigma counting uncertainty in percent.
- The first nuclide peak is one line below the applicable nuclide data.
- If the `b30winds.ini` “Zero Activity Isotope flag” flag is set to “T” (true), rejected nuclides and associated peaks are included in the table. The activity values are set to zero, but peak flags, MDA, and counting uncertainty are displayed (as well as branching ratio and half-life if applicable based on the “Unidentified Peak Summary and Library Peak Usage Format flag” flag setting). Uncertainty values may be set to a default value of zero (RENNPP) or 1E+03 (RENENV) for peaks that are rejected. This may be due to the nuclide being rejected prior to the Library Directed Fit process, the inability to physically fit a peak in the spectrum, or other peak rejection criteria. If this parameter is set to “F” (false), rejected nuclides are not displayed in this table.
- If **Directed Fit** is enabled on the Analysis tab, peak fit data associated with Directed Fit are displayed in this table. When using RENENV, all nuclides should be reported with an activity value. When using RENNPP, nuclides that fail the Key Line or Fraction Limit tests, or have interferences at key peaks, can still be reported with zero activity.
- Peak energies are listed in the library order regardless of the `b30winds.ini` parameter “Sort Nuclide Peaks by Energy flag” setting.
- If the `b30winds.ini` parameter “Zero Area Library Peak flag” is set to “T” (true), display all nuclide library peaks even if they did not pass the analysis settings criteria. If this flag is set to “F” (false), only the peaks that passed the analysis settings criteria will be displayed, and a message summarizing how many of the

library peaks were found will be displayed below the nuclide peak list (i.e., X of Y peaks found).

— **RENWAN, RENGAM, and RENROI:**

- Average Nuclide Activity is reported as Time of Count Total Activity in either μCi or Bq as selected on the System tab. This value has all corrections applied except for activity scaling factor (based on the **Multiplier**, **Divisor**, and sample **Size** entered on the System tab) and decay.
- Peak Activity is reported as Time of Count Total Activity in either μCi or Bq as selected on the System tab. This value has all corrections applied except for activity scaling factor (**Multiplier**, **Divisor**, and sample **Size**), decay, and Random Summing.
- Peak uncertainty is not reported.
- The first nuclide peak is on the same line as the nuclide data as shown in Fig. 207.

```

*****  S U M M A R Y    O F  L I B R A R Y    P E A K    U S A G E    *****
- Nuclide - Average      ----- Peak -----
Name Code Activity      Energy Activity Code MDA Value
      microCi      keV      microCi microCi      Comments
-----
Cs-137 I  1.4035E-01    661.62 1.374E-01 ( 6.631E-04 1.10E+04 8.46E+01 G
Co-60      8.3372E-02    1332.51 8.159E-02 (P 2.483E-03 1.93E+03 1.00E+02 G
          1173.23 1.507E-01 $ 3.187E-03          9.99E+01 GA

```

Figure 207.

- All nuclides are reported even when they are not identified (i.e., zero activity) regardless of the `b30winds.ini` “Zero Activity Isotope flag” parameter setting.
- If **Directed Fit** is enabled on the Analysis tab, peak fit data associated with Directed Fit are displayed in this table. When using RENWAN, nuclides that fail the Key Line or Fraction Limit tests, or have interferences at key peaks, can still be reported with zero activity.
- If the `b30winds.ini` “Sort Nuclide Peaks by Energy flag” flag is set to “T” (true), then nuclide peaks are listed in order of energy. If this parameter is set to “F” (false), then nuclide peaks are listed in the library order.

- All nuclide library peaks are displayed regardless of the `b30winds.ini` “Zero Area Library Peak flag” setting.

— All analysis engines:

- If the `b30winds.ini` “Unidentified Peak Summary and Library Peak Usage Format flag” parameter is set to “T” (true), the nuclide half-life (in days) is displayed under the COMMENTS header on the same line as the nuclide data, and the peak branching ratios are displayed in the right-most column before the peak flags. If this parameter is set to “F”, the nuclide half-life and branching ratios are omitted.
- If the `b30winds.ini` “Use Internal TCC Library Peaks” parameter is set to “T” (true), the nuclide peaks in this table (and throughout the analysis process) will be based on the internal TCC library including the peak list and peak order which may (and likely will) differ from the original analysis library. Additionally, any peak flags set in the library are discarded. This configuration may not generate optimal results for some applications. If this parameter is set to “F”, the peak list, peak order, and peak flags from the original library are used for analysis. Only the Branching Ratio is adjusted for the coincidence summing correction. This configuration allows for improved optimization of the analysis results.
- The legend of Nuclide Codes shown after the nuclide name, Peak Codes shown at the far right, and Peak Flags shown after the Peak Activity are reported after this table. These are explained in the following section.

6.7.7.1. Summary of Library Peak Usage Flags

This table (Fig. 208) is displayed after the Summary of ROI Peak Usage and Summary of Library Peak Usage sections of the report. The Nuclide and Peak Codes listed at the bottom of the table are based on flags set in the analysis library. The Peak Flags are defined as follows:

- (This peak was used in the average nuclide activity calculation (even if any other symbols are displayed). For more information on the Weighted Average Nuclide Activity, see Section 8.6.1.
- * The peak FW10M and FW25M were wider than the calibrated shape by more than 20% which would indicate that this might be a multiplet. However, deconvolution was not possible because only one peak was in the library.

```

( - This peak used in the nuclide activity average.
* - Peak is too wide, but only one peak in library.
! - Peak is part of a multiplet and this area went
  negative during deconvolution.
? - Peak is too narrow.
@ - Peak is too wide at FW25M, but ok at FWHM.
% - Peak fails sensitivity test.
$ - Peak identified, but first peak of this nuclide
  failed one or more qualification tests.
+ - Peak activity higher than counting uncertainty range.
- - Peak activity lower than counting uncertainty range.

= - Peak outside analysis energy range.
& - Calculated peak centroid is not close enough to the
  library energy centroid for positive identification.
P - Peakbackground subtraction

Nuclide Codes:                               Peak Codes:
T - Thermal Neutron Activation                G - Gamma Ray
F - Fast Neutron Activation                   X - X-Ray
I - Fission Product                          P - Positron Decay
N - Naturally occurring isotope              S - Single-Escape
P - Photon Reaction                          D - Double-Escape
C - Charged Particle Reaction                K - Key Line
M - No MDA Calculation                       A - Not in Average
R - Coincidence Corrected                    C - Coincidence Peak
H - Half-life limit exceeded

```

Figure 208.

- ! This peak was in an area that was deconvoluted and the area of this component was zero or negative. The peak was then removed as a component and the deconvolution redone. This usually indicates the peak was not present or the energy calibration needs adjustment.
- ? The peak FW25M is less than 80% of the calibration FW25M. This usually indicates that the peak has poor shape.
- @ The peak FW25M was wider than the calibrated shape by more than 20%, but the FWHM was within 20% of the calibrated FWHM. This indicates there might be a small peak near the main peak that may need to be included in the library.
- % The 1-sigma counting error was greater than the **Peak Cutoff** value set on the Analysis tab.
- \$ This peak was identified as belonging to this nuclide, but the first non-interfered peak for this nuclide was not identified or was disqualified. This may indicate that this peak was not generated by the respective nuclide.

- + The abundance for this peak was higher than the running average of those included at this point. For more information on the Weighted Average Nuclide Activity, see Section 8.6.1.
- The abundance for this peak was lower than the running average of those included at this point. For more information on the Weighted Average Nuclide Activity, see Section 8.6.1.
- = This peak was outside the user-specified limits for the analysis.
- & When the library-directed centroid was recalculated after background subtraction, the centroid value was outside the energy limits such that the peak could not be attributed to this nuclide. This may occur with very small peaks where the peak shape is not well defined, when the energy calibration needs adjustment, or if the library peak energies need to be corrected.
- } The peak area for this peak was derived using other peaks for this nuclide. This is enabled by the library-based peak stripping option.
- P Peak Background Subtraction was applied to this peak. (See Section 8.9.4 for details on peak background subtraction.)

6.7.8. Discarded Isotope Peaks

This table (Fig. 209) displays peaks associated with a nuclide that was rejected during the analysis due to a failed Key Line or Fraction limit test, with the clarifications below.

- Isotopes may be discarded when using RENWAN, RENROI, and RENNPP analysis engines because the rejection criteria are evaluated after the Library Directed Peak Search has associated peaks with a nuclide. For RENGAM and RENENV analysis engines, this table should be empty because the Key Line and Fraction Limit tests are implemented during the Library Reduction step at the beginning of the analysis process before the Library Directed Peak search, which assigns nuclide peaks.
- If the `b30winds.ini` parameter “Print Discarded Peak Table flag” is set to “T” (true), this table is displayed for all analysis engines except for RENGAM. If this parameter is set to “F” (false), this table is suppressed.

```

***** D I S C A R D E D   I S O T O P E   P E A K S *****
Nuclide Centroid  Background  Net Area   Intensity  Uncert    Activity
          Energy    Counts      Counts     Cts/sec   1 Sigma %
-----
Co-57    122.05    52140.    213398.    59.277    0.29    3.177E+03
Co-57    136.50    37910.    28373.     7.881     1.41    3.316E+03
P - Peakbackground subtraction

```

Figure 209.

6.7.9. Summary of Discarded Peaks

This table (Fig. 210) displays peaks that were evaluated during the Library Directed Peak Search and rejected from use in calculating Nuclide Activity, with the following notes:

```

***** S U M M A R Y   O F   D I S C A R D E D   P E A K S *****
122.07  Co-57    136.43  Co-57    1173.23 + Co-60    1460.75 % K-40

! - Peak is part of a multiplet and this area went
    negative during deconvolution.
? - Peak is too narrow.
@ - Peak is too wide at FW25M, but ok at FWHM.
% - Peak fails sensitivity test.
$ - Peak identified, but first peak of this nuclide
    failed one or more qualification tests.
+ - Peak activity higher than counting uncertainty range.
- - Peak activity lower than counting uncertainty range.
= - Peak outside analysis energy range.
& - calculated peak centroid is not close enough to the
    library energy centroid for positive identification.
P - Peakbackground subtraction

```

Figure 210.

- A peak may be rejected due to failing a peak test, rejection of the nuclide due to key line or fraction limit tests, peak activity outside the uncertainty range for the nuclide average activity, as well as other factors.
- This table is displayed only when the **Library peak matrix** option is *disabled* on the Report tab.
- See Section 6.7.7.1 for peak flag descriptions.

6.7.10. Summary of Nuclides in Sample

This table (Fig. 211) displays the final nuclide activity results with the clarifications below.

- The **Nuclide abundance** option must be enabled on the Report tab for this table to be displayed.
- If the library is not found or the spectrum is not calibrated, this table is suppressed.

```

*****  S U M M A R Y  O F  N U C L I D E S  I N  S A M P L E  *****
Nuclide  Time of Count  Time Corrected  Uncertainty  2 Sigma  MDA
          Activity      Activity          Counting      Total
          Bq/Kg         Bq/Kg           Bq/Kg         Bq/Kg
-----
Cs-137   5.2932E+05  5.2938E+05  1.5036E+03  1.8574E+05  2.832E+04
Co-57    5.8342E+04  5.8639E+04  4.2554E+02  2.1081E+04  1.802E+04
Co-60    6.1311E+05  6.1355E+05  1.3755E+03  2.1397E+05  3.399E+04
K-40    < 1.9763E+05  1.9763E+05
Mo-90    < 1.4860E+04  1.8922E+04
Y-88     3.4829E+05  3.5282E+05  1.9920E+03  1.2363E+05  4.062E+04
# - All peaks for activity calculation had bad shape.
* - Activity omitted from total
& - Activity omitted from total and all peaks had bad shape.
< - MDA value printed.
A - Activity printed, but activity < MDA.
B - Activity < MDA and failed test.
C - Area < Critical level.
F - Failed fraction or key line test.
H - Half-life limit exceeded
I - ISO NORM MDA ratio at maximum for one or more peaks

----- S U M M A R Y -----
Total Activity ( 36.0 to 2588.5 keV)  2.981E+06 Bq/kg
Total Decayed Activity ( 36.0 to 2588.5 keV)  1.4957548E+06 Bq/kg

```

Figure 211.

- Nuclide Activity Notes:
 - The “Time of Count” Activity column is weighted by the peak branching ratios as described in Section 8.9.2, and includes all corrections except for decay during collection and decay to collection time. Note that this includes **Decay During Acquisition**, which is set on the Decay tab.
 - The “Time Corrected Activity” column is weighted by the peak branching ratios as described in Section 8.9.3, and has all corrections applied including decay. It is only displayed in this table when **Decay During Collection** or **Decay to Collection Time** is enabled on the Decay tab.

- **Uncertainty Notes:**
 - Uncertainty Counting and Total Uncertainty data are reported in either percent or activity units as specified on the Report tab.
 - The Total Uncertainty column is only displayed if the Total Uncertainty option is specified on the Report tab.
 - If activity is set to zero, which may occur when using **Directed Fit**, the default percent uncertainty is 1000%.
 - Uncertainty is omitted, or set to zero for some analysis engines, if the nuclide activity is reported with the “<” flag (i.e. less than the calculated MDA value.)
- **MDA Notes:**
 - Nuclides that have the “No MDA Calculation” flag set in the library will not calculate an MDA value. If an activity value is not calculated, these nuclides will be omitted from this table.
 - When a nuclide is reported with the “<” flag, the MDA values are displayed in the Time of Count and Time Corrected Activity columns as applicable.
 - For all analysis engines except for RENGAM, if the `b30winds.ini` parameter “Print MDA flag” is set to “T” (true), the MDA value is reported in the far right column for nuclides that have an activity value calculated. If this parameter is set to “F” (false), nuclide MDA is not reported for nuclides that have an activity value calculated. The RENGAM analysis engine does not report MDA values when nuclide activity is calculated regardless of this flag setting.
 - The MDA Column header is determined by the `b30winds.ini` parameter “Nuclide Summary MDA Header,” which is set to “MDA” by default.
- Total Activity and Total Decayed Activity at the bottom of the table are the sum of the respective nuclide activity columns except that nuclides marked with the following flags are not included in the totals: *, &, <, B, F, (H for Decay Activity only).
- Some nuclide flags may not be reported if no nuclides in the list meet the specified criteria. Nuclide flags are defined as follows:

- # - All peaks for the activity calculation had bad shape. This does not invalidate the nuclide activity, but may indicate that the peaks may have interference, few counts (as may also be accompanied with high uncertainty), tails due to detector performance, or other anomalies that may warrant investigation.
- * - This nuclide activity was omitted from the total activity because the “Activity Not in Total” flag was set for this nuclide in the library.
- & - This nuclide activity was omitted from the total activity because the “Activity Not in Total” flag was set for this nuclide in the library, and all of the peaks had bad shape. This flag is a combination of the # and * flag conditions.
- < - The nuclide MDA is reported in the Time of Count and Decay Corrected activity columns as applicable.
- A - The nuclide activity is lower than the calculated MDA value. This condition does not necessarily mean that the nuclide activity is invalid or that the true activity must be below the detection limit. This condition may be due to a liberal peak acceptance criterion (i.e., **Peak Cutoff**), using **Directed Fit** in the analysis options for nuclides with no substantial peaks, or when nuclide activity is near the detection level depending on the MDA method specified on the System tab. Further investigation may be warranted for this condition.
- B - This flag is a combination of the “A” and “F” flags. Activity is less than the calculated MDA, and the Key Line or Fraction limit test failed.
- C - The nuclide activity is lower than the Critical Level MDA method, which is based on the MDA Method 2 described in Section 8.8.2.1. This condition may be due to a liberal peak acceptance criteria (i.e., **Peak Cutoff**), or when using **Directed Fit** in the analysis options for nuclides with no substantial peaks. Further investigation may be warranted for this condition.
- F - The Fraction Limit or Key Line test failed for this nuclide. Normally, nuclides that fail one of these tests would be reported as <MDA, but some conditions (i.e., **Directed Fit** or when using the RENWAN analysis engine) may result in nuclide activity being reported.
- H - The number of half-lives specified in the `b30winds.ini` file for the “Half lives decay cutoff” parameter has been exceeded for this nuclide. If this occurs, the Time of Count Activity is reported as “>X Halflives” and the Time of Count Activity is reported based on the analysis engine as follows:

- **RENWAN, RENROI, and RENENV:** Time of Count activity is reported.
- **RENGAM:** The “<” flag and MDA value are reported.
- **RENNPP:** Time of Count activity is omitted.

I - Not used in Renaissance.

7. THE NAI REPORT

A typical Renaissance report for NaI spectra is shown in Figs. 212 through 217. The exact details of the report depend on the options selected and the spectrum, calibration, and libraries.

7.1. First Page

The first page of the report (Fig. 212) shows all the bookkeeping data that are stored with the spectrum files along with other messages about the analysis.

```
ORTEC      S V - I ( 63) GSA      WIN7.32  21-NOV-2014 10:39:25 Page    1
ORTEC                                           Spectrum name: SN1250 1.5 cm

Sample description
Co-60, Co-57 & Cs-137, 20 ml bottles 1.5 cm from endcap SN1250

Spectrum Filename: C:\Dev\Gsa60\Gsa60VandVFiles\Eff Calib\SN1250 1.5 cm.An1

Acquisition information
Start time      22-Oct-2014 15:48:29
Live time       1872
Real time       1927
Dead time       2.82%
Detector/Geometry IDs      0 &      0

Detector system
JGUO-digiBASE-RH SN 5

Calibration
Filename: SN1250 1.5 cm away good peaks.Sp
Created: 19-Nov-2014 08:34:48 & 19-Nov-2014 08:48:23
Mixed gamma src calibration. SN 1250

Zero offset     -8.167 keV; Gain      1.932 keV/channel
Quadratic       0.141E-03 keV/channel^2
```

Figure 212. First Page of NaI Report.

PROGRAM NAME

The report-generating program's name is listed at the top of the report and does not change.

INPUT/REPORT CODE

The number in parentheses represents the operator input requests and the status on the program's ability to fulfill these requests. Normally, this code just confirms that the proper analysis was performed. In the case where the output report does not appear to be the correct form, this code can help locate the difficulty (see Section 6.1).

ANALYSIS VERSION NUMBER

As updates to the internal algorithms are made, this number is changed. It is only useful when requesting assistance for a particular spectrum.

ANALYSIS DATE AND TIME

Self-explanatory.

SAMPLE DESCRIPTION

The sample description is from the spectrum file. The **.SPC** file description is 128 characters (two lines) and the **.CHN** file description is 63 characters (one line).

SPECTRUM FILENAME

This is the input name for the original name of the **.SPC** file.

ACQUISITION INFORMATION

This information is derived from the spectrum file and includes the date the spectrum was collected; the live-time, real-time, and dead-time values; and information (if present) about the detector geometry.

DETECTOR SYSTEM

The detector description from the MCB Configuration program.

CALIBRATION

The calibration filename and description are from the spectrum file if it is an **.SPC** file. If the file is a **.CHN** file, a message is printed that the calibration is from MAESTRO. The **CREATED** field lists the date the calibration calculation was performed (not the collection date of the calibration spectrum).

In addition, the energy factors are the offset and slope and (where present) quadratic factor from the calibration file.

The rest of page 1 is shown in Fig. 213.

LIBRARY FILENAME

The analysis library filename is printed. If the library was not found, a “not found” message is printed here. If library-based peak stripping was used, a message is printed.

ANALYSIS PARAMETERS

This section includes the Analysis Range (stop/start channels) and background width (Background Type) on the Sample tab under **Analyze/ Settings/Sample Type...**; the activity scaling factor (Multiplier/Divisor), peak acceptance width (Match Width) and Fraction Limit on the System tab; and the MDA Factor and Decay Limit on the Analysis tab. Note that the activity scaling factor changes the output activities from the internal unit, becquerels, to the requested unit. A value of 1.0 leaves the activities in becquerels.

```

Library Files
  Main analysis library:      SM1250.lib
  Library based peak stripping used.

Analysis parameters
  Start channel      10 for an energy of  11.17keV
  Stop channel      1024 for an energy of 2117.92keV
  Activity scaling factor  1.0000E+00/( 1.0000E+00* 1.0000E+00)
                        = 1.0000E+00
  MDA Factor        2.5300000E+00
  Fraction limit    0.0000000E+00
  Decay limit       1.2000000E+01
  Background width  average of three points.

  Peak acceptance width  7.4000E-01

Corrections          Status      Comments
Decay correct to date      NO
Decay during acquisition   NO
Peaked background correction NO
Background stripping       YES  C:\User\NaI Bkg.Spc
Absorption (Internal)     NO

```

Figure 213. NaI Report Page 1, continued.

CORRECTIONS

All of the available corrections are listed along with the on/off status. If the decay correction was off, the decay-corrected activity is blank. If background stripping was enabled, the stripping file is printed. Note that if decay during acquisition was enabled, the correction may be very small due to the ratio of the half-life to the real time, thus the effect may not be obvious in the output activity.

7.2. Unidentified Peak Summary

Figure 214 shows the second page of the report. The first section of this page provides the peak/energy matrix of the unidentified peak summary. You can suppress this table.

```

***** UNIDENTIFIED PEAK SUMMARY *****
  PEAK CENTROID  BACKGROUND  NET AREA  EFFICIENCY  UNCERT   FWHM
  CHANNEL  ENERGY  COUNTS  COUNTS  * AREA  1 SIGMA %  keV
  +-----+-----+-----+-----+-----+-----+-----+-----+
    31.14   89.07   633650.  126686.  2.997e+05  0.93  31.113  -  sD
    283.49  913.49   72774.   3950.   6.249e+04  9.79  63.007  |

  s Peak fails shape tests.
  D Peak area deconvoluted.

```

Figure 214. Unidentified Peak Summary on Page 2.

PEAK CHANNEL

Peak channel as determined by the peak finder (see page 249). It is reported to two decimal places, but normal variation can be in the tenths of a channel.

CENTROID ENERGY

Peak centroid in energy if the spectrum is calibrated, zero otherwise. This is the first column converted to energy according to the energy coefficients in the calibration data. This, too, is reported to the nearest hundredth of a channel. Peaks are included in the unknown list if they are too far from a library peak, so these extra digits might be of use.

BACKGROUND COUNTS

The background under the peak.

NET AREA COUNTS

The fourth column shows the net area which is the gross area minus the background area. The area is calculated by the summation method for singlets and by the fitting method for multiplets.

EFFICIENCY * AREA

This column shows the peak area times the efficiency at this energy — *or* — the net area divided by the live time to yield the counts/second for the peak. To choose which will be printed, edit `g30winds.ini` (Section A.2.3).

UNCERTAINTY

The counting uncertainty for this net peak area, as selected on the Report tab under **Analyze/Settings/Sample Type...** The choice of 1-, 2-, or 3-sigma value is operator selected.

FWHM

The FWHM of the net peak area. This is in energy if the spectrum is calibrated, otherwise it is in channels.

The final column lists the peak flags (if any) for each peak channel. They are explained beneath the table. For acceptable peaks, or if the spectrum is not calibrated, the column is blank. The deconvolution symbol is listed if the peak is within the deconvolution range of a library peak or peaks. If this occurs, this region of the spectrum should be investigated to see if the line should be added to the library to ensure that the peak areas are correctly calculated. It can also mean that the system is not correctly energy calibrated.

7.3. Identified Peak Summary

The next section (Fig. 215) shows the peak/energy matrix for the library peaks. The library name is printed at the beginning of the list. They are arranged in ascending energy order. The list can be suppressed. It will not be generated if the library is not found or the spectrum is not calibrated.

```

-----
This section based on library: SN1250.lib

***** I D E N T I F I E D   P E A K   S U M M A R Y *****
NUCLIDE      PEAK CENTROID BACKGROUND NET AREA INTENSITY UNCERT FWHM
              CHANNEL  ENERGY  COUNTS  COUNTS  CTS/SEC  2 SIGMA % keV
-----
AM-241      34.32   58.31   617805.  317767.  169.718   0.80  12.603
CD-109      49.62   88.04   856505.  458802.  245.044   0.66  14.190
CO-57       67.37  122.63   556341.  176641.   94.344   1.30  15.677
CE-139      89.48  165.83   510784.  196655.  105.033   1.20  20.286
HG-203     147.80  280.44   407887.  180966.   96.653   1.31  36.979
SN-113     205.54  394.88   454045.  193409.  103.299   1.40  49.888
CS-137     339.63  664.23   418584.  154997.   82.783   1.94  74.212
Y-88       455.15  900.34   467835.  166350.   88.847   2.03  94.233
CO-60      586.43 1173.24   393307.   76534.   40.877   4.16  89.755D
CO-60      661.98 1332.50   611459.  117756.   62.893   4.13 166.062D
Y-88      891.72 1826.65  134139.   24462.   13.065   6.80  96.218s

s Peak fails shape tests.
D Peak area deconvoluted.
A Derived peak area.
    
```

Figure 215. Identified (Library) Peak List.

LIBRARY USED

Library file used for the peak list table.

NUCLIDE

Self-explanatory.

PEAK CHANNEL

Peak channel as determined by the peak finder (see page 249). If the peak centroid cannot be found, this is set to 0, along with the remaining entries on this line. It is reported to two decimal places, but normal variation can be in the tenths of a channel.

CENTROID ENERGY

Peak centroid in energy if the spectrum is calibrated, zero otherwise. This is the first column converted to energy according to the energy coefficients in the calibration data. This, too, is reported to the nearest hundredth of a channel. Peaks are included in the unknown list if they are too far from a library peak, so these extra digits might be of use.

BACKGROUND COUNTS

The background under the peak. In most cases this is the straight-line background, but can be the stepped background in a deconvoluted region.

NET AREA COUNTS

The gross area minus the background area. The area is calculated by the summation method for singlets and by the fitting method for multiplets.

INTENSITY CTS/SEC

The net area divided by the live time to yield the counts/second for the peak — *or* — the peak area times the efficiency at this energy. To choose which will be printed, edit `g30winds.ini` (Section A.2.3).

UNCERTAINTY

The counting uncertainty for this net peak area. All library peaks are reported, even if their error exceeds the input sensitivity cutoff.

PEAK WIDTH

The next column shows the FWHM of the net peak area.

The last column shows a symbol if the peak is too wide or too narrow as compared to the shape calibration, or a different symbol if the peak area was deconvoluted. Otherwise it is blank. The symbol explanations are printed at the bottom of the list.

7.4. Library Peak Usage

Figure 216 shows the isotope/peak matrix or summary of library peak usage. You can suppress this section. It is not available if the library is not found or the spectrum is not efficiency calibrated. If library-based peak stripping is enabled, there will be a separate list for the two analysis libraries. The library name is printed at the beginning of the list.

NUCLIDE

Arranged in library order.

AVERAGE ACTIVITY

In becquerels or other units. This number has not been normalized by the scaling factors, but does include the decay during acquisition correction.

PEAK ENERGY keV

Peak energies for each nuclide, in library order. This is the library energy.

```

***** SUMMARY OF LIBRARY PEAK USAGE *****
NUCLIDE      AVERAGE          PEAK
              ACTIVITY          -----
              Becquerels      ENERGY      ACTIVITY CODE      MDA VALUE
              Becquerels      keV          Becquerels      Becquerels      COMMENTS
+-----+-----+-----+-----+-----+-----+-----+-----+-----+
|
CO-57      9.70495E+02      122.07      9.705E+02      (      2.1755E+01
              136.43      0.000E+00      -      1.9842E+02

CO-60      3.45939E+03      1173.24      2.355E+03      [(      1.0375E+02
              1332.50      4.563E+03      (      1.3068E+02

CS-137      2.34540E+03      661.62      2.345E+03      (      4.4390E+01
              ( - This peak used in the nuclide activity average.

= - Peak outside analysis energy range.
P - Peakbackground subtraction
- - Peak activity lower than critical level.
[ - Fwhm is more than 20% from calibrated value
) - Peak is too close to another for the activity
   to be found directly.

```

Figure 216. Library Peak Use Summary.

PEAK ACTIVITY

The activity based only on this peak. For a nuclide with only one peak, this is the same as the entry in column 2.

PEAK CODE

The next column can contain a symbol which shows whether or not the peak passed various tests. These symbols can be used to determine how to change the analysis in order to obtain better results.

The symbols have the following meanings:

% The 1-sigma counting error was greater than the user-set sensitivity cutoff value.

- The abundance for this peak was lower than the critical level.

P Peak background subtraction was done on this peak.

The next column can contain a symbol, (, that indicates which peaks were used in the average activity calculation for this nuclide. There could be a symbol in the previous column indicating that the peak did not pass a test, but if the (is present, it was used in the activity calculation.

PEAK MDA

The MDA for this nuclide, based on this peak only.

PEAK HALF LIFE IN DAYS

The half-life in days. This column can be suppressed by modifying g30winds.ini.

PEAK BRANCHING RATIO

For this energy for this isotope. This column can be suppressed by modifying g30winds.ini.

COMMENTS

This column may overwrite the HALF LIFE and BRANCHING RATIO.

7.5. Summary of Nuclides in Sample

Figure 217 shows the last page of the report, which lists the activity in the sample.

```

*****  S U M M A R Y  O F  N U C L I D E S  I N  S A M P L E  *****
          TIME OF COUNT   UNCERTAINTY 2 SIGMA
NUCLIDE   ACTIVITY       COUNTING   TOTAL
          Bq/Kg
+-----+-----+-----+-----+
CD-109    6.1611E+04    6.6402E-01%  6.9451E+00%
AM-241    5.5002E+03    8.0145E-01%  6.9596E+00%
CO-57     9.7050E+02    1.3002E+00%  7.0345E+00%
CO-60     3.4594E+03    4.1447E+00%  7.5260E+00%
CS-137    2.3454E+03    1.9422E+00%  7.1810E+00%
  < - MDA value printed.
  A - Activity printed, but activity < MDA.
  B - Activity < MDA and failed test.
  C - Area < Critical level.
  F - Failed fraction or key line test.
  H - Halflife limit exceeded
----- S U M M A R Y -----
TOTAL ACTIVITY ( 11.2 to 2117.9 keV) 8.1146461E+04 Bq/Kg

Analyzed by: _____
              Callie Kitts

Reviewed by:  _____
              Supervisor

Laboratory:  ORTEC
    
```

Figure 217. Final Analysis Summary.

If the spectrum is not efficiency calibrated or the library is not found, this table is suppressed. The nuclides are arranged in library order. The activity is the average activity multiplied by the scale factor. The column label is entered by the operator. If decay correction is requested, the decay-corrected activity is also printed (decay correction is turned off in Fig. 217). If the nuclide is not found, the MDA value is printed with a < symbol after the nuclide name, and no error. The total activity is the scaled sum of the decay-corrected activity, if present, or the time-of-count activity. The MDA values are not included in the total.

8. ANALYSIS METHODS — GE

The Renaissance software incorporates five analysis engines from GammaVision. These programs provide the kernel of functions necessary for analysis of gamma-ray spectra acquired with HPGe detectors. Described here are the calculations performed and the algorithms employed by these analysis engines.

HPGe detector spectra are characterized by high-resolution peaks which results in separated peak areas and good signal-to-noise ratios. These engines were developed to analyze HPGe spectra. Their main features include: (1) peak search algorithms appropriate to HPGe spectra; (2) activity analysis algorithms for HPGe spectra for multiplet decomposition and identifying and quantifying the activities of nuclides present.

Renaissance analyzes spectrum files and produces a list of the background, net area, counting uncertainty, FWHM, and net count rate for all peaks in the spectrum. If possible, it also gives a list of the average activity of the nuclides in the sample, the activity of each nuclide based on each gamma-ray energy in the library, the MDA for each peak energy of all nuclides in the library, and the reasons the unacceptable peaks were not used for the activity calculation. Peaks that are not the correct shape (according to the calibration) are marked as such; peak areas that are the result of deconvolution of overlapping energies are also marked; gamma-ray energies not in the analysis library are reported as suspected nuclides if a suitable candidate is found in the suspected nuclide library.

The result is a report containing all the descriptions stored with the spectrum file, the analysis parameters, user inputs, and the list of peaks and nuclides found in the spectrum. The standard Renaissance HPGe report is discussed in Chapter 6.

8.1. The Analysis Engines

8.1.1. Analysis Engine Options

RENGAM includes five analysis engines, which are discussed in general terms below. Each one handles the analysis sequence in a slightly different manner. The traditional engines were RENWAN and RENGAM. RENNPP and RENENV were created in more recent years to meet applications for which RENWAN and RENGAM were not optimized. RENROI allows you to choose which spectral regions are to be analyzed, after which the unmarked parts of the spectrum are evaluated with a simplified RENWAN analysis. All five routines produce a report file (.RPT) and a binary output (.UFO) file. The following is a basic summary of processes used by each analysis engine. Section 8.1.2 contains a decision matrix to assist you in choosing an analysis routine.

8.1.1.1. RENWAN

RENWAN does a preliminary library-based peak search of the spectrum. The analysis assumes that all gamma-ray listed in the library exist in the spectrum so it tries to fit a peak at every energy listed in the library. The **Peak Cutoff** value specified in the Sample Defaults File (.SDF) is compared to the 1 sigma counting uncertainty for each peak to determine if that energy will be used for further analysis. With a large **Peak Cutoff** value (> 200), this engine can “find” false peaks. A Mariscotti peak search is then implemented on the remainder of the spectrum. For nuclides with no clean (well resolved) gamma rays **RENWAN** offers **Manual-Based** peak stripping.

8.1.1.2. RENGAM

RENGAM does a preliminary Mariscotti peak search of the spectrum and removes library nuclides for which sufficient energy peaks were not found based on **Fraction limit**. A library-based peak search is then performed using the reduced library. This analysis engine is used for specialized applications and generally should not be selected. **RENGAM** overcomes the false-positive weakness of “library-directed” analysis when the sample is completely unknown, and the activity-accuracy weakness of the traditional “matrix” method.

In most cases, the MDA for a nuclide will not be reported because all nuclides without gamma rays in the spectrum will have been removed from the library. In a few cases, the nuclide will be eliminated in the deconvolution step and the MDA will be reported for this case. To remove these possibilities, go to the System tab under **Analyze/Settings/Sample Type...** and select **Suppress Output** from the **MDA Type** droplist.

For information on library reduction during **RENGAM** analysis, see Section 8.1.3.

8.1.1.3. RENNPP

RENNPP does a preliminary library-based peak search like **RENWAN**. Gain shift corrections can be applied for an accurate determination of peak energy and associated nuclide activity. After the Library-based analysis is complete, a Mariscotti peak search is used to find any peaks that were not included in the library or did not pass the library peak search criteria. A **Directed Fit** can also be used to generate negative peak areas to meet environmental reporting requirements for singlet peaks. Standard reports have a “Summary of Peaks in Range” section that displays potential library matches and associated activity concentration for each peak found during analysis. **RENNPP** and **RENENV** do especially well with **Library-Based** peak stripping.

For the deconvolution of multiplets in the re-analysis phase, the peaks are allowed to shift in energy, up to two channels. The entire multiplet moves as a group. This gives more accurate peak areas when the energy shifts between the calibration and the sample spectrum. (Note that this is in addition to the recalibration for energy for the entire spectrum.)

8.1.1.4. RENENV

RENENV does a preliminary Mariscotti peak search of the spectrum and removes library nuclides for which sufficient energy peaks were not found. A library-based peak search is then performed using the reduced library. Gain shift corrections can be applied for an accurate determination of peak energy and associated nuclide activity. A **Directed Fit** can also be used to generate negative peak areas to meet environmental reporting requirements for singlet and multiplet peaks. Standard reports have a “Summary of Peaks in Range” section that displays potential library matches and associated activity concentration for each peak found during analysis.

For more information on library reduction during RENENV analyses, see Section 8.1.3.

8.1.1.5. RENROI

The RENROI analysis engine operates on the entire spectrum, performing an ROI analysis on user-marked ROIs and a modified RENWAN analysis (no peak stripping or directed fit) on unmarked regions. You can either mark ROIs on a live or retrieved spectrum, then use the **Analyze/Entire Spectrum in Memory** command; or use the **Analyze/Spectrum on Disk** command on a spectrum file in which ROIs have already been marked and saved.

ROI Analysis

- 1) The ROI center is used to calculate the ROI peak energy using the existing energy calibration. If the ROI peak energy is within the match width of a library peak, then the ROI will be used. *Otherwise, the ROI will be ignored.* In other words, **do not mark an ROI around unknown peaks.**
- 2) To calculate the ROI peak background, you can set the number of background points to be used at 1, 3 or 5 on the Sample tab under **Analyze/Settings/Sample Type....** *If Auto background is selected, then 5 points will always be used.* The background points to be used for the background calculation are within the selected ROI region, not adjacent and outside the ROI region.
- 3) The background of the ROI peak is calculated as:

$$B = \left(\frac{B_1 + B_2}{2 * N} \right) * (H - L + 1) \quad (20)$$

where:

L = the lowest-energy channel of the ROI

H = the highest-energy channel of the ROI

N = 1, 3, or 5, depending on the background method chosen, as discussed above.

and the sum of background counts on the low and high end of the ROI, B_1 and B_2 , respectively, are given by:

$$B_1 = \sum_1^N C_{LB}$$

$$B_2 = \sum_1^N C_{HB}$$
(21)

where

C_{LB} = counts per background channel at the low end of the ROI

C_{HB} = counts per background channel at the high end of the ROI

4) The gross counts within the ROI are calculated as:

$$G = \sum_L^H \text{Counts in ROI}$$
(22)

5) The net peak area is the adjusted gross counts minus the adjusted calculated background, as follows:

$$A_{ag} = G - (B_1 + B_2)$$
(23)

thus:

$$A = A_{ag} - B \left(\frac{H-L+1-2N}{H-L+1} \right)$$
(24)

where all parameters have been defined above. If the 3-point background method is chosen on the Sample tab (page ?), all three parameters calculated above — B , G , and A — should be the same as calculated with the **Peak Info** method (Section ?).

6) This simplifies to:

$$A = B - G$$
(25)

Additional Considerations

- If there are multiple ROIs defined for a nuclide, then only the first ROI peak is used to calculate the nuclide activity.
- In RENROI engine, if a nuclide has multiple peaks and only one peak is marked with a ROI, then the nuclide activity displayed is the activity of only the marked ROI peak.
- In the RENWAN analysis results section of the report, the nuclide activity is the same as the activity reported in the ROI Peak Summary section of the report.

8.1.2. Selecting an Analysis Engine — Decision Matrix

A library-based peak search looks for potential peaks for all gamma rays listed in the library.

Sensitivity is set by the **Peak-Cutoff** settings. A Mariscotti peak search uses a second differential method to identify peaks. Sensitivity is set by the **Peak-Search Sensitivity** setting. Mariscotti peak searches do a better job of identifying peaks within multiplets; library-based peak searches will do a better job of finding a weak or misshapen peak listed in the library.

Feature	ENV	WAN	NPP	GAM	ROI
Uses an initial Mariscotti peak search	✓			✓	
Uses an initial library-based peak search		✓	✓		✓
ROI peak search on user-marked peaks					✓
Library based peak stripping	✓	✓	✓		
Manual based peak stripping		✓			
Removes nuclides from library not found in a preliminary peak search	✓		✓	✓	
Reports MDA for removed nuclides	✓		✓		
Utilizes gain shift corrections	✓	✓	✓	✓	
Directed fit (negative or misshapen peak areas) option available	✓ ^a	✓ ^b	✓ ^b		
More sensitive in finding misshapen peaks		✓	✓		✓
Displays all possible library nuclide matches and calculates activity for all peaks found.	✓		✓		✓

^aSinglets and multiplets.

^bSinglets only.

8.1.2.1. Guidelines for Selecting an Analysis Engine

- 1) Decide which peak search method is best for your application.
- 2) Establish the sensitivity for the peak search (**Peak Cutoff** for library directed; **Sensitivity** for Mariscotti).
- 3) Decide if an accurate analysis of the multiplets is important. If so, select RENNPP or the RENENV analysis engine.
- 4) Notice if there are false negatives in your answers. That is nuclides have been initially detected and later dropped. If so, revert to the RENWAN analysis engine.

8.1.3. Library Reduction Based on Nuclide Rejection (RENENV and RENGAM Analysis Engines Only)

At the start of an analysis using the RENENV or RENGAM engine, a raw peak search is performed on the spectrum. The list of peaks found is compared to the peaks in the library, and the nuclides not likely to be present are removed from the library. After this library reduction step, a library-directed peak search is performed similar to RENNPP (for RENENV) or RENWAN (for RENGAM) to find and fit peaks, then quantify nuclide activity. After this analysis, the raw data (Mariscotti) peak search is run again to pick up any peaks not accounted for in the library-directed search. Finally, if **Directed Fit** is turned on, any peaks in the library that were previously rejected are now fitted using **Directed Fit** formulation (Section 8.2.2.2) and the activity is calculated for nuclides that were previously not reported. If the “ENV factor” in `b30winds.ini` (page 391) is zero, this test is not performed.

8.1.3.1. Details of Library Reduction

Following is a more detailed description of the library reduction phase of the RENENV and RENGAM analysis:

- 1) If the first peak for a nuclide in the library is not found meeting the peak cutoff, then that nuclide is removed from the analysis.
- 2) If the first peak for a nuclide in the library is found meeting the peak cutoff limit then each subsequent peak for that nuclide (to a maximum of three peaks per nuclide) is evaluated to determine if the nuclide should be removed from the analysis as follows:
- 3) For each subsequent peak i (to the maximum of three per nuclide), evaluate as follows:

If $(E_i * Br_i) \leq ENV * (E_1 * Br_1)$, then

Go to the next peak,

Else,

- a) Calculate the expected peak area for the i^{th} peak as:

$$A_i = A_1 \left(\frac{E_i * Br_i}{E_1 * Br_1} \right) \quad (26)$$

- b) Calculate the critical level L_c for the i^{th} peak as:

$$L_c = 2.33 * \sqrt{(B_i * W/M)} \quad (27)$$

If $A_i > L_c$ and the i^{th} peak is not a valid peak (that is, the peak is not found or the peak uncertainty is greater than the peak cutoff), then the nuclide is removed from the library.

Next peak i .

where:

E_1 = efficiency for the first valid peak

Br_1 = branching ratio for the first valid peak

E_i = efficiency for subsequent library peaks

Br_i = branching ratio for subsequent library peaks

A_1 = activity calculated for the first nuclide peak

A_i = activity calculated for subsequent library peaks

B_i = peak background for subsequent library peaks

W = peak width for subsequent library peaks

M = number of total points outside the peak used to calculate background

ENV = user-adjustable **ENV factor** from the `b30winds.ini` file located in `C:\Program Files\Renaissance` (see page 391 in Section A.2.2). The default setting is 0.2, but it can be set higher to keep more nuclides in the library by minimizing the number of subsequent peaks evaluated using the formulation above.

8.1.3.2. Details of Library Reduction Based on Key Line and Fraction Limit Test

Like the ENV test discussed above, this library reduction test is performed at the start of an analysis after a raw peak searched is performed. In this library reduction algorithm, both the key line and fraction limit tests are carried out for RENENV and RENGAM engines.

For the key line test, the first in-range peak for a nuclide is always considered as a key line, even if it is not marked as a key line. All key lines for a nuclide must be found in the spectrum, even if

the key line has overlap with another library peak. If any of the qualifying key lines is not found, the key line test fails and the nuclide is rejected.

If the fraction limit is not zero (the default value is zero), the fraction of the branching ratios is calculated. If the calculated fraction is less than the Fraction Limit set on the Analysis tab, the nuclide is rejected. Branching ratios of all qualifying in-range peaks for a nuclide are summed. Then sum of branching ratios for all qualified and identified peaks for a nuclide is summed as well. The ratio of the two sums is compared with the branching ratio limit. If it is less than the limit set, the nuclide is rejected.

If the “Fraction Limit Test flag” in `b30winds.ini` is False and **Directed Fit** is enabled on the System tab, the library peak flags are checked to determine if a peak is “qualified” for its branching ratio to be summed (in the total sum and the identified peak sum). Peaks with the “Not In Average” flag set in the library are excluded along with peaks outside the analysis range.

8.2. Calculation Details for Peaks

For all library peaks in the analysis energy range, the program attempts to calculate the net peak area and centroid of a peak at that channel. At this step in the analysis, each peak is considered to be a singlet. A singlet is a single, isolated peak; that is, it is far enough away from other peaks in the spectrum so that the spectrum is background on both sides of the peak (does not overlap another peak).

8.2.1. Background Calculation Methods

You can select the method from among these types: automatic, 5-point average, 3-point average, and 1-point minimum in the analysis options (see page 125).

8.2.1.1. Automatic

For the first pass, the peak centroid is the library energy (Fig. 218).

To calculate the first pass background on the low-energy side of the peak, the 5-point average of the channel contents is calculated for the region from the peak-centroid channel to the channel which is 6 times the library match width (normally 0.5) times the calculated FWHM (from the calibration) below the centroid. The 5-point average data at a given point is the sum of the data from two channels below the point to two channels above the point divided by 5. This is the same as smoothing the data with a smoothing width of 5 and coefficients of 0.2 for all points. The background value is the minimum value of the moving 5-point average and the background channel number is the center channel of the 5. If the minimum average value is within one sigma (counting statistics) of the actual channel value at the assigned channel point, this 5-point average is the low energy background value for this peak. If the average value is not within one

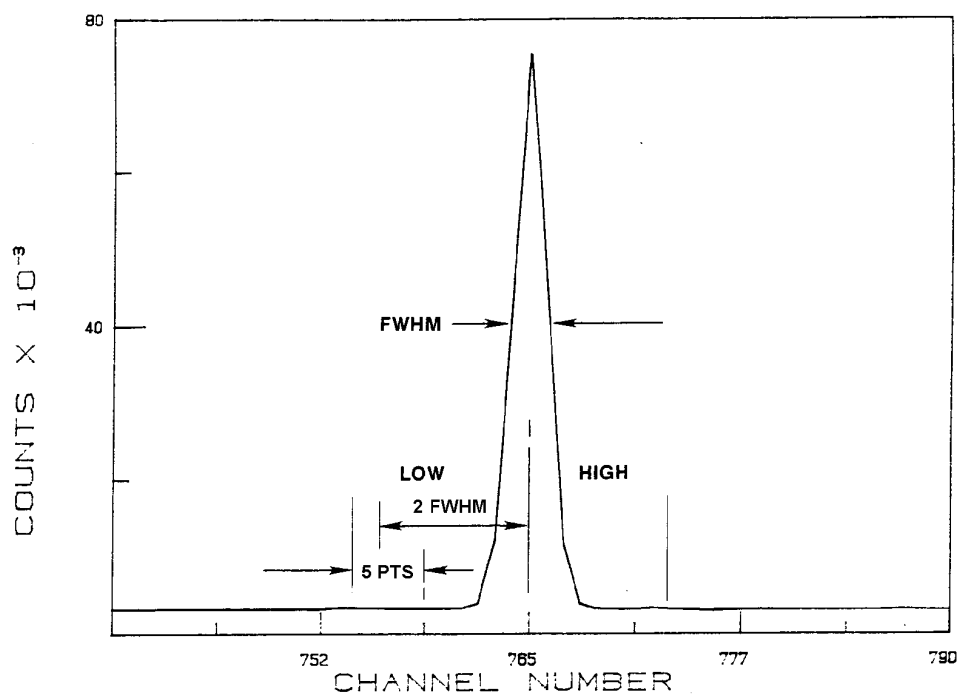


Figure 218. Background Calculation.

sigma of the actual data, a 3-point average is used instead of the 5-point average to calculate a new minimum value. This 3-point average minimum value is compared with the actual data at the assigned channel and is accepted if it is within 1 sigma of the actual data. If the 3-point average also fails this test, the data value at the assigned channel is used for the background.

The same process is repeated for the high-energy side of the peak to calculate the background value above the peak. The background under the peak is the straight line between these two values.

The net peak area and background are calculated from this first pass. Next, the width is reduced or increased depending on the peak-area-to-background ratio and the library match width. This adjustment makes two improvements: (1) it reduces the number of channels in the peak for small peaks (decreasing the uncertainty), and (2) it improves the area calculation for peaks moved from the library energy.

This background calculation method (that is, automatically selecting 5-, 3-, or 1-point averaging, depending on which method best approximates the spectrum data) has advantages, when there are closely spaced peaks, over other methods. For example, because the 1-point method will be used when a small peak is very near a large peak, a more accurate measure of the background will be obtained as compared to the 5- or the 3-point average (Fig. 219).

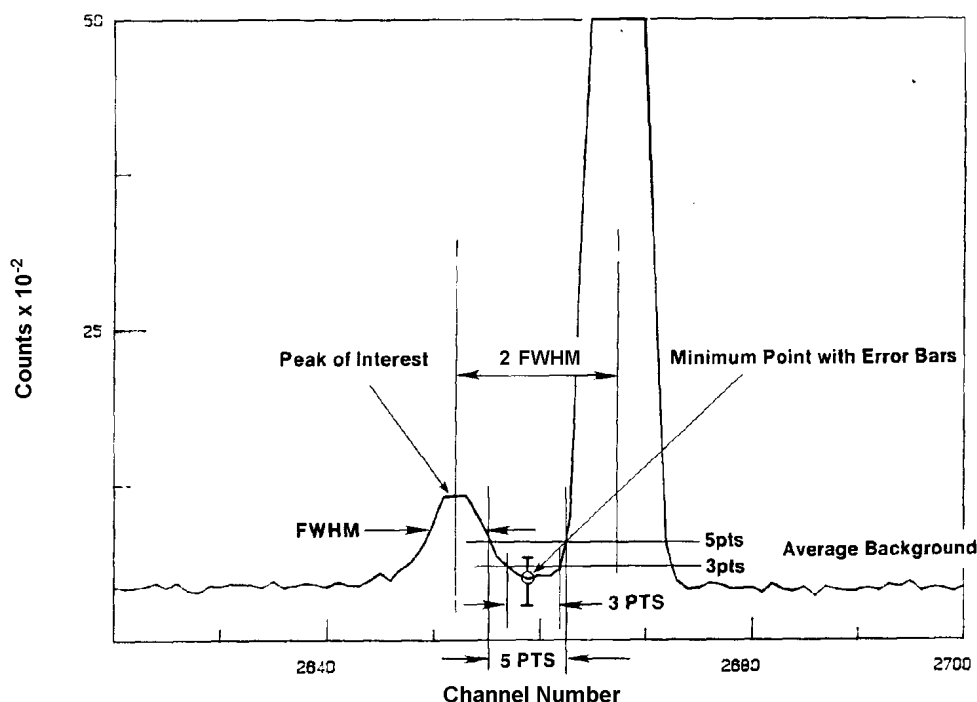


Figure 219. Background of a Small Peak Near Large Peak.

The background of the small peak is less affected by the other peak because the automatic method will tend toward the smaller values.

Even in the case of peaks that are further apart than those shown in Fig. 219, the background is less dependent on the scatter in the data when the 5-point method is used.

8.2.1.2. 5-Point Average

If the 5-point method is chosen, the minimum 5-point average channel value is chosen and is not compared with the actual data at the center channel. This can be useful for isolated peaks with high scatter in the channel-by-channel data.

8.2.1.3. 3-Point Average

If the 3-point method is chosen, the minimum 3-point average channel value is chosen and is not compared with the actual data. This is better than the 5-point method for close peaks and better than the minimum value for high scatter.

8.2.1.4. 1-Point

The 1-point method uses the minimum data point in the search width. This might not be the same value as the automatic method, because the automatic method uses the center channel of

the 3-point average as the background point (assuming the 5-point and 3-point tests have failed). This method has advantages in close peaks with good counting statistics.

If in doubt as to which method should be used, use the **Auto** selection, except when the spectrum has a low number of counts per channel and the peak width (in channels) is more than about 6. In this case, use the 5-point method.

8.2.1.5. Example Background

An example is shown in Fig. 220, with the spectrum printout in Table 2. The report section for this peak is shown in Fig. 221.

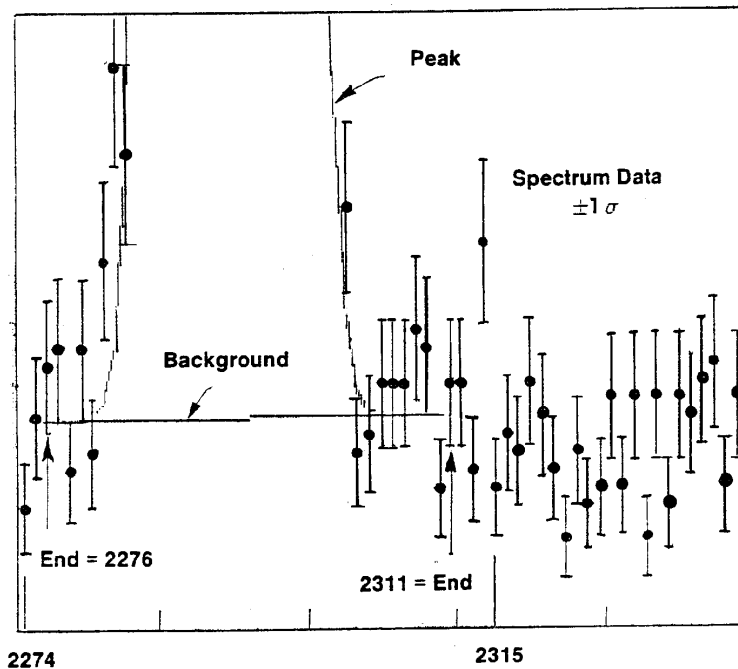


Figure 220. Example Peak Background Calculation.

The FWHM for this peak is 6.85 channels. The centroid is at channel 2292.16. The background search width is from channel 2271 to 2313. The 5-point averages are shown in Table 2, and the minima are 11.8 at channel 2276 and 12.2 at channel 2311. The background slope is +0.0114 and the offset is -14.4.

UNIDENTIFIED PEAK SUMMARY							
PEAK SUSPECTED CHANNEL	CENTROID ENERGY	BACKGROUND COUNTS	NET AREA COUNTS	INTENSITY CTS/SEC	UNCERT 1 SIGMA %	FWHM keV	NUCLIDE
2292.16	569.78	432.	17711.	59.04	.81	1.734	Bi-207

Figure 221. Peak Results for Previous Peak.

Table 2. Spectrum and Five-Point Smooth.

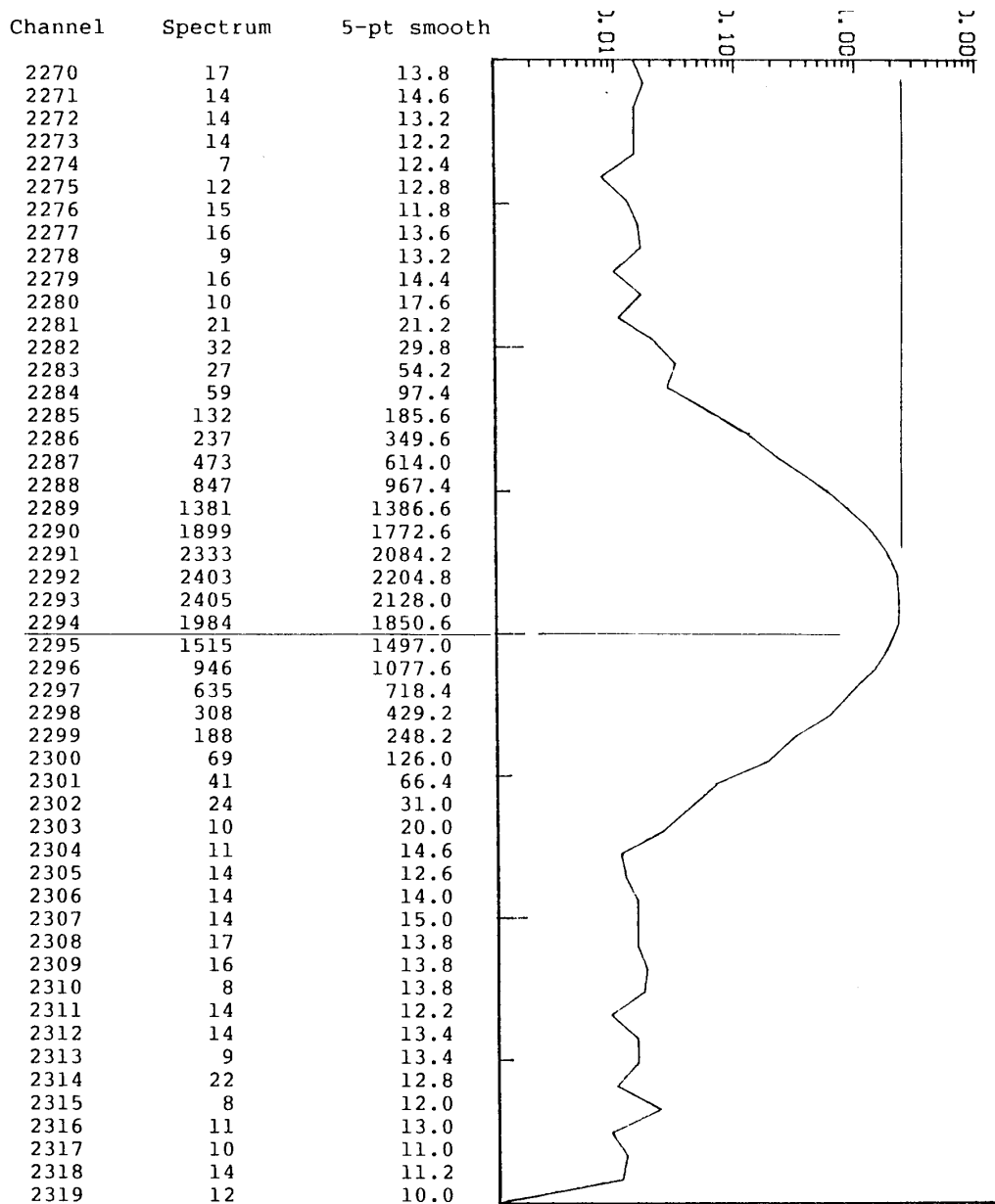


Fig. 222 shows an example of the differences among the four methods for determining the background.

PEAK CHANNEL	CENTROID ENERGY	BACKGROUND COUNTS	NET AREA COUNTS	INTENSITY CTS/SEC	UNCERT 1 SIGMA %	FWHM keV
+++++ Background width: best method (based on spectrum). +++++						
2939.64	718.00	1514.	79.	.009	70.82	1.517
Background width: average of five points.						
2939.64	718.00	1372.	12.	.001	422.37	1.517
Background width: average of three points.						
2939.64	718.00	1299.	43.	.005	119.77	1.517
Background width: minimum data point.						
2939.64	718.00	1214.	72.	.008	69.70	1.517

Figure 222. Example of Different Background Method Results.

8.2.2. Peak Area — Singlets

8.2.2.1. Total Summation Method

The gross area of the peak is the sum of the contents of each channel between the background channels (including the two background channels) as follows:

$$A_g = \sum_{i=l}^h C_i \quad (28)$$

where:

A_g = the gross area

C_i = the data value of channel i

l = the center channel of the background calculation width at the low energy side of the spectrum

h = the center channel of the background calculation width at the high energy side of the spectrum

This peak area calculation method (referred to as total summation) maintains precision as the peak gets smaller, is less sensitive to random fluctuations in the data, and is less sensitive to the differences between the spectrum peak shape and the calibrated peak shape.

Refer to Fig. 220, Fig. 221, and Table 2 to calculate the gross area for the example peak. The integral from channel 2276 to 2311 is 18143 counts.

The net area is the gross area minus the background in those channels (Fig. 223).

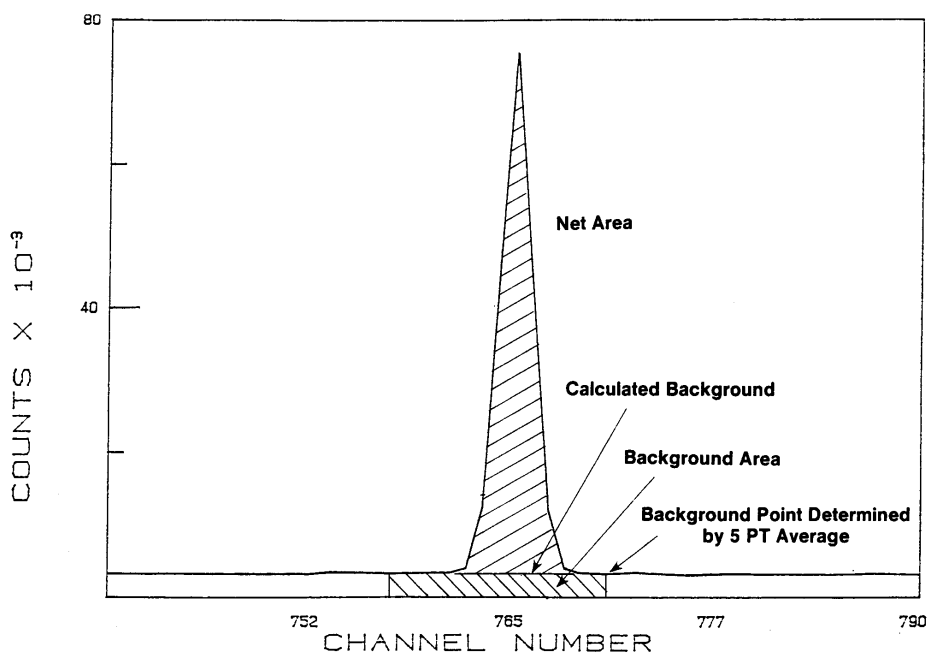


Figure 223. Gross and Net Peak Area.

$$A_b = \frac{B_l + B_h}{2} \times W \quad (29)$$

where:

A_b = the background area

B_l = the background on low side of peak

B_h = the background on high side of peak

W = the peak width

If the PBC correction is enabled, the calculation is performed as discussed in Section 8.9.4.

8.2.2.2. Directed Fit Method

In some cases the total summation method does not produce the desired answer for the peak area and does not produce negative peak areas. Another method of obtaining the peak area for a particular energy is to fit the spectrum region with a background plus peak shape function. This so-called “directed fit” — enabled on the Analysis tab — can be applied to peaks and has the ability to produce negative peak areas. The negative peak area will produce a negative activity and this will be reported. Negative activities are required by some reporting agencies for statistical purposes.

The directed fit to the library peak area is performed if the following are true:

- 1) The option is enabled.
- 2) The spectrum is energy calibrated.
- 3) The peak was rejected for any test by the total summation method.
- 4) The peak is a singlet (multiplets allowed in RENENV).

If all these conditions are met, the spectrum region is fit for 3 times the calibration FWHM, centered on the peak energy. The function is the background plus a Gaussian peak shape. The five parameters are peak amplitude, peak centroid, and a quadratic background function. The initial values and uncertainties are taken from the spectrum.

The fit is iterated until the reduced chi square for the fit changes by less than 1% from the previous iteration, to a maximum of 10 iterations. Most cases will converge in 3 to 4 iterations. If the fit fails, the peak values are set to the total summation values. If the fit converges, the background and peak area are calculated from the fit values.

8.2.3. Example Peak Area

8.2.3.1. Total Summation Method

Again, refer to Fig. 220, Fig. 221, and Table 2 to calculate the background for this peak (PBC correction disabled). Substituting in the above formulas yields:

$$\begin{aligned} \text{Background area} &= \frac{11.8 + 12.2}{2} \times (2311 - 2276 + 1) \\ &= 432 \end{aligned} \tag{30}$$

and

$$\text{Net area} = 18143 - 432 = 17711 \tag{31}$$

8.2.3.2. Directed Fit Method

A section of a spectrum with a negative peak is shown in Fig. 224. The raw data values and the generated fit are shown. In this case the, background at the low energy end of the peak is 1170 counts per channel and on the high end is 1173 counts per channel. This gives a total background of 35145 counts and the net peak of -133 counts.

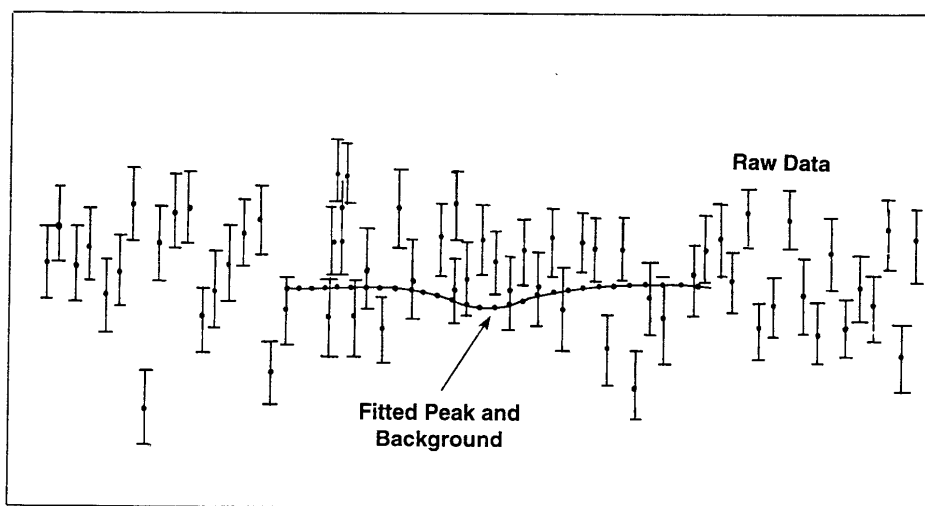


Figure 224. Example of Directed Fit.

Since these values are derived from a fitting process, it is difficult to redo the calculations manually.

8.2.4. Peak Uncertainty

The counting statistical uncertainty is the uncertainty in the gross area and the uncertainty in the background added in quadrature. The uncertainty in the gross area is the square root of the area. The uncertainty in the background is not as simple because the background is a calculated number. The background area uncertainty is the uncertainty in the channels used to calculate the end points of the background multiplied by the ratio of the number of channels in the peak to the number of channels used to calculate the background. For wide peaks and low counts per channel, there is high uncertainty in the calculated background.

$$bkg\ error = \left(\frac{(background\ area)\ (peakwidth)}{(width\ of\ low\ average\ +\ width\ of\ high\ average)} \right)^{1/2}$$

$$gross\ area\ error = \sqrt{gross\ area} \quad (32)$$

$$net\ area\ error = \sqrt{(gross\ area\ error)^2 + (background\ error)^2}$$

If the PBC correction is enabled, the uncertainty calculation is performed as discussed in Section 8.12.10.

PBC correction is disabled for the following example. Referring back to Fig. 220, Fig. 221, and Table 2, the background uncertainty is:

$$\begin{aligned} \text{Background error} &= \sqrt{\frac{(432)(2311 - 2276 + 1)}{5 + 5}} \\ &= 39.4 \end{aligned} \tag{33}$$

$$\begin{aligned} \text{Net area error} &= \sqrt{(18143 + 1552.4)} \\ &= 140.4 \text{ or } 0.8\% \text{ of net peak area} \end{aligned}$$

The peak width is calculated at the half maximum, tenth maximum, and twenty-fifth maximum for the net peak shape. The peak width points are linearly interpolated between the two channels that bracket the respective height value.

8.2.4.1. Peak Uncertainty in ZDT Spectra

The ORTEC zero dead-time (ZDT) mode¹⁹ is discussed in the hardware manuals for supported MCBs.

8.2.5. Peak Centroid

The peak centroid channel in total summation is the center-of-moment of the peak and is calculated as the weighted channel number of the peak. That is, the peak centroid is the sum of the net channel contents times the channel number divided by the sum of the channel contents. The centroid is calculated as:

$$\text{Peak centroid} = \frac{\sum_{i=l}^h i \cdot C_i}{\sum_{i=l}^h C_i} \tag{34}$$

where:

- l, h = the peak low and high channels
- i = the channel number
- C_i = net contents of channel i

¹⁹U.S. Patent 6,327,549.

For the directed fit method, the centroid can be refined from the fitting process.

From the Table 2 values and the calculated background, the net spectrum is shown in Table 3, continuing the example calculation on this peak.

The FW.04M is 2.2 times the FWHM for a Gaussian peak. The peak integration channels are then 2284 to 2300. The channel numbers are rounded to the nearest integers. The centroid for this example is $4.0366 \times 10^7 / 1.761 \times 10^4 = 2292.16$.

8.2.6. Energy Recalibration

The spectrum energy calibration can be redone “on the fly” for the spectrum being analyzed. This improves the analysis results and adjusts for small changes in the hardware gain. Energy recalibration is first performed using singlet peaks only. Then, after deconvolution, the spectrum is recalibrated using all the peaks. If the energy calibration changes, the spectrum is reanalyzed.

For all peaks in the library, the peak centroid energy in the spectrum is compared with the library energy. If the difference between the library energy and the centroid energy is less than 0.5 keV, or the current **Match Width** (the FWHM multiplier entered on the System tab under **Analyze/Settings/Sample Type...**), or one channel — whichever is greater — that centroid is associated with that library energy. The FWHM multiplier can be changed. If it is within this limit and has counting error less than 10% or the input sensitivity value (whichever is less), it is a qualified recalibration peak.

The energy range is split into two parts and the number of qualified library peaks in each

Table 3. Example Net Spectrum.

Channel	Background	Net Spectrum
2270	11.7152	5.284
2271	11.7266	2.273
2272	11.7380	2.262
2273	11.7494	2.250
2274	11.7608	-4.760
2275	11.7722	0.227
2276	11.7836	3.216
2277	11.7950	4.205
2278	11.8064	-2.806
2279	11.8178	4.182
2280	11.8292	-1.829
2281	11.8406	9.159
2282	11.8520	20.148
2283	11.8634	15.136
2284	11.8748	47.125
2285	11.8862	120.113
2286	11.8976	225.102
2287	11.9090	461.091
2288	11.9204	835.079
2289	11.9318	1369.068
2290	11.9432	1887.057
2291	11.9546	2321.046
2292	11.9660	2391.034
2293	11.9774	2393.023
2294	11.9888	1972.011
2295	12.0002	1503.000
2296	12.0116	933.988
2297	12.0230	622.977
2298	12.0344	295.965
2299	12.0458	175.954
2300	12.0572	56.942
2301	12.0686	28.931
2302	12.0800	11.920
2303	12.0914	-2.091
2304	12.1028	-1.102
2305	12.1142	1.885
2306	12.1256	1.874
2307	12.1370	1.863
2308	12.1484	4.851
2309	12.1598	3.840
2310	12.1712	-4.171
2311	12.1826	1.817
2312	12.1940	1.806
2313	12.2054	-3.205
2314	12.2168	9.783
2315	12.2282	-4.228
2316	12.2396	-1.239
2317	12.2510	-2.251
2318	12.2624	1.737
2319	12.2738	-0.273

region is counted. If there are more than the user-set number of qualified recalibration peaks in both regions of the spectrum, these spectrum centroids and library energies are used to recalculate the energy calibration for the spectrum. The default energy is 0 keV and the number of peaks is 1000 below and 1000 above. Only this analysis is affected and the calibration in the spectrum file is not changed. If the energy recalibration is performed, a notice is written on the report, even if the recalibration had little or no effect. The new coefficients are printed on the output report.

Since this energy recalibration is dependent on the library and the spectrum, changes in the library can affect the calibration, and hence the peak energies reported. Only the energy factors are changed. The shape coefficient and efficiency coefficients are not altered. While the automatic energy recalibration will correct for small changes in the calibration, it is not intended as a substitute for accurate calibrations or as a correction for systems suffering from stability problems.

For an accurately calibrated spectrum, this recalibration will have little effect. Its effect will be most pronounced on deconvolutions of multiplets; this is discussed in Section 8.4.

Because of this recalibration feature, the analysis results of spectra can change when a library is changed, or if the peak sensitivity is changed to a value under 10% (see fixed cutoff above). Such changes between analyses can result in the recalibration being enabled in one case and disabled in the other case. This can result in the analyses being different in several different ways. The peak areas and backgrounds can be different because the integration limits for each peak will change slightly. This change is usually very small, but in a spectrum with very few counts it can be a high percentage of the total peak. In a given spectrum, some peak areas might change and others might be constant. Some peaks might move from the identified list to the unknown list (or the reverse) because the uncorrected centroid is too far from the library energy for validation.

In addition, an energy difference for all good library peaks is calculated. This is the sum of the absolute value of the difference between the peak centroid energy (before recalibration) and the library energy, expressed as a fraction of the FWHM, divided by the number of peaks in the sum. This yields a number between 0 and 1 for good 3-point (or more) calibrations, with 0 being the best calibration. For 2-point calibrations, this number can be much larger than 1.0 because the calculated FWHM (which is a linear function) does not fit the spectrum FWHM at the ends of the spectrum. If high values are reported, and the analysis results are unacceptable, a better calibration should be made. The calibration section can be used to produce a multi-point calibration which will reduce the energy difference.

$$QUALITY FACTOR = \frac{\sum_{i=1}^n \frac{|E_{pi} - E_{Li}|}{FWHM_{Li}}}{n} \quad (35)$$

where:

- E_{pi} = the energy of the i th peak in the spectrum
- E_{Li} = the energy of the corresponding peak in the library
- $FWHM_{Li}$ = the calculated FWHM of the peak at the library
- n = the number of peaks in a spectrum with matching library peaks

This “energy-normalized difference” is printed on the report. For a complex spectrum this number will range from 0.1 to 0.3. A large value indicates that a new calibration should be performed or that the library does not match the spectrum well. Smaller values are usually associated with fewer peaks or a better calibration.

If an energy recalibration has occurred, the library peak list is reanalyzed with the new energy calibration. This results in more accurate peak values for centroid and area.

8.2.7. Peak Search

After the library peaks are located, the spectrum is searched for any other peaks. This is needed, even if the list of unknown peak values is not requested, for correct calculation of the peak background near peak multiplets and for determination of the peak centroids for deconvolution of multiplets not in the library. The stepped background test compares the background above the peak area to the background of the peak area (see “Background for Multiplets,” Section 8.4.2).

The peak search method is based on the method proposed by Mariscotti. In this method it is assumed that the spectrum, $C(n)$, is continuous and the background is a linear function of the channel number in the vicinity of a peak. This implies that the second derivative is zero for background regions and non-zero in the peak regions. In order to reduce the effect of statistical fluctuations, the smoothed second difference is used (see Fig. 225).

The second difference can be represented as:

$$C''(n) = \sum_{i=0}^{2j} k_i C(n - j + i) \quad (36)$$

where:

- k_i = the smoothed second difference weighting functions
- $2j + 1$ = the smoothing width

For regular peaks, $j = 4$; for wide peaks, $j = 9$. There are nine coefficients for regular peaks and 19 for wide peaks. The criterion for using the wide-peak filter is that the spectrum resolution in keV per channel at the center of the spectrum is <0.15 keV/channel.

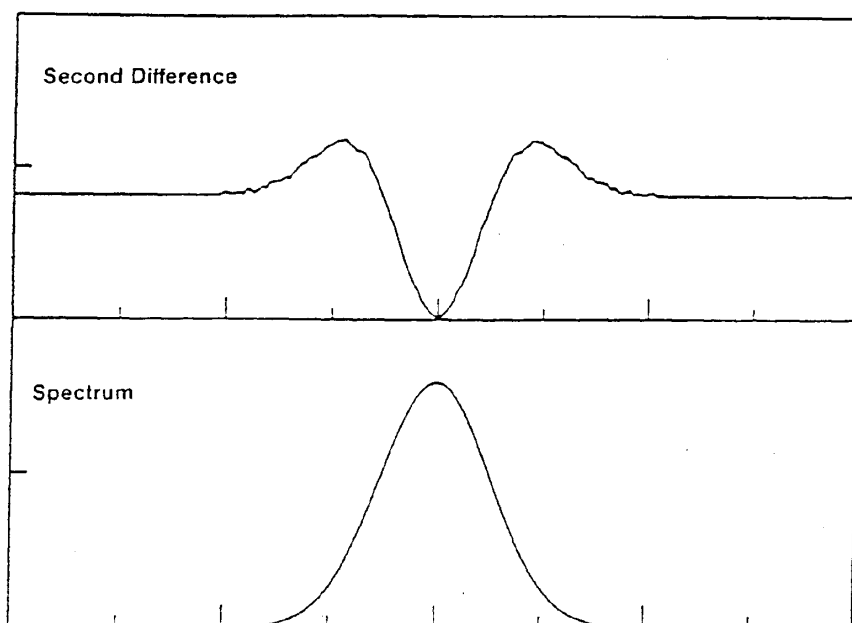


Figure 225. Second Difference.

The peaks are located where the second derivative varies significantly from zero.

A typical gamma-ray spectrum is shown in Fig. 226. This gamma-ray spectrum is far from the ideal spectrum of a well-formed peak on a smooth background. Shown are seven features that can be distinguished and accounted for in the peak-detection algorithm.

- 1) The full-energy photopeak that results from the complete capture of all the photon energy in the detector and is the most well-defined feature
- 2) The Compton edge for the full-energy peak
- 3) The Compton plateau
- 4) The backscatter peak
- 5) The pulse pileup or sum peaks from the addition of the peak energies in the detector or electronic processing
- 6) The single-escape peak
- 7) The double-escape peak

Not all of these will appear in a given spectrum. For example, escape peaks cannot occur for photons less than about 1 MeV.

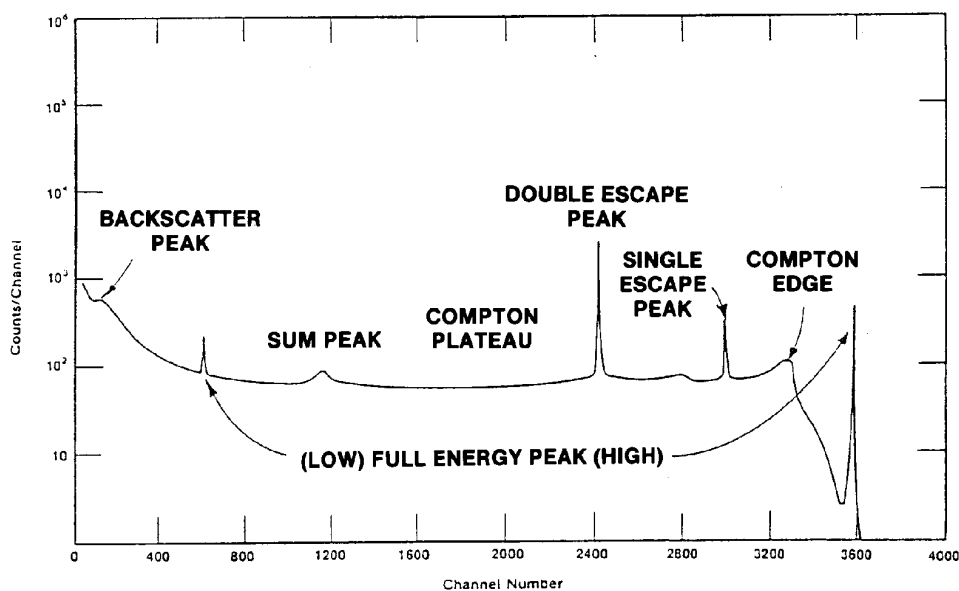


Figure 226. A Typical Gamma-Ray Spectrum.

The shape of the second derivative can be used to reject Compton edges and other non-peak structure in the data (Fig. 227).

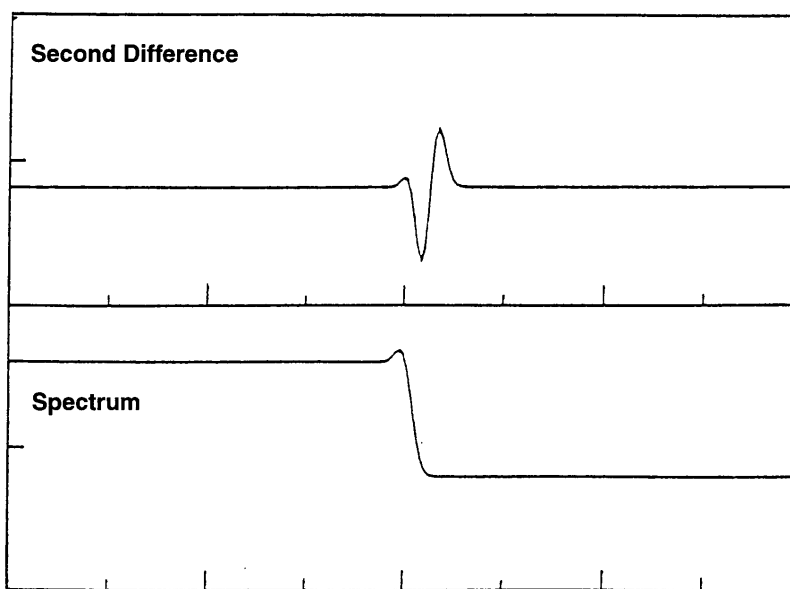


Figure 227. Second Difference for a Compton Edge.

8.2.7.1. Peak Acceptance Tests

The second difference must pass the following tests to be considered a peak.

$$C''(n) < -G \sqrt{C(n)} \quad (37)$$

where G is related to S , the **PEAK SEARCH SENSITIVITY** factor, set on the System tab under **Analyze/Settings/Sample Type...**, as follows:

$$G = (0.35 * S + 1.45) * 13.03 * F \quad (38)$$

where:

G = a constant proportional to the resolution of the detector

F = 1.35 for the wide-peak filter and 1.0 for the regular-peak filter

In addition, the spectrum data at the channel indicated by the second derivative must pass these tests.

$$\begin{aligned} C''(n+1) &> C''(n) \\ C''(n-2) &> C''(n-1) \end{aligned} \quad (39)$$

where:

$C(n)$ = the channel data of the n th channel

$C''(n)$ = the second difference at the n th channel

If the wide-peak filter is used, the second derivatives must also meet the following criterion:

$$C''(n-1) > C''(n) \quad (40)$$

The peak centroid is calculated using the weighted channel sum method as follows:

$$P = \frac{\sum_{i=1}^h i * C_i}{\sum_{i=1}^h i} \quad (41)$$

where:

P = peak centroid in channels

C_i = net contents of channel i

i = channel number

- l = peak low limit
- h = peak high limit

Once a peak is located, it is recorded and the peak search starts again.

After a peak has been located, if it is not in the library, the peak background, net area, and uncertainty are calculated in the same manner as library peaks. If the peak uncertainty is less than the sensitivity threshold level you entered, the peak is added to the list of unknowns. If the peak is within the deconvolution width (approximately 3.3 times the FWHM) of a library peak, then the peak is marked on the output list. The unknown peaks are included in a deconvolution when they are close enough to affect the peak area calculation.

If a peak is located in the spectrum and the library peak is a subsidiary peak, where the major peak has not been found, the peak will be maintained in the unknown list.

8.2.8. Narrow Peaks

The peak width is compared to the calibration width at the half and tenth maximum. If the peak is too wide or too narrow it is marked to show this in the output report. If the peak is too narrow, it is not used in the abundance calculation unless the “accept-low-peaks” or “accept-all-peaks” switch ($T=accept\ low\ peaks$, page 387, 395) is turned on. If accept-all-peaks is on, all are accepted. If accept-low-peaks is on, the peak is further tested. If the peak area is less than 200 counts, it is accepted. If the peak area is between 200 and 300 counts and the background is less than half the peak area, the peak is accepted. If the peak area is over 300 it is rejected.

8.3. Suspected Nuclides

The suspected nuclides feature will identify peak energies in the unknown peak list, based on a second gamma-ray library. The unknown peak list is the list of all peaks located in the spectrum that are not in the analysis library. It is intended to help identify unexpected peaks or can be used to note peaks that are always present but for which no analysis is desired (e.g., ^{40}K or 511 keV). The name for the suspected nuclide library is specified on the System tab under **Analyze/Settings/Sample Type...**

For each energy listed in the unknown peak list, the nuclide with the closest energy within four times the FWHM is listed. In the event that two energies are found with the same difference, the lowest energy entry in the library is printed. If none is found, a symbol is printed. In addition, the same symbol is printed if the suspected library is not found, a read error occurs, or the spectrum is not calibrated.

The suspected nuclide feature can be used with calibrated spectrum files (and no analysis library) to obtain a quick list of nuclides in the sample and their peak count rates.

8.4. Locating Multiplets

A peak is considered to overlap if its start or end channels are within another peak region. The peak overlap range factor in `b30winds.ini` (in units of peak FWHM; see page 392) determines whether two peaks close in energy will be deconvoluted as a multiplet or stripped. The lowest setting for this parameter is 1.0; the default value is 3.5. If you change its `b30winds.ini` entry to less than 1.0, the analysis uses a value of 1.0.

If the library energies are less than 10 eV apart, only the lowest energy peak is included in the deconvolution. The peak areas for the other peaks (within 10 eV) are set to zero. The conflicting peaks are marked as energy-conflicting peaks. This message appears on the report and the individual peaks are labeled in the comment field of the nuclide/peak matrix. See the discussion of library-based peak stripping, Section 8.4.5.

All peaks found by the peak search routine and not in the library are included in the deconvolution regardless of the sensitivity setting, unless all the deconvolution candidates are unknown peaks with uncertainty greater than the sensitivity setting, in which case the region is ignored.

8.4.1. Defining a Multiplet Region for Deconvolution

After a list of peaks is determined from the library-directed and Mariscotti peak searches, multiplets are identified. Note that peaks which are found by the Mariscotti peak search but do not pass the sensitivity (peak cutoff) test are flagged for further multiplet consideration. For each located peak, the energy of the next peak is checked to see if it is less than or equal to 3.08 times the FWHM of the peak currently being processed. If so, the two peaks are marked as a multiplet. The energy of successive peaks is checked, using the same criteria, to determine if they belong in the multiplet. After the last peak in the multiplet is identified, the multiplet is flagged for peak deconvolution.

Because a multiplet identified in this way might contain a combination of library peaks and unidentified peaks, the analysis engine processes it as follows:

- If library energies are less than 10 eV apart, the lowest-energy peak is included in the deconvolution and the other peaks within 10 eV are set to zero.
- If all the peaks in the multiplet are unidentified (i.e., not listed in the library) and do not meet the sensitivity criterion, the entire region is ignored.

The width of the multiplet region is from 1.5 times the FWHM below the lowest peak to 1.5 times the FWHM above the highest-energy peak (Fig. 228).

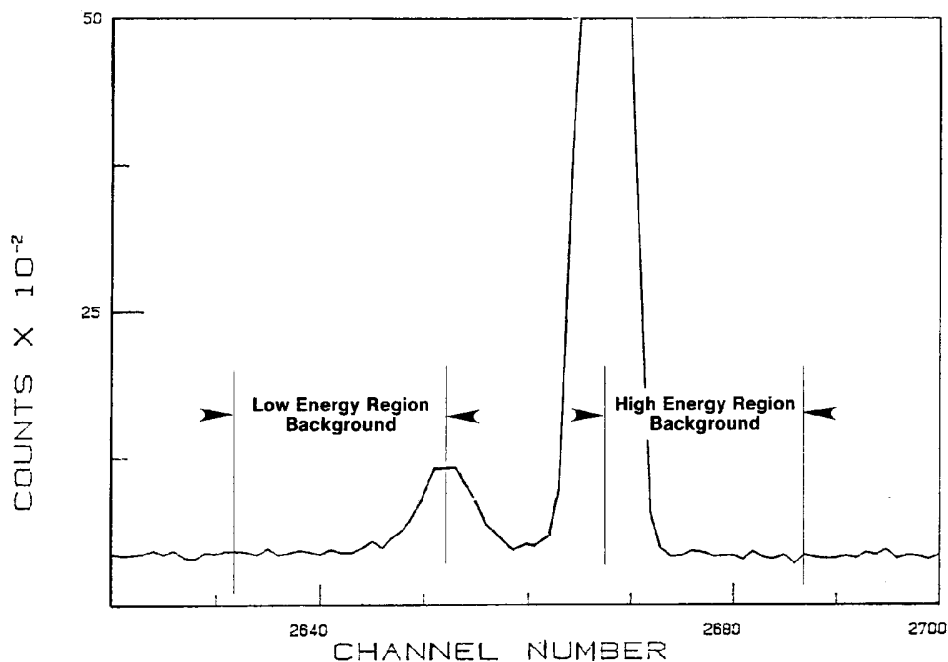


Figure 228. Background for Multiplets.

8.4.2. Establishing Multiplet Background

Three background types are used for multiplets: *stepped*, *parabolic*, and *straight-line*. Selection of the background type depends on the shape of the peak background.

- 1) Stepped background is used if the slope of the peak background across the peak area is less than the slope of the background adjacent to the high-energy side of the peak. That is, if the background under the peak is declining faster than the background above the highest-energy peak in the background, the stepped background is selected; see Fig. 229.
- 2) Parabolic background is selected if:
 - The background on the low-energy side of the multiplet is less than the background on the high-energy side.
 - At least three contiguous points in the lower 75% of the multiplet region are less than the straight-line background.
 - The energies of the peaks are less than 200 keV.
 - The peak sensitivity is 2 or higher; see Fig. 231.

3) Straight-line background is selected if the other two background methods do not apply.

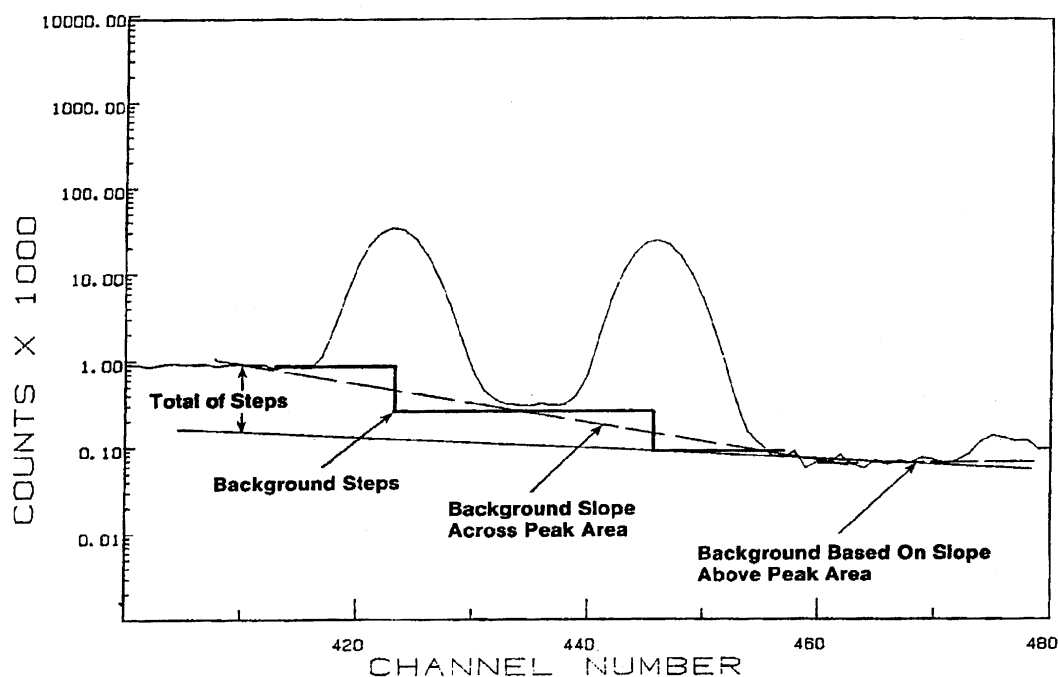


Figure 229. Stepped Background.

8.4.2.1. Stepped Background

The total height of the background steps is the difference between the background below the peak region and the value of the peak background above the peak region projected back to the background point at the low-energy end of the multiplet; see Fig. 229. The size of the step inserted at each peak centroid is proportional to the height of the peak. The result is then smoothed. This background is calculated after the deconvolution, the net spectrum is recalculated, and the deconvolution is repeated.

A real spectrum with stepped background is shown in Fig. 230. The two components of the doublet are of equal size.

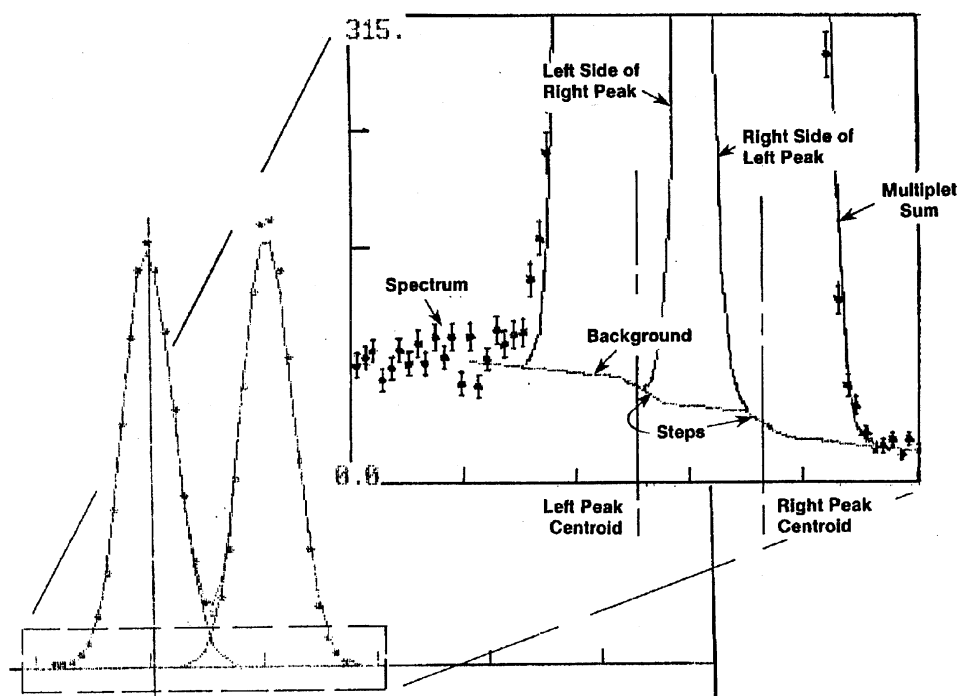


Figure 230. Stepped Background.

8.4.3. Parabolic Background

The parabolic background is calculated as the least squares fit to the actual spectrum data at the low-energy background data point, the spectrum data point at the channel most below the straight-line background and the spectrum data at the high-energy background data point. This parabolic form is calculated channel-by-channel and subtracted from the original spectrum to obtain the net spectrum for the fit.

Figure 231 shows this case for an actual spectrum.

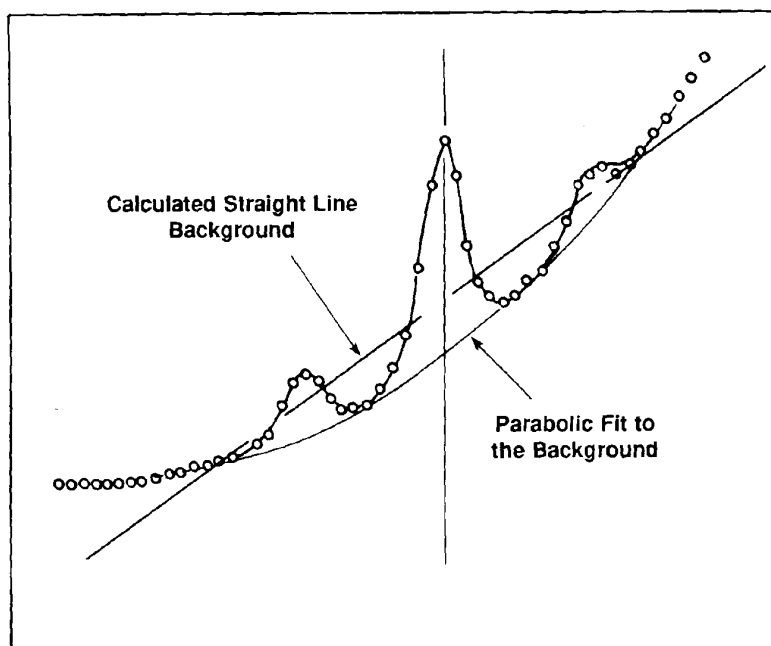


Figure 231. Parabolic Background.

8.4.4. Total Peak Area

The net spectrum, which is the composite of the contributions of the individual peaks, can be represented as a weighted sum of the Gaussian peak shapes. The weighting factors of each component are proportional to the area of that component peak.

The peaks to be included in the deconvolution are each positioned at the library energy or the peak finder energy of the component. The shape is calculated for the peak at the given energy even though the change in shape with energy within the energy range of the multiplet is small. The calibration peak shape is used. The contribution of a unit-height peak is calculated for each channel in the multiplet range for each candidate energy. This matrix of peak amplitudes multiplied by the weighting factors and summed is equal to the net spectrum. For RENNPP and RENENV, the peak centroids are allowed to vary in the fitting. The peak positions for all peaks are allowed to shift in the fitting process to obtain a reduced chi-square. The library peaks are all shifted the same, while unknown peaks each shift independently. The weighting factors are determined by solving the matrix equation. The final result, that is, the area of the individual components of the multiplet, is the corresponding weighting factors times the unit-height area of the peaks at their respective positions.

If any of the weighting factors (and therefore the peak areas) are negative or zero as a result of the deconvolution, that peak candidate is deleted from the list and the remaining candidates are re-fit. Peak areas for deleted peaks are set to zero. The fitting process is repeated until no peak areas are negative or there is only one peak remaining. If there is only one peak remaining, the

peak parameters for this peak are recalculated as if this peak were a singlet. The peak shape parameters and energy are set to the calculated peak parameters.

The background reported for each component peak in a multiplet is the gross area for three times the FWHM centered at the peak centroid minus the component peak area (Fig. 232). This means that for each peak the areas of the other peaks in the multiplet are treated as background. By including all the area not associated with the actual peak in the region of the peak, the uncertainty due to the background is more accurately calculated.

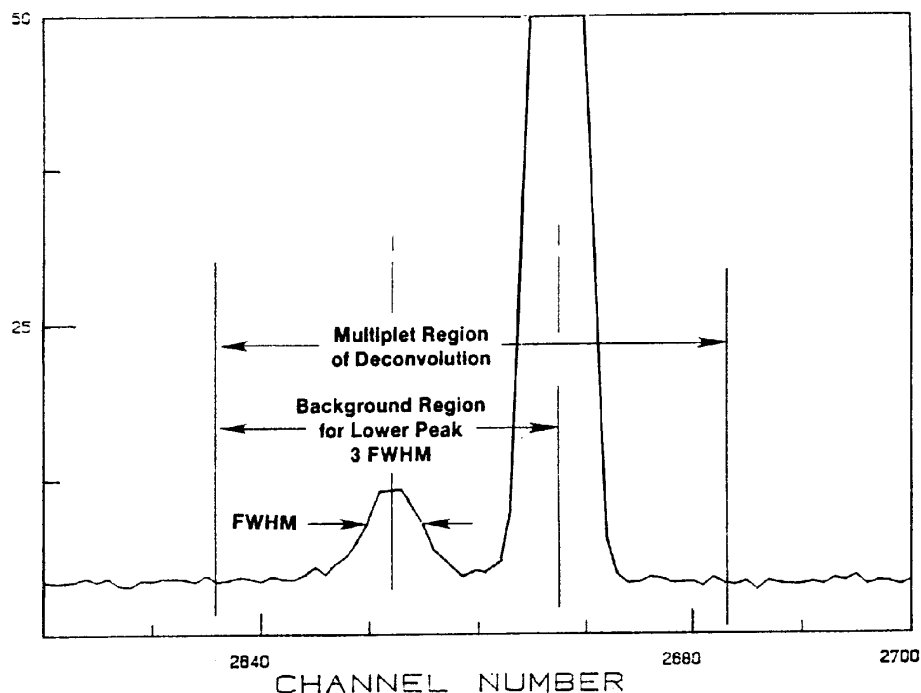


Figure 232. Background for Multiplet Components.

In the case of a multiplet, the sum of the reported backgrounds and net peak areas will be more than the sum of the gross spectrum for the same region because the background and some (if not all) of the net peak counts will be counted more than once.

The energy recalibration affects the multiplets in two ways. For inclusion in the list of deconvolution candidates, the first peak for this nuclide must be present. If the first peak has not been found because it failed the centroid test (see above), then subsequent peaks are not used. The deconvolution will then be performed with fewer candidates. Secondly, the library energies are used to define the location of the multiplet component library peaks. The peak finder energies are derived from the channel number, so although the reported energy might change, the position relative to the actual data does not change. A mismatch of these will result in an inaccurate fit, and a different fit when the peak channels are shifted relative to the spectrum.

8.4.5. Library-Based Peak Stripping

In a few cases, all of the gamma-rays emitted by one isotope are very close in energy to gamma-rays emitted by other isotopes in the sample. The peaks from the two gamma rays cannot be separated correctly using conventional analysis, so the activity for one isotope cannot be correctly determined. This alternative to deconvolution can be used to obtain peak areas of the components of a multiplet. It uses peak areas from other parts of the spectrum to determine the areas of some of the components and calculates the remaining areas. It is also referred to as peak-interference correction.

When enabled on the System tab under **Analyze/Settings/Sample Type...**, the program can operate automatically using only one library, or manually using three user-defined libraries detailing the peak overlaps.

8.4.5.1. Automatic Peak Stripping

In the automatic or library-based method, Renaissance automatically identifies the isotopes in the library that are too close together and calculates their activities indirectly. This method is simpler to use than the manual method.

The first step is to search the library for isotopes with severely overlapping gamma rays. The criterion for severe is that the peaks are within two channels of one another (regardless of the energy per channel). For peaks that are this close, the peak areas will be more accurate if they are found indirectly. Any such peaks are marked in the library as being too close together.

For example, the only useful gamma ray emitted by ^{226}Ra is 185.99 keV. The peak overlaps the 185.72 keV peak of ^{235}U . If these two isotopes are both in the library, ^{226}Ra and the 185.72 keV ^{235}U peak are flagged when the library is read. Table 4 shows some other common examples. These energies are from Erdmann and Soyka. Other references might have different energies, but the overlaps will still occur.

The spectrum is then analyzed as described with one exception: any peaks that are marked as too close are not used in the isotope activity calculations. Instead, the activity of one isotope is based on other gamma rays from that isotope. That activity is then used to calculate the contribution to the overlapped peak of this isotope. That contribution is subtracted from the total peak area to obtain the peak area due to the other isotope.

In the example above, the activity of ^{235}U is calculated from the area of the peak at the next most probable energy, i.e., 143 keV. Then the area of the 185.72 keV ^{235}U peak is calculated using the branching ratio of that gamma ray, the efficiency, and the activity. The ^{235}U area is subtracted from the area of the peak at 185 keV to give the area due to ^{226}Ra . From this, the activity of ^{226}Ra in the sample is calculated.

Table 4. Gamma Peak Overlap Examples.

Isotope	Energy (keV)	Probability	Isotope with close energy
^{99m} Tc	140.99	89.3	⁹⁹ Mo
²²⁴ Ra	241.00	3.90	⁹² Sr
²²⁶ Ra	185.99	3.28	²³⁵ U
²⁴¹ Am	26.35	2.5	²³⁷ U
²⁴¹ Am	33.20	0.11	¹⁴⁴ Ce
²⁴¹ Am	59.54	36.3	²³⁷ U

8.4.5.2. Manual Peak Stripping

The manual method of analysis uses three libraries. The first is the working analysis library with the severely overlapped peak multiplets removed. Multiplets that can be deconvoluted by fitting should remain in the first library. The **Second Library** contains the peaks that are to be stripped from the overlapped doublet. The amount to be stripped is based on the analysis from Library 1. The nuclide name for the stripped peak must be the same in both libraries, as this is how the program determines which peak areas to use. The **Third Library** contains the nuclides with the other peak in the overlapped doublets. The computations for the third library are the same as the first library except that deconvolutions are not performed and MDAs are not calculated for the third-library nuclides. You have complete control over the three libraries and can choose which peaks to use in each step. Nuclides that appear in both Libraries 1 and 3 are reported twice on the report.

For example, consider the case in which a spectrum contains nuclides A, B, C, D, E, and F. Nuclide D has energies of 200 keV and 500 keV, and nuclide F has only one peak at 500 keV. Let Library 1 contain five nuclides labeled A, B, C, D, and E. Let Library 2 contain nuclide D, and Library 3 contain nuclide F. In Library 1, nuclide D is listed with only the energy at 200 keV. In Library 2, nuclide D is listed with only the energy at 500 keV.

The analysis of the spectrum using Library 1 will give an activity for nuclide D based on the peak at 200 keV (as well as activities for A, B, C, and E). Using this activity, the peak count rate for the nuclide D peak at 500 keV will be calculated using Library 2 and the calibration and corrections, if any. This peak count rate will be converted to a peak shape function (a Gaussian) based on the calibration peak shape and the counting time. This peak will be subtracted channel by channel from the net spectrum. This new net spectrum will then be analyzed using Library 3.

The results of all the calculations (that is, the equivalent peak areas and gross areas) will be shown on the full report. If Library 1 or 3 does not contain any peaks in the energy range being

analyzed, this option is turned off. If Library 2 does not contain any peaks in the energy range or any peaks in Library 1, the subtraction of peak areas does not take place, but the analysis using Library 3 is still performed. This can be an easy way to obtain a report with MDA for some nuclides (those in Library 1) and without MDA for other nuclides (those in Library 3).

8.5. Fraction Limit

To verify the identification of a particular nuclide in a spectrum, the number of identified peaks is compared to the number of possible peaks, where “identified” peaks are those with a 1-sigma counting uncertainty less than the **Peak Cutoff** value, and the possible peaks include only those within the low-/high-energy analysis range. Peaks with the “Not in Average” flag set as NOT TRUE in the library are excluded. It is expressed as follows:

$$Fraction = \frac{\sum_{l=1}^n Br_l}{\sum_{p=1}^m Br_p} \quad (42)$$

where Br is the branching ratio for the peak for the given nuclide, adjusted for TCC where applicable; l is the sum over the located peaks; and p is the sum over the possible peaks. This fraction is between 100 for all peaks located and 0 for no peaks located.

This value is compared to the Fraction Limit, entered on the System tab under **Analyze/Settings/Sample Type...**, to determine whether this nuclide’s peaks are present in sufficient measure to say the nuclide is present. The *fraction limit test* is passed if the fraction is above the selected value.

To disable the fraction limit test, enter a limit of zero on the System tab.

8.6. Nuclide Activity

The nuclide activity is calculated for all peaks in the library whose energy is between the energy limits you have selected for the analysis (in-range). There are several methods of determining if a nuclide is present or not, and if MDA should be reported.

A nuclide is reported with an activity value under the following conditions:

- 1) If more than one peak is listed for the nuclide, the following apply:

- The first in-range peak that is not marked as “Not in Average” and not closely overlapping another library peak, such that peak stripping would be applied, must be identified.²⁰
- All peaks marked as key lines must be identified.
- The Fraction Limit Test must be satisfied.
- For RENGAM and RENENV, the Library Reduction requirements must be satisfied (see Section 6.2.3.)

2) If only one peak is listed for the nuclide, the following apply:

- If the peak does not closely overlap another library peak, it must be identified in the analysis range.
- If the “Not in Average” flag is set for this peak, the nuclide is automatically rejected when using all analysis engines except for RENWAN, which ignores the “Not in Average” flag under this condition.
- If the peak closely overlaps another library peak such that peak stripping would be applied, the uncertainty of the area remaining after peak stripping must be less than the **Peak Cutoff**.

3) **Directed Fit** forces an activity to be reported for nuclides that do not meet the preceding criteria.

If a nuclide is not reported with an activity value, and the “No MDA Calculation” flag is not set in the library, the MDA value will be reported in the Summary of Nuclides in Sample. Otherwise, the nuclide will be omitted from the Summary of Nuclides in Sample.

The nuclide activity (in becquerels or curies), based on the peak at energy E , is given by:

$$A_{Ei} = \frac{N_{Ei} * TDC * Mult * RSF * GeoFac * A_c}{LT * \epsilon_E * Br * Div * s} \quad (43)$$

where:

- A_{Ei} = the activity of nuclide i based on energy E
- N_{Ei} = net peak area for peak at energy E
- TDC = decay corrections, incorporating DDA , DC , and DDC as defined in Sections 8.9.1 through 8.9.3.
- $Mult$ = multiplier entered on the System tab.
- RSF = random summing correction factor (Section 8.11).
- LT = live time.

²⁰“Identified” in this discussion indicates the peak counting uncertainty at 1 sigma is less than the **Peak Cutoff** value.

- ε_E = detector efficiency at energy E (Section 5.3.5); this efficiency factor is stored in the .CLB record of the .SPC spectrum file.
 Br = peak branching ratio from library.
 $GeoFac$ = geometry correction factor as described in Section 8.9.5.
 A_c = attenuation correction (Section 8.9.6.1).
 Div = divisor entered on the System tab.
 s = sample quantity entered on the System tab.

This “peak activity” is reported in the nuclide peak matrix (if requested). If there is more than one peak in the energy analysis range for a nuclide, then an attempt to average the peak activities is made. The result of the average is the average nuclide activity.

8.6.1. Average Activity

The average activity for the nuclide is calculated by first calculating a gammas/disintegration weighted average of the first and second library peak activity, if the activity of the second peak is within N times the uncertainty of the first peak activity, where N is the **Activity range factor** in `b30winds.ini` (Section A.2.2, page 388; the default value is 2) if the activity of the second peak is within two times the uncertainty of the first peak activity. Only peaks that (1) *do not* have the “Not in Average” flag set and (2) have been positively identified per the criteria in Section 8.6 (and their associated branching ratios) are included in this summation.

The uncertainty in the first peak activity includes counting uncertainty of the first peak, uncertainty in the library entries, and uncertainty in the calibration. Subsequent peaks are likewise included in a running average if their activity is within two times the uncertainty of the running average activity. The averaged activity is weighted by the branching ratio and is calculated as:

$$A_{avg} = \frac{\sum_{i=1}^n A_{Ei} Br_E}{\sum_{i=1}^n Br_E} \quad (44)$$

where:

- A_{Ei} = the activity of nuclide peak i at energy E per Eq. 43
 Br_i = the gamma/disintegration of the i th peak
 n = the number of peaks included in the activity

8.6.2. Nuclide Counting Uncertainty Estimate

Many radioisotopes have more than one peak useful for calculating the measured activity of the isotope. The uncertainty caused by counting statistics can vary widely among those peaks. This variation can be caused by differences in the net counting rates in the peaks or the background levels under the peaks. Renaissance utilizes a relatively simple yet statistically rigorous method for choosing the peaks to achieve optimum precision. When more than one peak is available, the software performs two assessments:

- 1) It finds the peak with the smallest percent standard deviation.
- 2) It computes the percent standard deviation for the linear average of all peaks detected according to the criteria in Section 8.6.

The option which yields the lowest percent standard deviation is the method used to calculate the nuclide counting uncertainty for the radioisotope. The mathematical process for this selection is summarized as follows:

Assume σ_A is the reported nuclide counting uncertainty, σ_{Pi} is the counting uncertainty for the i^{th} peak and n is the total number of peaks used to calculate the nuclide activity. All the uncertainties are relative. Furthermore, let us define σ_{Pmin} as the minimum counting uncertainty of all the n peaks:

$$\sigma_{Pmin} = \text{MIN}(\sigma_{Pi}), \quad i = 1, \dots, n \quad (45)$$

where *MIN* is the minimum function which returns the minimum value from a list of values in the parenthesis (from 1 to n above).

The averaged nuclide counting uncertainty σ_{avg} is calculated from:

$$\sigma_{avg} = \frac{\sqrt{\sum \sigma_{Pi}^2}}{n} \quad (46)$$

The reported nuclide counting uncertainty is calculated at 1 sigma and reported at 1, 2, or 3 sigma, depending on the **Confidence level** setting on the Report tab. It is calculated as:

$$\sigma_A = \text{MIN}(\sigma_{Pmin}, \sigma_{avg}) \quad (47)$$

Renaissance compares the averaged peak counting uncertainty and the minimum peak counting uncertainty and reports the smaller value as the nuclide counting uncertainty.

8.7. Total Activity (RENROI32 Analysis Engine Only)

Total activity represents the summed activity calculated for all nuclides found in the sample. It is calculated as follows and printed immediately after the Summary of ROI Nuclides table in the analysis report.

$$A_{tot} = \sum_{n=1}^{Nuclides} A_{avg} \quad (48)$$

where A_{avg} is calculated per Section 8.6.1. Note that if MDA is reported for A_{avg} for a particular nuclide, that nuclide's contribution is not included in A_{tot} .

8.8. MDA

The Minimum Detectable Activity (MDA) is a measure of how little activity could be present and not be detected by the analysis. There are many factors affecting the MDA, which is reported in activity units such as becquerels. The calibration geometry, the backgrounds (system- and source-induced), the detector resolution, and the particular nuclide all substantially affect the MDA reported.

In most instances, the MDA value is calculated based on the background value of the peak. If the peak area was not used in the activity calculation because it failed the sensitivity test, or a shape test, the peak area is added to the background for the MDA calculation unless the MDA defines the background separately. If the background is 0, it is set to 1 for the MDA calculation. The background will still be reported as 0 on the report. By reviewing the individual MDA values (which are printed on the nuclide/peak matrix) you can determine how relevant the selected MDA value is to the physical situation. The MDA reported for the nuclide is the value for the first peak in the library.

8.8.1. Computing MDA Values

MDA values for many methods depend on area and background values. Area and background determination varies from method to method. The information needed to validate the MDA results can be found in the peak analysis Details dialog (Fig. 233); the analysis options (.SDF file) for the spectrum (Section 5.5.1); reports (Chapter 6); and manual integration of the spectrum peaks.

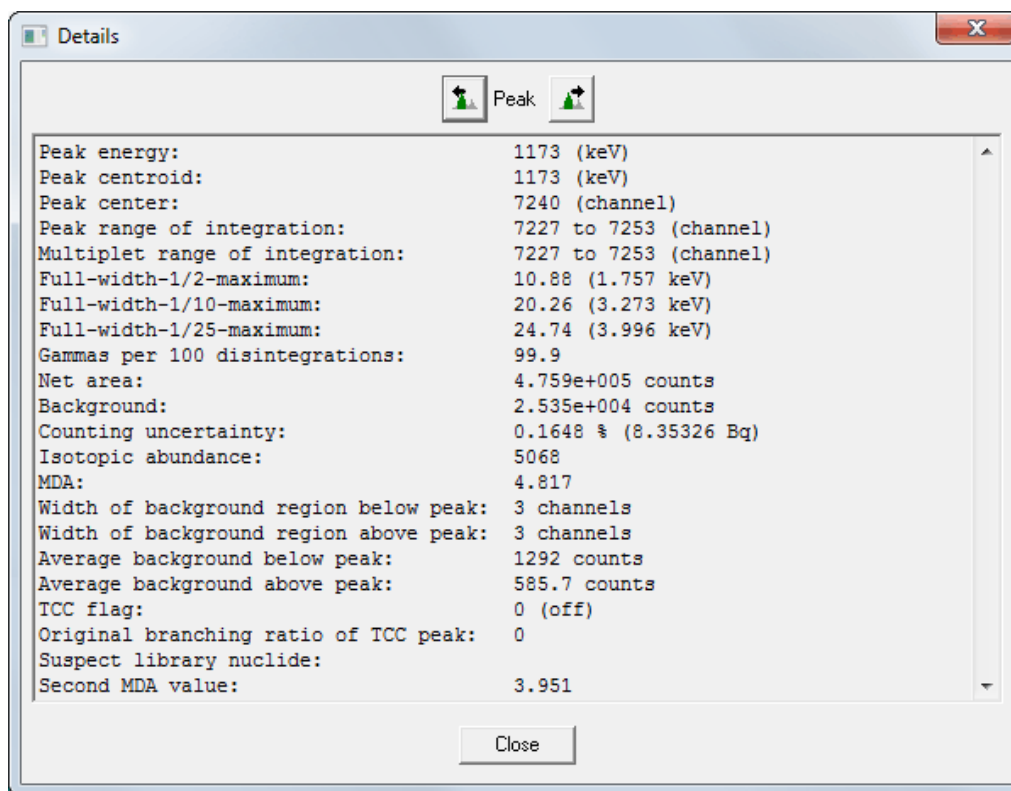


Figure 233. Peak Analysis Details Dialog is One Source of Data for the MDA Calculation.

8.8.1.1. Area Methods

A₁ Gross area under the peak determined by integrating the peak with a width of 2.5 times FWHM (counts). Areas computed in this manner are used in Methods 4, 11, and 14 below.

To determine the area:

- 1) Determine the (decimal representation) centroid energy of the peak.
- 2) Determine the (decimal representation) channel of this centroid (based on the energy calibration).
- 3) Determine the (decimal representation) FWHM of this peak (based on the FWHM calibration at the centroid channel).
- 4) Determine half of the FWHM range (denoted as I_L), which is calculated as the integer representation of $(1.25 * FWHM + 0.5)$. Note that this value is capped at 100.

- 5) Determine the centroid for integration (denoted as C_I), which is simply the centroid channel determined in step (2) rounded to the closest whole (integer) number.
- 6) Determine a lower channel of integration (denoted as C_{Low}) as follows. This value has a minimum value of 1.

$$C_{Low} = C_I - I_L$$

- 7) Determine an upper channel of integration (denoted as C_{High}) as follows:

$$C_{High} = C_I + I_L$$

- 8) A_1 is then simply the sum of all channels from C_{Low} to C_{High} .

- A₂** Net peak area reported on the Identified Peak Summary Report or peak Details dialog (counts). Areas computed in this manner are used in Methods 9 and 10 below.
- A₃** Gross area under the peak determined by integrating the peak with a width of 2.5 times FWHM minus one channel on the high- and low-energy side of the peaks. Areas computed in this manner are used in Method 13 below.

To determine the gross area:

- 1) Determine the (decimal representation) centroid energy of the peak.
- 2) Determine the (decimal representation) channel of this centroid (based on the energy calibration).
- 3) Determine the (decimal representation) FWHM of this peak (based on the FWHM calibration at the centroid channel).
- 4) Determine half of the FWHM range (denoted as I_L), which is calculated as the integer representation of $(1.25 * FWHM + 0.5)$. Note that this value is capped at 100.
- 5) Determine the centroid for integration (denoted as C_I), which is simply the centroid channel determined in step (2) rounded to the closest whole (integer) number.
- 6) Determine a lower channel of integration (denoted as C_{Low}) as follows. This value has a minimum value of 4.

$$C_{Low} = C_I - I_L + I$$

- 7) Determine an upper channel of integration (denoted as C_{High}) as follows:

$$C_{High} = C_I + I_L - 1$$

- 8) A_3 is then simply the sum of all channels from C_{Low} to C_{High} .

8.8.1.2. Background Methods

- B₁** Background reported in the Identified Peak Summary (counts). These backgrounds are used in Methods 1, 2, 5, 6, 7, 8, 12, and 16 below. For some MDA methods, if the peak fails validity tests, $B_I = B_I + peak\ area$.
- B₂** The average of three high-energy channels and three low-energy channels as part of peak area method A_3 (counts). Backgrounds computed in this manner are used in Method 13 below.
- B₃** The sum of the counts on the high-energy portion of the peak and the low-energy portion of the peak. The boundary of the peak is established as described for A_1 . Backgrounds computed in this manner are used in Methods 14 and 15 below.

To determine the area:

- 1) Determine the (decimal representation) centroid energy of the peak.
- 2) Determine the (decimal representation) channel of this centroid (based on the energy calibration).
- 3) Determine the (decimal representation) FWHM of this peak (based on the FWHM calibration at the centroid channel).
- 4) Determine the integer value representation of the centroid channel (denoted as C_{Int}) simply by rounding the centroid channel down to the closest whole (integer) number.
- 5) Determine the width of 2.5 times the FWHM (denoted as I_B , range 4 to 100), then round to next integer; e.g., round 5.0 to 5, and 5.0001 to 6.0 to 6. This value is calculated as follows:

$$I_B = (Integer) 2.5 * FWHM + 0.9999$$

- 6) Determine half the I_B range (denoted as L) as follows and rounded down to the next closest whole integer:

$$L = (\text{Integer}) I_B / 2$$

- 7) Determine the start channel of the main peak region (denoted as Pk_{Start}). This value is set at the minimum value of 1, and is calculated as:

$$Pk_{Start} = C_{Int} - (\text{integer}) (-0.45 + IB / 2)$$

- 8) Determine the end channel of the main peak region (denoted as Pk_{End}) as follows:

$$Pk_{Start} = C_{Int} + L$$

- 9) Determine the starting channel for $N1$ integration (denoted as $N1_{Low}$) as follows:

$$N1_{Low} = Pk_{Start} - L$$

- 10) Determine the ending channel for $N1$ integration (denoted as $N1_{High}$) as follows:

$$N1_{High} = Pk_{Start} - 1$$

- 11) $N1$ is then the summation of all counts from channel $N1_{Low}$ to $N1_{High}$.

- 12) Determine the starting channel for $N2$ integration (denoted as $N2_{Low}$) as follows:

$$N2_{Low} = Pk_{Start} + 1$$

- 13) Determine the ending channel for $N2$ integration (denoted as $N2_{High}$) as follows:

$$N2_{High} = Pk_{Start} + L$$

- 14) $N2$ is then the summation of all counts from channel $N2_{Low}$ to $N2_{High}$.

- 15) The final value B_3 is then simply the sum of $N1$ and $N2$.

8.8.1.3. Computing MDA

The MDA methods are computed from count rates, CR_{mda} . To convert CR_{mda} from counts to activity, a conversion factor MDA_{conv} is used that contains detector efficiency, branching ratio, and activity correction factors.

$$MDA_{conv} = \frac{1.0}{\xi * LT} \quad (49)$$

where LT is the live time and ξ is defined as:

$$\xi = \frac{TDC * Mult * RSF * GeoFac * A_c}{LT * \epsilon_E * Br * Div * s} \quad (50)$$

where:

- TDC = decay corrections, incorporating DDA , DC , and DDC as defined in Sections 8.9.1 through 8.9.3.
- $Mult$ = multiplier entered on the System tab.
- RSF = random summing correction factor (Section 8.11).
- LT = live time.
- ϵ_E = detector efficiency at energy E (Section 5.3.5); this efficiency factor is stored in the `.CLB` record of the `.SPC` spectrum file.
- Br = peak branching ratio from library.
- $GeoFac$ = geometry correction factor as described in Section 8.9.5.
- A_c = attenuation correction (Section 8.9.6.1).
- Div = divisor entered on the System tab.
- s = sample quantity entered on the System tab.

8.8.2. Renaissance MDA Methods

By default, Renaissance Supervisor and Operator use MDA Method 12 (Section 8.8.2.11, 8.8.2.11). This cannot be changed in the analysis options. To use a different MDA method, edit the **MDA type, T=Allow change** line in the `B30winds.ini` file (page 387) so the first value is the MDA method and the true/false flag must be set to **F**. For instance, the following edit changes the MDA type to Method 10.

10 F

MDA type, T=Allow change

This MDA method is used for all spectrum analyses in both Supervisor and Operator.

Method 1: Traditional ORTEC

$$CR_{mda} = \frac{\frac{100}{SENS} * \left(\sqrt{2 * B_1 + \frac{2500}{SENS^2} + \frac{50}{SENS}} \right)}{LT} \quad (51)$$

where:

$SENS$ = **Peak Cutoff** value (%) on the Analysis tab or in the .SDF file

LT = live time (sec)

NOTE If the peak is rejected, the peak area is added to the background term B_l .

8.8.2.1. Method 2: Critical Level ORTEC

$$CR_{mda} = 2.33 * \frac{\sqrt{B_1}}{LT} \quad (52)$$

Critical level (CL) is defined as the smallest concentration of radioactive material in a sample that will yield a net count (above background) that will be detected with a 95% probability.

NOTE If B_l is computed as zero, it is assigned a value of 1 for CL calculations.

8.8.2.2. Method 3: Suppress MDA Output

The MDA is not calculated and is set to zero.

8.8.2.3. Method 4: KTA Rule

$$CR_{mda} = \frac{\sigma * \sqrt{\frac{A_1}{N} * FWHM}}{LT} \quad (53)$$

where:

- N = number of channels under peak A_1 (channels)
- $FWHM$ = full width at half maximum (in channels, where channels is rounded to the nearest integer); use the Details dialog for the proper value
- σ = **Confidence Level** on the System tab or in the .SDF file (1, 2, or 3 sigma)

8.8.2.4. Method 5: Japan 2 Sigma Limit

$$CR_{mda} = 2 * \frac{\left(1 + \sqrt{1 + 2B_1}\right)}{LT} \quad (54)$$

8.8.2.5. Method 6: Japan 3 Sigma Limit

$$CR_{mda} = 4.5 * \frac{\left(1 + \sqrt{1 + 0.8888 * B_1}\right)}{LT} \quad (55)$$

8.8.2.6. Method 7: Currie Limit

$$CR_{mda} = 1.645 * \frac{\sqrt{B_1}}{LT} \quad (56)$$

NOTE If B_1 is computed as zero, it is assigned a value of 1 for MDA calculations.

8.8.2.7. Method 8: RISO MDA

$$CR_{mda} = 4.65 * \frac{\sqrt{B_1}}{LT} \quad (57)$$

NOTE If B_1 is computed as zero, it is assigned a value of 1 for MDA calculations.

8.8.2.8. Method 9: LLD ORTEC

$$CR_{mda} = 4.66 * \frac{\left(\frac{\sigma_p}{100} * A_2 \right)}{LT} \quad (58)$$

where σ_p is the counting uncertainty (%). This value is found in the peak Details dialog.

8.8.2.9. Method 10: Peak Area

This method is useful if negative peak areas are expected.

$$CR_{mda} = \frac{A_2}{LT} \quad (59)$$

8.8.2.10. Method 11: Air Monitor — GIMRAD (also called DIN 25 482 Method)

$$CR_{mda} = \frac{1.35 * \left(1.0 + \sqrt{1.0 + 2.96 * A_1 * \frac{FWHM}{N}} \right)}{LT} \quad (60)$$

where $FWHM$ is in channels, derived from the $FWHM$ calibration. Unlike the KTA Method (Section 8.8.2.3), $FWHM$ here is a decimal, not the whole-integer representation.

8.8.2.11. Method 12: Regulatory Guide 4.16

This is a frequently used method in the USA.

$$CR_{mda} = \frac{2.71 + 4.66 \sqrt{B_1}}{LT} \quad (61)$$

8.8.2.12. Method 13: Counting Lab — USA

This method is used when a minus MDA is needed in situations when the background is greater than the peak area.

$$CR_{mda} = \frac{A_3 - B_2 N}{LT} \quad (62)$$

where N is the number of channels included in the integration of the peak (channels)

8.8.2.13. Method 14: Erkennungsgrenze (Detection Limit) DIN 25 482.5

This method is described in the German DIN 25 482 teil 5. It is designed to establish a critical value for the spectrum.

$$CR_{mda} = \frac{1.96^2 * N_A * \left(1 + \sqrt{1 + \left(\frac{4 * B_3}{1.96^2} \right) \left(\frac{N_A}{2N_B} \right) \left(1 + \frac{2N_B}{N_A} \right)} \right)}{4 * LT * N_B} \quad (63)$$

where:

N_A = number of channels in the peak rounded up using the A_1 peak method (page 270).

N_B = number of channels in the background regions above and below the peak. Usually, this number is approximately half of the number of peak channels, N_A (channels). It is calculated as follows:

- 1) Determine the peak centroid channel as a whole (integer) number.
- 2) Determine the FWHM at this channel, based on the FWHM calibration.
- 3) Determine the integration channel range (I_B , ranging from 4 to 100) by multiplying 2.5 by the FWHM and rounding up to the next integer (i.e., such that 5.0 is 5 and 5.0001 to 6.0 is 6).
- 4) N_B is then simply $I_B / 2$ and rounded up as described in (3).

8.8.2.14. Method 15: Nachweisgrenze DIN 25 482.5

This method represents the lowest true value of activity that can be reliably reported with similar samples. Its value is approximately twice the value computed for Erkennungsgrenze (Section 8.8.2.13), where N_A and N_B are defined.

$$CR_{mda} = \frac{2 * 1.96 * \sqrt{B_3 * \left(1 + \frac{N_A}{2N_B} \right)}}{LT} + \frac{(2 * 1.96)^2 * \left(1 + \frac{N_A}{2N_B} \right)}{4 * LT} \quad (64)$$

8.8.2.15. Method 16: EDF — France

This method is defined for the EDF and CEA in Rapport CEA-R-5506, *Determination du Seuil de la Limite de Detection en Spectrometrie Gamma*.

$$CR_{mda} = 6.2 * \frac{\sqrt{B_1}}{LT} \quad (65)$$

NOTE If B_1 is computed as zero, it is assigned a value of 1 for MDA calculations.

8.8.2.16. Method 17: NUREG 0472

$$CR_{mda} = 4.66 * \frac{\sqrt{B_1}}{LT} \quad (66)$$

8.9. Corrections

If enabled, the following corrections are made on a nuclide-by-nuclide or peak-by-peak basis.

8.9.1. Decay During Acquisition

The decay during acquisition correction is used to correct the activity of nuclides whose half-life is short compared to the spectrum real time.

The correction is:

$$DDA = \frac{\ln 2 \times \frac{Real\ time}{half-life}}{1 - e^{-\left(\ln 2 \times \frac{Real\ time}{half-life}\right)}} \quad (67)$$

where:

- DDA = the decay correction factor
- $Real\ time$ = the spectrum real time (in seconds)
- $half-life$ = the half-life of the nuclide of interest

This can be viewed as scaling up the activity measured to the value of the activity at the start of the measurement. The correction goes to 1 (no change) as acquisition time becomes much smaller than the half-life.

The decay during acquisition technique is superior to making use of a hardware dead-time correction. For example, suppose a sample contains two nuclides, one with a short half-life and one with a long half-life. The count rate of the short half-life nuclide will be higher at the beginning of the count time than at the end of the count. This means more counts per unit time will be accepted at the beginning of the count time than at the end. So even if the count time is extended by the hardware to compensate for the lost counts at the beginning of the counting period, the count rate is so low at the end of the count that not enough counts will be added in. For the long half-life nuclide, the count rate does not change during the count time, so the live-time correction will correctly account for the lost counts during the count time.

8.9.2. Decay Correction

If disabled on the Decay tab or in the .SDF file, the decay correction is set to 1.0. If enabled, this correction projects the activity at the time of count back to the time the sample was collected. This is useful when there is a long time, relative to the half-life, between the sample collection time and the sample count time. The sample collection time is entered on the Decay tab (alternatively, the number of half-lives can be set in `b30winds.ini`; see Section A.2.2). If the time is greater than 12 half-lives, the correction is not made and the message is printed out. Twelve half-lives corresponds to a decay factor of about 4000. Both the time of count and decay-corrected values are presented on the report. The total activity is the decay-corrected activity.

Decay correction is determined as follows:

$$DC = e^{\left(\frac{\ln(2) \Delta T}{T_1}\right)} \quad (68)$$

where

$$\Delta T = T_{Count} - T_{Collection}$$

8.9.3. Decay During Collection

If the sample was collected over an extended time (see page 127), this correction will account for the buildup or increase of activity in the sample during the collection time. The correction is given by:

$$DDC = \frac{\ln(2) \times \frac{\textit{Elapsed time}}{\textit{half-life}}}{1 - e^{-\left(\ln(2) \times \frac{\textit{Elapsed time}}{\textit{half-life}}\right)}} \quad (69)$$

8.9.4. Peaked Background Correction

The Peaked Background Correction (PBC) is used to correct for the presence of peaks in the background spectrum that also occurs in the sample. If the peak is not of interest in the analysis results, there is no need to make this correction. The values in the PBC table are the counts per second at each library energy. These count rates are multiplied by the sample live time to calculate background counts, and the resulting background counts are added to the respective peak background. *Note that this background subtraction may raise the peak uncertainty above the peak cutoff such that a peak is no longer considered as identified.*

This section describes how peaks are qualified for PBC correction. The correction and uncertainty calculations are covered in Section 8.12.10.

8.9.4.1. PBC Match Width

The PBC is applied only if the nuclide name is the same as the nuclide defined in the PBC file *and* the two peak energies are within the **Match Width** specified on the Correction tab. The default PBC match width is 0.2 times the peak FWHM. For backward compatibility with earlier versions of Renaissance, if the match width is found to be zero, the default match width is used. The minimum match width is 0.1. If you specify a non-zero **Match Width**, it is used as follows.

For each peak at energy E_0 , the PBC match width in keV is calculated first:

$$\Delta E = f_{PBC} * FWHM \quad (70)$$

where $FWHM$ is the calibrated peak FWHM at that energy and f is the **Match Width** value specified on the Correction tab. Then the energy range from E_1 to E_2 is considered for PBC matching width:

$$E_1 = E_0 - \Delta E, \quad E_2 = E_0 + \Delta E \quad (71)$$

A PBC peak is considered a matching peak if the PBC peak energy is within this energy range. The PBC uncertainty calculation is discussed in Section 8.12.10.

8.9.5. Geometry Correction

The geometry correction is used to adjust the activities reported in a sample of a given source/detector geometry when the system was calibrated using a different source/detector geometry. This is useful when many different geometries are used in a laboratory and calibrated sources are not available for all the geometries used. For more information, see Section ?.

The correction factor multiplies the peak activity for each peak in the library as shown in Eq. 72. The factors are stored as a function of energy.

$$A_{Geo} = A * GeoFac \quad (72)$$

where:

- A_{Geo} = corrected activity for a given energy
- A = uncorrected activity for a given energy
- $GeoFac$ = the correction factor for that energy

The correction is not applied to unknown peaks. The peak values in the isotope/peak list in the output report are uncorrected values. The peak uncertainty is maintained as a constant percentage. The factor is linearly interpolated between the points in the table and linearly extrapolated outside the energy range of the table points.

The geometry correction table is stored in the spectrum file (.SPC). The correction can be enabled or disabled for a specific analysis.

8.9.5.1. Example

As an example of this correction, two spectra were taken of the same point source (Fig. 234). In case 1, the source was about 4 cm from the end cap and on-axis of the detector. The second geometry (case 2) is with the source about 7.5 cm from the center of the detector in a position in the plane of the end cap of the detector.

Table 5 shows the analysis of the two spectra for the peaks due to ^{154}Eu . The ratio of the peak count rates is shown in

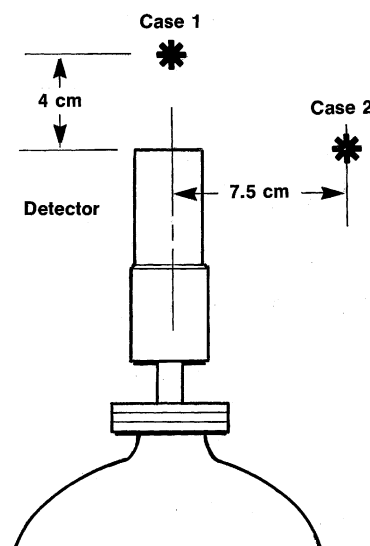


Figure 234. Example Geometries Used.

column 4. These values are entered into the geometry table. The spectrum was re-analyzed with the geometry correction turned on. The comparison of all three analyses is shown in Table 6.

Table 5. Geometry Correction Table.

Energy (keV)	Peak Count Rate		ratio
	Case 1	Case 2	
123.14	63.23	51.07	1.238
591.74	3.31	2.19	1.511
723.3	11.50	7.47	1.539
873.20	5.75	3.79	1.517
1004.76	7.71	4.91	1.570
1274.45	10.29	6.07	1.695

Note that the ^{155}Eu activity is not corrected as much as needed. This is primarily due to all of the ^{155}Eu gamma-ray lines falling below the lowest energy in the correction table. It is in these low energies that the differences in the geometries is most noticeable.

The geometry correction table can be made automatically using analysis results files (.UFO) of the pairs of geometries or manually by entering the correction factor and energy pairs.

Table 6. Geometry Correction Results.

Nuclide	Activity		
	Case 1	Case 2 no correction	Case 2 correction
^{154}Eu	12750	7730	13000
^{155}Eu	8020	5180	6300
^{125}Sb	2900	1956	2840

8.9.6. Absorption

The absorption factor is used to correct for the absorption of gamma-rays by material between the detector and the source. The factors are stored as a function of energy in the *attenuation database*, *Atd.mdb*, in C:\User. Materials that are always present (such as the detector end cap) will be accounted for in the efficiency calibration. Source containers will not normally be accounted for, nor will an absorbing matrix such as soil. In these cases, the absorption of the gamma-rays will cause low values for the isotopic abundances to be reported unless the absorp-

tion correction is made. One of two types of absorption correction (as defined in ASTM E181-82)²¹ can be selected. External absorption is for cases where all the source gamma-rays pass through the absorber. Internal absorption is for cases where the radioisotope is mixed with the absorber so that some of the gamma-rays go through a lot of absorber and some only go through a small amount of absorber.

8.9.6.1. External Absorption

The external absorption is used when the source is separate from the absorber, as in a source in a metal can. All of the gamma rays from the source must pass through all of the absorber before reaching the detector. The corrected peak areas are the spectrum peak areas multiplied by the correction as:

$$A_c = A * e^{\mu x} \quad (73)$$

where:

A = the peak area at energy E

μ = the table value at energy E ; normally the mass attenuation coefficient

x = the absorption factor; a function of the sample weight, density, or thickness such that it is in inverse units of μ (**Length**, entered on the Corrections tab)

For values between the table values, the μ are linearly interpolated between the table values using the natural logarithms of the μ values and their associated energies when using the coefficient table. If the spectrum is being used to calculate the μ values, linear interpolation is used on the μ values and their associated energies to obtain μ between energies. The correction value is always 1 or greater.

8.9.6.2. Internal Absorption

The internal absorption is used when the source and the absorber are mixed together, such as soil or sand samples. Some of the gamma rays pass through no part of the absorber and some pass through the entire sample. The following formula for the corrected areas assumes that the absorbing matrix is homogeneous and that the source is uniformly distributed in the matrix.

$$A_c = A * \frac{\mu x}{1 - e^{-\mu x}} \quad (74)$$

²¹“Standard General Methods for Detector Calibration and Analysis of Radionuclides,” ASTM E181-82, also ANSI N42.14-1978, IEEE, NY, NY.

where:

A = the peak area at energy E

μ = the table value at energy E ; normally the mass attenuation coefficient

x = the absorption factor; a function of the sample weight, density or thickness such that it is in inverse units of μ (**Length**, entered on the Corrections tab)

Internal Absorption Correction

For other absorbing conditions, these approximations might not apply. The corrections should be checked against a known situation to ensure that these conditions are met for the current analysis situation.

The absorption table values can be constructed from mass attenuation coefficients or by ratioing unattenuated spectrum results with attenuated spectrum results. The ratio method is difficult to apply to the internal absorption correction because of the difficulty in obtaining appropriate spectra.

The mass attenuation coefficients are available from many sources. For mixtures not listed in the table, use the molecular weight fractions to obtain an average attenuation coefficient. For example, for water, multiply the hydrogen coefficient by 2.016, the oxygen coefficient by 16 and divide the sum by 18.016.

The table will contain the attenuation coefficients for the absorber being used. The x-factor, which you enter, is in inverse units of the attenuation coefficient. If the coefficient is entered in cm^2/g , then the factor must be in g/cm^2 , which is the density (g/cm^3) times the thickness of the sample.

The linear attenuation coefficients can also be used. In this case the input factor will be the thickness. It might be more convenient to use the linear attenuation coefficients so that the input factor can be directly related to the sample.

To use the ratio of two spectra, take at least two spectra with and without the absorber. It is not necessary that the peaks be listed in the library, only that the peaks be defined in the spectra. The half-life of any nuclide used should be very long compared to the time of measurement of both spectra, so that decay corrections will not have to be made. The program calculates the ratio of the peak areas from the absorber-in and absorber-out analysis output files. This will give a table of energies (peak energies) and multipliers. The program now stores the natural log of the multipliers to obtain a table of energies and coefficients. The coefficients are divided by the thickness of the absorber (**Length**, entered on the Corrections tab, Fig. 115), so that the factor you have entered is the sample thickness.

8.9.6.3. Example — Ratio Method

The following is an example of calculating the absorption factor using the ratio of two spectra. The results of the spectrum analysis without an absorber is shown in Fig. 235. The ¹⁵⁴Eu peaks are used because they are distributed over the range of interest.

The results with an absorber are shown in Fig. 236. The intensity (activity) columns from both figures have been transferred to Table 7, which also shows the ratio of the two sets of intensities and the logarithm of the ratio.

The logarithm values and the energies were entered into the absorption table. The absorption file records were saved in the “absorber-in” spectrum.

The spectrum was energy and efficiency calibrated using the point source (SRM 4275). The results of the analysis of the three conditions (no absorber, uncorrected absorber, and corrected absorber) are shown in Table 8.

NUCLIDE	PEAK CHANNEL	CENTROID ENERGY	BACKGROUND COUNTS	COUNTS	NET AREA CTS/SEC	INTENSITY	UNCERT 1 SIGMA %	FWHM keV
EU-154	205.56	42.83	21567.	81517.	81.52	.56	1.386s	
EU-154	600.95	123.08	3702.	63228.	63.23	.46	1.096	
EU-154	1216.09	247.92	2387.	7803.	7.80	1.93	1.172	
EU-154	1240.28	252.83	842.	66.	.07	77.62	.431s	
EU-154	2909.92	591.69	1386.	3309.	3.31	3.67	1.490	
EU-154	3516.06	714.71	1248.	258.	.26	47.25	1.071s	
EU-154	3558.06	723.24	1344.	11503.	11.50	1.45	1.577	
EU-154	4296.98	873.20	920.	5748.	5.75	2.21	1.631	
EU-154	4902.96	996.19	869.	4710.	4.71	2.33	1.685	
EU-154	4944.77	1004.67	987.	7712.	7.71	1.81	1.841	
EU-154	6273.55	1274.35	77.	10292.	10.29	1.02	2.028	
EU-154	7860.55	1596.44	4.	296.	.30	6.21	1.297s	

s Peak fails shape tests.
D Peak area deconvoluted.

Figure 235. No Absorber Analysis.

NUCLIDE	PEAK CENTROID		BACKGROUND		NET AREA	INTENSITY	UNCERT	FWHM
	CHANNEL	ENERGY	COUNTS	COUNTS	CTS/SEC		1 SIGMA %	keV
EU-154	205.11	42.74	13258.	27358.	27.36	1.12	1.407s	
EU-154	600.85	123.06	4562.	40707.	40.71	.68	1.090	
EU-154	1215.85	247.88	2402.	5359.	5.36	2.56	1.230	
EU-154	1244.33	253.66	1757.	208.	.21	43.82	.317s	
EU-154	2910.12	591.73	1334.	2679.	2.68	4.42	1.569	
EU-154	3517.08	714.92	1205.	278.	.28	38.89	.354s	
EU-154	3558.02	723.23	1185.	8792.	8.79	1.47	1.628	
EU-154	4296.72	873.15	602.	4686.	4.69	2.01	1.697	
EU-154	4903.03	996.20	718.	3682.	3.68	2.62	1.690	
EU-154	4944.84	1004.69	799.	6249.	6.25	2.00	1.824	
EU-154	6273.41	1274.33	85.	8654.	8.65	1.13	2.100	
EU-154	7860.54	1596.44	0.	256.	.26	6.25	1.780s	

s Peak fails shape tests.
D Peak area deconvoluted.

Figure 236. Absorber-In Analysis.

All three isotopes in the sample are affected by the correction (see columns 3 and 4). The ^{154}Eu and ^{125}Sb are corrected to the no-absorber value. The ^{155}Eu activity is not corrected enough because all the lines used in the analysis of ^{155}Eu are below the lowest energy in the absorption table and the program uses a linear interpolation between the table values and linear extrapolation outside the table values. This underestimates the correction below the lowest energy because the attenuation is logarithmic in form.

Table 7. Absorption.

Energy	Without	With	Ratio	Log(ratio)
123.14	63.23	40.71	1.553	0.440
248.04	7.80	5.36	1.455	0.375
591.74	3.31	2.68	1.235	0.211
723.3	11.50	8.79	1.308	0.269
873.20	5.75	4.69	1.226	0.204
1004.76	7.71	6.25	1.234	0.210
1274.45	10.29	8.65	1.190	0.174

Table 8. Results — Measured Correction.

Nuclide	No Absorber	Uncorrected Absorber	Corrected Absorber
¹⁵⁴ Eu	12750 Bq	10900 Bq	12750 Bq
¹⁵⁵ Eu	8020	4813	7621
¹²⁵ Sb	2900	2190	2890

8.9.6.4. Example — Table Values

The same spectrum example can be used to show the calculated coefficients. Using the mass attenuation coefficients table²² for silicon and oxygen, the linear attenuation coefficients can be calculated for the sand absorber. Any other materials in the sand are ignored in this case, but might not be in the general case. Table 9 shows the mass attenuation coefficients for oxygen, silicon and sand (SiO₂).

The sand value can be calculated using the mass ratios. In this case it is also given in the hand-book tables. The density of the sand was measured to be 1.67 g/cm³. The fifth column in the table is the coefficient in column 4 multiplied by the density. These numbers are entered into the SOR table. This is the linear attenuation factor in 1/cm.

In the analysis, the absorption factor is entered as 1.6, because this is the thickness of the sand in cm. The result of the analysis using this table is shown in Table 10. Note that the calculated correction is more accurate below 100 keV than the measured correction so ¹⁵⁵Eu is more accurately corrected. Figure 237 shows the two correction files. The vertical scales have been adjusted to account for the difference in the input factor of 1.6.

²²“Radiological Health Handbook,” January 1970, U.S. Dept. of Health, Education and Welfare.

Table 9. Calculated Coefficients.

Energy	mu/rho			mu Sand
	Oxygen	Silicon	Sand	
30	.372	1.41	.859	1.43
40	.257	.696	.463	.773
50	.213	.437	.318	.531
60	.191	.322	.252	.421
80	.168	.224	.194	.324
100	.156	.184	.169	.282
150	.136	.145	.140	.234
200	.124	.128	.126	.210
300	.107	.108	.108	.180
400	.0957	.0962	.0959	.160
500	.0873	.0875	.0874	.146
600	.0808	.0808	.0808	.135
800	.0708	.0707	.0707	.118
1000	.0637	.0635	.0636	.106
1500	.0518	.0518	.0518	.0865
2000	.0446	.0448	.0447	.0746

Table 10. Results — Calculated Correction.

Nuclide	No absorber	Uncorrected absorber	Corrected absorber
¹⁵⁴ Eu	12750 Bq	10900 Bq	12450 Bq
¹⁵⁵ Eu	8020	4813	7965
¹²⁵ Sb	2900	2190	2776

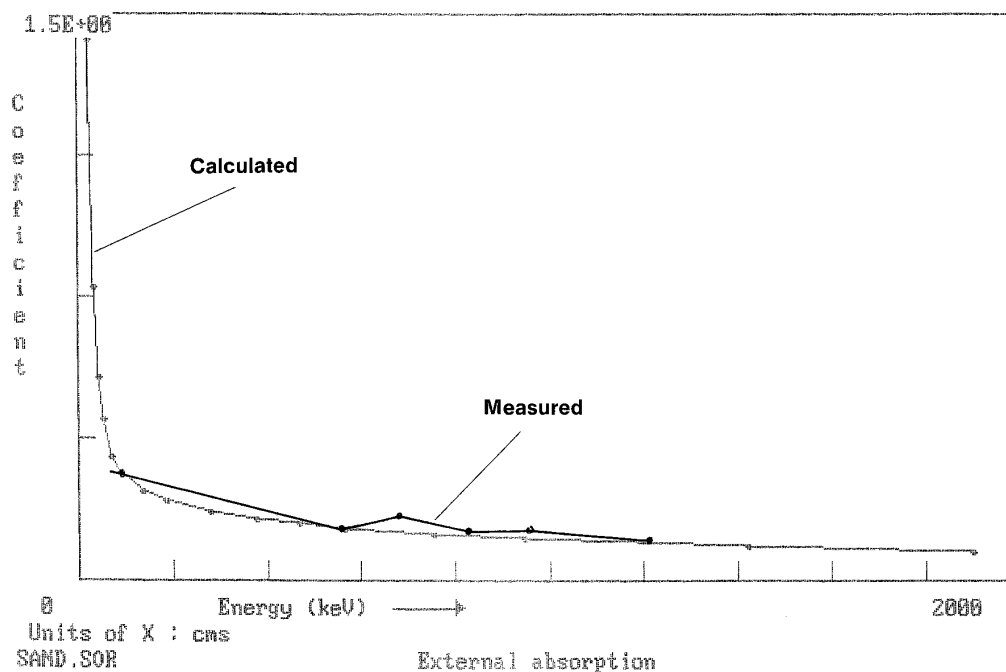


Figure 237. Comparison of Measured and Calculated Absorption Factors.

8.10. Chest Wall Thickness Correction

The chest wall thickness correction is used to account for the absorption of the gamma-rays by the chest wall tissue. The wall thickness used here is based on the work of several groups, including Watts, et al.,²³ which bases the thickness on the height and weight of the person. The attenuation correction is based on this thickness, the absorption coefficients selected, and the correction formula selected. You can select from three equations or the operator can enter the values (see the Renaissance Operator user manual).

One of the two types of absorption correction (as defined in ASTM E181-82)²⁴ can be selected. External absorption is for cases where all the source gamma-rays pass through the absorber. Internal absorption is for cases where the radioisotope is mixed with the absorber so that some of the gamma-rays go through a lot of absorber and some only go through a small amount of absorber.

²³J.R. Watts, J.M. Barber, G.R. Rao, and M.C. McFee, "Chest-wall Thickness Predictions for Actinide Lung Counting." 42nd Annual Conference on Bioassay, Analytical, and Environmental Radiochemistry, 1996.

²⁴"Standard General Methods for Detector Calibration and Analysis of Radionuclides," ASTM E181-82, also ANSI N42.14-1978, IEEE, NY, NY.

8.10.1. External Absorption

The external absorption is used when the source is separate from the absorber, as in a source in a metal can. All of the gamma rays from the source must pass through all of the absorber before reaching the detector. The corrected peak areas are the spectrum peak areas multiplied by the correction as:

$$A_c = A e^{\mu x} \quad (75)$$

where:

- A = the peak area at energy E
- μ = the table value at energy E and is normally the mass attenuation coefficient
- x = the absorption factor and is a function of the sample weight, density, or thickness such that it is in inverse units of μ . This is entered by the operator.

For values between the table values, the μ are linearly interpolated between the table values. The correction value is always 1 or greater.

8.10.1.1. Internal Absorption

The internal absorption is used when the source and the absorber are mixed together, such as soil or sand samples. Some of the gamma-rays pass through no part of the absorber and some pass through the entire sample. The following formula for the corrected areas assumes that the absorbing matrix is homogeneous and that the source is uniformly distributed in the matrix:

$$A_c = A \frac{\mu x}{1 - e^{-\mu x}} \quad (76)$$

where:

- A = the peak area at energy E
- μ = the table value at energy E and is normally the mass attenuation coefficient
- x = the absorption factor and is a function of the sample weight, density or thickness such that it is in inverse units of μ . This is entered by the operator.

In these formulas, the “ x ” is the chest wall thickness CWT. The CWT is given by:

$$CWT = 0.4657 + 4.731 \cdot \left(\frac{wt}{ht} \right) \quad (77)$$

where:

wt = the weight in kg

ht = the height in cm

The weight and height are converted to kg if entered in lbs/inches.

8.11. Random Summing

If more than one gamma-ray photon signal is absorbed by the detector during a pulse sampling cycle, the sum of the energies of the two (or more) is recorded in the spectrum. Since the two gamma rays are not related in any way, this is random coincidence. Random coincidence sum peaks can be formed at double the energy of the primary peaks (Fig. 238). Any full-energy photon that is summed with another pulse is not recorded in the single photon peak and represents a loss of counts or efficiency. This loss is count-rate dependent.

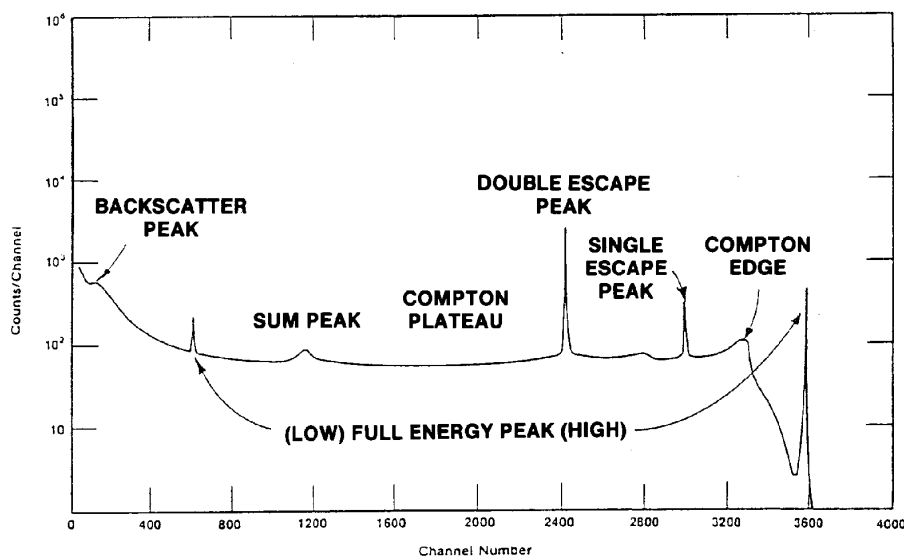


Figure 238. Random Summing. The Sum Peak Is the Sum of Two Coincident Low Full-Energy Peaks.

The random summing correction factor is:

$$RSF = \frac{1}{1 - \frac{\sum Ct}{F * LT_1}} \quad (78)$$

where:

- RSF = the random summing factor (multiplier)
- Ct = the contents of all channels
- F = the user-entered slope of the correction curve
- LT_1 = the live time

This value is set to 1.0 if it is calculated at less than or equal to zero.

8.11.1. Random Summing Correction

The uncorrected peak area is multiplied by RSF to obtain the corrected peak area. This is done before the peak area is converted to activity.

The slope of the correction curve is dependent on the detector and the source/detector geometry. It is experimentally determined by the following simple procedure. The procedure requires two radioactive sources: one of low activity and high energy, and one of high activity and a lower energy. The energy of the high-activity source must be chosen so that it will not interfere with the high-energy peak, i.e., it should be less than half the energy. Two such sources are ^{88}Y and ^{137}Cs .

Position the high-energy source in front of the detector so that the count rate is low and collect a spectrum with a small counting statistical error (e.g., 100000 counts in the peak area). Measure the net peak area of the high energy gamma ray and the total counts in the spectrum (see Section 5.4.2, **Calculate/Peak Info...**). Now position the low-energy source in front of the detector to increase the count rate and collect a second spectrum for the same live time as the first spectrum. Again measure the net peak area and total counts in the spectrum. More spectra can be collected by moving the low-energy source closer to the detector to increase the count rate.

For example, six spectra were collected and the results are shown in Table 11.

Table 11. Random Summing Data.

Count Rate	Peak Area	Ratio
200	100000	1.00
2000	98850	0.98
4000	97200	0.97
6200	95900	0.95
8000	94800	0.94
9500	93700	0.937

Using the lowest and highest count rate values, the slope is calculated as:

$$\begin{aligned}
 SLOPE &= \frac{200 - 9500}{1.0 - 0.937} \\
 &= -147619
 \end{aligned}
 \tag{79}$$

The negative of this slope is the factor you enter as the **Random Summing** factor on the Sample tab under **Analyze/Settings/Sample Type...**

8.12. Reported Uncertainty

The uncertainty printed on the report can be either counting or total uncertainty. They can be printed at 1, 2, or 3 sigma. The counting uncertainty is the uncertainty of the peak area due to statistical uncertainty, and was discussed earlier. For a peak net area, the counting uncertainty can be expressed in percent of the peak area. This same percent is used to express the percent counting uncertainty in the activity values.

8.12.1. Total Uncertainty Estimate

The total uncertainty estimate (1 sigma) is determined by summing in quadrature the individual uncertainties from the various analysis components.

$$\sigma_t = \sqrt{\sigma_{count}^2 + \sigma_{nor}^2 + \sigma_{rsum}^2 + \sigma_{abs}^2 + \sigma_{nuc}^2 + \sigma_{eff}^2 + \sigma_{geo}^2 + \frac{\sigma_{sys}^2}{3}}
 \tag{80}$$

where:

- σ_{count}^2 = counting uncertainty estimate (Section 8.2.4). If PBC is enabled, this term includes the PBC uncertainty calculated per Section 8.12.10.
- σ_{nor}^2 = additional normally distributed uncertainty estimate (Section 8.12.3)
- σ_{rsum}^2 = random summing uncertainty estimate (Section 8.12.4)
- σ_{abs}^2 = absorption uncertainty estimate (Section 8.12.5)
- σ_{nuc}^2 = nuclide uncertainty estimate (Section 8.12.6)
- σ_{eff}^2 = efficiency uncertainty estimate (Section 8.12.7)
- σ_{geo}^2 = geometry uncertainty estimate (Section 8.12.8)
- σ_{sys}^2 = systematic (uniformly distributed) uncertainty estimate (Section 8.12.9)

All components of uncertainty estimates except σ_{uni} are computed at the 1-sigma level. The uncertainty estimate for a uniformly distributed error is used at the full range. If a correction factor is not used, the uncertainty estimate is zero for that component.

8.12.2. Counting Uncertainty Estimate

This is discussed in Section 8.2.4.

8.12.3. Additional Normally Distributed Uncertainty Estimate

$Input_{nor}$ is obtained based on the **Random** setting in the **Additional Error** section of the Analysis tab.

$$\sigma_{nor}^2 = \left(\frac{Input_{nor}}{100} \right)^2 \quad (81)$$

where:

- σ_{nor}^2 = variance of additional normally distributed uncertainty (% 1 sigma)
- $Input_{nor}$ = user input for normally distributed uncertainty (% 1 sigma)

8.12.4. Random Summing Uncertainty Estimate

$$\sigma_{rsum}^2 = \frac{|CF_{rs} - 1|}{100} \quad (82)$$

where:

$$\begin{aligned}\sigma_{rsum}^2 &= \text{variance of random summing error estimate} \\ CF_{rs} &= \text{random summing correction factor}\end{aligned}$$

8.12.5. Absorption Uncertainty Estimate

$$\sigma_{abs}^2 = \frac{|CF_{ab} - 1|}{100} \quad (83)$$

where:

$$\begin{aligned}\sigma_{abs}^2 &= \text{variance of attenuation error estimate} \\ CF_{ab} &= \text{absorption correction factor}\end{aligned}$$

8.12.6. Nuclide Uncertainty Estimate

$$\sigma_{nuc}^2 = \left(\frac{Input_{nuc}}{200} \right)^2 \quad (84)$$

where:

$$\begin{aligned}\sigma_{nuc}^2 &= \text{variance of nuclide error estimate} \\ Input_{nuc} &= \text{user uncertainty input for nuclide (\% 2 sigma). This is the uncertainty in the yield (branching ratio) for the first gamma ray in the library for each nuclide.}\end{aligned}$$

8.12.7. Efficiency Uncertainty Estimate

The efficiency uncertainty is computed differently depending on the type of fit used for the efficiency calculation. The components used for efficiency include the errors due to uncertainty of the calibration source, uncertainty of the calibration fit, and the counting uncertainty of the calibration.

The total efficiency uncertainty, σ_{eff} , is calculated as:

$$\sigma_{eff}^2 = \sigma_c^2 + \sigma_p^2 \quad (85)$$

where σ_c is the calibration fit uncertainty and σ_p is the calibration counting uncertainty, both discussed in the sections below.

8.12.7.1. Calibration Counting Uncertainty

When an efficiency calibration is performed, the counting uncertainty is calculated and stored in the calibration record. In general, there is an above-the-knee counting uncertainty and a below-the-knee counting uncertainty, both calculated and saved to the calibration data record.

For polynomial and TCC-polynomial type calibrations, the counting uncertainty above the knee is calculated as the averaged counting uncertainty of all calibration peaks involved, regardless of the knee energy, as shown below:

$$\sigma_{ca} = \frac{1}{N} \sum_{i=1}^N \sigma_{ci} \quad (86)$$

where σ_{ci} is the counting uncertainty of the i -th calibration peak, and N is the total number of calibration peaks used. The counting uncertainty below the knee is always set to zero for these two calibration types:

$$\sigma_{cb} = 0 \quad (87)$$

For all other calibration types, the above-the-knee counting uncertainty is calculated as the averaged counting uncertainty of all the calibration peaks with energy greater than or equal to the knee energy, as shown below:

$$\sigma_{ca} = \frac{1}{NI} \sum_{i=1}^{NI} \sigma_{ci}, \quad \text{with } E_i \geq E_{knee} \quad (88)$$

where NI is the number of calibration peaks whose energies are greater than or equal to the knee energy.

The below-the-knee counting uncertainty is calculated as the averaged counting uncertainty of all the calibration peaks with energy less than the knee energy:

$$\sigma_{cb} = \frac{1}{N2} \sum_{j=1}^{N2} \sigma_{cj}, \quad \text{with } E_j < E_{knee} \quad (89)$$

where $N2$ is the number of calibration peaks with energies less than the knee energy. If $N2$ is zero, the counting uncertainty is zero.

For polynomial and TCC-polynomial type calibrations, the calibration counting uncertainty σ_p is always equal to the counting uncertainty above the knee:

$$\sigma_p = \sigma_{ca} \quad (90)$$

For all other calibration types, σ_p is calculated as:

$$\begin{aligned} \sigma_p &= \sigma_{cb}, & E > E_{knee} \\ \sigma_p &= \sigma_{ca}, & E \leq E_{knee} \end{aligned} \quad (91)$$

NOTE For calibrations performed before Renaissance 7, the above-and below-the-knee counting uncertainties are both zero. To take into account the counting uncertainty discussed here, update the efficiency calibration with Renaissance 7 so the new uncertainties will be calculated and stored in the calibration file. Then, when a spectrum is analyzed, the final reported activity uncertainty will take into account the added uncertainty in calibration.

8.12.7.2. TCC-Polynomial

The calibration variance is the averaged variance of all the calibration points in the certificate file:

$$\sigma_c = \sqrt{\frac{\sum_{i=1}^N \sigma_i^2}{N}} \quad (92)$$

where:

σ_c = the calibration uncertainty

σ_i = the uncertainty of the i^{th} calibration point from the certificate

N = the total number of calibration points

8.12.7.3. Interpolative

For this calculation, the calibration points are sorted in ascending order by energy. If energy E is less than the first (lowest-energy) calibration point, E_i and E_{i+1} are the two lowest-energy calibration points. If energy E is greater than the last (highest-energy) calibration point, E_i and E_{i+1} are the two highest-energy calibration points. For all other cases, $E_i < E < E_{i+1}$:

$$\sigma_c = \frac{\sigma_i(E_{i+1} - E) + \sigma_{i+1}(E - E_i)}{(E_{i+1} - E_i)} \quad (93)$$

where:

σ_i = the uncertainty (*not* the fractional uncertainty) associated with energy E_i from the certificate.

This calculation is also used when energy E is less than the first calibration point, the efficiency fit is polynomial, and the detector is N-type.

8.12.7.4. Linear, Quadratic or Polynomial

In general, the efficiency curve (or efficiency fit) can be expressed as:

$$\ln \varepsilon = \sum a_k x^n, \quad k = 1, \dots, m \quad (94)$$

where:

ε = the efficiency at energy E

a_k = the k^{th} fitting parameter

The parameters x , n , and m depend on the type of efficiency curves:

- For linear/quadratic fits:

$$\begin{aligned} x &= \ln E \\ n &= k - 1 \\ m &= 2 \text{ (linear) or } 3 \text{ (quadratic)} \end{aligned} \quad (95)$$

- For polynomial fits:

$$\begin{aligned} x &= E \\ n &= 2 - k \\ m &= 6 \end{aligned} \quad (96)$$

If the energy x is lower than the lowest two calibration points, the analysis engine performs an interpolated fit instead of a polynomial fit. The summation in Eq. 94 is the sum over all the fitting parameters, $k = 1, \dots, m$, not the sum over all the calibration points.

Now let us define a parameter y as $y = \ln \varepsilon$. This yields:

$$y = \sum a_k x^n, \quad k = 1, \dots, m \quad (97)$$

The fitted efficiency at any point x_i (as defined in Eqs. 95 and 96 above) is:

$$y_i(x_i) = \sum a_k x_i^n, \quad k = 1, \dots, m \quad (98)$$

Matrix Solution

Equation 98 above is Eq. 7.12 in Bevington,²⁵ except that the function $f_k(x_i)$ has been replaced by x_i^n , a particular type of polynomial:

$$f_k(x_i) = x_i^n \quad (99)$$

where x_i and n are defined in Eqs. 95 and 96.

From Eq. 7.14 in Bevington, the β matrix is calculated using Eq. 99 above:

$$\beta_k = \sum (1/\sigma_i^2) y_i x_i^n, \quad i = 1, \dots, N \quad (100)$$

where σ_i and N are defined in Eq. 92, y_i is defined in Eq. 98, and x_i is defined in Eqs. 95 and 96.

From Eq. 7.15 in Bevington, the α matrix is calculated by:

$$\alpha_{nk} = \sum (1/\sigma_i^2) x_i^{(n_1+k_1)}, \quad i = 1, \dots, N \quad (101)$$

where for a linear/quadratic fit:

$$\begin{aligned} n_1 &= n - 1 \\ k_1 &= k - 1 \end{aligned}$$

and for a polynomial fit:

$$\begin{aligned} n_1 &= 2 - n \\ k_1 &= 2 - k \end{aligned}$$

The σ_i factor is the fractional uncertainty at the i^{th} calibration point (as defined for Eq. 92). σ_i is not the absolute uncertainty because the actual curve being fitted is not the efficiencies themselves but the natural log of the curve.

²⁵Bevington, Philip R. and D. K. Robinson. *Data Reduction and Error Analysis for the Physical Sciences*, 2nd ed., McGraw-Hill, 1992.

Matrix Inversion

From Eq. 7.20 in Bevington, the n^{th} fitting parameter in our Eq. 97 or Eq. 94 can be calculated as:

$$a_n = \sum \beta_k \delta_{kn}, \quad k = 1, \dots, m \quad (102)$$

where δ is the *inverse matrix* of α :

$$\delta = \alpha^{-1} \quad (103)$$

The δ matrix is called the *error matrix* because its diagonal elements are the variances of the fitting parameters, and the off-diagonal elements are the covariances of the fitting parameters (see Eq. 7.25 in Bevington):

$$\sigma_{a_i a_j}^2 = \delta_{ij}, \quad i, j = 1, \dots, m \quad (104)$$

If $i = j$, $\sigma_{a_i a_j}^2$ is the variance for the fitting parameter a_i . If $i \neq j$, $\sigma_{a_i a_j}^2$ is the covariance between the fitting parameter a_i and a_j .

Uncertainty of the Fit

From Eq. 3.13 in Bevington, the polynomial fit uncertainty is given by:

$$\sigma_y^2 = \sum \sum \delta_{ij} (\partial y / \partial a_i) (\partial y / \partial a_j) \quad i, j = 1, \dots, m \quad (105)$$

where y is the polynomial given in Eq. 97 and a_i is the i^{th} fitting parameter. The error matrix δ_{ij} has been used instead of $\sigma_{a_i a_j}^2$ for clarity. Equation 105 does not use the factor 2 before the covariance terms, as is done in Bevington Eq. 3.13. This is due to the double-summation notation used in Eq. 105 and because the error matrix is symmetric ($\delta_{12} = \delta_{21}, \dots$). The diagonal elements are not double-counted in the above equation. (In Bevington Eq. 3.13, $\sigma_{a_i a_j}^2$ is denoted as $\sigma_{a_i}^2$.)

From Eq. 97, since $\partial y / \partial a_i = x^{i_1}$, we have:

$$\sigma_y^2 = \sum \sum \delta_{ij} x^{(i_1+j_1)} \quad i, j = 1, \dots, m \quad (106)$$

where for a linear/quadratic fit:

$$\begin{aligned} i_1 &= i - 1 \\ j_1 &= j - 1 \end{aligned}$$

and for a polynomial fit:

$$\begin{aligned} i_1 &= 2 - i \\ j_1 &= 2 - j \end{aligned}$$

Finally, the calibration uncertainty is:

$$\sigma_c = \varepsilon \sigma_y \quad (107)$$

where ε is the fitted efficiency at energy E (from Eq. 94), and σ_y is calculated from Eq. 106. If σ_c is zero, then the “sigma above” (σ_a) or “sigma below” (σ_b) value described in the following paragraphs is used.

If the fit type is neither polynomial nor TCC-polynomial, the calibration uncertainty is calculated as:

$$\sigma_c = \sigma_a \quad \text{for } E > E_{knee} \quad (108)$$

$$\sigma_c = \sigma_b \quad \text{for } E \leq E_{knee} \quad (109)$$

where σ_a and σ_b are defined as follows.

If the energy $E > E_{knee}$,

$$\sigma_a^2 = \frac{\sum [(\varepsilon_i - f_i) / f_i]^2 - \left(\sum |(\varepsilon_i - f_i) / f_i| \sum |(\varepsilon_i - f_i) / f_i| \right) / N_a}{N_a - 1} \quad (110)$$

If $E \leq E_{knee}$,

$$\sigma_b^2 = \frac{\sum [(\varepsilon_i - f_i)/f_i]^2 - \left(\sum |(\varepsilon_i - f_i)|/f_i \sum |(\varepsilon_i - f_i)|/f_i \right) / N_b}{N_b - 1} \quad (111)$$

where:

- ε_i = the measured efficiency at energy E_i
- f_i = the calculated efficiency at E_i from Eq. 94
- E_{knee} = the efficiency knee energy

N_a is the number of efficiency points above the knee energy and N_b is the number of efficiency points below the knee energy. Both N_a and N_b must be greater than 1. If σ_a or σ_b is zero, the default uncertainty of 1.5% is used.

If the fit type is polynomial but not TCC-polynomial, the calibration uncertainty is calculated as:

$$\sigma_c = \sigma_a \quad (112)$$

For polynomial fits, E_{knee} is always ignored.

Sometimes, the efficiency pairs might be missing from the calibration file but the fit parameters and fit type are stored in the file. In these cases, the σ_a or σ_b value is used.

8.12.8. Geometry Uncertainty Estimate

This value, σ_{geo}^2 , is based on the geometry uncertainty estimate entered on the geometry correction sidebar.

$$\sigma_{geo}^2 = \left(\frac{Input_{geo}}{100} \right)^2 \quad (113)$$

If the uncertainty is 0 or no value is entered, or if using a .GEO file from an earlier version of Renaissance, a fixed value of 1.5% is used.

8.12.9. Uniformly Distributed Uncertainty Estimate

This is based on the **Systematic** error entered on the System tab and saved in the .SDF file.

$$\sigma_{sys}^2 = \left(\frac{Input_{sys}}{100} \right)^2 \quad (114)$$

where:

σ_{sys}^2 = uncertainty estimate for a uniformly distributed uncertainty estimate
 $Input_{sys}$ = user input for full range (%)

8.12.10. Peaked Background Correction and Uncertainty Calculations

8.12.10.1. Single PBC Subtraction

If the PBC net count rate at energy E is R_p (in cps), the live time is LT (in seconds), and the fractional uncertainty of the net PBC peak count rate is σ_p , then the corresponding PBC counts N_p and the associated absolute uncertainty σ_{absp} in counts can be calculated from the following:

$$N_p = LT * R_p \quad (115)$$

$$\sigma_{absp} = N_p * \sigma_p \quad (116)$$

If N_0 is the peak area in counts before PBC, σ_0 is the corresponding fractional uncertainty, and σ_{abs0} is the corresponding absolute uncertainty for the net peak area before PBC (see Eq. 32, page 248), the absolute peak area uncertainty before PBC is:

$$\sigma_{abs0} = N_0 * \sigma_0 \quad (117)$$

The PBC corrected peak area N (in counts) is calculated as:

$$N = N_0 - N_p \quad (118)$$

If, after PBC, the net peak area is <0 , it is set to 0 unless **Directed Fit** is enabled (because negative peak area is not physical). After PBC, the subtracted PBC area is added to the peak background. If B_0 is the peak background before PBC, the peak background after PBC is:

$$B = B_0 + N_p \quad (119)$$

After PBC, the variance of the peak net area counts has contributions from the PBC subtraction as well as from the change in the peak background discussed above. The variance from the PBC subtraction is simply σ_{absp}^2 .

The variance due to the change in the peak background is taken to be the increase in the peak background, N_p . Therefore, after PBC, the total absolute uncertainty (in counts) for the net peak area is calculated as:

$$\sigma_{absN} = \sqrt{\sigma_0^2 + \sigma_{absp}^2 + N_p} \quad (120)$$

Note that for PBC, only the absolute uncertainties (not relative) are added in quadrature. After the PBC correction, the relative uncertainty in percent is calculated as:

$$\sigma_N = \sigma_{absN} / Abs(N), \quad \text{if } N < > 0 \quad (121)$$

If the PBC corrected area is exactly zero, the relative uncertainty is set at 1000% (or 10.0), the default value used in all cases where the activity is zero.

Note that when PBC is enabled, the counting uncertainty for a peak always has PBC contributions. That is, the counting uncertainty calculated before PBC (σ_0 in Eq. 117) is not saved in the .UFO file. The same holds for the peak area; it is always the PBC corrected value, and the net peak area before PBC is not saved in the .UFO file.

8.12.10.2. Multiple PBC Subtraction

If there are multiple PBC peaks under a peak, that peak is subject to multiple PBC subtractions. The sum of the PBC net areas is simply the sum of individual PBC areas (for comparison, see Eq. 115 for single PBC subtraction):

$$N_p = \sum_{i=1}^m (LT * R_{p-i}) \quad (122)$$

where LT is the live time, R_{p-i} is the PBC count rate for the i -th PBC, and m is the total number of PBC peaks.

The total PBC uncertainty is calculated from the following (compare to Eq. 116):

$$\sigma_{absp}^2 = \sum_{i=1}^m \sigma_{absp-i}^2 \quad (123)$$

where σ_{absp-i} is the absolute uncertainty of each PBC peak in counts. After calculating N_p and σ_{absp} for the combined PBC subtraction with multiple PBC the rest of the calculations can be applied the same way as for a single PBC (that is, all equations in this section except Eqs. 115 and 116 can be applied the same way for both single and multiple PBC subtractions).

8.13. True Coincidence Correction

In the case where a nuclide emits multiple cascade gamma rays when it decays, these multiple gamma rays can be detected individually or together as one gamma ray. An example decay is ^{60}Co , as shown in Fig. 239.

The two gamma rays (1173.2 and 1332.5 keV) are emitted in cascade or one after another. The lifetime of the intermediate state is very short so that it appears that the two gamma rays are emitted in coincidence (i.e., at the same time).

Since the two gamma rays can interact in the detector in a time short compared to the response time of the detector and the resolving time of the electronics, the two gamma rays are recorded as a single gamma ray.

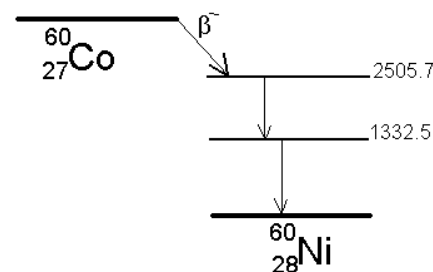


Figure 239. ^{60}Co Decay to ^{60}Ni .

When the two gamma rays are detected as one, it effects the spectrum in two ways. One way is the creation of a “sum” peak that is the sum of the amplitudes of the two individual full-energy peaks. The second way is to remove counts from the full-energy peak. The first creates extra peaks in the spectrum. The second reduces the peak area of these gamma rays and thus the reported activity of the nuclide.

The reduction of the peak area due to summing is more important than the creation of the “sum peak.” The sum peak requires the addition of two full-energy pulses to get the summed energy. The reduction of the peak area only requires that there be a full-energy interaction at the same time as another interaction from the other members of the cascade. Recall that most of the interactions in the detector do not produce full-energy peaks, but produce partial-energy interactions

(the Compton background). A summing with any of the partial-energy signals will result in the full-energy pulse being removed from the full-energy peak. Further details can be found in many references.^{26,27,28}

The *true coincidence correction* (TCC) is the correction necessary to account for all of the pulses removed from the full-energy peak. This correction is a simple divisor of the net peak area, that is the net peak area is increased by the correction factor. The correction factor is detector and sample geometry dependent. The correction factor depends on the full-energy efficiency, that is the ability of the detector to detect the total energy of the gamma ray, and the total efficiency, that is the ability of the detector to detect any part of the gamma ray energy.

²⁶ Glenn F. Knoll, *Radiation Detection and Measurement*, 3rd edition, p. 323, Wiley and Sons, 2000.

²⁷ Gilmore, G., and J.D. Hemingway, *Practical Gamma-Ray Spectrometry*, p. 156, Wiley and Sons, 1995.

²⁸ “Calibration and use of Germanium Spectrometers for the measurement of gamma-ray emission rates of radionuclides,” ANSI N42.14-1991.

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9. ANALYSIS METHODS — NAI

The Renaissance analysis engine, RENGSA, uses `GSA.DLL` from ScintiVision™. This provides the kernel of functions necessary for analysis of gamma-ray spectra acquired with NaI detectors. This chapter describes the calculations performed and the algorithms employed by this analysis engine. The ROI analysis engine, RENROI32, is discussed in Section 8.1.1.5.

NaI detector spectra are characterized by significantly poorer resolution (caused by fewer ADC channels combined with broader peaks) and, therefore, more interference (overlapping peak areas) along with poorer signal-to-noise ratios than corresponding HPGe spectra. Therefore, NaI spectra inherently require significantly different algorithms for proper peak extraction and activity analysis. `GSA.DLL` was developed with such limitations of NaI spectra in mind. Its main features include:

- Peak-search algorithms appropriate to NaI spectra.
- Activity-analysis algorithms appropriate to NaI spectra for multiplet decomposition and for identifying and quantifying the activities of nuclides present.

9.1. Peak Search

Each peak is located in a spectrum using a variable-Gaussian cross-correlation method (discussed below), whereupon a working model of the background is obtained based on the endpoints of the peak envelope detected. Estimates for the background-subtracted net area and centroid are computed based on this model and the counts in the spectrum in that vicinity. The only inputs required are

- Spectrum data to be searched.
- An estimate of the FWHM of the peaks (this can be a full FWHM calibration or just a single-constant FWHM value approximating the expected width of peaks to be found).

The peak search provides:

- A list of peak centroids.
- Initial estimates of the background and peak area(s), computed as if these peaks were pure Gaussian singlets superimposed on a simple linear background.

Note that these centroids are accurate only for pure singlets; therefore, subsequent peak fitting (see below) is normally recommended for complete peak information in all cases.

9.1.1. Peak Search Algorithm

The spectrum is smoothed, then a filtered spectrum F is calculated at channel i from the smoothed spectrum S :

$$F(i) = S(i) - 0.5 \times (S(i + FWHM(i)) - S(i - FWHM(i)))$$

where $FWHM(i)$ is the calibrated FWHM value at channel i .

Around a Gaussian peak, the filtered spectrum has a maximum when the center point of the window coincides with the center point of the peak (i.e., when $i = \text{center of peak}$). If the smoothed spectrum contains a peak, then the filtered spectrum will contain a minimum on each side of the peak. These minima are negative. The maxima obtained in this filtering process identify possible peak locations. These “peak candidates” are further processed as discussed below.

9.1.2. Background Method and Initial Peak Estimates

Peak limits are obtained during the peak search at the point where the filtered spectrum drops below zero on either side of the peak. We assume that background is defined by three points above and below these peak limits. An average at each of these endpoints is computed and a straight-line is “drawn” between these endpoints to model the background across the peak region.

An initial estimate of the FWHM of the peak can be obtained from the width of the region of the filtered spectrum that is greater than zero. The peak location is set to the maximum.

Finally, the area is obtained from the background-subtracted data using the formula for a perfect Gaussian:

$$Area = Fit\ Height \times FWHM \times \frac{\sqrt{2\pi}}{2.35} \quad (125)$$

where:

$$\begin{aligned} Fit\ Height &= F(i_1) - F(i_2) \\ i_1 &= \text{channel where } F \text{ is maximum} \\ i_2 &= \text{channel where } F \text{ is minimum} \end{aligned}$$

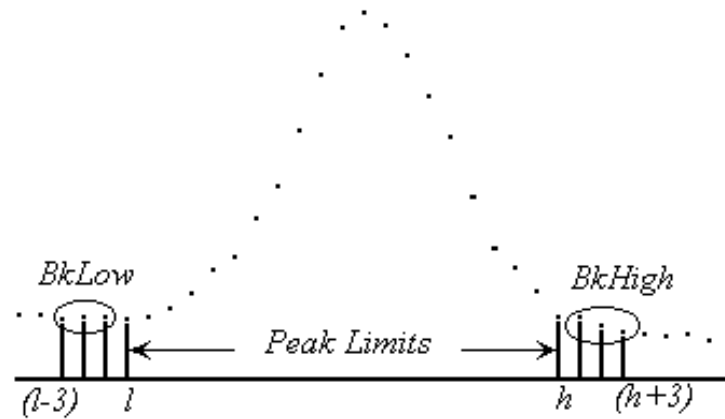


Figure 240. Peak Limits and Background Points.

9.1.3. Peak Statistics

The uncertainty (1 sigma) in the net area of the peak is computed as follows:

$$\text{Net Uncertainty} = \sqrt{\text{Background Variance} + \text{Gross Area}} \quad (126)$$

where the *Background Variance* was computed as follows:

$$\text{Background Variance} = \left(\frac{\text{Background}}{(\text{Channels})(\text{BackLo} + \text{BackHi})} \right) \quad (127)$$

where:

- Channels = number of channels in peak
- BkLo = background per channel at low end of peak
- BkHi = background per channel at high end of peak

9.1.4. Critical Level/Peak Rejection Criteria

Peaks can be rejected for use in subsequent analysis steps if they do not meet the minimum criterion expressed by the *Critical Level*:

$$\text{Critical Level} = 2.33\sqrt{\text{Background Variance}} \quad (128)$$

The net area of each peak is tested against this value and marked as “PRESENT” only if it exceeds this level. In the case of peaks involved in multiplets, the test will be repeated as necessary after the peaks have been deconvoluted.

9.2. Peak Fitting

After locating the peaks, the FWHM must be more accurately determined, as well as the position and net area for each peak.

The list of peaks found in the peak search is combined with the library list for further fitting. Library peaks not located in the peak search are inserted into the peak list positions and FWHMs calculated with the calibration coefficients. The first step in peak fitting is to divide the spectrum into regions containing one or more overlapping peaks. Peaks and background in these regions are fitted alternately, the appropriate type of background being determined by the energy and number of peaks in the region. The peak amplitude, width, and position are found by minimizing χ^2 .

9.2.1. Background Fit

Two types of backgrounds are used in fitting NaI spectra: polynomial and stepped. At low energies the background is typically represented by a polynomial with up to 4 coefficients calculated by a weighted least-squares fit. At higher energies the background is linear, with steps added at the centroid of each peak in a multiplet. The **Analyze/Settings/Sample Type...** dialogs let you choose an automatic determination of the best type of background fit, or to set the energy at which the background switches from polynomial to linear. In most cases, the automatic setting will give a better result.

At this time, the peak centroid, height, starting point, and ending point are the values from the peak fitting routine.

9.2.1.1. Linear Backgrounds

Singlets

Singlets are fitted with a linear background using the spectrum values at the end points of the peak. The number of values used in the average is set by the user in the **Analyze/Settings/Sample Type...** dialog to 1, 3, or 5. To calculate the background on the low energy side of the peak with 5 points, the 5-point average of the channel contents is calculated for the region below the start of the peak. This is the same as smoothing the data with a smoothing width of 5 and

coefficients of 0.2 for all points. The calculation is repeated in the region above the end of the peak, and the background is:

$$\text{Background} = B_L + \frac{(B_H - B_L) \times (C_H - C_L)}{C_H - C_L} \quad (129)$$

where:

- B_L = low background
- B_H = high background
- C_H = high channel
- C_L = low channel

Multiplets

In high energy regions the background is roughly linear, and the background for peak multiplets is calculated in an analogous manner to singlets. If the slope above the peak region is less than the slope below the region, (that is, if the background under the peaks is declining faster than the background above the peaks), a step is inserted at the centroid of each peak (see Fig. 241).

The total height of the steps is equal to the difference between the background above and below the peak area. The steps are smoothed over the width of the peak, and the height of each step is proportional to the height of the peak.

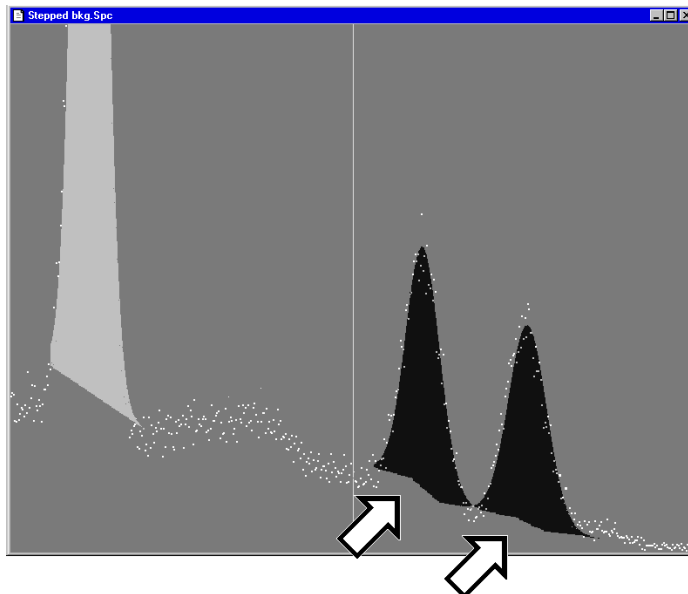


Figure 241. Stepped Background.

Polynomial Backgrounds

In low-energy regions, the background is best represented by a polynomial. To obtain the best background fit in non-peak regions, the fitted peaks are subtracted from the spectrum before the background fit is performed. If this is not the first time the region has been fitted, a weighted least-squares fit is used, with data below the current background level weighted more heavily than data above the current background. This gives a better estimate of the background in the presence of peaks. Coefficients are calculated for linear, quadratic, and cubic fits, and the polynomial that gives the smallest value of χ^2 is returned.

Sparse Peak Regions

If the peaks in a multiplet overlap by only a few channels, the background is fitted as a polynomial. It is also appropriate to fit small peaks at low energies with a polynomial background. At high energies, if this is a refit, points with a background above the array value are weighted more heavily than points with background below the array value. In the example shown below, the background is a parabola:

$$B = (169.242 - 1.87175 \times (C - C_{Start})) + (0.002288748 \times (C - C_{Start})^2) \quad (130)$$

where:

- B = background in channel C
- C = channel
- C_{Start} = start channel = 111

The constant values are calculated by the program based on the fit to the spectrum data.

9.2.2. The Peak Fit

Before the peaks are fitted, the background is subtracted from the spectrum. The error in the peak fit can be represented by:

$$\chi^2 = \sum_{i=Min}^{Max} \frac{(F_i p(i) - b(i))^2}{w_i} \quad (131)$$

where F_i is the spectrum data at channel i , $b(i)$ is the fit to the background, $p(i)$ is the fit to the peak, and w_i is the weight. The sum is over the entire fitting region. The peaks are represented by Gaussians, so

$$p(i) = \sum_{j=1}^N c_j e^{-(x-x_j)^2/2\sigma_j^2} \quad (132)$$

where N is the number of peaks in the multiplet. The best values of the constant c_j , position x_j , and FWHM ($2.53\sigma_j$) of each peak are those that minimize χ^2 . The uncertainties of the constant, position, and FWHM are also calculated.

Starting with the values found in the peak search, the background and peak fit is repeated at most three times. If the region has been fitted to the noise level, the fit is saved. Otherwise, peaks are added or removed at the channel with the largest residual.

9.2.2.1. Adding and Removing Peaks

The channel with the largest residual value is found, and if the residual is positive, and if adding a peak improves the fit, a peak will be added there. If the largest residual is negative, the peak closest to that channel might be removed. Up to ten peaks can be added to, or subtracted from, a fitting region. After the region is fitted, χ^2 is calculated. If the new fit has not changed χ^2 by more than $0.1 \times (\text{the largest residual} - \text{convergence limit})^2$, the fit is saved and the program moves to the next fitting region. The convergence limit is set in the `B30WINDS.INI` file (see Section ?).

9.2.2.2. Directed Fit Method

Another method of obtaining the peak area for a particular energy is to fit the spectrum region with a background plus peak shape function. This so-called “directed fit” can be applied to peaks and has the ability to produce negative peak areas. The negative peak area will produce a negative activity and this will be reported. Negative activities are required by some reporting agencies for statistical purposes.

The directed fit to the library peak area is done if the following are true:

- 1) The option is enabled.
- 2) The spectrum is energy calibrated.
- 3) The peak area was zero in the regular analysis.

If all these conditions are met, the spectrum region for 2 times the calibration FWHM, centered on the peak energy, is fit as above, but with the area allowed to go negative.

9.3. Library-Based Peak Stripping

In a few cases, all of the gamma-rays emitted by one isotope are very close in energy to gamma-rays emitted by other isotopes in the sample. The peaks from the two gamma rays cannot be separated correctly using conventional analysis, so the activity for one isotope cannot be correctly determined. Renaissance can perform library-based peak stripping, as an alternative to deconvolution, to obtain peak areas of the components of a multiplet. This alternative method (also referred to as peak-interference correction) uses peak areas from other parts of the spectrum to determine the areas of some of the components and calculates the remaining areas. Library-based peak stripping uses the library specified on the Sample tab under **Analyze/Settings/Sample Type...**

As the first step, Renaissance searches the library for isotopes with severely overlapping gamma rays. The criterion for severe overlap is that the peaks are within approximately one FWHM of one another (regardless of the energy per channel). For peaks this close, the peak areas will be more accurate if they are found indirectly. Any such peaks are automatically marked in the library as being too close together.

For example, the only useful gamma ray emitted by ^{226}Ra is 185.99 keV. The peak overlaps the 185.72-keV peak of ^{235}U . If these two isotopes are both in the library, ^{226}Ra and the 185.72-keV ^{235}U peak are flagged when the library is read. Table 12 shows some other common examples. These energies are from Erdmann and Soyka. Other references might use different energies, but the overlaps will still occur.

Table 12. Gamma Peak Overlap Examples.

Isotope	Energy (keV)	Probability	Isotope with close energy
$^{99\text{m}}\text{Tc}$	140.99	89.3	^{99}Mo
^{224}Ra	241.00	3.90	^{92}Sr
^{226}Ra	185.99	3.28	^{235}U
^{241}Am	26.35	2.5	^{237}U
^{241}Am	33.20	0.11	^{144}Ce
^{241}Am	59.54	36.3	^{237}U

The spectrum is then analyzed as described with one exception: *any peaks that are marked as too close are not used in the isotope activity calculations*. Instead, the activity of one isotope is based on other gamma rays from that isotope. That activity is then used to calculate the contribution to the overlapped peak of this isotope. That contribution is subtracted from the total peak area to obtain the peak area due to the other isotope.

In the example above, the activity of ^{235}U is calculated from the area of the peak at the next most probable energy, i.e., 143 keV. Then the area of the 185.72-keV ^{235}U peak is calculated using the branching ratio of that gamma ray, the efficiency, and the activity. The ^{235}U area is subtracted from the area of the peak at 185 keV to give the area due to ^{226}Ra . From this, the activity of ^{226}Ra in the sample is calculated.

9.4. Peak Identification

After the peaks in a spectrum have been properly located and measured using the searching and fitting procedures discussed above, the next step is to identify these peaks with the emitting nuclides, and ultimately to compute the activities of these nuclides.

9.4.1. Peak Identification

Using (1) the energy-calibrated spectrum, (2) a list of peaks from the peak search and fit, and (3) a nuclide library, each peak can be assigned to a nuclide by finding the best match(es) between the energies of peaks found in the spectrum and the library energies.

9.4.2. Fraction Limit Test

In order to verify the identification of a particular nuclide to a given peak, the number of located peaks is compared to the number of possible peaks. This is expressed as the fraction figure:

$$Fraction = \frac{\sum_{l=1}^n BranchingRatio_l}{\sum_{p=1}^n BranchingRatio_p} \quad (133)$$

where *BranchingRatio* is the branching ratio for the peak for the given nuclide, *l* is the sum over the located peaks, and *p* is the sum over the possible peaks. This fraction is between 1.00 for all peaks located and 0 for no peaks located. This value is compared to a limit value to determine whether this nuclide's peaks are present in sufficient measure to say this nuclide is present. The *Fraction Limit Test* is passed if the fraction (as percent) is above the value entered on the System tab under **Analyze/Settings/Sample Type....**

9.4.3. Decay Limit Test

Another test for the validity of a nuclide identification is to reject nuclides that have decayed between the collection time for the sample and the spectrum time. If the time elapsed between sample and data collection is too large, this nuclide will have decayed away. This determination is referred to as the *Decay Limit Test*, and the limit is entered on the Analysis tab under **Analyze/Settings/Sample Type....**

9.4.4. Nuclide Activity

After all the peaks have been properly identified and decomposed, the nuclide activity is calculated.

The individual *peak activities* are calculated first, starting with the net area of each peak divided by the acquisition live time, to give the counts per second detected. This is then adjusted by the calibrated efficiency supplied to yield the disintegrations per second at the source. This is then divided by the branching ratio for the peak to give the activity in becquerels. The attenuation correction is also applied.

The *nuclide activity* is computed as an average of the individual peak activities, weighted by the branching ratios of these peaks as follows:

$$\text{Nuclide Activity} = \frac{\sum (\text{Peak Activity} \times \text{Branching Ratio})}{\sum \text{Branching Ratio}} \quad (134)$$

The *uncertainty* in this value is computed by adding the peak uncertainties in quadrature as follows:

$$\text{Uncertainty} = \sqrt{\frac{\sum (\text{Peak Uncertainty})^2}{\text{Number of Peaks}}} \quad (135)$$

The nuclide activity can also be *decay corrected*, which is based on the time elapsed between sample collection and data acquisition and the nuclide half-life.

9.4.5. Statistical Detection Limits

These are only used in connection with library peaks not found in the spectrum, to provide a lower limit for activities, based upon the counting statistics of the data detection.^{29,30}

Peaks marked as type MDA will be processed differently in that their peak limits are determined as a multiple of the expected FWHM rather than being determined by the peak search as described earlier. Otherwise, the background calculations are the same, only using these artificially determined peak boundaries.

9.4.5.1. MDA (Minimum Detectable Activity)

The first step in calculating the MDA is to calculate the Minimum Peak Area (MPA) that could be undetected. The MPA is given by the following formula:

$$\text{MPA} = 2.71 + 3.29\sqrt{2(\text{Bkg Variance})} \quad (136)$$

where *Bkg Variance* is calculated in Eq. (127) if the peak is located; or is calculated in Eq. (137) when the peak is too small for Poisson statistics (not located).

²⁹“The Minimum Detectable Activity Concept,” Joseph C. Lochamy, *Measurements for the Safe Use of Radiation*, NBS 75th Anniversary Symposium, March 1976.

³⁰*Detection Limits for Radioisotopic Counting Techniques*, page 10, J.K. Hartwell, ARH-2537, June 1972.

$$Bkg\ Variance = \sum_{i=l}^h C_i \quad (137)$$

where:

- C_i = the channel contents of channel i
- l = the peak lower limit
- h = the peak higher limit

The peak high and low limits are (MDA factor/2 × FWHM) above and below the centroid energy, for a total width of (MDA factor × FWHM). The **MDA Factor** is entered on the Analysis tab under **Analyze/Settings/Sample Type...** (page 146). The FWHM is calculated from the calibration FWHM formula.

The MDA is then given as the following formula:

$$MDA = \frac{MPA}{\epsilon \times T \times \gamma_d} \quad (138)$$

where:

- ϵ = the efficiency at the peak energy
- T = the live time of the acquisition
- γ_d = the branching ratio

It should be noted that the MDA value will not always represent the maximum activity of a particular nuclide that might be present in a sample. Rather, it measures the limit of detection for that particular nuclide. Theoretically, if a nuclide activity exceeds the detection limit, the peak will be found by the peak search, and will be matched with a nuclide and/or be reported as an unknown peak, with an actual activity being reported as much greater than the MDA.

The subtraction of the PBC area and the recalculation of the percent error can result in the new net peak area being below the sensitivity cutoff and thus eliminating this peak from being used in the activity calculation. If the first library peak is rejected, the MDA is reported.

9.5. Peak Background Correction

The Peak Background Correction (PBC) is used to correct for the presence of an isotope in the background spectrum that also occurs in the sample. If the isotope is not of interest in the analysis results, there is no need to make this correction. The correction subtracts peak counts in the background spectrum from the peak counts in the sample.

The PBC values in the PBC table are the counts-per-second at each library energy and these values are subtracted from the counts-per-second values of the sample spectrum before the above corrections. The PBC value is added to the background and the new error is calculated by multiplying the percent error by the ratio of the uncorrected area to the corrected area.

This method improves on older PBC methods because the peak count rates are stored in the PBC table for each energy in the spectrum and not the average rate for an isotope. This removes the dependence on the efficiency calibration in the PBC table, yielding more accurate results because the nuclides in the background are not in the same geometry as the sample, meaning that the efficiency calibration is not the one to be used.

9.6. Chest Wall Thickness Correction

The chest wall thickness correction is the same for both NaI and Ge spectra, and is discussed in Section 8.10.

10. QUALITY ASSURANCE

10.1. Introduction

The accuracy and reproducibility of results of a data acquisition system should be verified on a periodic basis. Quality assurance (QA) in Renaissance supplies a means for doing this in accordance with ANSI N13.30 and N42.14. The detector-shield background, detector efficiency, peak shape, and peak drift can be tracked with warning and acceptance limits. All of these but detector-shield background use a check source. The QA results are stored in the Renaissance QA database, `RenpQA32.Mdb` (stored by default in `c:\User`) and can be displayed and charted. The database can be accessed with commercially available database products, including Microsoft Access. The information stored in the database for each detector includes:

- **Total Background** count rate (counts/sec), which is taken without a source.
- **Total Activity** of all nuclide(s) for a given calibration source (decay corrected).
- **Average FWHM ratio** ($\text{FWHM}_{\text{Spectrum}}/\text{FWHM}_{\text{Calibration}}$) for a list of peaks in a library from a calibration source.
- **Average FWTM** (full width at tenth maximum) **ratio** ($\text{FWTM}_{\text{Spectrum}}/\text{FWTM}_{\text{Calibration}}$) for a list of peaks in a library from a calibration source (Ge spectra only).
- **Average peak shift** average of the deviation of actual peak centroids from expected library energies within a specified range (the **Match Width** entered on the System tab under **Analyze/Settings/Sample Type...**).
- Optionally, the **Actual centroid energies** of all the library peaks.

The background should be monitored to verify that the detector and shield have not been contaminated by radioactive materials. The value stored is the total count rate which is independent of the count time and any specific nuclide contamination. A background analysis report is printed after the analysis completes.

The total activity of a calibration or check source will check the efficiency calibration currently in use and the general operating parameters of the system, including source positioning, contamination, library values, and energy calibration. To ensure that the total system is checked, this activity calculation uses the analysis engine specified in the analysis options file for the QA acquisition and analysis.

The FWHM and FWTM values will check the electronic noise and pole-zero adjustment of the amplifier. The peak shift checks to verify that the system gain and zero offset are satisfactory.

CAUTION Running the MCB Configuration program can affect QA as well as other Renaissance functions. *Be sure to read Section 2.4!*

10.1.1. Setting Up QA for Renaissance Operator

Before performing sample and background QA in the Operator program, the QA settings for each Detector must be established as discussed in the next section. In addition, you must create an operator scan type (.OPR) file for *each Detector group*. This file will control acquisition and analysis in Operator. If you wish, the same scan type file can be used for both QA measurements. QA is always detector-specific so it cannot be performed on a summed spectrum.

Note that background QA measurements use the **BACKGROUND Acquisition** time entered in the Quality Assurance Settings dialog. However, the presets for sample QA are determined in the analysis options (.SDF/.SVD) file specified on the Scan Settings page of the Operator Scan Type wizard (see Section 5.7.8.2) or in the analysis options files for individual detectors, as defined on the Spectrum Settings page (Section 5.7.8.6). If a detector-specific .SDF or .SVD files is not entered on the Spectrum Settings page, the analysis options file from the Scan Settings page will be used.

Should you wish to obtain additional peak information from Operator QA measurements, set the reporting option to **Printer** in the analysis options file. Renaissance will print a standard Supervisor analysis report in addition to the QA Report.

See Section 5.7.8 for a more detailed discussion on creating scan type files.

10.1.2. Changing to Default Path of the Renaissance QA Database

The QA database is determined by the DSN called [RenPQA32](#), which can be modified using the **ODBC Administration** function in Windows Control Panel. The default path is [C:\User\RenpQA32.mdb](#).

10.2. QA Submenu

Figure 242 shows the QA submenu (under the **Acquire** menu).

The three parts of QA in Renaissance are:

- 1) Establishing the QA settings for each Detector, including warning and alarm limits for background and sample measurements.

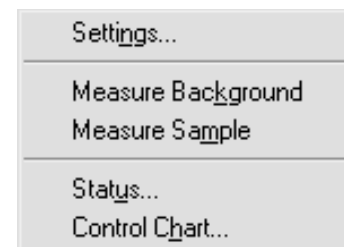


Figure 242. QA Menu.

- 2) Measuring background and sample. This is performed periodically, and it is automatically logged into the QA database by Renaissance.
- 3) Analyzing the QA data and generating reports. This includes the **Status** and **Control Chart** features, which allow you to view the current status of measurements for the detector and/or view and print the data stored in the database as a control-chart display.

10.2.1. Settings...

Use the Quality Assurance Settings dialog (Fig. 243) to configure the settings for QA measurements in the Supervisor program.

NOTE If the QA settings are not set up in Supervisor, the count presets for background QA measurements in the Operator program will be set to zero (infinite acquisition time) and the analysis engine will not be able to start.

The dialog box is titled "Quality Assurance Settings" and is divided into three main sections:

- BACKGROUND Acquisition / Count Rate Limits:**
 - Real: 10.00 S. Minimum: 0, Low: 0.00010, High: 1e+006, Maximum: 1e+007
 - Live: 10.00 S.
 - Buttons: OK, Cancel
 - Options: Create Background Report , Print On Completion
- SAMPLE Type Analysis Settings File:**
 - File path: c:\user\qutoqa.sdf
 - Buttons: Browse..., Edit...
 - Options: Don't Clear at Start , Peak Records in Database , Lock Acquire on Violation(s)
 - QA File Prefix: QA
 - QA File Sequence: 0
- SAMPLE Analysis Parameter Limits:**
 - Check Limits:
 - Total Activity (Bq)
 - Av Peak Shift (keV)
 - Av FWHM Ratios
 - Av FWTM Ratios
 - Parameter Limits Table:

	Minimum	Low	High	Maximum
Total Activity (Bq)	0	0	0	0
Av Peak Shift (keV)	0	0	0	0
Av FWHM Ratios	0	0	0	0
Av FWTM Ratios	0	0	0	0
 - Button: Suggest

Figure 243. QA Settings Dialog.

Several preliminary steps must be taken to determine the QA settings:

- 1) Backgrounds must be counted to determine reasonable levels.
- 2) Samples must be counted for total activity to obtain expected values, since total activity is detector and QA source dependent.
- 3) A QA library containing only the nuclides in the QA source must be created using the nuclide library editor (see Section 5.6).
- 4) An analysis options file (.SDF for Ge, .SVD for NaI) must be created which contains the defaults for the QA acquisition and analysis (see Section 5.5.1.1 [Ge] and 5.5.1.2 [NaI]). We recommend that the same file be used in the .OPR file that will govern QA measurements in the Operator program; this will ensure that QA is the same in both programs.

NOTE All parameters on this dialog *except* **SAMPLE Type Analysis Settings File** are used for this Detector's QA measurements in both the Supervisor and Operator programs. The .SDF or .SVD file entered here *controls only the Supervisor program's sample QA analysis*. The .SDF or .SVD file for sample QA analysis in Operator can only be specified in the operator scan type (.OPR) files discussed in Section 5.7.8. However, to maintain consistency, we recommend that the .SDF/.SVD file used for a particular detector in Supervisor QA also be used in Operator QA.

- 5) A database to contain the QA results must exist. The QA database, `RenpQA32.Mdb`, is installed by default in the `C:\User` folder. However, if you select the **Settings...** command and Renaissance cannot find `RenpQA32.Mdb` (or if the database file cannot be used for some reason), a warning message will ask if you wish to create a QA database. Click **OK** to start the QA database setup wizard and go to Section 10.3, page 331, for instructions. When the database has been successfully created, you will be automatically returned to the Quality Assurance Settings dialog.

The **BACKGROUND Acquisition** time and **Count Rate Limits** are entered using the information gathered in Step 1 above. Enter the **Real** time or **Live** time in seconds. For background spectra the dead time is near zero, so these are usually equal. *Note that the **BACKGROUND Acquisition** time for this detector is also used for background QA measurements in the Operator program.*

The **Count Rate Limits** include the upper and lower radionuclide activity limits which, when exceeded, indicate that the system is not operating correctly. There are two levels of limits. The **warning** limits are determined by the settings in the **Low** and **High** fields. The **alarm** limits are those outside of the **Minimum** and **Maximum** fields. If the result of a QA measurement is

outside the warning limits, a warning dialog is displayed. If the QA result is outside the alarm limits, a violation dialog is displayed. In addition, if the **Lock Acquire on Violation(s)** box is marked, the violation must be corrected and the QA measurement repeated before the out-of-limits Detector can be used to collect more data in Renaissance.

Generally, after setup these levels should not be changed without careful consideration.

The **Create Background Report** and **Print on Completion** checkboxes allow you to generate and/or print the report after the analysis is completed.

The **SAMPLE Type Analysis Settings File** is the **.SDF** file, for Ge, or **.SVD** file, for NaI, created for QA in Step 4 using **Analyze/Settings/Sample Type...** Click on **Browse...** to select the analysis options file. To edit the analysis options file, click on **Edit...** This will open the Analysis Options dialog (see Section 5.5.1.1 [Ge] and 5.5.1.2 [NaI]).

On the left of the **SAMPLE Analysis Parameter Limits** section are checkboxes for marking the limits to be tracked. **Total Activity (Bq)**, **Average Peak Shift (keV)**, **Average FWHM Ratios**, and **Average FWTM Ratios** (Ge only) are the choices. Click on the ones to be tracked. The first time Renaissance QA is set up, click on the **Suggest** button (on the right) to enter factory-set limits. After this, use the **Suggest** button with caution, because clicking on it again will reset all the limits to the factory settings. The actual limits can be determined from the samples counted in Step 2 above.

Click on **OK**. Renaissance will check the measurement limits to determine if they are set consistently. If they are, the dialog will close. If not, a dialog will open indicating that the limits are not properly set and the dialog will remain open so the limits can be changed. QA data can now be collected using **Acquire/QA/Measure Background** and **Acquire/QA/Measure Sample**.

10.2.2. Measure Background

This command opens the dialog in Fig. 244, to verify that all sources have been removed from the Detector before proceeding. Confirm that all sources have been removed for a background measurement, click on **OK–Start**. The remaining functions are performed automatically.

Mark the **Overwrite (repeat) previous background measurement** check box (by clicking on it) if the previous measurement was in error. For example, if a problem was detected, fixed, and this run is to verify the repairs, check the box so the “bad” value is not kept in the database.

Click **OK**.

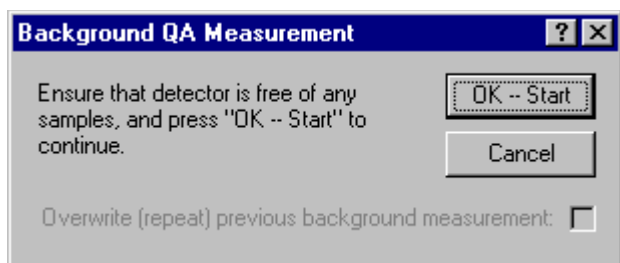


Figure 244. Begin Count for Background QA.

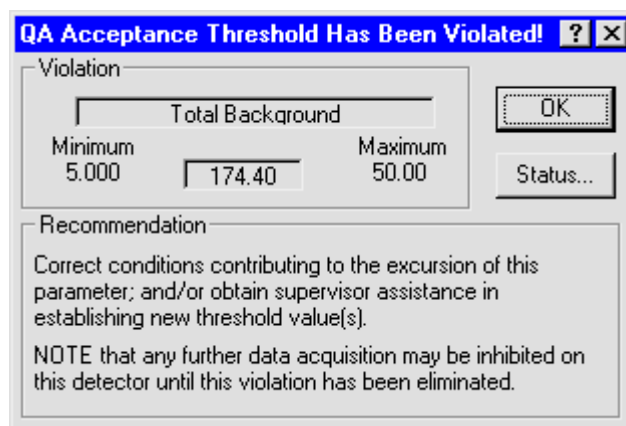


Figure 245. Background Warning Message.

NOTE If a sample QA has been run since the background QA, the previous background run cannot be overwritten.

If the background is outside the minimum/maximum limits, a warning similar to Fig. 245 is displayed.

10.2.3. Measure Sample

This command opens the Sample QA Measurement dialog (Fig. 246). It contains a reminder to place the QA source on the Detector. Click on **Overwrite** to replace the last measurement. Click **OK--Start** to begin the count.

The QA source spectra are collected for the preset time and analyzed automatically. The analysis results are compared with the limits. If the result is outside the limits, a warning is displayed. The results are also stored in the QA database.

10.2.4. Status...

The QA status for the currently selected Detector is displayed as shown in Fig. 247. Click on **OK** to close the dialog.

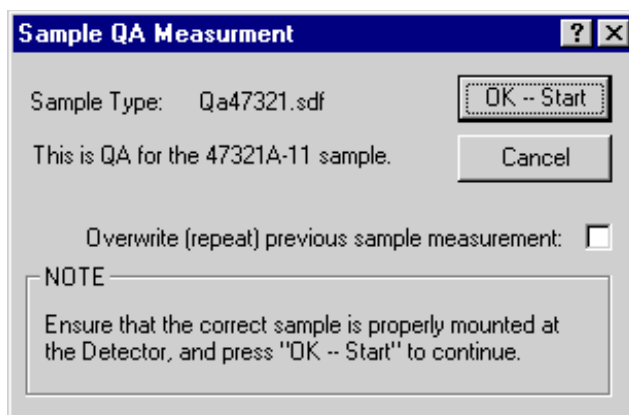


Figure 246. Starting Sample Type QA Measurement.

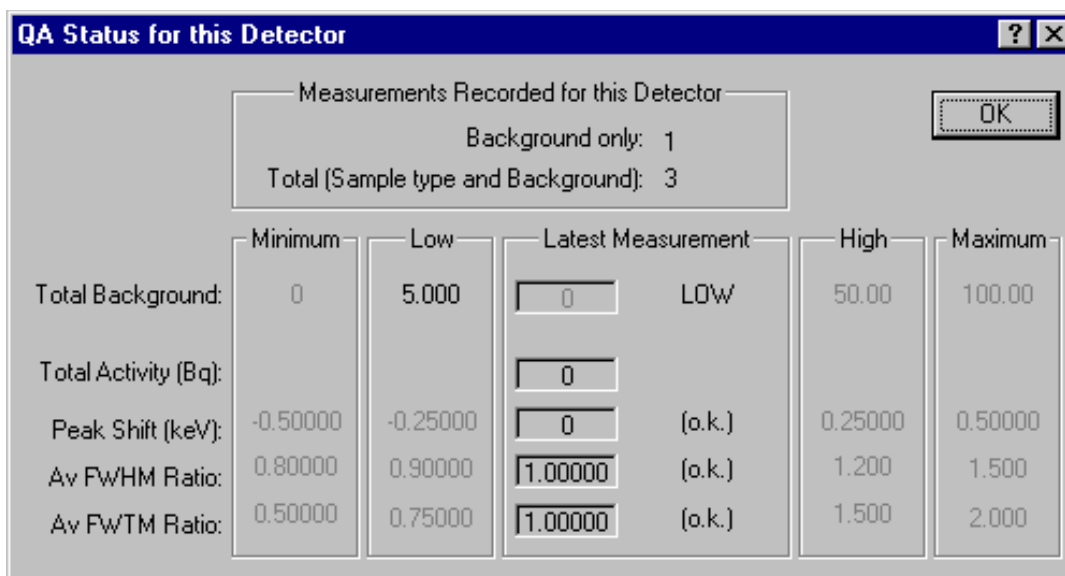


Figure 247. Showing Status of QA Measurements for a Detector.

10.2.5. Control Chart...

The Control Chart...

commands display the data stored in the QA database as a control chart. The displayed data can be scrolled backward or forward across the screen so that all collected data can be viewed. A typical chart is shown in Fig. 248. The short dashed lines represent the warning limits and the long dashed lines represent the acceptance threshold limits.

Figure 249 shows the control chart **File** menu, which contains the **Print Graph** command for printing the current graph. This command opens

a standard Windows printer setup dialog that lets you choose the printer and settings such as paper size, image orientation, and number of copies. The **Exit** command closes the QA Chart Program (this duplicates the Close box on the upper-right corner of the chart display). The **About** box provides version information about the chart program.

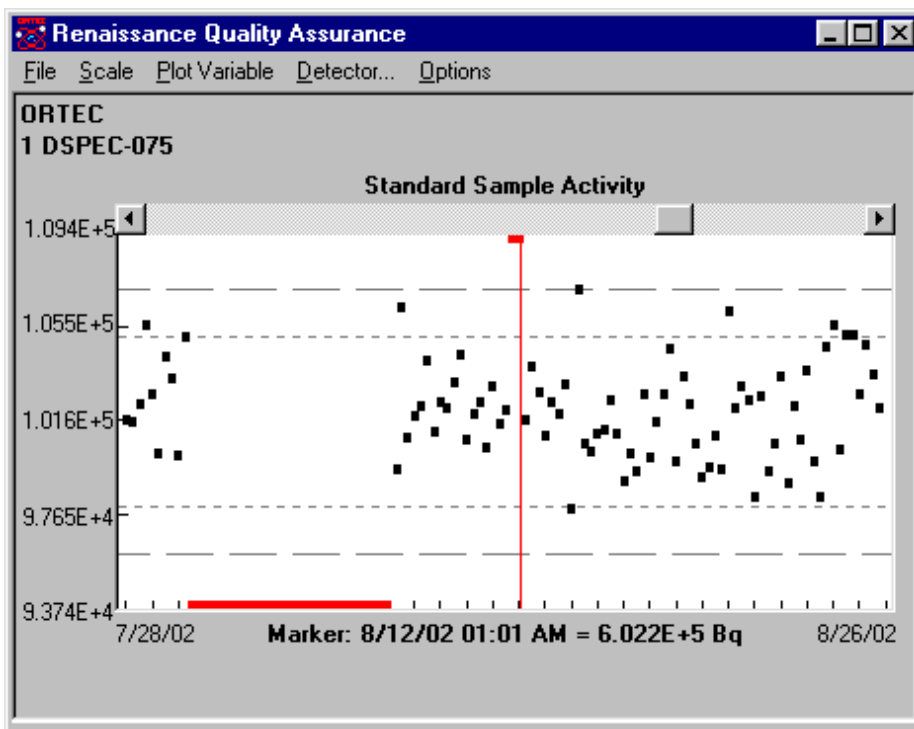


Figure 248. Control Chart Example.

Choose the chart time period (**Week**, **Month**, or **Quarter**) from the **Scale** menu (Fig. 250).

The **Plot Variable** menu (Fig. 251) contains functions for selecting **Activity**, **Peak Energy**, **Peak Width @ Half Max**, **Peak Width @ Tenth Max**, or **Background**.

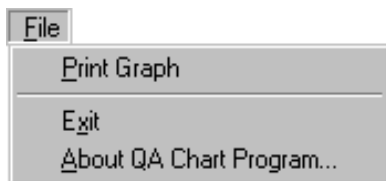


Figure 249. QA Chart File Menu.

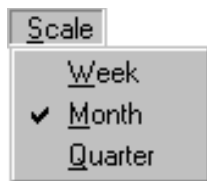


Figure 250. Scale Menu.

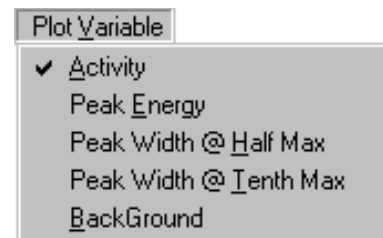


Figure 251. Plot Variable Menu.

The **Detector** menu item opens the list of Detectors for which background and sample measurements have been made (Fig. 252). Select a Detector for this control chart and click on **OK**.

Off-line processing of the QA database (including detailed trend analyses) can be done outside of Renaissance. The database format is well-documented and compatible with a number of popular software products including Microsoft Access.

NOTE *We strongly recommend that you back up any Renaissance database files before performing manipulations on them outside of Renaissance.*

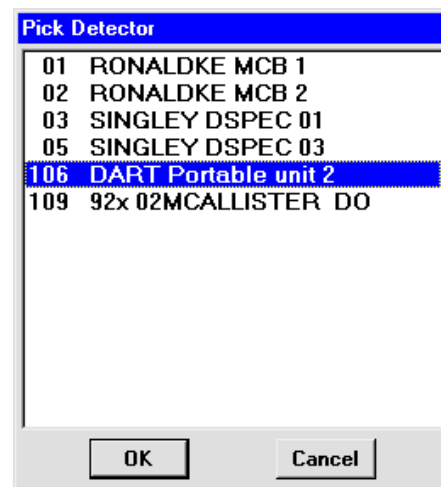


Figure 252. Detector Pick List.

The **Options** menu (Fig. 253) includes an **Always On Top** command, which keeps the QA window on top of all other windows, no matter which window (in Renaissance or any other program) might be active.

The **Fixed Vertical Scale** command adds flexibility in displaying control charts both on-screen and on printouts, for comparison with other charts.

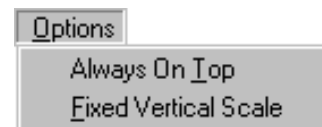


Figure 253. QA Chart File Menu.

- **Fixed Vertical Scale Off** (no check mark) — In this mode, the vertical scale of the graph is adjusted so that all points are shown to scale. All points are black. If one or more data points are substantially out of range, the graph might be quite compressed vertically.

- **Fixed Vertical Scale On** (check mark) — In this mode, the vertical scale of the graph is set to show the upper and lower alarm limits as full scale. The data points within the alarm limits are colored black. Out-of-range points are displayed in red at the lower or upper limits of the graph, at the proper horizontal coordinate. The out-of-range points are printed as a question mark (?).

To switch between the two display modes, click on the menu item to mark it with a checkmark or unmark it.

Figures 254 through 257 show the screen and printout for a QA data set with **Fixed Vertical Scale** on, then off. Compare the location of the points that exceed alarm limits in Figs. 254 and 255 to the location of the question marks in Figs. 256 and 257.

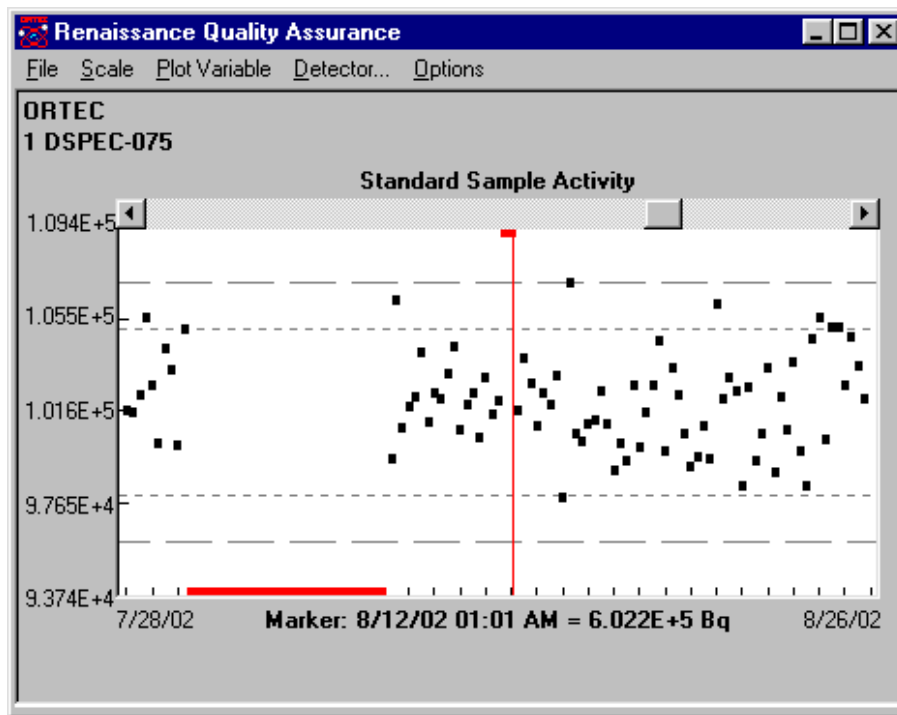


Figure 254. Control Chart On Screen with Fixed Vertical Scale On.

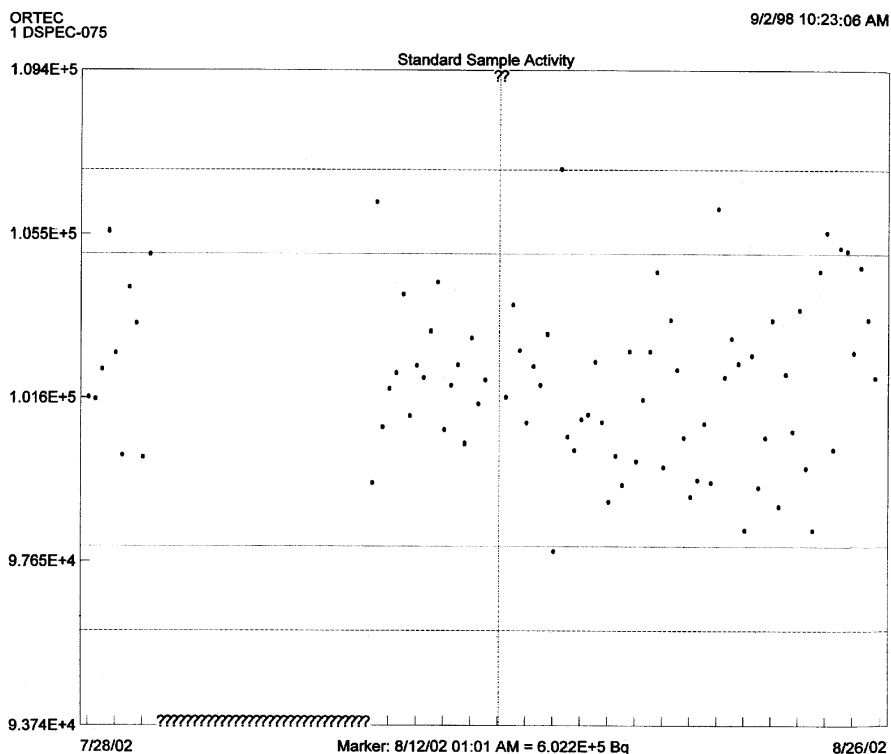


Figure 255. Printout of Control Chart with Fixed Vertical Scale On.

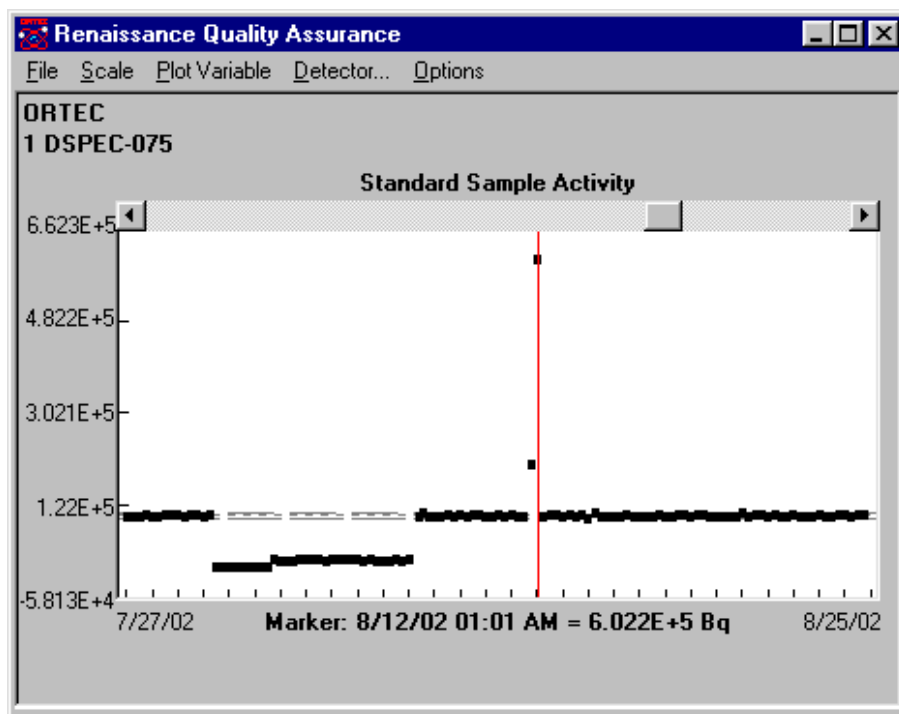


Figure 256. Control Chart On Screen with Fixed Vertical Scale Off.

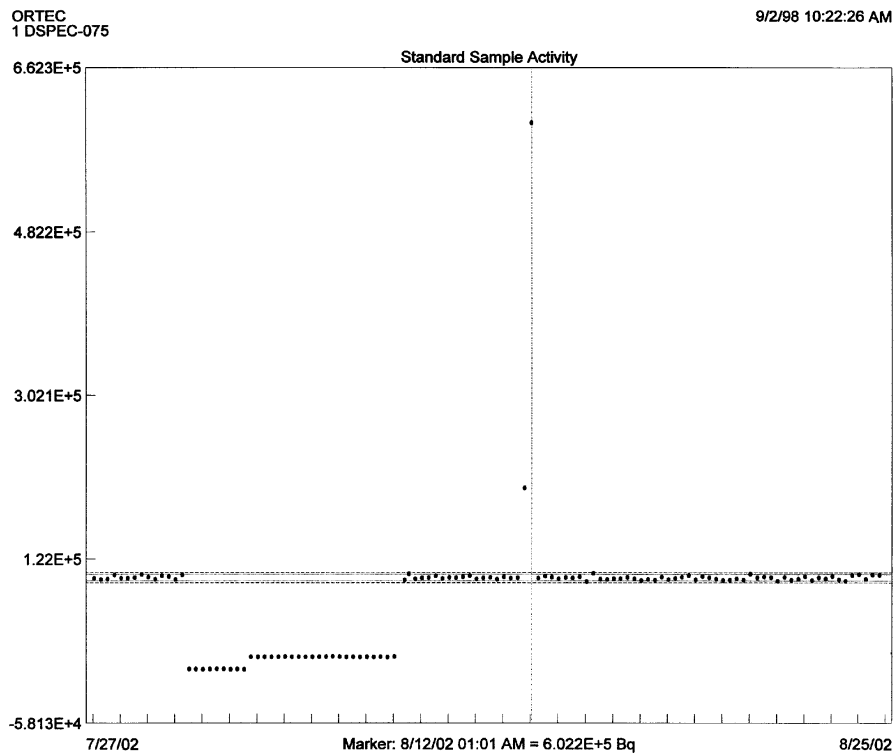


Figure 257. Printout of Control Chart with Fixed Vertical Scale Off.

10.3. Creating the QA Database

If Renaissance cannot find the QA database file, `RenpQA32.Mdb`, the QA database setup wizard will allow you to locate or create it. Figure 258 shows the first wizard screen. Mark the **second** radio button, **User Data Source (Applies to this machine only)**. Click on **Next**.

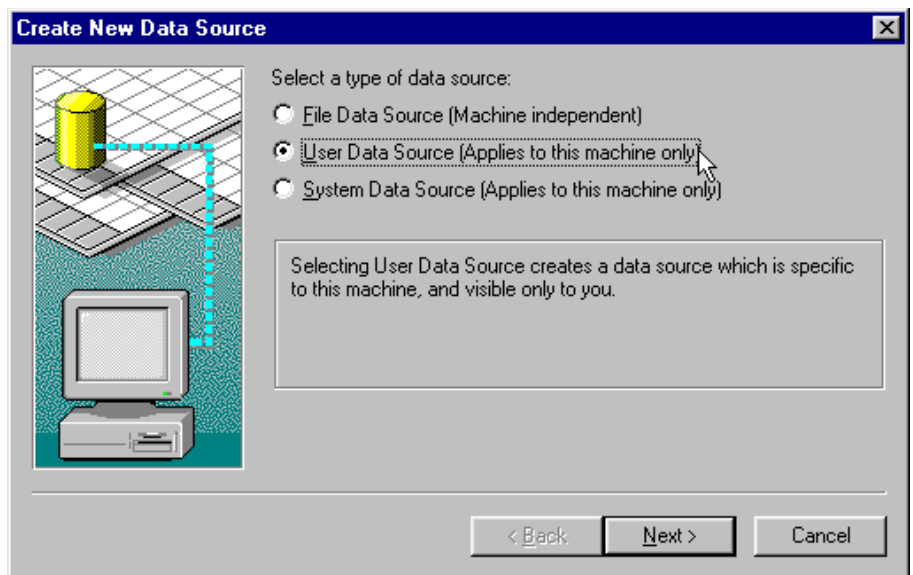


Figure 258. First QA Database Wizard Screen.

The second wizard screen is shown in Fig. 259. Scroll down the list and highlight **Microsoft Access Driver (*.mdb)**, then click on **Next**.

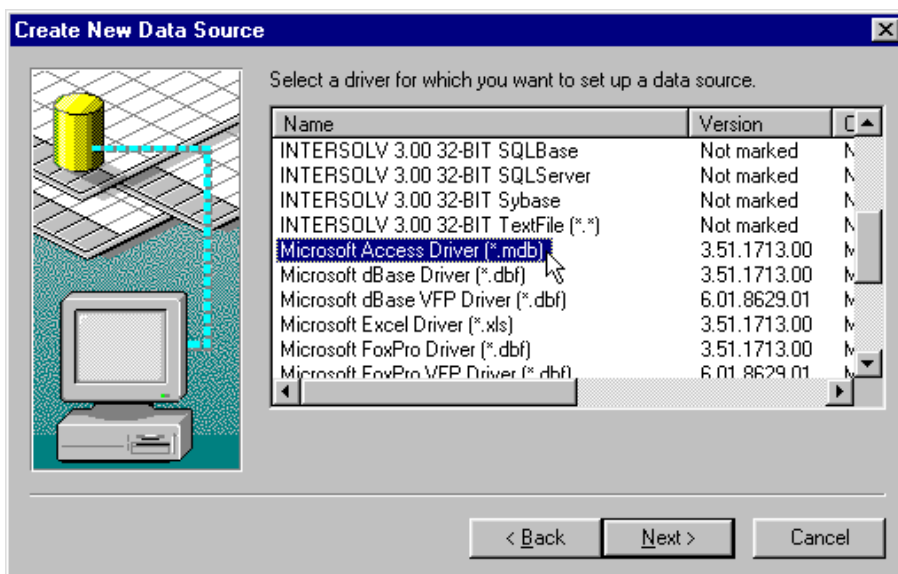


Figure 259. Second QA Database Wizard Screen.

Figure 260 shows the setup summary on the final wizard screen. Click on **Finish**.

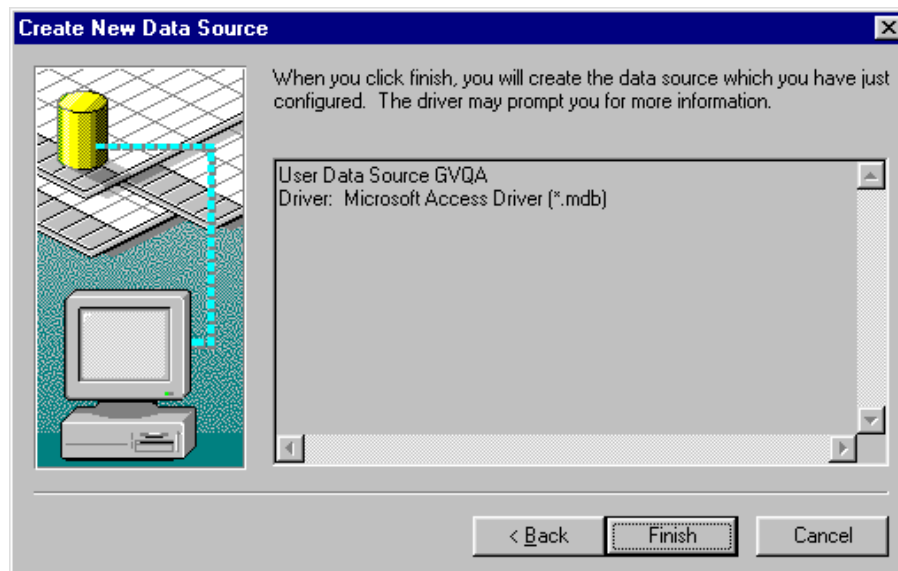


Figure 260. Final Wizard Screen.

When the wizard closes, an ODBC setup dialog (Fig. 261) will open. In the **Database** section of the dialog, Renaissance will display the location where it expects to find `RenpQA32.Mdb` (this is `C:\User` in the accompanying figure). If Renaissance was installed on another drive, the path will reflect that drive name (for example, if Renaissance was installed on drive `E:\`, the **Database** path will default to `E:\User\RenpQA32.Mdb`).

Click on **Select...** to try to locate the database file. The Select Database dialog (Fig. 262) will open, displaying all `.MDB` files in the current directory. Use the **Drives** and **Directories** fields to find the location of `RenpQA32.Mdb`, if it exists, then click on **OK**.

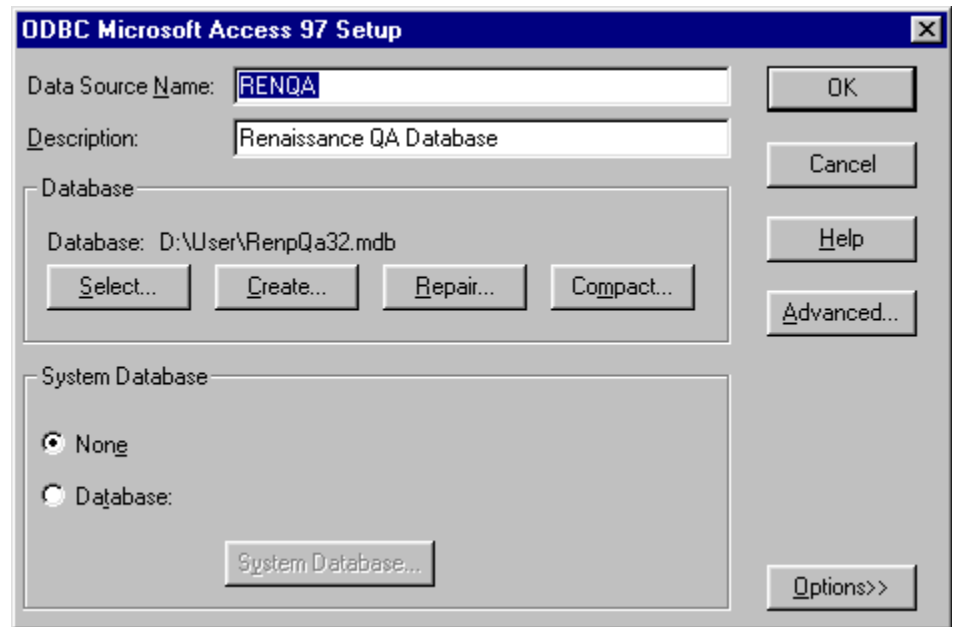


Figure 261. Select a Database.

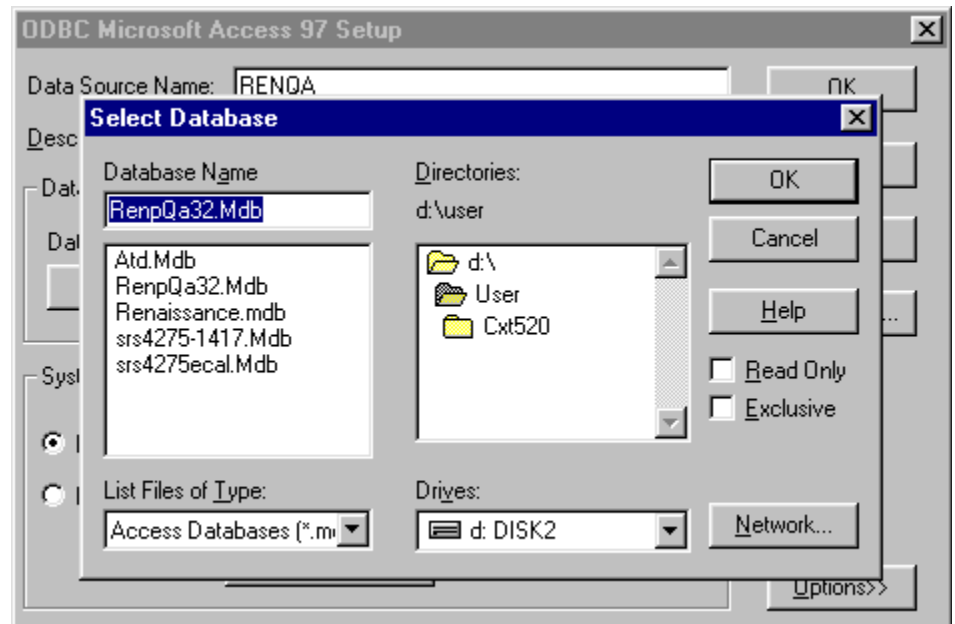


Figure 262. Locate the Renaissance QA Database.

If the database file is not in the current directory, you will receive an error message. Click on **Cancel** to return to the ODBC setup dialog, then click on **Create...** This will open the New Database dialog, shown in Fig. 263.

In the **Database Name** field, enter **RenpQA32.Mdb**, then click on **OK**. to return to the ODBC setup dialog. Click again on **OK**.

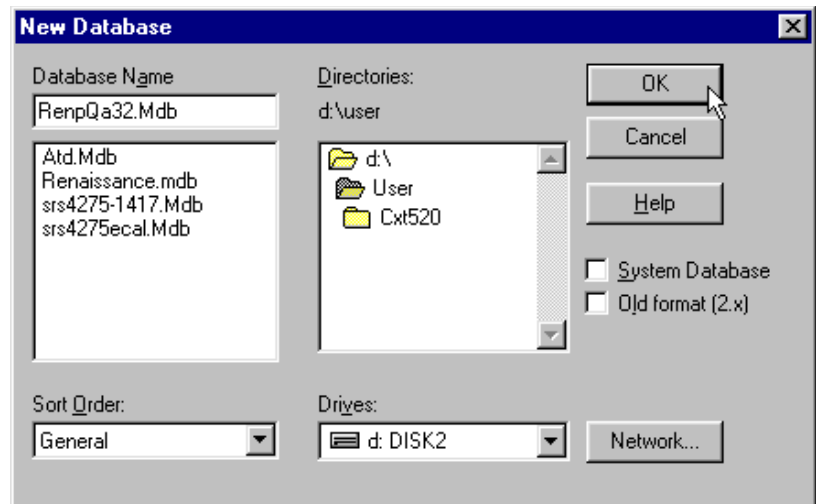


Figure 263. Create a New QA Database.

The Quality Assurance Settings dialog (Fig. 243) will now open. At this point, the database is ready and you're ready to begin taking QA setup and measurements.

11. KEYBOARD ACCELERATORS

This chapter describes the Renaissance accelerator keys. The keys described in this section are grouped primarily according to location on the keyboard and secondarily by related function.

11.1. Introduction

Table 13 provides a quick reference to all of the Renaissance keyboard and keypad functions. These accelerators are also illustrated in Fig. 264, and discussed in more detail in the remainder of the chapter.

The accelerators operate only in the active window (click in the window you wish to activate). The title bar must be highlighted with the active title bar color (as set up in Windows Control Panel). In addition, the active cursor — or input *focus* — must be in one of the spectrum windows. Similar to other Windows applications, the focus can be switched between Renaissance and other applications by clicking on the Windows Taskbar, pressing <Alt + Tab>, or, if the inactive window is visible, pointing with the mouse at some spot in the inactive window and clicking.

The multi-key functions, such as <Alt + 1> or <Shift + →>, are executed by holding down the first key (e.g., <Alt>, <Shift>, or <Ctrl>) while pressing the key that follows the “+” sign in the brackets, then releasing both keys simultaneously. Functions that use the keypad keys begin with the word **Keypad**, e.g., **Keypad<5>**.

As usual for any Windows application, the menus are accessed by clicking on them with the mouse, or by using the **Alt** key plus the key that matches the underlined letter in the menu item name. For example, the multi-key combination to open the **F**ile menu is <Alt + F>.

Note that the Renaissance accelerator keys do not interfere with Windows menu operations or task switching. For example, when a menu is active (i.e., pulled down), the <←>/<→> and <↑>/<↓> keys revert to their normal Windows functions of moving across the menu bar and scrolling up/down within a menu, respectively. As soon as the menu is closed, they behave as Renaissance accelerators again.

11.2. Marker and Display Function Keys

11.2.1. Next Channel

<←>/<→>

When not in rubber-rectangle mode, the right and left arrow keys move the marker by one displayed pixel in the corresponding direction. This can represent a jump of more than one spectral data memory channel, especially if the horizontal scale in channels is larger than the width in pixels of the window (see the discussion in Section 4.1).

Table 13. Quick Reference to GammaVision Keyboard Commands.

Key	Function
<↓> or <F5>	Change vertical scale so spectrum peaks are smaller.
<↑> or <F6>	Change vertical scale so spectrum peaks are larger.
<↓>	In rubber rectangle mode, shift rectangle down (toward baseline) one pixel
<↑>	In rubber rectangle mode, shift rectangle up (away from baseline) one pixel.
<←>	Move marker to higher channel. In rubber rectangle mode, shift rectangle right one pixel.
<→>	Move marker to lower channel. In rubber rectangle mode, shift rubber rectangle left one pixel.
<←> or <F7>	Narrow the horizontal scale.
<→> or <F8>	Widen the horizontal scale.
<Ctrl + →>	Jump to next higher peak.
<Ctrl + ←>	Jump to next lower peak.
<Shift + →>	Jump to next higher ROI.
<Shift + ←>	Jump to next lower ROI.
<Alt + →>	Advance to next library entry.
<Alt + ←>	Recede to previous library entry.
<PageUp>	Jump to higher channel number in 1/16th-screen-width increments.
<PageDown>	Jump to lower channel number in 1/16th-screen-width increments.
<Home>	Jump to first channel of the full spectrum.
<End>	Jump to last channel of the full spectrum.
<Ctrl + Fi>	Select Detector i (i = 1 to 12, in pick list order).
<F2>	Switch ROI bit control from OFF to SET to CLEAR.
<F3>	In supported digital spectrometers, switch between the two spectra stored in ZDT mode.
<Shift + F3>	In supported digital spectrometers, switch the disk spectrum to compare normal to disk ZDT spectrum or ZDT spectrum to disk normal spectrum.
<F4> or <Alt + 6>	Switch between displaying selected Detector and buffer.
<F5> or <↓>	Change vertical scale so that spectrum peaks are smaller.
<F6> or <↑>	Change vertical scale so that spectrum peaks are larger.
<F7> or <←>	Narrow the horizontal scale.
<F8> or <→>	Widen the horizontal scale.
<Alt + F7>	Reset both horizontal and vertical scaling to view complete spectrum.
Keypad<←>	Zoom out.
Keypad<→>	Zoom in.
Keypad<5>	Center expanded display on cursor.
Keypad</>	Switch to logarithmic vertical scale.
Keypad<*>	Switch to auto vertical scale.
Insert<Ins>	Mark the peak region around the cursor as an ROI.
Delete	Clear the ROI.
<Shift + ↑>	Shift the compare spectrum upwards.
<Shift + ↓>	Shift the compare spectrum downwards.
<Alt + 1>	Start acquisition in selected Detector.
<Alt + 2>	Stop acquisition in selected Detector.
<Alt + 3>	Clear data in selected Detector.
<Alt + 5>	Copy data in the selected Detector to the buffer.
<Alt + 6> or <F4>	Switch between displaying selected Detector and buffer.
<Alt + ->	Decrease amplifier fine gain by smallest increment (where supported).
<Shift + Alt + ->	Decrease amplifier fine gain by several increments.
<Alt + +>	Increase amplifier fine gain by smallest increment.
<Shift + Alt + +>	Increase amplifier fine gain by several increments.
<PrintScreen>	Capture screen to Windows Clipboard.

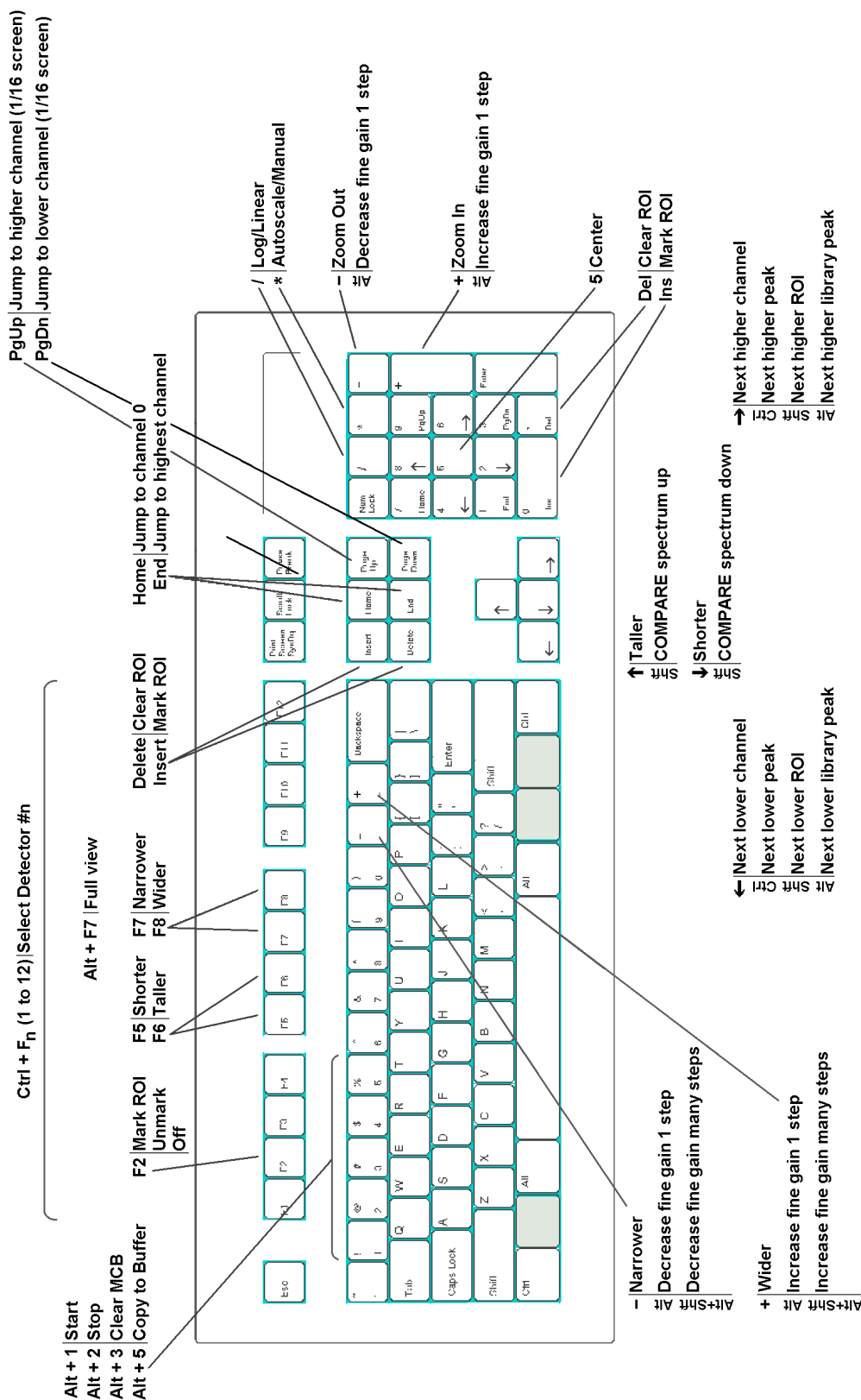


Figure 264. Renaissance Keyboard and Keypad Accelerators.

If the horizontal scale is expanded, when the marker reaches the edge of the spectrum window, the next key press past the edge shifts the window to the next block of channels in that direction such that the marker is now in the center of the display.

When the ROI mode is set to **Mark**, the <→>/<←> keys cause the channels to be marked as the marker moves. Similarly, they clear the ROI bits while the ROI mode is **UnMark**. (See Section 5.8.)

11.2.2. Next ROI

<Shift + →>/<Shift + ←>

The <Shift + →> or <Shift + ←> move the marker to the beginning of the next higher channel ROI, or the end of the preceding ROI, respectively, of the displayed spectrum. These functions are duplicated by the **ROI** indexing buttons on the Status Sidebar.

11.2.3. Next Peak

<Ctrl + →>/<Ctrl + ←>

The <Ctrl+ →> and <Ctrl+ ←> keys perform a peak search on the spectrum in the higher or lower channel direction, respectively, and move the marker to the first peak found. If no peak is found, the program displays the “**No More Peaks**” message and the marker does not move. If the spectrum is energy-calibrated and the library loaded, the system displays the best match from the library within two FWHMs of the peak centroid. If there is no match within this range, the “**No Close Library Match**” message is displayed. These functions are duplicated by the **Peak** indexing buttons on the Status Sidebar.

11.2.4. Next Library Entry

<Alt + →>/<Alt + ←>

These keys move forward or backward through the nuclide library to the next closest library entry. Each button press advances to the next library entry and moves the marker to the corresponding energy. Also, instead of indexing from a previously identified peak, the marker can be positioned anywhere in the spectrum and these keys used to locate the entries closest in energy to that point. If a warning beep sounds, it means that all library entries have been exhausted in that direction, or that the spectrum is not properly calibrated for reaching the energy with the marker. In any case, if an appropriate peak is available at the location of the marker, data on the peak activity are displayed on the Marker Information Line. These functions are duplicated by the **Library** indexing buttons on the Status Sidebar.

11.2.5. First/Last Channel

<Home>/<End>

These keys move the marker to the first or last channel of the spectrum.

11.2.6. Jump (Sixteenth Screen Width)

<PageDown>/<PageUp>

<PageDown> and <PageUp> jump the marker position to the left (to lower channel numbers) or right (to higher channel numbers), respectively, 1/16 of the window width, regardless of the horizontal scale. The status of the ROI bit is not altered when the marker is moved with these keys, that is, the **Mark/UnMark/Off** state is ignored. The marker channel contents and Marker Information Line are continuously updated as the marker jumps, so when the jump is complete, the marker information is up-to-date for the current channel.

11.2.7. Insert ROI

<Insert> or Keypad<Ins>

These keys mark an ROI in the spectrum, at the marker position, in one of two ways:

- 1) If the spectrum is calibrated, the region is centered on the marker with a width of three times the calibrated FWHM. There does not need to be a peak at the marker position.
- 2) If the spectrum is not calibrated, the region is centered on the peak, if any, located within two channels of the marker and is as wide as the peak. If the peak search fails, or if the peak is not well-formed, no ROI is marked. There is no limit on the size of a peak or ROI; therefore, in some uncalibrated spectra, large ROIs could be marked.

These accelerators duplicate the function of the **Mark ROI** Toolbar button and the **ROI/Mark Peak** menu selection (see Section 5.8).

NOTE <Insert> and Keypad<Ins> work conveniently in combination with <Ctrl + ←> and <Ctrl + →> to rapidly set peak ROIs.

11.2.8. Clear ROI

<Delete> or Keypad

<Delete> and Keypad clear the ROI bits of all ROI channels contiguous to the channel containing the marker. These accelerators duplicate the function of the **Clear ROI** button on the Toolbar and the **ROI/Clear** menu selection (see Section 5.8).

11.2.9. Taller/Shorter

<↑>/<↓>

When not in rubber-rectangle mode, the <↑> and <↓> keys decrease or increase the vertical full scale of the displayed spectrum so the peaks appear taller or shorter, respectively. The minimum is 16 counts-full-scale; the maximum is 1024 million counts. Each successive key press doubles or halves the full scale until the maximum or minimum is reached. Whenever the maximum full-scale value is reached, the next <↑> key press switches to logarithmic scale. If the display is already in logarithmic scale, the display switches to linear scale. In either case, the vertical full-scale value is always shown on the Toolbar.

Note that if the number of counts exceeds the full-scale value, the data points will be displayed at the full-scale value. These keys duplicate the function of the <F6>/<F5> keys.

11.2.10. Move Rubber Rectangle One Pixel

<↑>/<↓>/<←>/<→>

In rubber-rectangle mode (see Section 4.3.3), the arrow keys move the rubber rectangle one channel or one pixel at a time.

11.2.11. Compare Vertical Separation

<Shift+↑>/<Shift+↓>

In Compare mode, the <Shift + ↑> or <Shift + ↓> keys decrease or increase the vertical separation between the two spectra. Each successive key press will increase or decrease the separation by moving the spectrum read from disk. The spectrum from disk can be moved below the first spectrum if it has fewer counts.

11.2.12. Zoom In/Zoom Out With No Change in Log/Lin Scale

Keypad<+>/<->

Keypad<+> and **Keypad<->** respectively contract the x-axis (making peaks look broader) and expand it (making peaks look narrower) by a factor of two without affecting the vertical scale or switching between logarithmic and linear scaling. The scale value for both axes is always displayed on the Toolbar.

11.2.13. Fine Gain

<Alt + +>/<Alt + ->

These accelerators step the internal amplifier up or down by one increment of fine gain on the selected Detector, if it has a software-controlled amplifier. The new fine gain setting is shown on the Supplemental Information Line at the bottom of the screen. If the gain stabilizer is active, the display of the histogram data might not change. The fine gain can also be set with **Acquire/ MCB Properties...** (Section 5.2.9), <Shift + Alt + +>/<Shift + Alt + -> on the keyboard, and **Keypad<Alt + +>/<Alt + ->**.

11.2.14. Fine Gain (Large Move)

<Shift + Alt + +>/<Shift + Alt + ->

<Shift+Alt+ +> and <Shift+Alt+ -> step the internal amplifier of the selected Detector (if it has a software-controlled amplifier) up or down by a large increment of fine gain. If the gain stabilizer is active, the display of the histogram data might not change. The fine gain can also be set using **Acquire/MCB Properties...** (Section 5.2.9), <Alt+ +>/ <Alt+ -> on the keyboard, and **Keypad<Alt + +>/ <Alt + ->**.

11.3. Keyboard Number Combinations

NOTE Only the *keyboard* numbers will function in the following combinations. The *keypad* number keys will *not* perform these functions.

11.3.1. Start

<Alt + 1>

<Alt + 1> starts the acquisition in the selected Detector. Any presets desired must be entered before starting acquisition. This accelerator duplicates the **Start** Toolbar button, the **Start** command on the right-mouse-button menu, and **Acquire/Start**.

11.3.2. Stop

<Alt + 2>

<Alt + 2> stops acquisition in the selected Detector. This duplicates the **Stop** Toolbar button, the **Stop** command on the right-mouse-button menu, and **Acquire/Stop**.

11.3.3. Clear

<Alt + 3>

<Alt + 3> clears the displayed Detector histogram data and its descriptors (e.g., real time, live time). This accelerator duplicates the **Clear Spectrum** Toolbar button, the **Clear** command on the right-mouse-button menu, and **Acquire/Clear**.

11.3.4. Copy to Buffer

<Alt + 5>

<Alt + 5> copies the histogram data from the selected Detector to the buffer, along with its descriptors (e.g., live time, real time), and displays the spectrum in a new window. This duplicates the **Copy to Buffer** command on the right-mouse-button menu and **Acquire/Copy to Buffer** (Section 5.2.5).

11.3.5. Detector/Buffer

<Alt + 6>

<Alt + 6> switches the display between the histogram of the spectrum in the selected Detector and the spectrum in the buffer. The buffer will have the memory size of the spectrum that was last transferred from Detector or disk file. The Detector list on the right side of the Toolbar indicates whether the buffer or a particular Detector is currently displayed, and the Status Sidebar shows the presets for the displayed data. This duplicates <F4> and **Display/Detector/Buffer**; see Section 4.6.2.

11.3.6. Narrower/Wider

<+>/<->

The <+> key increases the horizontal scale of the Expanded Spectrum Window so the peaks appear wider, while the <-> key decreases the horizontal scale, making the peaks look narrower. The horizontal and vertical scale values are displayed on the Toolbar. These functions are duplicated by <F7>/<F8>.

11.4. Function Keys

11.4.1. ROI

<F2>

The <F2> key switches the ROI marker status among the **Mark**, **UnMark**, and **Off** conditions, so the arrow keys are used to set or clear the ROI bits for particular channels or groups of channels, or return the marker to normal usage. The current ROI marking status (**Marking**, **Unmarking**) is shown in at the extreme right of the Menu Bar (**Off** mode is shown as blank). ROI bits are changed by using the keyboard to move the marker to a channel, as follows:

- **Mark** The channel is marked (set) as an ROI with the marker.
- **UnMark** The channel is removed from the ROI (reset) with the marker.
- **Off** The ROI status is unchanged with the marker.

11.4.2. ZDT/Normal

<F3>

For supported digital spectrometers in ZDT mode, the <F3> key switches between the normal (LTC) or uncertainty (ERR) spectrum and the ZDT corrected spectrum. It duplicates the **Acquire/ZDT Display Select** command.

11.4.3. ZDT Compare

<Shift+F3>

For supported digital spectrometers in Compare mode, this accelerator switches the compare spectrum between the ZDT spectrum and its accompanying LTC or ERR spectrum. It is used in combination with <F3> or **Acquire/ZDT Display Select** to display the normal-to-ZDT, uncertainty-to-ZDT, ZDT-to-normal, or ZDT-to-uncertainty comparisons.

11.4.4. Detector/Buffer

<F4>

The <F4> key switches between the display of the data in the Detector and the data in the buffer. It duplicates the function of <Alt + 6> and **Display/Detector/Buffer**; see Section 11.3.5.

11.4.5. Taller/Shorter

<F5>/<F6>

These keys decrease or increase the vertical full scale of the displayed spectrum so the peaks appear taller or shorter, respectively. They duplicate the function of the <↑> and <↓> keys. The vertical scale value is always shown on the Toolbar.

11.4.6. Narrower/Wider

<F7>/<F8>

These keys increase or decrease the horizontal scale of the data display so the peaks appear narrower or wider, respectively. They duplicate the function of <-> and <+> keys. The horizontal scale value is always shown on the Toolbar.

11.4.7. Select Detector

<Ctrl + F1> through <Ctrl + F12>

These keys display the spectrum for the specified Detector **n** (where **n** = 1 to 12, corresponding to **<Ctrl+ Fn>**, in the order that the Detectors are defined in the Detector pick list; see Fig. 10). The selected Detector name (or the buffer) is shown on the Toolbar.

These keys duplicate the function of the Detector pick list on the Toolbar, and the **Detector...** dialog under the **Display** menu. An error message box will appear if the selected Detector is invalid. In systems with more than 12 Detectors, use **Display/Detector...** or the drop-down list on the Toolbar.

11.4.8. Full View

<Alt + F7>

This key will force the expanded spectrum window for the active spectrum to be the full spectrum width. This is duplicated by the **Display/Full View**.

11.5. Keypad Keys

11.5.1. Log/Linear

Keypad</>

Keypad</> toggles the active spectrum window between logarithmic and linear vertical display. This is duplicated by the **Log** Toolbar button. The vertical scale can be controlled with the **Zoom In/Zoom Out** Toolbar buttons, **Keypad<+>/<->**, the **<↑>** and **<↓>** keys, and **<F7/F8>**.

11.5.2. Auto/Manual

Keypad<*>

Keypad<*> switches the spectrum window between automatic and manual vertical full scale (see the discussion in Section 5.9.2). This is duplicated by the **Vertical Auto Scale** button on the Toolbar.

11.5.3. Center

Keypad<5>

Keypad<5> forces the marker to the center of the screen by shifting the spectrum without moving the marker from its current channel. This is duplicated by the **Center** button on the Toolbar. For more information, see Section 5.9.6.

11.5.4. Zoom In/Zoom Out With No Change in Log/Lin Scale

Keypad<+>/<->

Keypad<+> and **Keypad<->** respectively contract the x-axis (making peaks look broader) and expand it (making peaks look narrower) by a factor of two without affecting the vertical scale or switching between logarithmic and linear scaling. The scale value for both axes is always displayed on the Toolbar.

11.5.5. Fine Gain

Keypad<Alt + +>/<Alt + ->

These accelerators step the internal amplifier up or down by one increment of fine gain on the selected Detector, if it has a software-controlled amplifier. The new fine gain setting is shown on the Supplemental Information Line at the bottom of the screen. If the gain stabilizer is active, the display of the histogram data might not change.

The fine gain can also be set with **Acquire/MCB Properties** (Section 5.2.9) and **Keypad<Shift + Alt + +>/ <Shift + Alt + ->**; and keyboard **<Alt + +>/<Alt + ->** and **<Shift + Alt + +>/<Shift + Alt + ->**.

12. JOB FILES

12.1. Introduction

The Renaissance `.JOB` file consists of one or more lines of ASCII text representing a series of commands that can automate most of the functions described earlier in this manual. The details of the commands and the required syntax are given in this chapter. A `.JOB` file can be started from **Services/Job Control...**, or by including the name of the `.JOB` file (e.g., `GVDEMO.JOB`) on the command line when Renaissance is first started (see Section A.1).

`.JOB` files are used for the following types of functions:

- Performing a repetitive task, such as running a sequence of experiments without user intervention.
- Defining initial conditions at startup (useful in preloading presets after a power loss for the 916/916A/917/918/918A each time Renaissance is run).

This version of Renaissance is compatible with `.JOB` files written for MAESTRO or Gamma-Vision. The text versions of these files will work on new Detectors as well as older models, with the exception of new commands and deleted commands.

12.1.1. JOB Command Functionality

12.1.1.1. Loops

Renaissance can run repetitive loops. Furthermore, the current loop count can be included as a variable in any string, including filenames, program parameters, and text. Data can thus be stored with unique filenames and labeled with unique descriptions.

12.1.1.2. Errors

If an error is encountered in running a `.JOB` file, the execution of the file stops and control returns to Renaissance. An error code appears in the **JOB Control...** dialog box; these are described in Appendix D.

12.1.1.3. Ask on Start and Ask on Save

If the appropriate **Ask on Start** or **Ask on Save** fields are turned on (see **Acquire/Acquisition Settings...** and **File/Settings...**, respectively), Renaissance will ask the corresponding questions when `START` or `SAVE` commands are executed in the `.JOB` file. This means that execution of the `.JOB` file stops until the entry is made.

The ASK commands will also stop the .JOB file and prompt you to enter the requested information. The .JOB file will continue when you click on **OK** or press <Enter> on the dialog. The input is used or stored immediately, before the next JOB instruction, except for the ASK_SPECTRUM command.

NOTE If you choose **Cancel** when responding to an ask-on-start or ask-on-save prompt, the JOB will terminate at that point.

12.1.1.4. Password-Locked Detectors

When .JOB files are used with locked Detectors, the first time a destructive command is used on the locked Detector, you will be prompted for the password. Alternatively, you can use the ASK_PASSWORD command at the beginning of the JOB. From then on while the .JOB file executes, the password is retained and you will not receive a prompt. When the .JOB file quits, the password will be forgotten.

12.1.2. JOB Command Structure

In the command descriptions in Sections 12.2 and 12.5, a variable filename or text is enclosed in “...” and a variable number is enclosed in <...>; anything enclosed in square brackets [...] is optional.

12.2. Summary of JOB Commands

This section provides a quick reference to the JOB commands; for more detailed information, see Section 12.5.

ANALYZE [“spectrum filename”]

Analyzes the spectrum in the same manner as the menu commands.

ASK_CALIBRATION

Asks for the internal calibration filename, then reads the file and loads the calibration.

ASK_COLLECTION

Asks for the date and time for the decay correction.

ASK_CONFIRM [“text”]

This displays “text” and waits for the user to click on **OK**.

ASK_DESCRIPTION

Asks for sample description.

ASK_LIBRARY

Asks for the name of the internal library, then loads it.

ASK_OPERATOR

Asks for the user name.

ASK_OPTIONS

Asks for the sample description filename of the analysis options.

ASK_PASSWORD

Asks for password (used to lock Detectors).

ASK_PBC

Asks for the name of the Peak Background Correction file, then loads it.

ASK_PRESET

Asks for the presets to be set in the detector.

ASK_SPECTRUM

Asks for the spectrum filename to be used in following SAVE commands.

ASK_WEIGHT

Asks for the sample size and units.

BEEP <freq>,<duration>

Produces an audible sound of <freq> Hz, lasting <duration> milliseconds.

BEEP ID

A numerical ID is given based on a desired system event.

BEEP “String”

String can be a .WAV file or any event defined in the Registry.

CALIBRATE_AUTO

This command executes the automatic energy calibration.

CALIBRATE_EFFICIENCY “file.eft”

Performs an efficiency calibration using the active spectrum and the data in file.eft.

CALIBRATE_ENERGY “file.ent”

Performs an energy calibration using the active spectrum and the data in file.ent.

CALL “file.job”

Executes another .JOB file as a subroutine.

CHANGE_SAMPLE

Provides sample changer hardware handshake.

CLEAR

Clears the data and descriptors in the active Detector.

DESCRIBE_SAMPLE “text”

Enters the text into the sample description to be saved with the spectrum.

END_LOOP — see LOOP**EXPORT “file”**

This command executes the Export function with the filename specified.

FILL_BUFFER

Transfers the data from the active Detector to the buffer.

IMPORT “file”

This command executes the Import function with the filename specified.

LOAD_LIBRARY “file”

Loads the specified .LIB- or .MDB-format nuclide library.

LOAD_PBC “file.pbc”

Loads the specified PBC file.

LOCK “Pwd” [,“Name”]

This command locks the current Detector using “Pwd” as the password. If the optional “Name” parameter is missing, the Locked name defaults to “Job”.

LOOP <reps>...END_LOOP

Executes all the commands between LOOP and END_LOOP, <reps> number of times.

LOOP SPECTRA...END_LOOP

This command executes the commands within the loop once for each spectrum stored in the Detector hardware.

MARK_PEAKS

Sets ROIs on all peaks in the buffer.

QABACKGROUND

This command executes the background QA test without displaying prompts or violations.

QASAMPLE

This command executes the sample QA test without displaying prompts or violations.

QUIT

Terminates this copy of Renaissance.

RECALL “file”

Reads the spectrum data file into the buffer.

RECALL_CALIB “file”

Loads both the energy and efficiency calibration data from the disk file to the selected memory calibration parameters. The spectrum is not changed.

RECALL_EFFICIENCY “file”

Loads the efficiency calibration data from the disk file to the selected memory calibration parameters. The spectrum is not changed.

RECALL_ENERGY “file”

Loads the energy calibration data from the disk file to the selected memory calibration parameters. The spectrum is not changed.

RECALL_OPTIONS “file”

Sets the analysis options from the table in the specified **.SDF** (Ge) or **.SVD** (NaI) file.

RECALL_ROI “file.roi”

Sets the ROIs from the table in the file.

REM [Text]

This line is a comment (remark) and is ignored during command processing.

REPORT “file”

Writes the ROI-marked peak report (not the analysis report) to the disk filename or to the printer (PRN:).

RUN “program”

Executes a Windows application program or non-Windows application. See the Microsoft documentation for more details.

RUN_MINIMIZED “program”

Same as the **RUN** command above, except that the application is run initially as an icon (minimized), rather than as a normal window.

SAVE “file” [,n]

Saves the current spectrum to disk in the format (.CHN or .SPC) specified in the **File/Settings** menu.

SAVE_CALIBRATION “file.clb”

Saves the current energy, efficiency, and TCC calibrations to the specified .CLB file.

SAVE_ROI “file.roi”

Saves the table of ROIs in the display to the specified disk file.

SEND_MESSAGE “text”

Sends the text as a command to the Detector.

SET_BUFFER

Selects the buffer, same as SET_DETECTOR 0.

SET_DETECTOR <number>

Selects the Detector or buffer (0).

SET_NAME_STRIP “file”

Sets the strip file to the specified .SPC or .CHN file. See STRIP below.

SET_PRESET_CLEAR

Clears all presets in active spectrum.

SET_PRESET_COUNT <n>

Sets the ROI Count preset to <n> counts.

SET_PRESET_INTEG <n>

Sets the ROI Integral preset to <n> counts.

SET_PRESET_LIVE <t>

Sets the live-time preset to <t> seconds.

SET_PRESET_REAL <t>

Sets the real-time preset to <t> seconds.

SET_PRESET_UNCERTAINTY <limit>,<low chan>,<high chan>

Sets the statistical preset to the uncertainty based on the counts in the region between the low and high channels. (Not valid on all MCBs.)

SMOOTH

Smooths the spectrum in the buffer.

START

Starts the selected Detector.

START_OPTIMIZE

Starts the optimize function for the Detector (for digital MCBs only).

START_PZ

Starts the PZ function for the Detector. It is automatically included in the optimize function.

STOP

Stops the selected Detector.

STOP_PZ

Stops the PZ function for the detector.

STRIP <factor>,[“file”]

Strips a spectrum file from the buffer.

UNLOCK “Pwd”

This command unlocks the current Detector using “Pwd” as the password.

VIEW “i”

This command moves the “i”th stored spectrum to position 0.

WAIT [<seconds>]

Waits a fixed number of seconds or until the active detector stops counting (if no seconds specified).

WAIT “program”

Waits until the named program, e.g., started by the RUN command, stops execution.

WAIT_AUTO

Waits until the optimize function is complete (for digital MCBs only).

WAIT_CHANGER

Waits until the sample ready signal on the rear panel is present.

WAIT_PZ

Waits until the PZ function is complete.

WAIT_QA

This command waits until QA is complete.

WAIT_SERIAL

This command is used to control serial devices such as sample changers.

ZOOM <i>

Changes the size of the Renaissance window to icon, normal, or maximum.

ZOOM: <x,y,w,h>

Changes the position and size of the Renaissance window to the stated values.

12.3. .JOB File Variables

Variables have been added to the .JOB file features to allow more flexibility and control of the JOBS. These variables are defined by the program or by user entries. They can be used anywhere in the .JOB file.

For example:

```
$(FullPath)= D:\USER\SOIL\SAM001.SPC
```

then:

```
$(FullBase) = D:\USER\SOIL\SAM001
$(FileExt) = SPC
$(FileDir) = D:\USER\SOIL
$(ShortPath) = SAM001.SPC
$(ShortBase) = SAM001
```

The following variables are expanded in .JOB file strings:

\$(FullPath)	Full pathname of the spectrum file
\$(FullBase)	Full pathname of the spectrum without the “.” and extension
\$(FileExt)	File extension of the spectrum file without the “.”
\$(FileDir)	Directory of the spectrum file without the last backslash (\)
\$(McaDir)	Renaissance directory without the last backslash
\$(CurDir)	Starting (current) directory of Renaissance
\$(Loop)	Current value of the loop counter (zero based)
\$(Loop1)	Loop counter plus 1
\$(Bel)	ASCII bell character
\$(CR)	ASCII carriage return character
\$(FF)	ASCII form feed character
\$(LF)	ASCII line feed character
\$(ESC)	ASCII escape character
\$(AutoFile)	Create an automatic filename based on the Start/Save/Report settings
\$(ShortPath)	Relative pathname of the spectrum file
\$(ShortBase)	Relative pathname of the spectrum without the “.” and extension
\$(Password)	Value entered in ASK_PASSWORD command
\$(Owner)	Value entered in ASK_PASSWORD command

The filename variables are updated each time a READ operation is performed. The READ operations are:

ANALYZE “file”	LOAD
ASK_CALIBRATION	RECALL
ASK_LIBRARY	RECALL_CALIBRATION
ASK_OPTIONS	RECALL_EFFICIENCY
ASK_PBC	RECALL_ENERGY
ASK_SPECTRUM	RECALL_OPTIONS
CALIBRATE_EFFICIENCY	RECALL_ROI
CALIBRATE_ENERGY	STRIP

The filename is not updated for WRITE commands.

The following sample .JOB file will produce a set of files in which the last character of the filename is a digit that increments with each loop.

```
ASK_SPECTRUM
LOOP 5
SAVE "$(FULLBASE)$(LOOP1).$(FILEEXT)"
END_LOOP
```

12.4. JOB Programming Example

A common operation that is ideal for a .JOB file is the collection of many consecutive sample spectra without user intervention. An example of this is the collection of a series of spectra to show the radioactive decay in a particular sample.

This process can be described as follows:

- 1) Set the Detector parameters, such as live time.
- 2) Start the acquisition.
- 3) Wait for the acquisition to stop.
- 4) Integrate the nuclide peak.
- 5) Record the peak area.
- 6) Repeat this for the required number of samples.

By looking at the list of steps above and the explanations below, the necessary commands can be determined and written down.

The first step in the process is to initialize the Detector to the condition needed of 1000 seconds live time. These are:

```
SET_DETECTOR 1
SET_PRESET_CLEAR
SET_PRESET_LIVE 1000
CLEAR
```

Note that all the presets were cleared before setting the live-time preset. This is to ensure that no previous presets (left over from other users) will interfere with this analysis.

Now start the acquisition and wait for completion of the live time.

```
START
WAIT
```

During this time the display manipulation keys are active so that the spectrum can be studied while collection is taking place.

Now move the spectrum from the Detector to the buffer. Select the buffer for the computational step.

```
FILL_BUFFER
SET_DETECTOR 0
```

In this step, the nuclide peak of interest is being marked by reading in an .ROI file. This .ROI file has been previously defined by looking at the spectrum and marking the peak (or the region around the peak). This ROI data is saved on the disk under the name DECAYPK.ROI. This .JOB file will work on different peaks or nuclides just by changing the .ROI file.

```
RECALL_ROI "DECAYPK.ROI"
```

The peak areas of the marked peak or peaks is printed on the printer by this command.

```
REPORT "PRN"
```

This gives a list of the peak areas and count rates for the marked peak. If the library (LIB.MCB) has a peak near this energy then the peak identity will also be printed.

The set of instructions, as written so far, will only collect and report once. There are two ways to make the process repeat itself for a series of samples. The first and hardest is to write one set of the above instructions for every sample in the series. A much more efficient way is to use the

LOOP command. To use this, put LOOP before CLEAR and END_LOOP after REPORT. The whole .JOB file now looks like this:

```
SET_DETECTOR 1
SET_PRESET_CLEAR
SET_PRESET_LIVE 1000
LOOP 10
CLEAR
START
WAIT
FILL_BUFFER
SET_DETECTOR 0
RECALL_ROI "DECAYPK.ROI"
REPORT "PRN"
SET_DETECTOR 1
END_LOOP
```

Note that an additional SET_DETECTOR 1 has been inserted after REPORT, so the loop will operate on the desired Detector.

Now select **Services/Job Control**. Click once on an existing .JOB filename then click the **Edit File** button. This will display the contents of that file in Windows Notepad. Now overwrite the existing instructions with the above set of commands. However, save the new instructions to a

new file named **SAMPDATA.JOB** using the **File/Save As** function (do not use **Save** or the original file will be lost).

This new **.JOB** file can then be executed in Renaissance from the **Services** menu by selecting **Job Control...** to display the **Run JOB File** dialog. Select **SAMPDATA.JOB** from the list of files and click on **Open**.

12.4.1. Improving the JOB

This **.JOB** file can be improved by adding a save step for each spectrum collected. This is done by inserting the **SAVE** command in the **.JOB** file. The spectrum sample description is also entered here. This sample description is saved with the spectrum and is printed by the **REPORT** command. Note that the loop counter (the **???** in the **.JOB** file text) is used in the **SAVE** and **DESCRIBE_SAMPLE** commands.

The new **.JOB** file is:

```
SET_DETECTOR 1
SET_PRESET_CLEAR
SET_PRESET_LIVE 1000
LOOP 10
CLEAR
START
WAIT
FILL_BUFFER
SET_DETECTOR 0
DESCRIBE_SAMPLE "This is sample ???."
SAVE "DECAY???.CHN"
RECALL_ROI "DECAYPK.ROI"
REPORT "PRN"
SET_DETECTOR 1
END_LOOP
```

Spooling the report might take some time. To overlap the data collection with the analysis, the logic of the **.JOB** file needs to be modified to restart the acquisition after the data have been moved to the buffer. All of the analysis is performed on the buffer spectrum so the Detector spectrum can be erased and the next one started.

Insert **CLEAR** and **START** after **FILL_BUFFER**, as shown here:

```
SET_DETECTOR 1
SET_PRESET_CLEAR
SET_PRESET_LIVE 1000
CLEAR
START
```



```
LOOP 10
WAIT
FILL_BUFFER
CLEAR
START
SET_DETECTOR 0
DESCRIBE_SAMPLE "This is sample ????"
SAVE "DECAY???.CHN"
RECALL_ROI "DECAYPK.ROI"
REPORT "PRN"
SET_DETECTOR 1
END_LOOP
```

These few examples have shown some of the possibilities of the JOB language in Renaissance.

12.5. JOB Command Details

ANALYZE ["spectrum file"]

This analyzes the spectrum in the same manner as the menu commands. With no argument, the spectrum in the display (either the MCB or the buffer) is analyzed according to the settings in the **Analyze/Settings/Sample Type...** dialog. With a spectrum filename as argument, the spectrum on disk is analyzed according to the settings in the spectrum file. The filename can include any of the variables shown in Section 12.3.

To change the settings used in an analysis, load the spectrum into the buffer using the **RECALL** command, recall the new settings using the **RECALL_SETTINGS** command, then **ANALYZE** the spectrum in memory (no filename).

The complete entry is passed to **WAN32** as the command line, so any of the command line options of **WAN32** can be used.

The **.JOB** file does not wait until the analysis is complete before proceeding to the next command, however the results will be automatically output according to the settings (printed, file or program) when the analysis is complete. To force the **JOB** to wait until the analysis is complete, put a **WAIT "WAN32.EXE"** command after the **ANALYZE** command.

The **JOB** command might exit after the **ANALYZE** command, but the **QUIT** command should not be used, as the results will not be printed if Renaissance is not running.

ASK_CALIBRATION

This asks for the name of a file containing the calibration to be used as the internal calibration. After entering the filename, the file is read and the calibration is loaded.

ASK_COLLECTION

This asks for the date and time for the decay correction. If any **Ask on Start Options** are marked, the START command in the .JOB file will also open this dialog. Note that if you select **Cancel** in response to an ask-on-start question, the JOB will terminate.

ASK_CONFIRM <“text”>

This opens a dialog showing the text, and waits until you click on **OK**.

ASK_DESCRIPTION

This asks for the sample description to be put in the spectrum file and on the report. It is the same as the sample description entry in the **Acquire/Acquisition Settings...** dialog and the sample description entry in the **File/Settings...** menu. If the **Ask on Start** option is marked, the START command in the .JOB file will also open this dialog. If the **Ask on Save** option is marked, the SAVE command in the .JOB file will also open this dialog. Note that if you select **Cancel** in response to an ask-on-start or ask-on-save question, the JOB will terminate.

ASK_LIBRARY

This asks for the name of the library to be used as the internal library. After you enter the filename, the library file is loaded.

ASK_OPERATOR

This asks for the operator name to be included in the spectrum file and on the report. It is also stored in the Registry.

ASK_OPTIONS

This asks for the name of the .SDF or .SVD (analysis options) file, which is created in the **Analyze/Settings/Sample Type...** dialog. It is the same as the sample type entry in the **Acquire/Acquisition Settings...** dialog. If **Ask on Start** is marked, the START command in the .JOB file will also open this dialog. Note that if you select **Cancel** in response to an ask-on-start question, the JOB will terminate.

ASK_PASSWORD

This is used to define the password to be used in the .JOB file. This command can be to lock an unlocked detector, unlock and use one that is locked, or lock one for the duration of the job and then unlock it. The actual lock/unlock is done with LOCK and UNLOCK, respectively.

This command is to set the internal password variable, \$(PASSWORD), to the user input so the password will be available for use in the JOB. The \$(OWNER) variable is only used when locking detectors. Following is an example:

ASK_PASSWORD
 LOCK "Pwd", "Name"

ASK_PBC

This asks for the name of the peak background correction to be used. After entering the filename, the Peak Background Correction file is loaded.

ASK_PRESET

This asks for the presets to be set in the Detector. It is the same as the preset entry in the **Acquire/Acquisition Settings...** dialog. If **Ask on Start** is marked, the START command in the .JOB file will also open this dialog. Note that if you select **Cancel** in response to an ask-on-start question, the JOB will terminate.

ASK_SPECTRUM

This asks for the spectrum filename to be used in the next and subsequent **SAVE** commands. See **SAVE** command below. This is stored in the variables \$(FullPath), \$(FullBase), \$(FileExt), and \$(FileDir).

ASK_WEIGHT

This asks for the sample size and units to be stored in the spectrum file and used in the analysis. It is the same as the sample size entry in the **Acquire/Acquisition Settings...** dialog and the sample size entry in the **File/Settings...** menu. If **Ask on Start** is marked, the START command in the .JOB file will also open this dialog. Similarly, if **Ask on Save** is marked, the SAVE command in the .JOB file will open this dialog. Note that if you select **Cancel** in response to an ask-on-start or ask-on-save question, the JOB will terminate.

BEEP <freq>,<duration>

Functions on computers without a sound card. This produces an audible tone at a pitch of <freq> Hertz, lasting for <duration> milliseconds. For example, BEEP 1000,1000 is a nicely annoying alarm, while BEEP 50,50 is a short "burp."

BEEP ID

Functions on computers without a sound card. A numerical ID is given based on a desired system event. For example, **BEEP 7** will exit Windows.

<u>ID</u>	<u>Event</u>
0	Beep Speaker
1	Default Beep
2	Start Windows
3	Asterisk
4	Exclamation

- 5 Critical Stop
- 6 Question
- 7 Exit Windows

BEEP “String”

String can be a .WAV file or any event defined in the Registry.

CALIBRATE_AUTO

This executes the automatic energy calibration on the active spectrum with the working library.

CALIBRATE_EFFICIENCY “file.eft”

Performs an efficiency calibration using the active spectrum and the data in file.eft. The filename can include any of the variables defined in Section 12.3.

CALIBRATE_ENERGY “file.ent”

Performs an energy calibration using the active spectrum and the data in file.ent. The filename can include any of the variables defined in Section 12.3.

CALL “file.job”

Executes another .JOB file as a subroutine. The filename can include any of the variables defined in Section 12.3.

CHANGE_SAMPLE

This is used to control the CHANGE SAMPLE output and SAMPLE READY input BNC signals on the rear panel of most MCBs, and is intended to initiate a hardware handshake sequence for advancing a sample changer. The SET_OUTPUT_HIGH command is sent to the currently selected Detector, then the sample-ready status is monitored (for at least 120 seconds) until the input is low, then finally the SET_OUTPUT_LOW command is sent and input is monitored until it returns to the high level again before proceeding.

Note that if the sample changer controls are not able to make the SAMPLE READY input go high very soon after the CHANGE SAMPLE signal is set (i.e., the normal state of the SAMPLE READY is low; it is expected to go high immediately after the CHANGE SAMPLE condition is set and remain high while the sample changer is moving, and returns to low when the sample changer is at its new position), then it might be necessary to use the SEND_MESSAGE command to send a SET_OUTPUT_HIGH command, then pause (with WAIT or some other time-consuming command), and then send the CHANGE_SAMPLE command. The following example demonstrates this:

```
SET_DETECTOR 1  
LOOP 5
```

```
CLEAR  
START  
WAIT  
FILL_BUFFER  
SEND_MESSAGE "SET_OUTPUT_HIGH"  
SET_DETECTOR 0  
SAVE "MONTE???.CHN"  
SET_DETECTOR 1  
CHANGE_SAMPLE  
END_LOOP
```

CLEAR

This clears (erases) the data, the real time and the live time for the selected Detector. The presets are not changed. This command has the same function as the CLEAR function under the ACQUIRE menu. The command would logically be preceded by the SET_DETECTOR commands as follows:

```
SET_DETECTOR 1  
CLEAR
```

DESCRIBE_SAMPLE “description”

This accepts a 63-character description of the sample being analyzed. This description is saved with the spectrum using the SAVE command function, and is included in the REPORT printout. This performs the same function as **Services/Sample Description**.

The loop count value can be included in any text by typing three question marks in the text where the loop count is to be inserted. The loop count replaces “???” with three characters wherever it appears.

END_LOOP — see LOOP

EXPORT “file”

This executes the Export function with the filename specified. The remainder of the options are defined on the Export tab under **File/Settings...**. The filename can include any of the variables defined in Section 12.3.

FILL_BUFFER

This transfers the active Detector data to the buffer. This command has the same function as **Copy to Buffer** under **Acquire**.

IMPORT “file”

This executes the Import function with the filename specified. The remainder of the options are defined on the Import tab under **File/Settings**. The filename can include any of the variables defined in Section 12.3.

LOAD_LIBRARY “file”

This loads the .LIB- or .MDB-format nuclide library specified, and duplicates the function of **Select File...** under the **Library** menu. The filename can include any of the variables defined in Section 12.3.

LOAD_PBC “name.pbc”

This loads the Peak Background Correction specified, and duplicates the function of **Analyze/Settings/Peak Background Correction/Select PBC...** The filename can include any of the variables defined in Section 12.3.

LOCK “Pwd” [,”Name”]

This locks the current Detector using “Pwd” as the password. If the optional “Name” parameter is missing, the Locked name defaults to “Job”.

This password is retained in the .JOB file and used with any .JOB commands so that the user does not need to re-enter the password.

LOOP <repetitions> ... **END_LOOP**

This pair executes multiple times all the commands between LOOP and END_LOOP. The number of execution times is specified by <repetitions>. Each command must be given on a separate line. A value of 0 executes once. A LOOP with no END_LOOP statement executes once.

The loop count value can be included in any text by typing three question marks in the text where the loop count is to be inserted. The loop count replaces “???” with three characters using leading zeros if necessary.

The loop variables, \$(Loop) and \$(LOOP1), can be included in any text. The loop count will be inserted with leading zeros suppressed.

The following is an example:

```
SET_DETECTOR 1
SET_PRESET_LIVE 20
LOOP 3
SET_DETECTOR 1
CLEAR
```

```
START
WAIT
FILL_BUFFER
SET_DETECTOR 0
SAVE "TEST???.CHN"
END_LOOP
```

The above commands run three 20-second acquisitions and store the data on a disk in TEST001.CHN, TEST002.CHN and TEST003.CHN.

If the SAVE command is replaced with SAVE "TEST\$(Loop).CHN," then the following files will be saved: TEST0.CHN, TEST1.CHN, and TEST2.CHN.

LOOP SPECTRA...END_LOOP

This executes the commands within the loop once for each spectrum stored in the Detector hardware. This command only works for hardware that supports Field Mode.

MARK_PEAKS

This performs a Mariscotti-type peak search (see Section ?) on the spectrum in the selected data memory. The peak search sensitivity is chosen on the System tab under **Analyze/Settings/Sample Type...** Each peak found is marked with an ROI. If the selected data memory is calibrated, the width of the ROI is three times the calculated FWHM of the peak. If the selected data memory is not calibrated, the width of the ROI equals the width of the peak as determined by the peak search function. Overlapping or close peaks might have contiguous ROIs. Existing ROIs are not cleared, therefore, you might wish to clear them before issuing this command.

The following is an example of the MARK_PEAKS command used with REPORT. It performs a peak-search-directed report of nuclides found.

```
MARK_PEAKS
REPORT "TESTDAT.RPT"
```

QABACKGROUND

This executes the background QA test without displaying prompts or violations.

QASAMPLE

This executes the sample QA test without displaying prompts or violations.

QUIT

This unconditionally terminates the Renaissance program and returns control to Windows.

RECALL “file”

This reads a disk filename to the buffer. The disk file must be in the format created by SAVE. Any DOS filename, including the drive and subdirectory, can be used. The resultant horizontal size of the buffer is the same as the file. If the spectrum file has calibration information, the calibration parameters in the spectrum file are used to set the calibration for the buffer.

This command has the same function as **Recall...** under the **File** menu.

The loop count value can be included in the above filename, as in any text, by typing three question marks in the text where the loop count is to be inserted. The loop count replaces “???” wherever they appear. The filename can include any of the variables defined in Section 12.3.

RECALL_CALIB “file “

This loads both the energy and efficiency calibration data from the specified file to the calibration data for the selected Detector. If the file is a pure calibration file (.CLB), then all the information, including any energy or efficiency tables, are replaced in the selected spectrum data memory. If the file is a spectrum data type file .CHN, only the calibration parameters from the calibration data stored with a spectrum are loaded.

The filename can include any of the variables defined in Section 12.3.

This command can be used in generating reports that include library nuclide identification. The following is an example:

```
RECALL_CALIB "CALIB001.clb"  
MARK_PEAKS  
REPORT "NEWDATA.RPT"
```

The report NEWDATA.RPT includes nuclide identification using the energy calibration contained in CALIB001.clb.

RECALL_EFFICIENCY “file “

This loads the efficiency calibration data from the specified file to the calibration data for the selected Detector. If the file is a pure calibration file (.CLB), then all the information, including any efficiency tables, are replaced in the selected spectrum data memory. The filename can include any of the variables defined in Section 12.3.

RECALL_ENERGY “file “

This loads the energy calibration data from the specified file to the calibration data for the selected Detector. If the file is a pure calibration file (.CLB), then all the information, includ-

ing any energy tables, are replaced in the selected spectrum data memory. If the file is a spectrum data type file `.CHN`, only the calibration parameters from the calibration data stored with a spectrum are loaded. The filename can include any of the variables defined in Section 12.3.

RECALL_OPTIONS “file.sdf”

This loads the acquisition and analysis parameters into the working set for the selected Detector or buffer. This is the same as recalling a `.SDF` or `.SVD` file in the **Analyze/Settings/Sample Type...** type menu. The filename can include any of the variables defined in Section 12.3.

RECALL_ROI “file.roi”

This marks the ROI channels in the selected data memory or Detector to conform to the table in the disk file, which can be an `.ROI`, `.UFO`, `.SPC`, or `.LIB` file. The data contents of the Detector or buffer are not altered by this operation. The previous ROIs are cleared. The filename can include any of the variables defined in Section 12.3.

This command has the same function as **Recall File...** under **ROI**.

This command can be used in generating reports that look for specific nuclides (library-directed as opposed to peak-search-directed). For example, a calibration spectrum is run containing ^{57}Co and ^{137}Cs , and ROIs marked on the 122-keV and 662-keV peaks.

The calibration is saved as spectrum file `COBCS.SPC` and as `.ROI` file `COBCS.ROI`. The command sequence is:

```
RECALL_CALIB "COBCS.SPC"
RECALL_ROI "COBCS.ROI"
REPORT "COBCS.RPT"
```

These commands report the values only for the 122-keV and 662-keV peaks. Compare with the example for `MARK_PEAKS`.

As usual, the loop count value can be included in any text by typing three question marks in the text where the loop count is to be inserted.

REM [Text]

This line is a comment (remark) and is ignored during command processing. The **REM** command allows entering descriptive comments into script files or disabling commands during testing of scripts.

REPORT “file”

This command generates a report containing the list of areas, activities, and peak shapes for all the ROIs marked in the spectrum. See **File/Print** (Section 5.1.6) for more information on the report format and contents. The ROI data will be presented in either columns or paragraphs, according to the format most recently selected in the ROI Report dialog (therefore, you can choose a format before executing the JOB file). If you do not specify a filename, the report will be sent to the default Windows printer for this PC. If you specify a filename, the report will be sent to an ASCII text file that can be used by other programs or printed later. The loop count value can be included in the filename by typing three question marks in the text where the loop count is to be inserted. The loop count replaces “???” in the filename. The filename can include any of the variables defined in Section 12.3.

RUN “program”

This executes an application named “program.” This is typically an .EXE filename. Note that the program will not run to completion before returning to Renaissance, unless it is run at higher priority or the WAIT command is used. The filename can include any of the variables defined in Section 12.3. Any arguments to the program can be included in the quotation marks.

RUN_MINIMIZED “program”

Same as the RUN command above, except that the application is run initially as an icon (minimized), rather than as a normal window.

SAVE “[d:][\path\]file[.spc]” [n]

This saves the active Detector or the selected data memory in a disk file. It has the same function as **Save As...** under the **File** menu. The file type is determined in the **File/Settings...** dialog. The disk filename (in quotation marks) can be any valid DOS filename; the drive [d:], path [\path\] and extension [.spc] are optional. If an extension is not supplied, the default extension is automatically determined by the file settings selection. Also, the current drive and directory are used by default when the optional path specification is not supplied. The loop count value can be included in the filename by typing three question marks in the text where the loop count is to be inserted. The loop count replaces “???” wherever it appears. The filename can include any of the variables defined in Section 12.3.

The optional argument n specifies the spectrum number to save for a .CHN or .SPE file. For supported digital spectrometers in ZDT mode zero, a value of zero will switch the display to the normal spectrum before the data is saved and a value of 1 will switch the spectrum to the ZDT spectrum before the save. For the instrument in ZDT mode one, a value of 1 will switch the display to the ZDT spectrum before the data is saved and a value of zero will switch the spectrum to the Error spectrum before the save. This parameter is ignored if the MCB is not

in ZDT mode. This parameter is not used when saving data to an **.SPC** file since both spectra are automatically saved.

The **Ask on Save** questions as defined in **File/Settings...** will be asked each time a **SAVE** command is executed. This will stop execution of the **.JOB** file until the question is answered. Note that if you **Cancel** an ask-on-save prompt, the **JOB** will terminate. As is the case for the **Save As** function, the real time, live time, start of acquisition, and, if available, calibration data, detector description, and sample description will be stored with the spectrum.

If the **ASK_SPECTRUM** command has been executed in this **.JOB** file prior to this **SAVE** command, the filename is stored in **\$(FullPath)**.

SAVE_CALIBRATION “[d:][\path\]file[.clb]”

This saves the current working energy and efficiency calibrations to a **.CLB** file. It has the same function as **Save Calibration...** under the **Calibrate** menu. The contents of the spectrum are not altered by this operation. The disk filename (in quotation marks) can be any valid filename, with optional elements as described for the **SAVE** command, above. The default extension is **.CLB**. The loop count value can be included in the filename by typing three question marks in the text where the loop count is to be inserted. The loop count replaces “???” wherever it appears. The filename can include any of the variables defined in Section 12.3.

SAVE_ROI “[d:][\path\]file[.roi]”

This saves a table of channel numbers that have the ROI set for the active Detector or selected data memory in a disk file. It has the same function as **Save File...** under the **ROI** menu. The contents of the spectrum are not altered by this operation. The disk filename (in quotation marks) can be any valid filename, with optional elements as described for the **SAVE** command, above. The default extension is **.ROI**. The loop count value can be included in the filename by typing three question marks in the text where the loop count is to be inserted. The loop count replaces “???” wherever it appears. The filename can include any of the variables defined in Section 12.3.

SEND_MESSAGE “command”

This is used to send NIM-488 commands to the active Detector. This can be used to perform any operations of the Detector that are desired. The text must be in the syntax expected by the Detector. If the response from the Detector does not end with a command-accepted message, then this command will exit with error.

Specific Detector commands and syntax are described in the technical manual associated with each specific Detector.

The following is an example of using this command to set the fine and coarse gain to a total value of 50 (the product of the fine [= 0.5] and coarse [= 100] gains):

```
SET_DETECTOR 1
STOP
CLEAR
SEND_MESSAGE "SET_GAIN_FINE 2048"
SEND_MESSAGE "SET_GAIN_COARSE 100"
```

SET_BUFFER

This selects the buffer. It is the same as SET_DETECTOR 0.

SET_DETECTOR <number>

This selects the active Detector or the buffer. The Detector number can be 1 to 999 according to the Detector configuration, or 0 for the buffer. Also, SET_DETECTOR without an argument is used to switch to the previously selected Detector. If a Detector is selected that does not exist, no change is made. The Detector number is the number shown on the Toolbar and the Detector pick list.

This command (for values 1 to 12) has the same function as <Ctrl+ F1> through <Ctrl+ F12>. For value 0 or no argument at all, it duplicates the **Detector/Buffer** toggle under the **Display** menu, <F4>, and <Alt+ 6>.

SET_NAME_STRIP "file"

This can be used before STRIP to select a disk filename to be used subsequently by the STRIP command. (It is not necessary to use this command, because the filename can be supplied as part of the STRIP command itself; however, the command is included for backward compatibility with MAESTRO II command files.) No other action is taken by this command. The filename can include any of the variables defined in Section 12.3.

SET_PRESET_CLEAR

This clears the presets for the active Detector. The clearing should be done to ensure that unwanted presets are not used by the Detector when the Detector is started.

NOTE For the Models 916/17/18 Detectors, the new presets (including CLEAR) can be loaded at any time, but are not put into effect until the Detector goes from STOP to START. For most other MCBs, the presets can only be changed when the unit is not counting.

The Detector should be selected by the SET_DETECTOR commands before the SET_PRESET_CLEAR command is given, as in the following:

```
SET_DETECTOR 1
STOP
SET_PRESET_CLEAR
START
```

SET_PRESET_COUNT <counts>

This sets the ROI peak count preset for the active Detector. The preset is set to the entered value. With this preset condition, the Detector stops counting when any ROI channel content reaches this value. If no ROIs are marked in the Detector, then that Detector never meets this condition. This command has the same function as the **ROI Peak Count** field on the Presets tab under **Acquire/MCB Properties...** (Section 5.2.9); refer to the discussion describing that dialog for additional information.

The JOB processor expects one or more numerals as the argument to this command, entered with or without quotation marks (e.g., you can enter the numerals 1000 or the string "1000"). The JOB processor will also accept the loop counter as an argument to the function *as long as it is set in quotation marks*. For example, you could use the loop counter to collect a series of spectra with increasing ROI peak counts by appending zeroes to the loop counter to obtain 1000 counts, then 2000, and so on.

SET_PRESET_INTEGRAL <counts>

This sets the ROI Integral Count preset value for the active Detector. The preset is set to the entered value. With this preset condition, the Detector stops counting when the sum of all counts in all channels marked with an ROI reaches this limit. If no ROIs are marked in the Detector, then that Detector never meets this condition. This command has the same function as the **ROI Integral** field on the Presets tab under **Acquire/MCB Properties...** (Section 5.2.9); refer to the discussion describing that dialog for additional information.

The JOB processor expects one or more numerals as the argument to this command, entered with or without quotation marks (e.g., you can enter the numerals 1000 or the string "1000"). The JOB processor will also accept the loop counter as an argument to the function *as long as it is set in quotation marks*. For example, you could use the loop counter to collect a series of spectra with increasing ROI peak counts by appending zeroes to the loop counter to obtain 1000 counts, then 2000, and so on.

SET_PRESET_LIVE <seconds>

This sets the live-time preset for the active Detector. The preset is set to the entered value. With this condition, the Detector stops counting when the live time reaches this limit. The live time is the real time minus the dead time. This command has the same function as the **Live Time** field on the Presets tab under **Acquire/MCB Properties...** (Section 5.2.9); refer to the discussion describing that dialog for additional information.

The JOB processor expects one or more numerals as the argument to this command, entered with or without quotation marks (e.g., you can enter the numerals 1000 or the string "1000"). The JOB processor will also accept the loop counter as an argument to the function *as long as it is set in quotation marks*. For example, you could use the loop counter to collect a series of spectra with increasing ROI peak counts by appending zeroes to the loop counter to obtain 1000 counts, then 2000, and so on.

SET_PRESET_REAL <seconds>

This sets the real-time preset for the active Detector. The preset is set to the entered value. With this preset condition, the Detector stops counting when the real time reaches this limit. This command has the same function as the **Real Time** field on the Presets tab under **Acquire/MCB Properties...** (Section 5.2.9); refer to the discussion describing that dialog for additional information.

The JOB processor expects one or more numerals as the argument to this command, entered with or without quotation marks (e.g., you can enter the numerals 1000 or the string "1000"). The JOB processor will also accept the loop counter as an argument to the function *as long as it is set in quotation marks*. For example, you could use the loop counter to collect a series of spectra with increasing ROI peak counts by appending zeroes to the loop counter to obtain 1000 counts, then 2000, and so on.

SET_PRESET_UNCERTAINTY <limit>,<low chan>,<high chan>

This sets the statistical preset to the uncertainty based on the counts in the region between the low and high channels. This is only available in some MCBs (e.g., DSPEC, 92X-II). See Section 4.2.1.1 for details on the calculation. The low channel must be greater than 1 and the high channel must be greater than the low channel plus 7.

SMOOTH

This smooths the data in the buffer; its function is the same as **Smooth** under the **Calculate** menu. A five-point, area-preserving, binomial smoothing algorithm is used. The original contents of the buffer are lost.

START

This initiates data collection in the selected Detector, and is the same as **Start** under the **Acquire** menu.

The **Ask on Start** questions, as defined in **Acquire/Acquisition Settings...**, will be asked each time a START command is executed. This will stop execution of the .JOB file until the question is answered. Note that if you select **Cancel** in response to an ask-on-start question, the JOB will terminate.

START_OPTIMIZE

This starts the optimize function for the Detector.

START_PZ

This starts the PZ function for the detector. It is automatically included in the optimize function. This command is only available for MCBs with internal amplifiers.

STOP

This stops data collection in the active Detector. If the Detector has already been stopped, no operation occurs. This command has the same function as **Stop** under the **Acquire** menu.

STOP_PZ

This stops the PZ function for the detector. Note that the PZ function is not complete when this is used. The PZ function should be allowed to complete automatically. This command is only available for MCBs with internal amplifiers.

STRIP <factor>,[“file”]

This strips the disk spectrum specified in the SET_NAME_STRIP command or in the command itself (either way is acceptable; the filename is optional in this command) from the spectrum in the buffer and stores the results in the buffer. The disk and selected data memory spectra must be the same size. The disk spectrum can be scaled up or down by <factor> (a constant) or, if <factor> is zero, by the ratio of the live times of the two spectra. The filename can include any of the variables defined in Section 12.3.

UNLOCK “Pwd”

This unlocks the current Detector using “Pwd” as the password.

VIEW “i”

This moves the “i”th stored spectrum to position 0. This command is only valid in MCBs with Field Mode.

WAIT [<seconds>]

This suspends execution of the JOB to wait until either the active Detector stops counting (in the case where the <seconds> argument is not included), or for a fixed number of seconds.

WAIT “program”

This suspends execution of the JOB to wait until the named program stops execution. If the program does not stop, this JOB will not continue. It is good practice to put a WAIT 2 command between the RUN “program” and WAIT “program” commands to give Windows time to start the program before the status is checked. The “program” name must agree with the name used in Windows, and must include the .EXE extension.

WAIT_AUTO

For digital MCBs only; this waits until the optimize function is complete.

WAIT_CHANGER

This waits until the sample ready signal on the rear panel is present. It is used in conjunction with the SEND_COMMAND function for more control over the sample changer than is provided by the CHANGE_SAMPLE command.

WAIT_PZ

This waits until the PZ function is complete.

WAIT_QA

This waits until QA is complete.

WAIT_SERIAL “Command”, timeout[,”Response”]

This is used to send and receive commands on the serial port of MCBs. It is designed to be used to control sample changers with RS-232 controls. “Command” are the characters sent to the changer to make it operate. Timeout is the maximum time to wait for a response before error. “Response” is the reply from the changer when it has finished the “Command.”

The first operation is to send “Command” out the serial port for the selected Detector. It then waits for a response or timeout according to these entries:

1. If a response string is provided, the length of the response string determines the exact number of characters to wait for.
2. If a response string is not provided, any character input will generate a success.
3. If a response string is provided, and the characters do not match, an Invalid Response message is generated and the JOB terminates.
4. If a timeout occurs, a Timeout Message is generated and the JOB terminates.

Example:

```
SET_DETECTOR 1
LOOP 3
    WAIT_SERIAL "$(Loop1)L$(CR)", 300, "$(BEL)"
    BEEP 5
END_LOOP
```

This code does the following:

1. Sends **1L**↵ and waits 5 minutes for an ASCII Bell Character. Beeps 5 after ASCII bell is received.
2. Sends **2L**↵ and waits 5 minutes for an ASCII Bell Character. Beeps 5 on success.
3. Sends **3L**↵ and waits 5 minutes for an ASCII Bell Character. Beeps 5 on success.

The ← is the \$(CR) (carriage return) character.

ZOOM <i>

Changes the size of the Renaissance window. Selects one of icon, normal, or maximum according to the argument. The arguments are:

- 1 = minimize (icon on Taskbar)
- 0 = normal (size determined by last use)
- +1 = maximize (full screen)

ZOOM: <x,y,w,h>

Changes the position and size of the Renaissance window. The arguments are:

- x = x position of upper-left corner of window (0 is left)
- y = y position of upper-left corner of window (0 is top)
- w = width of window in pixels, starting at x and going right
- h = height in pixels, starting at y and going down

Since these arguments are in pixels, experimentation is the best way to determine the desired size.

[Intentionally blank]

13. UTILITIES

13.1. WinPlots

This program prints any type of ORTEC spectrum file in a fixed format with many user-set optional variations (such as grid lines) available. In the interactive mode, a preview of the spectrum plot is automatically displayed on the screen and updated as changes are made to the display parameters. The formatting and contents of the plot can be specified, such as: start and stop channels or energy range for the plot, the printer to be used, whether the plot will be in logarithm mode or linear mode, and whether to specify the scale maximum in linear mode or use automatic scaling. If a color printer is selected, the colors of the different parts of the plot can be selected.

The sample, detector, and acquisition descriptions in the file can be plotted or suppressed. ROIs can be plotted when stored in the spectrum (.SPC) file or in a separate .ROI file.

To start WinPlots, enter `winp` in the “*Search programs and files*” box on the Windows start menu, then click the **WinPlots** search result; or open the Windows Start menu and click **Renaissance** then **WinPlots**. You can also run WinPlots in command line mode for use in .JOB files, or directly from other Windows programs (see Section 13.1.3). In this mode, you can either specify the settings or use the defaults.

The spectrum files are associated with WinPlots by the installation program, so double-clicking on a spectrum file-name within Windows Explorer will start WinPlots and display that spectrum.

The main WinPlots display is shown in Fig. 265.

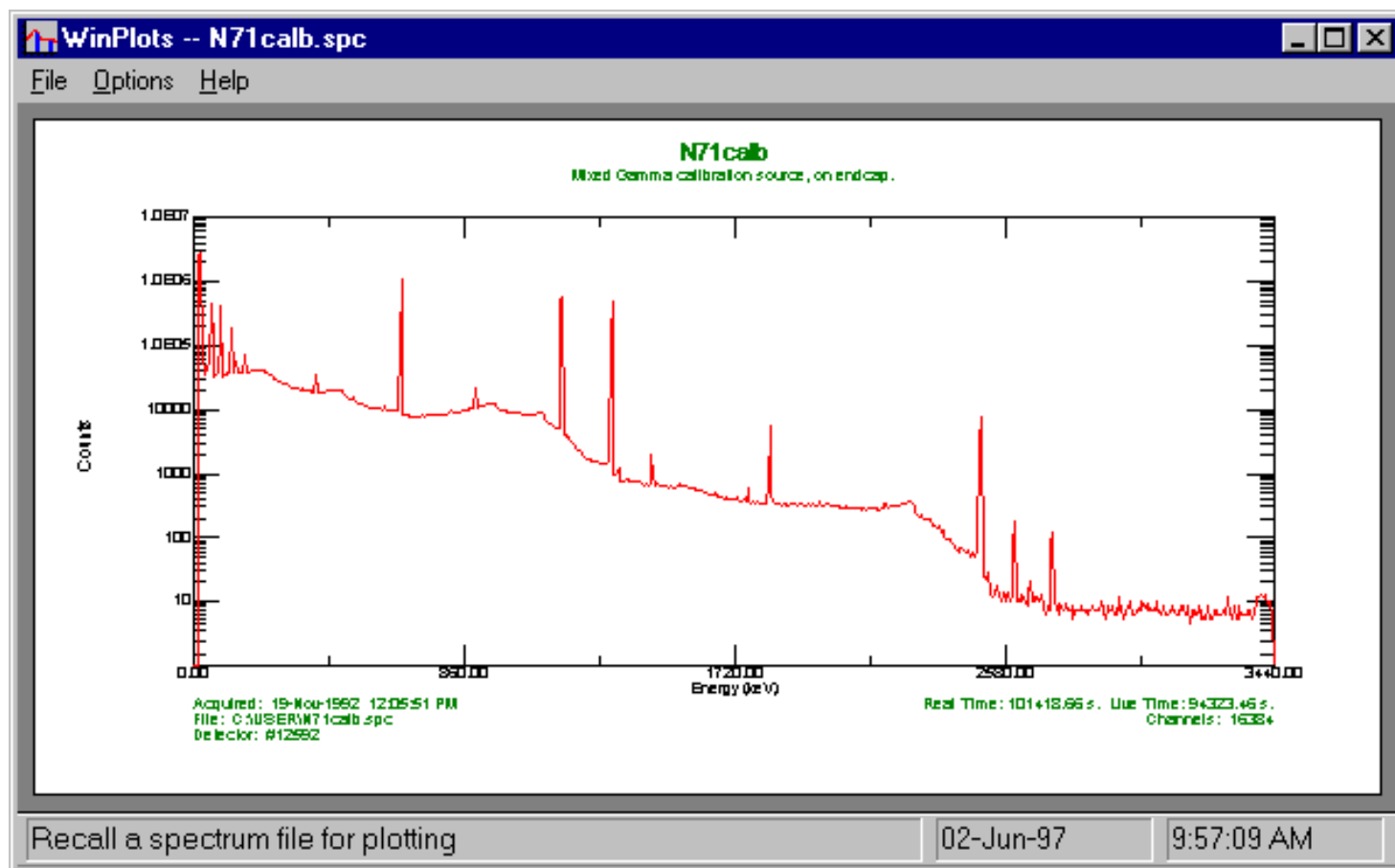


Figure 265. The Main WinPlots Display.

13.1.1. File

Figure 266 shows the **File** menu. These menu items select the spectrum and ROI to be displayed, read and write the settings file, and actually make the plot.

Once a file has been selected using the **Recall Spectrum...** function (see the file recall dialog shown in Fig. 267), it is automatically previewed using the current settings. This is the exact plot that will be printed. There are minor differences between display and printer fonts and colors.

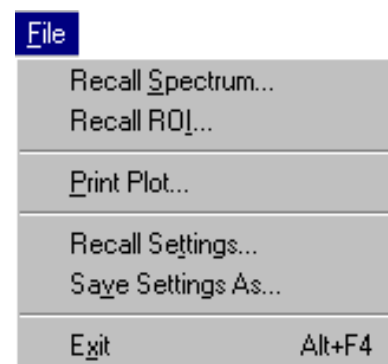


Figure 266. The File Menu.

The sample description, format, and number of channels are shown at the bottom of the dialog to aid in selecting the correct file.

Figure 267 shows the **Recall a settings file** dialog. All of the settings specified on the **Options/**

Plot... dialog can be saved in the settings file. The file is saved in the **Save Settings** menu item. Various groups of settings can be saved and recalled here to make the desired plots or to be used in the command line mode.

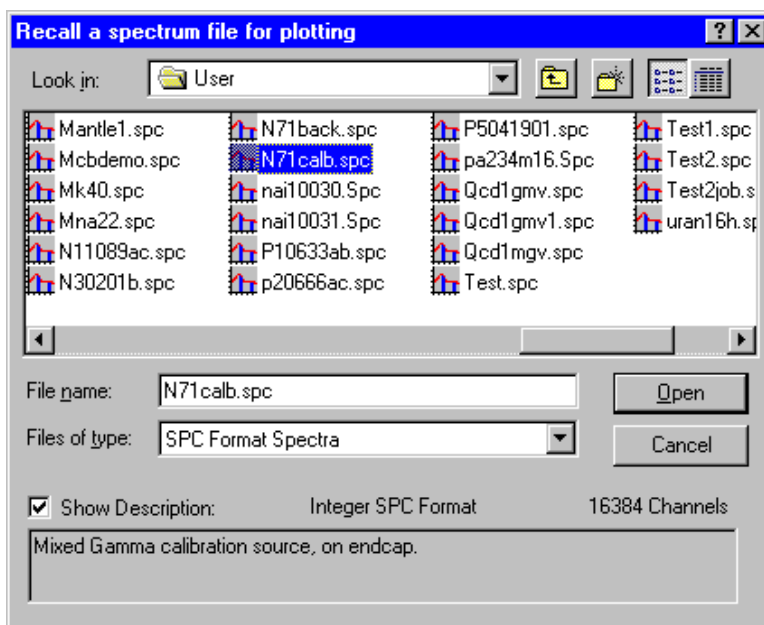


Figure 267. The Recall Spectrum File for Plotting Dialog.

The **Print Plot...** dialog (Fig.268) is used to select a printer and specify the **Number of copies** to be printed (this number is reset to 1 after every print session). Click **Properties** to change the print options.

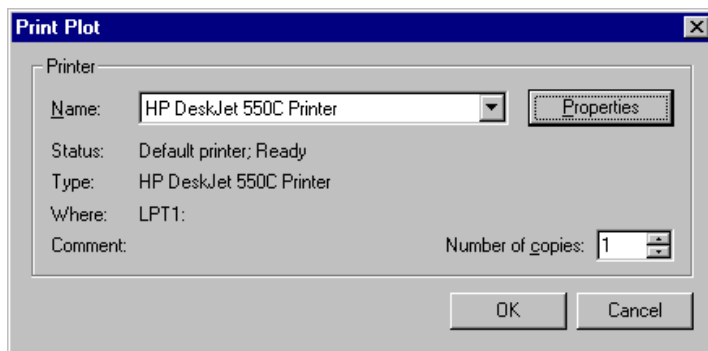


Figure 268. The Print Plot Dialog.

13.1.2. Options

The **Options** menu is shown in Fig. 269. These menu items control the plot settings and WinPlots operation.

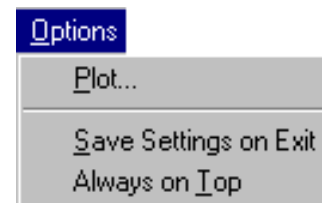


Figure 269. The Options Menu.

13.1.2.1. Plot...

The **Plot Options** dialog is shown in Fig. 270. These settings are all stored in the default settings file and reloaded when WinPlots is next started. The **Title** is printed at the top of every plot (just above the sample description). If no title is specified, a default title composed of the spectrum and .ROI file names is generated. The **Printer** is selected from the list of available printers in Windows.

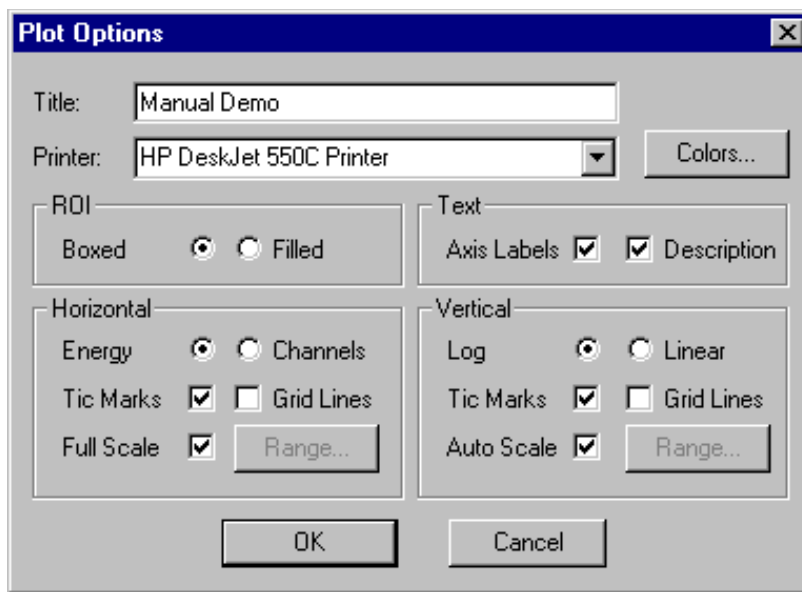


Figure 270. The Plot Options Dialog.

If the printer supports color printing, the **Colors...** button will be enabled. Clicking on it will display Fig. 271. If monochrome prints are desired from a color printer, check the **Monochrome** box. The five different plot areas can have different colors. Select the desired color from the drop down list for each area. These are the Windows colors defined for the selected printer and might not duplicate the actual colors printed.

ROI

The ROIs can be **Boxed**, that is, represented as “boxes” drawn from the start to the stop channel (or energy) and from the baseline to above the spectrum. The **Filled** selection will “fill” the region under the spectrum data with a cross hatch. It is not completely filled in and does not extend above the data.

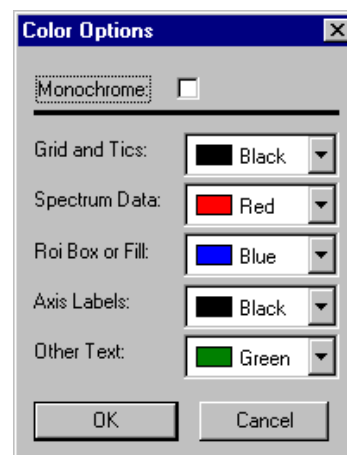


Figure 271. The Color Options Dialog.

Text

The **Axis Labels** and the text **Description** from the file can be printed. The description includes the sample, detector, and acquisition description.

Horizontal

If the spectrum to be plotted is calibrated, the plot can be either in **Energy** or **Channel** numbers. If the spectrum is not calibrated, this value is set to channel and cannot be altered.

Tic Marks (small lines indicating the scale on the axes) can be included. Including them makes the plot more readable. **Grid Lines** can also be included. The grid lines are lines across the complete width of the plot at the major tic marks.

The plot can either be the complete spectrum or any part of the spectrum. Unmarking **Full Scale** will enable the **Range** button. Selecting **Range** will open the dialog shown in Fig. 272 where the limits for the plot are set. The range of the plot can be either in **Channels** or **Energy** (independent of the plot labeling). In order to easily compare spectra, the energy can be set to values below the first channel in the spectrum. In this case the data below channel 0 are plotted as 0.

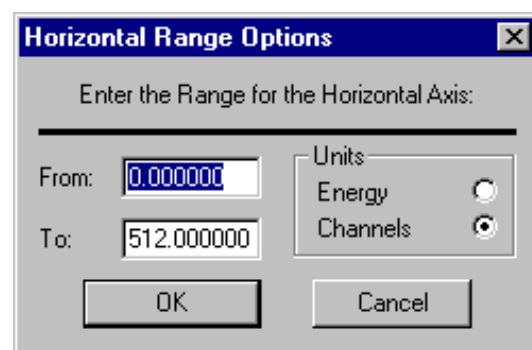


Figure 272. Horizontal Range Options Dialog.

Vertical

One of the two choices, **Log** and **Linear**, can be selected by clicking on the appropriate radio button. The linear scale is set by clicking on **Range...**

Tic Marks (small lines indicating the scale on the axes) can be included. Including them makes the plot more readable. **Grid Lines** can also be included. The grid lines are lines across the complete height of the plot at the major tic marks.

When **Auto Scale** is selected, the plot vertical axis is adjusted so that the largest count in the spectrum is near the top of the plot region.

When **Auto Scale** is clicked off, the **Range** button is enabled. Clicking on **Range** will display the dialog shown in Fig. 273. The value entered will be the value for the top of the plotted region. Any counts above this value will be plotted at this value.

13.1.3. Command Line Interface

The WinPlots command line interface will support options available in the interactive mode as shown below:

```
WINPLT32<spectrum> -R <roi_file> -S <set_file> -P
```

where:

- <spectrum>** Specifies the spectral data file (.SPC, .An1, or .CHN). The extension must be included.
- R <roi_file>** Specifies the .ROI file. The extension must be included.
- S <set_file>** Specifies the settings file. The extension must be included.
- P** Causes the program to print the plot and exit automatically. Used mainly in .JOB files or the Export function.

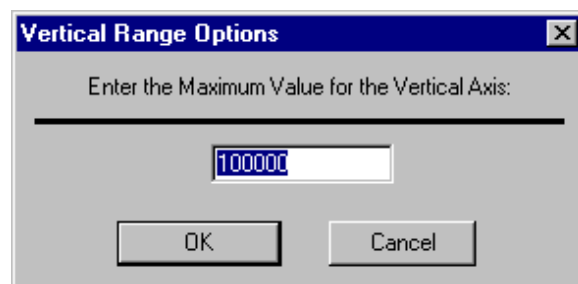


Figure 273. Vertical Range Options Dialog.

APPENDIX A. STARTUP AND CONFIGURATION

To start Renaissance Supervisor, enter `supe` in the “Search programs and files” box (Fig. 274) then click the **Renaissance Supervisor** search result; or open the Windows Start menu and click **Renaissance**, and **Renaissance Supervisor**. You can also start Supervisor by entering `run` in the search box and choosing the **Run** search result; or (in XP) by selecting **Run...** from the Start menu. The Run option allows you to start up from the command line, with or without arguments, as described below.

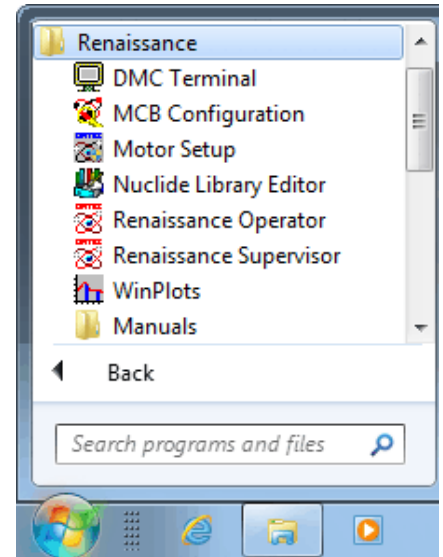


Figure 274. Renaissance Menu.

A.1. Command Line Options

Renaissance is run with the following command line properties:

```
RENSUPR [-d[n]] [-L file.lib] [-p pick] [-t] [-1] [-B] [-z] [file.job]
```

All of the arguments are optional; one or more can be omitted. Thus, at a minimum, Renaissance can be executed without any arguments at all, in which case certain defaults apply for the Detector list and nuclide library, as described below. All of the switches (e.g., `-d`, `-z`) can be upper- or lowercase (e.g., `-d` or `-D`, `-z` or `-Z`).

- [n]** An optional parameter for the `-d` switch to enable debugging output mode at a specified level (values are 1 or 2; no argument is equivalent to 1). Default is no debugging. Debug mode is not recommended for general use.
- file.lib** An optional nuclide library (`-L` option) to be loaded at startup. The default is the library loaded when Renaissance exited.
- pick** An optional Detector pick list name (use with `-p` option). The pick list name must be 5 characters or less. If a pick list is not specified, `M32REN.CFG` is used by default. The list created with the **Edit Ge List** command is named `M32RGE.CFG`, and that created with **Edit NaI List** is `M32RNAI.CFG`. The current pick list name is

displayed above the Pick List column in the Detector List Editor dialog (**Services/ Edit Detector List...**). If the pick list name specified by `pick` does not exist then one is created. This new list will contain all available detectors included in the Master Detector List. If the pick list already exists, only the detectors defined in that list are displayed in the Detector droplist on the Toolbar. Changes made to the pick list with the **Edit Detector List...** command are stored with the active pick list filename. Therefore, to create multiple pick lists, use the `-p` option with the pick list name and then edit the list to contain only the desired Detectors.

- t Forces Renaissance to be “Always on Top.” The default is the normal Windows display.
- 1 Allows one and only one instance to run. This is the numeral one.
- B Startup in the buffer. This should be used if the PC is on a network and no MCBs are connected anywhere in the system.
- z The “zoom” switch with several variations:
 - z or -z: With no arguments, causes the previously stored “ZOOM:” parameters (see page 373) to be used to position and size the Renaissance window.
 - z:x,y,w,h Changes the position and size of the Renaissance window. The arguments (which are the same as for the ZOOM: profile variables, page 373) are:
 - x = x position of upper-left corner of window (0 is left)
 - y = y position of upper-left corner of window (0 is top)
 - w = width of window in pixels, starting at x and going right
 - h = height in pixels, starting at y and going down
 - z0 Forces position and size to be determined by Windows tiling algorithm.
 - z+1 Forces Renaissance to be maximized.
 - z-1 Forces Renaissance to be minimized.
- file.job An optional .JOB file to be executed at start-up.

Certain defaults apply if any one or more of these arguments is omitted. The initial Detector list is named `M32REN.CFG`. The nuclide library is the last library used. And no JOB is automatically executed unless the `file.job` argument is included.

A.2. Analysis Setup

All of the analysis engines have several options that can be specified in a disk file (`b30winds.ini` for Ge and `g30windw.ini` for NaI) and the report output text can be specified in a disk file (`b30win.txt` for Ge and `g30win.txt` for NaI). These files are loaded during installation, but if they are not found or cannot be read, the internal defaults are used. As supplied, the files are the same as the internal defaults.

These files should only be changed after careful consideration of the impact of the changes.

A.2.1. RENWAN, RENGAM, RENNPP, and RENENV (Ge Analysis)

The RENWAN, RENGAM, RENNPP, and RENENV analysis engines perform the analysis of a complete Ge spectrum. These programs are run by Renaissance and can also be run by other programs. These programs read the command line to control the analysis. The command line (shown here for RENWAN only) is:

`RENWAN file.SPC [DEBUG] [file.INI]`

- | | |
|-----------------------|---|
| <code>file.SPC</code> | This is the spectrum filename and it must be the first argument. For a complete analysis it must contain all the analysis parameters and calibrations. The output files are the input file name with the extension of <code>.UFO</code> for the binary output and the extension of <code>.RPT</code> for the text output. |
| <code>DEBUG</code> | This optional parameter controls the output of debugging information on the RENWAN Window. Renaissance sets this parameter when Renaissance is run in debug mode. This produces considerable output and significantly slows the execution. It must be the second or third argument. |
| <code>file.INI</code> | This optional file is the <code>.INI</code> file (such as <code>b30winds.ini</code>) for controlling the analysis. It overrides the normal default file. If the file cannot be found or read, the default file name is used. If the default file cannot be found or read, the internal options are used. By selecting different <code>.INI</code> files for different spectra, different analyses can be produced. |

A.2.2. B30winds.ini (Ge Analysis)

The `b30winds.ini` file (Fig. 275) contains initial or default values for the analysis engine. It is read by the engine before the spectrum file is read. The contents are shown below. The filename can be specified on the command line. If the specified file cannot be found in the default directory (as defined by Windows) the `\MESSAGE` directory on the default drive is searched. If it is not found there or cannot be read, then the internal values are used. Some of these values can only be set in this file.

NOTE The parameters in `b30winds.ini` are read sequentially from the file and none can be omitted even if they will not be used. Doing so would offset the parameters as they are read in, and all subsequent settings would be incorrectly interpreted.

```

B30WIN.TXT      Message file name
YES NO         spellings
JANFEBMARAPR...MAYJUNJULY...AUGSEPOCTNOVDEC  spellings of months, no longer used as of GV 6.08
D              Deconvol. character
S              Shape character
M              Multiplet character
-              Unknown suspect
C:\User\EBAR.TBL  EBAR table filename
C:\User\IEQT.TBL IEQ table filename
F              EBAR on/off
F              IEQ on/off
T              Unidentified Peak Summary and Library Peak Usage Format flag (T=print eff cor peakarea)
1000          Minimum Good Peaks Above Dividing Energy for Energy Recalibration (5 Minimum)
1000          Minimum Good Peaks Below Dividing Energy for Energy Recalibration (5 Minimum)
0.0           Energy Recalibration Dividing Energy
1.0           Activity scaling Factor
2.0           Unidentified Peak Match width Factor
60            Page length
T             save ufo File Flag (F=Erase UFO file)
T             MDA type, T=Allow change
F             PBC F=off and filename
F             MPC F=off and filename
F             Directed Fit Flag (T=enable directed fit)
F             NO LONGER USED
T             Accept Small Peaks Flag (T=Accept low peaks)
A            Derived Peak Area character
T            Print discarded peak table
T            Maximum Half-lives Cutoff
12           Peak Activity range factor
2            Activity Range Test Flag (T=Perform activity range test)
T            Zero Area Identified Peak Flag (T=Print 0 area peaks)
F            Zero Activity Isotope flag (T=Print 0 activity isotopes)
F            Minimum Step Background Energy
0.0         Fraction Limit Test Flag (T=Do frac. test on all peaks)
T            Use Narrow Peaks for Nuclide Activity Flag (T=Use all narrow peaks in act.)
T            Zero Area Library Peak Flag (T=Print 0 act. pks. in nuc. tab.)
T            Use Peak Cutoff Flag (T=Use peak cutoff)
T            second MDA type, T=calculate
F            Sort Nuclide Peaks by Energy Flag (T=sort by energy)
2.0         Multiplet channel shift limit
0.0         Background width/FWHM for MDAs
T            Print MDA in Nuclide Summary Flag (T=Print MDA)
F            Maximum Half-life to unknowns Flag (T=Peaks for Nuclides > max halfives are unidentified)
MDA         Nuclide summary MDA Header
0.0         ENV factor
0.05        ISO NORM Probability alpha
0.05        ISO NORM Probability beta
0.05        ISO NORM Probability gamma
T            ISO NORM Print MDA Flag (T=Print MDA in ISO NORM table if Activity < Critical Level)
3.0         Maximum ISO NORM MDA Ratio factor
3.50        Peak overlap range in units of peak FWHM (Peaks within this range are deconvoluted)
1000        Directed Fit Minimum Background Counts for Quadratic Peak Fit
0.80        Directed Fit Peak Region Width Factor
25.0        Dominant Background Peak Cutoff and Override Flag (T=Override using analysis_settings peak_cutoff value)
1.20        Dominant Background Peak Width Factor and Flag (Units of FWHM, Flags: T=use factor, F=use gv peak range)
4.50        Non-dominant Background Peak width Factor and Flag (Units of FWHM, Flags: T=use factor, F=use gv peak range)
F            TCC Internal Library Flag (T=use internal TCC Library Peaks, F=use only analysis library peaks)
T            Regional Decimal Settings (T=use decimal symbol in Regional Settings, F=use only English/American format(periods))
  
```

Figure 275. The `b30winds.ini` File in Notepad.

A.2.2.1. Contents

Except where indicated, all discussion of analysis settings refers to the current (working) settings on the **Analyze/Settings/Sample Type...** tabs or in the selected `.SDF` file.

Message file name

B30WIN.TXT

The name of the file that defines the standard analysis report format.

spellings

YES NO

Spelling of Yes and No displayed on analysis report under the Corrections Status column. Alternates to English can be substituted.

spellings of months

NO LONGER USED.

Deconvol. character

D

The character in the peak tables indicating that this peak is part of a deconvolution.

Shape character

s

Bad-peak-shape indicator in the peak tables.

Multiplet character

M

The peak table character indicating this peak is part of a multiplet.

Unknown suspect

-

The character in the unknown peak table indicating that this peak was not found in the Suspect Library.

EBAR table filename

NOT USED IN RENAISSANCE

IEQ table filename

NOT USED IN RENAISSANCE

EBAR on/off

NOT USED IN RENAISSANCE

IEQ on/off

NOT USED IN RENAISSANCE

Unidentified Peak Summary and Library Peak Usage Format flag (T=print eff cor peakarea)

T

T = Print efficiency corrected peak area for unknown peaks instead of net peak count rate and include the nuclide half-life and peak branching ratios in the Library Peak Usage section.

F = Print net peak count rate for unknown peaks instead of efficiency corrected peak area and omit the nuclide half-life and peak branching ratios in the Library Peak Usage section.

Minimum Good Peaks Above Dividing Energy for Energy Recalibration (5 Minimum)

1000

This flag does not function in ROI32. Number of good peaks above the energy calibration dividing point required for an automatic energy recalibration during analysis. The maximum value is 9999.

Minimum Good Peaks Below Dividing Energy for Energy Recalibration (5 Minimum)

1000

This flag does not function in ROI32. Number of good peaks below the energy calibration dividing point required for an automatic energy recalibration during analysis. The maximum value is 9999.

Energy Recalibration Dividing Energy

0.0

This flag does not function in ROI32. Energy calibration dividing point (energy). This value must include a decimal point.

Activity Scaling Factor

1.0

Scaling factor multiplied times nuclide activity in addition to the **Multiplier**, **Divisor**, and **Weight** values specified in the analysis settings. This value must include a decimal point.

Unidentified Peak Match Width Factor

2.0

Range multiplier for listing suspect nuclides in the unknown peak table. For peaks listed in the unknown peak table, the suspect nuclide in the unknown peak table is determined by choosing the closest energy match to the unknown peak that is within *Range Multiplier* * *FWHM* of each peak. This value must include a decimal point.

Page length

60

Page length (in lines) of analysis report.

Save UFO File flag

T

If the .UFO file is deleted upon completion of the analysis, some features in GVPlot, the **Display Analysis Results...** command, and updating PBC files will not be available because these functions rely on information stored in the .UFO file.

T = Do not delete .UFO file after analysis is complete.

F = Erase .UFO file after analysis is complete.

MDA Type, T = Allow change

1 T

T = Allow change and use the **MDA Type** specified in the analysis settings.

F = Do not allow change and always use the MDA number specified on this line, regardless of the analysis settings. The MDA number is based on the order in which MDA methods are listed on the System tab.

PBC F=off and filename

F PBCTEST.PBC

T = Use the PBC file specified here unless a different PBC file is given in the analysis settings. The file must include the full path and is limited to 32 characters total.

F = Do not use a PBC file unless one is specified in the analysis settings.

MPC F=off and filename

NOT USED IN RENAISSANCE

Directed Fit flag (T=enable directed fit)

F

T = Perform directed fit regardless of analysis setting.

F = Do not perform directed fit unless the option is turned on in the analysis settings.

F

NO LONGER USED

Accept Small Peaks flag (T=Accept low peaks)

T

If the following three conditions are all true, then an MDA is reported for the peak. Otherwise, an activity calculation for the peak is attempted.

Condition 1 — The peak is too narrow (FWHM or FWTM too narrow)

Condition 2 — This condition is TRUE if the Narrow Peak for Activity Calculation flag is off.

Condition 3 — This condition is TRUE if any one of the following conditions is true:

- a) If the area is less than 200 AND the Accept Small Peaks flag is off.
- b) The peak area is greater than 300.
- c) The background is more than twice the peak area.

Derived Peak Area character

A Character displayed in the unidentified and identified peak summaries.

Print Discarded Peak Table

T

T = Discarded Isotope Peaks table is displayed on the report for all analysis engines except GAM32. (See Section 6.7.8 for more detail related to the Discarded Isotope Peaks Table.)

F = Discarded Isotope Peaks table is suppressed.

Maximum Half-lives Cutoff

12 The Decay-Corrected Activity is flagged as exceeding the half-life cutoff instead of calculating a decay-corrected activity value. The same type of flag is displayed in the Summary of Peaks in Range section. The maximum value is 9999.

Peak Activity range factor

2.

A peak is used in the nuclide activity average if:

- Peak Activity * (1 - A) < activity of first peak in the library for that nuclide and
- Peak Activity * (1 + A) > activity of first peak in the library for that nuclide

where:

$$A = \text{Activity Range Factor} * \sqrt{\text{count uncert}^2 + \left(\frac{\text{nuclide uncert}}{100}\right)^2 + \left(\frac{\text{calib source uncert}}{196}\right)^2}$$

Note that this value must be followed by a decimal point.

Activity Range Test flag (T=Perform activity range test)

T

T = Use the Activity Range Factor in the previous parameter to determine if a nuclide peak is used to calculate the weighted average nuclide activity.

F = Use all peaks that meet the uncertainty cutoff in determining the weighted average nuclide activity.

Zero Area Identified Peak flag (T=Print 0 area peaks)

F

T = Show peaks that are not found in the spectrum (i.e. fail the Peak Cutoff test) in the Identified Peak Summary with the following qualifications for specific analysis engines:

- **WAN32 and ROI32** — Peak data is displayed for all peaks in the library.
- **GAM32** — Peak data is displayed for all peaks reported, but all library peaks may not be reported depending on peak quality, library content, and analysis settings.
- **NPP32** — Deconvoluted peaks that are rejected may not be included in the peak list. Only the peak background and FWHM is displayed for peaks that do not meet the peak cutoff criteria.
- **ENV32** — Some rejected peaks may be included in the list, but no peak data are displayed.

F = Only show peaks in the Identified Peak Summary that meet the Uncertainty cutoff limit.

Zero Activity Isotope flag (T=Print 0 activity isotopes)

F

This flag functions only for the NPP32 and ENV32 analysis engines.

The GAM32, WAN32, and ROI32 analysis engines show all nuclides (even if zero activity) regardless of this flag setting.

T = Show nuclides with no activity reported in the Summary of Library Peak Usage table. This would include all nuclides in the library that were not found during analysis.

F = Only show nuclides in the Summary of Library Peak Usage table that were identified in the analysis. This includes nuclides that had zero activity because the associated peaks were found but moved to the Discarded Peaks Table.

Minimum Step Background Energy

0.0

Sets the lowest energy to use for a stepped background under a multiplet. Typically, this parameter is set greater than zero only when multiplet peaks are found on the rising edge of a peak or continuum that is not compatible with the stepped-background fitting methodology required for fitting small peaks on the high side of larger peaks. This value must include a decimal point.

Fraction Limit Test flag (T=Do frac. test on all peaks)

T

This flag functions only in ENV32.

T = All nuclide peaks are used for the fraction limit test.

F = Nuclide peaks flagged as “do not include in the average activity” in the library are not used for the fraction limit test.

Use Narrow Peaks for Nuclide Activity flag (T=Use all narrow peaks in act.)

T Operates in conjunction with the “Accept Small Peaks” flag (page 387).

Zero Area Library Peak flag (T=Print 0 act. pks. in nuc. tab.)

T *This flag applies only to the NPP32 and ENV32 analysis engines. The WAN32, GAM32, and ROI32 analysis engines always display all library peaks.*

T = Show peaks with no area in the Summary of Library Peak Usage table. This would include all library peaks that did not pass the analysis settings criteria.

F = Only show peaks in the Summary of Library Peak Usage table that passed the analysis settings criteria, and summarize how many library peaks were found as compared to the number listed in the library for that nuclide (i.e., “X of Y peaks found”) under nuclide peak list.

Use Peak Cutoff flag (T=Use peak cutoff)

T

T = Use Peak Cutoff specified in the analysis settings file to limit peaks used in the analysis to only those that meet the Peak Uncertainty Cutoff limit.

F = Ignore the Peak Cutoff value in the analysis settings and use all peaks found regardless of uncertainty in the analysis.

Second MDA type, T=Calculate

2 T Second MDA Type (see MDA Type above). If set to T, the second MDA type is stored in the .UFO file but it is not printed on the analysis report.

Sort Nuclide Peaks By Energy flag (T=Sort by energy)

F *This flag applies only to the WAN32, GAM32, and ROI32 analysis engines. The NPP32 and ENV32 analysis engines always sort peak energy by the library order.*

T = Sort peaks in the Summary of Library Peak Usage table by energy

F = Sort peaks in the Summary of Library Peak Usage table by library order.

Multiplet channel shift limit

2.0 The maximum number of channels that multiplet peaks can be shifted in the peak-fit optimization. This value must include a decimal point.

Background width/FWHM for MDAs

0.0 Use this value times the peak FWHM to determine the background area for calculating the MDA. If set to zero, the entire background area for the peak is used to calculate the MDA. (Use zero for old method.) This value must include a decimal point.

Print MDA in Nuclide Summary (T=Print MDA)

T *This parameter does not function in GAM32.* GAM32 does not report MDA for nuclides that have an activity value calculated.

T = Include the MDA in the Summary of Nuclides in Sample table when a nuclide activity value is calculated.

F = The nuclide MDA is not included in the Summary of Nuclides in Sample table when a nuclide activity is calculated.

Maximum Half-life to Unknowns flag

F

T = Treat peaks associated with nuclides exceeding the half-life limit as unknowns.

F = Treat peaks associated with nuclides that exceed the half-life limit as identified peaks rather than unknowns.

Nuclide Summary MDA Header

MDA MDA column header in “Summary of Nuclides in Sample” section of report. This column header is displayed only if the nuclide MDA column is included in the Summary of Nuclides in Sample table (see the “Print MDA in Nuclide Summary” flag above).

ENV factor

0.0 *This flag functions only in ENV32 and GAM32.* Nuclide rejection factor. In the library reduction algorithm, it is used to remove nuclides from the analysis library. If set to a lower value, more nuclides will likely be removed/dropped from the library (see Section 8.1.3 for details on how this factor is used). This value must include a decimal point.

ISO NORM Probability alpha

NOT USED IN RENAISSANCE

ISO NORM Probability beta

NOT USED IN RENAISSANCE

ISO NORM Probability gamma

NOT USED IN RENAISSANCE

ISO NORM Print MDA flag (T=Print MDA in ISO NORM table if Activity < Critical Level)

NOT USED IN RENAISSANCE

Maximum ISO NORM MDA Ratio factor

NOT USED IN RENAISSANCE

Peak overlap range in units of peak FWHM (Peaks within this range are deconvoluted)

3.5 This value must include a decimal point. The minimum value is 1.0. If you assign a value less than the minimum, the analysis automatically defaults to 1.0.

Directed Fit Minimum Background Counts for Quadratic Peak Fit

1000

Directed Fit Peak Region Width Factor

0.80 This value must include a decimal point. The maximum value is 9999.

Dominant Background Peak Cutoff and Override flag (T=Override using analysis settings peak cutoff value)

NOT USED IN RENAISSANCE

Dominant Background Peak Width Factor and flag (Units of FWHM, Flags: T=Use factor, F=Use GV peak range)

NOT USED IN RENAISSANCE

Non-dominant Background Peak Width Factor and flag (Units of FWHM, Flags: T=Use factor, F=Use GV peak range)

NOT USED IN RENAISSANCE

TCC Internal Library Flag (T=Use Internal TCC Library Peaks, F=Use only analysis library peaks)

F

A.2.3. G30winds.ini (NaI Analysis)

The `g30winds.ini` file contains initial or default values for the RENGSA analysis engine for NaI. It is read by the engine before the spectrum file is read. The contents are shown below. The file-name can be specified on the command line. If the specified file cannot be found or cannot be read, then the internal values are used. Some of these values can only be set in this file.

A.2.3.1. Contents

G30WIN.TXT	Message file name
Report Definition Filename. The name of the file that defines the standard analysis report format.	
YES NO	spellings
Spelling of Yes and No displayed on analysis report under the Corrections - Status column. Alternates to English can be substituted.	
JANFEBMARAPRMAYJUNJULAUGSEPOCTNOVDEC	spellings of months
Three character month spellings using for dates displayed on analysis reports.	
D	Deconvol. charact
The character in the peak tables indicating that this peak is part of a deconvolution.	
s	shape character
The character in the peak tables indicating that this peak had bad shape.	
M	Multiplet char.
The character in the peak tables indicating that this peak is part of a multiplet.	
-	Unknown suspect
Not-in-Suspect-Library character. The character in the unknown peak table indicating that this peak was not found in the Suspect Library.	
D:\A27\EBAR.TBL	Ebar table filename
NOT USED IN RENAISSANCE	
D:\A27\IEQT.TBL	IEq table filename
NOT USED IN RENAISSANCE	
F	Ebar on/off
NOT USED IN RENAISSANCE	

- F** IEq on/off
NOT USED IN RENAISSANCE
- T** T=print eff cor peakarea
Unidentified Peak and Library Table Format Flag
T = Print efficiency corrected peak area for unknown peaks instead of net peak count rate and include the nuclide half-life and peak branching ratios in the Library Peak Usage section.
F = Print net peak count rate for unknown peaks instead of efficiency corrected peak area and omit the nuclide half-life and peak branching ratios in the Library Peak Usage section.
- 15** # of pks/eng recal high (5 default)
Number of good peaks above the energy calibration dividing point (see below) required for an automatic energy recalibration during analysis.
- 0** # of pks/eng recal low
Number of good peaks below the energy calibration dividing point (see below) required for an automatic energy recalibration during analysis.
- 0.0** recal energy dividing
Energy calibration dividing point (energy).
- 1.0** scaling factor on activ
Additional Scaling Factor. Scaling factor multiplied times nuclide activity in addition to the **Multiplier**, **Divisor**, and **Weight** values specified in the SDF.
- 2.0** range multiplier
Range multiplier for listing suspect nuclides in the unknown peak table. For peaks listed in the unknown peak table, the suspect nuclide in the unknown peak table is determined by choosing the closest energy match to the unknown peak that is within the Range Multiplier * FWHM of each peak.
- 60** Page length
Page length (in lines) of analysis report.
- T** F = erase UFO file
Save UFO File Flag
T = Do not delete .UFO file after analysis is complete.
F = Erase .UFO file after analysis is complete.

NOTE If the .UFO file is deleted upon completion of the analysis, some features in WinPlots, the **Display analysis results...** command, and updating PBC files will not be available because these functions rely on information stored in the .UFO file.

- 09 T** MDA type, T=Allow change
NaI analysis in Renaissance uses the MDA method discussed in Section 9.4.5.1, so this option has no effect.
- F PBCTEST.PBC** PBC F=off and filename
PBC Flag
T = Use the PBC file specified here unless a different PBC file is given in the analysis options. The file must include the full path and is limited to 32 characters total.
F = Do not use a PBC file unless one is specified in the analysis options.
- F d:\a27\MPCTABLE.MPC** MPC F=off and filename
Not used in Renaissance.
- F** T=do directed fit
Directed Fit Flag
T = Perform directed fit regardless of analysis options setting.
F = Do not perform directed fit unless the option is turned on in the analysis options.
- F** T=Halt WAN1 on error
T = Halt WAN1 on error (this parameter is no longer used by Renaissance).
- T** T=Accept low peaks
NOT USED IN RENAISSANCE
- A** Derived peak area char
Derived Peak Area Character. Character displayed in the unidentified and identified peak summaries.
- 1.3** Multiplet FWHM limit
If two peaks are farther apart than the multiplet FWHM limit * FWHM, the analysis engine separates the peaks; otherwise, it is left as a multiplet.
- T** Adjust peak width and position
Allows the peak fit part of the program to adjust width and position of peaks found during the peak search. *In almost all cases, this should be set as true.*

- T** Add peaks in peakfit
Allows peak fit part of program to split peaks found in peak search into doublets, and add small peaks that might have been missed by peak search. *In almost all cases, this should be set as true.*
- F** Library based peak stripping
NOT USED IN RENAISSANCE
- T** T = Print 0 area peaks
Zero Area Identified Peak Flag
T = Show peaks with no area in Identified Peak Summary. This would include all library peaks that were not found in the spectrum.
F = Only show peaks in the Identified Peak Summary that meet the Uncertainty cutoff limit.
Do not show peaks with no area.
- T** T = Print 0 activity isotopes
Zero Activity Isotope Flag
T = Show nuclides with no activity in the Library Usage Summary. This would include all nuclides in the library that were not found during analysis.
F = Only show nuclides in the Library Usage Summary that were identified in the analysis. This includes nuclides that had zero activity because the associated peaks were found but moved to the Discarded Peaks Table.

APPENDIX B. THE MOTOR SETUP PROGRAM

The Motor Setup program (**Start, Programs, Renaissance, Motor Setup**) lets you adjust the home position, maintenance position, scan length, and scan speed of motorized counting stations; and move the bed into maintenance position.

IMPORTANT Once the parameters in these dialogs are set, *we recommend that you not change them unless absolutely necessary, or unintended consequences might result.* For example, if your efficiency calibrations are all performed at one scan length, changing to another scan length will require you to perform new efficiency calibrations.

The **Start Count, Extend Count, Abort Count, and Motor Return** buttons in Renaissance Operator directly control the motorized bed so there is no need to run the Motor Setup program while counting subjects. However, the supervisor will have to use Motor Setup and the Supervisor program simultaneously in order to calibrate the motorized bed.

Figure 276 shows the Motor Selection tab.

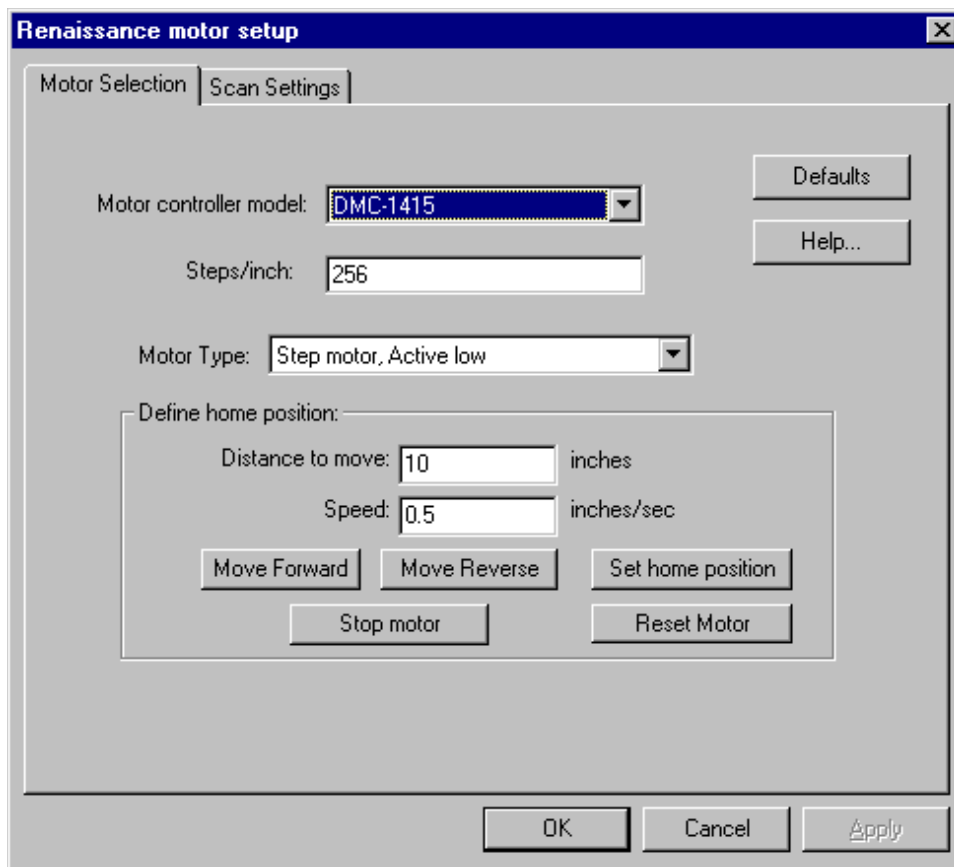


Figure 276. Motor Selection and Home Position.

Only one motor can be connected to the controlling PC.

The **Steps/inch** setting depends on the **Motor Type**; these fields are typically set by the factory, but can be adjusted as follows:

- Enter an estimated **Steps/inch** value.
- Set the **Distance to move** to at least 1 inch.
- Click on **Move Forward** or **Move Reverse** to move the motor the specified distance.
- Measure the actual movement distance.
- Adjust the **Steps/inch** value and repeat the preceding steps until the actual movement distance is within an acceptable range of the target distance.

To **Define home position** (the position from which subject counts, including extended counts, begin), use the **Move Left**, **Move Right**, and **Stop Motor** buttons to move the bed to the desired position, then click on **Set home position**. This setting will be retained until you change to a different home position. The **Distance to move** and **Speed** fields govern motor activity when defining home position, and do not affect the scan speed during subject measurements in Renaissance Operator. Scan speed (inches per second) during data acquisition can be determined by dividing the **Scan Length** by the real-time preset.

To test new settings without putting them into full effect, click on **Apply**. To return to the factory settings for all fields on this screen, click on **Defaults**.

Use **Reset Motor** if the motor is not responding correctly. This resets the firmware according to the settings on this tab.

Click on the Scan Settings tab (Fig. 277).

The **Position** fields allow you to set the **Scan length** and **Maintenance** position, both of which are set in relation to the **Home** position. **Scan Length** can be a maximum of +200 inches. The **Maintenance** position can be +/-200 inches.

The **Move to position** buttons allow you to quickly position the bed. **End** moves the bed to the end-of-scan position, according to **Scan Length**. The progress indicator below the **Stop** button shows the bed position relative to the scan length.

The **Change moving direction** button allows you to select the direction in which the motor turns for each operation. Each time you click on this button, Motor Setup must be closed and restarted and you must reset the **Home** position.

To reposition the motor after an Operator scan, be sure to mark the **Automatically return motor when reaches End position** box. Otherwise, the operator will have to click on the **Motor Return** button to move the motor back to the home position after each scan.

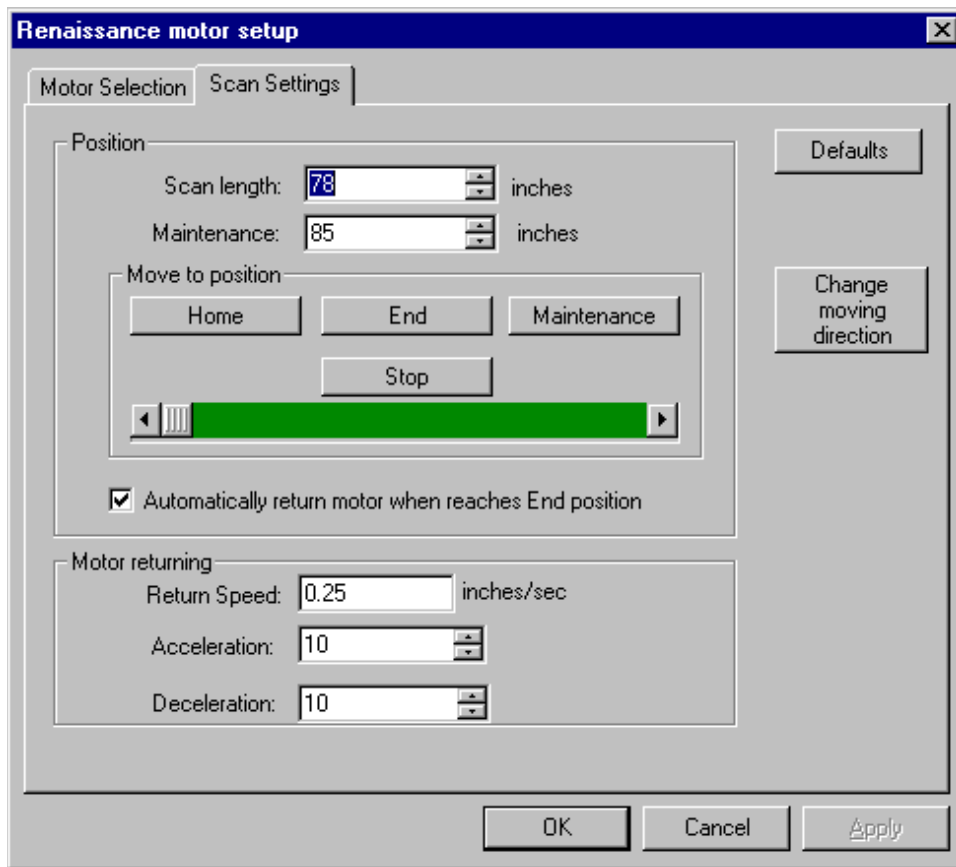


Figure 277. Adjusting Scan Parameters and Maintenance Position.

In the **Motor returning** section, the **Return Speed** setting determines the speed at which the bed returns to home position at the end of a scan, and must not exceed 5.9 inches per second. See the manual for the motor for the acceptable **Return Speed**, **Acceleration**, and **Deceleration** rates.

[Intentionally blank]

APPENDIX C. FILE TYPES AND DATABASE TABLES

This appendix describes the file types created with and used in Renaissance, as well as the structure of the tables in the QA and results databases. See the *File Structures Manual* for complete descriptions of the formats for the file types discussed below, including .SPC, .CHN, and .UFO files.

C.1. Renaissance File Types

C.1.1. Detector Files

- .CFG “Configuration”; System Detector configuration information used by `GV32.EXE`; binary format.
- .SDF “Analysis Options Files” for detectors identified as germanium within **Services/Edit List Ge...**; created with the **Analyze/Settings/Sample Type...** menu function; binary format.
- .SVD “Analysis Options Files” for detectors identified as sodium iodide within **Services/Edit List NaI...**; created with the **Analyze/Settings/Sample Type...** menu function; binary format.

C.1.2. Spectrum Files

- .CHN “Channels”; MAESTRO-style spectral data file; binary format.
- .SPC “Spectrum”; spectrum with full analysis settings, calibration, descriptions, etc; “Inform” type binary format.
- .AN1 Alternate name for spectrum files used for analysis, when the .SPC name is already in use; same format as .SPC.
- .ROI “ROI”; channel pairs created by the **ROI/Save File...** function; binary format.

C.1.3. Miscellaneous Files

- .CLB “Calibration”; full energy/efficiency calibration; “Inform” style binary format.
- .LIB “Library”; nuclide library; “Inform” style binary format.
- .UFO “Unformatted Output”; analysis results; “Inform” style binary format.

- .EFT “Efficiency Table”; used for efficiency **Calibrate/Recall Calibration...** function (and created with the **Save...** button on the Efficiency Calibration Sidebar); formatted ASCII text (also, lines that do not begin with numeric values are ignored).
- .ENT “Energy Table”; used for energy **Calibrate/Recall Calibration...** function (and created with the **Save...** button on the Energy Calibration Sidebar); formatted ASCII text (also, lines that do not begin with numeric values are ignored).
- .RPT “Report”; output of analysis engine; ASCII text.
- .TXT “Text”; general ASCII text files used by **File/Print...**
- .JOB ASCII text providing commands for **Services/JOB Control...** function.
- .PBC “Peak Background Correction”; table values for the PBC.

C.1.4. QA Database Files

- .MDB Microsoft Access database file extension.

C.2. Database Tables for Renaissance QA

Note that you can use Microsoft Access to examine the table structure.

C.2.1. QA Detectors Table

(Only one of these tables for entire database; one record for each detector being monitored for QA, with fields defined as follows.)

<u>Field Name</u>	<u>SQL Data Type</u>	<u>Description</u>
Detector	SQL_LONG	Detector ID number. (Primary Key)
DetName	SQL_CHAR (64)	Detector Pick List Name
DetDesc	SQL_CHAR (64)	Detector Description
Creation	SQL_TIMESTAMP	Date/Time this record created
NumMeas	SQL_LONG	Measurement counter (all types) for this detector
NumBack	SQL_INTEGER	Background type only Measurement counter for this detector
SamFile	SQL_CHAR (128)	Sample Type File Name
SamType	SQL_CHAR (80)	Sample Type Description
LibFile	SQL_CHAR (128)	Nuclide Library File Name

<u>Field Name</u>	<u>SQL Data Type</u>	<u>Description</u>
Setup	SQL_SMALLINT	Setup Flagword
Limits	SQL_SMALLINT	Limit Settings Flagword
MinBack	SQL_REAL	Min. Background CPS Acceptance Limit
LowBack	SQL_REAL	Low Background CPS Excursion Warning Level
BigBack	SQL_REAL	High Background CPS Excursion Warning Level
MaxBack	SQL_REAL	Max. Background CPS Acceptance Limit
MinActivity	SQL_REAL	Min. Total Activity Acceptance Limit
LowActivity	SQL_REAL	Low Total Activity Excursion Warning Level
BigActivity	SQL_REAL	High Total Activity Excursion Warning Level
MaxActivity	SQL_REAL	Max. Total Activity Acceptance Limit
MinShift	SQL_REAL	Min. Average Peak Shift Acceptance Limit
LowShift	SQL_REAL	Low Average Peak Shift Warning Level
BigShift	SQL_REAL	High Average Peak Shift Warning Level
MaxShift	SQL_REAL	Max. Average Peak Shift Acceptance Limit
MinFWHM	SQL_REAL	Min. Average FWHM Ratio Acceptance Limit
LowFWHM	SQL_REAL	Low Average FWHM Ratio Warning Level
BigFWHM	SQL_REAL	High Average FWHM Ratio Warning Level
MaxFWHM	SQL_REAL	Max. Average FWHM Ratio Acceptance Limit
MinFWTM	SQL_REAL	Min. Average FWTM Ratio Acceptance Limit
LowFWTM	SQL_REAL	Low Average FWTM Ratio Warning Level
BigFWTM	SQL_REAL	High Average FWTM Ratio Warning Level
MaxFWTM	SQL_REAL	Max. Average FWTM Ratio Acceptance Limit
Operator	SQL_CHAR(64)	User name last entered on the System tab under Analyze/Settings/Sample Type... at start of latest measurement

C.2.2. Application Information Table

(One of these tables for entire database; one record for Renaissance.)

<u>Field Name</u>	<u>SQL Data Type</u>	<u>Description</u>
ModelNumber	SQL_LONG	Product model number (i.e., 66)
SerialNumber	SQL_CHAR(32)	Product serial number
AppName	SQL_CHAR(16)	Application Name (i.e., "Renaissance")
AppVersion	SQL_CHAR(8)	Version/Revision (i.e., "4.0" or greater)
Laboratory	SQL_CHAR(64)	Laboratory name entered under Renaissance system dialog

C.2.3. M...d Measurements Table(s)

(Where "...d" is the detector number in decimal from the Detectors table above. There is one of these tables for each detector, covering all measurements, whether background or standard sample type. The total number of records in this table is denoted by NumMeas in the Detectors table, which is also the measurement number of the last record in this table. The records are stored sequentially by measurement number.)

<u>Field Name</u>	<u>SQL Data Type</u>	<u>Description</u>
Measurement	SQL_LONG	Measurement number (primary key)
MeasTime	SQL_TIMESTAMP	Date/Time for this measurement
MeasType	SQL_SMALLINT	Activity analysis (1) or Background (0)
LiveTime	SQL_REAL	Acquisition live time in seconds
CountRate	SQL_REAL	Background CPS (only for Background measurement)
Activity	SQL_REAL	Total activity
PeakShift	SQL_REAL	Average peak shift
FWHMRatio	SQL_REAL	Average FWHM ratio
FWTMRatio	SQL_REAL	Average FWTM ratio

C.2.4. P...dmmmm Peaks Table(s)

(Where "...d" is the detector number in decimal, "m...m" is the measurement number to 4 places. There is one of these tables for each measurement in the table above, but only if the output of actual centroid energies is enabled.)

<u>Field Name</u>	<u>SQL Data Type</u>	<u>Description</u>
PeakNumber	SQL_LONG	Peak number counter (primary key)
PeakFlags	SQL_LONG	Analysis results flags
Nuclide	SQL_CHAR(8)	Library nuclide name this peak belongs to
Energy	SQL_REAL	Library energy
Centroid	SQL_REAL	Actual centroid energy
CalFWHM	SQL_REAL	Expected (calibrated) FWHM at this energy
FWHM	SQL_REAL	Actual FWHM
FWTM	SQL_REAL	Actual FWTM (Ge only)
Area	SQL_REAL	Net counts in peak
Background	SQL_REAL	Background counts

C.3. The Renaissance v7.0 Database

C.3.1. Key Tables for Working with the Renaissance Database

C.3.1.1. Table: RenResults

This table is the top of the analysis results chain. It contains links to the subject history and analysis group tables.

C.3.1.2. Table: SubjectHistory

This table contains the subject height, weight, CWT, comments entered by the operator, and the optional entries. It also contains the date the comment was entered or edited. (The most recent comment can be edited by the operator.)

C.3.1.3. Table: Subject

A list of name, badge, and social security numbers. The badge numbers need not be unique if the key is the name or social security number.

C.3.1.4. Table: RenLimits

This table contains the activities, MDAs, and uncertainties listed on the Renaissance Operator report. It also contains links to the AnalysisGroup table and AnalysisResults table. (The AnalysisResults table contains the analysis results for individual spectra.) The RenLimits table also contains the alarm and warning limits used in writing the Renaissance Operator report.

- Average results — When results obtained by analyzing several spectra are averaged, the AnalysisResultsID value in this table is zero.

- Nuclide activities — Nuclide name is displayed in the Nuclide column and LibEnergy and Energy are zero.
- Unknown peaks — Nuclide column is blank and LibEnergy is zero.
- When the AnalysisResultsID is not zero, the peak and nuclide activity values will be identical to those in the Peak and Nuclide tables.

C.3.1.5. Table: AnalysisGroup

This table contains links to the AnalysisResults table, as well as flags indicating whether an alarm or warning level of activity was discovered during the analysis. A scan that uses several detectors will have one AnalysisGroupID value. Each individual spectrum will have its own AnalysisResultsID value, and the average results will have 0 for the AnalysisResultsID. When several spectra are summed and the sum is analyzed, the AnalysisResultsID will be -1 for the individual spectra and a value for the sum. This was done so that the individual spectrum names would be listed in the database.

C.3.1.6. Table: AnalysisResults

This table contains links to the Spectra, AnalysisParams, EnergyCal, and EffCal tables. The AnalysisResultsID is used in the Peaks and Nuclides tables.

C.3.1.7. Table: AnalysisParams

This table contains the contents of the sample defaults file (.SDF file for germanium spectra and .SVD file for sodium iodide spectra). Its key is the AnalysisID value used in the AnalysisResults table.

C.3.2. List of Tables in the Renaissance Database

Table	Comment	Key	Keys to Other Tables in this Table
ActivityLimits	Alarm and warning limits by peak and nuclide	LimitID	
AnalysisGroup		AnalysisGroupID	AnalysisResultsID
AnalysisParams	Analysis parameters	AnalysisID	AbsorptionID GeoID IEQID (IodineEQID) EBARID (AverageEnergyID) DACID ReportParamsID
AnalysisResults	Standard analysis results	AnalysisResultsID	SpectrumID

Table	Comment	Key	Keys to Other Tables in this Table
			AnalysisID EnergyCalID EffCalID
Attenuation	Attenuation calculated with two spectra	AttenuationID	DetectorID RefAnalysisID (an AnalysisResultsID value) CurAnalysisID (an AnalysisResultsID value)
AttenuationCoefficients	Energy, Linear and Mass coefficients		AttenuationMaterialID
AttenuationMaterials	Material name, formula, density, and weight	AttenuationMaterialID	
AverageEnergy	EBAR values	AverageEnergyID	
ChestWallThickness	Chest wall thickness parameters	CWTID	
DAC	DAC values	DACID	
Detectors	Detector information	DetectorID	
EffCal	Efficiency calibration	EfficiencyID	DetectorID CertificateID
EffCalPeaks	Efficiency calibration peaks	EfficiencyID and Energy	EfficiencyID
EffCertificate	Efficiency Certificate values	CertificateID and Peak Energy	
EnergyCal	Energy calibration	EnegyID	DetectorID
EnergyCalPeaks	Energy calibration peaks	EnergyID and Peak Energy	EnergyID
Geometry	Geometry correction calculated from two spectra	GeometryID	DetectorID RefAnalysisID (an AnalysisResultsID value) CurAnalysisID (an AnalysisResultsID value)
IodineEquivalence	IEQ values	IodineEQID	
Nuclides	Standard analysis results	NuclideID	AnalysisResultsID
Peaks	Standard analysis results	PeaksID	AnalysisResultsID, ShapeID
PkShapeCal	Peak shape calibration	PkShapeID	DetectorID, ECalID
RenLimits	Renaissance weighted activity, warning and alarm	RenLimitID	AnalysisGroupID, AnalysisResultsID

Table	Comment	Key	Keys to Other Tables in this Table
	limits		
RenResults	Renaissance analysis results	RenResultsID	HistoryID (SubjectHistory table), AnalysisGroupID
ReportParams	Report settings	ReportParamsID	
Spectra	Spectrum name, detector, calibration	SpectrumID	DetectorID, EnergyID, EfficiencyID
Subject	Subject name, badge, SSN	SubjectID	
SubjectHistory	Height, weight, cwt, comments, optional fields	HistoryID	SubjectID, CWTID

C.3.3. Renaissance Database Table Descriptions

C.3.3.1. Table: ActivityLimits

Properties

Date Created:	5/7/03 3:43:36 PM	Def. Updatable:	True
Last Updated:	5/7/03 3:43:36 PM	OrderByOn:	False
Orientation:	0	RecordCount:	1

Columns

Name	Type	Size	Description/Attributes
LimitID	Number (Long)	4	
Nuclide	Text	8	Nuclide name
Energy	Number (Double)	8	Peak energy (keV)
AlarmLimit	Number (Double)	8	Alarm limit on activity (Bq)
WarningLimit	Number (Double)	8	Warning limit on activity (Bq)

C.3.3.2. Table: AnalysisGroup**Properties**

Date Created:	5/7/03 3:43:36 PM	Def. Updatable:	True
Last Updated:	5/7/03 3:43:36 PM	OrderByOn:	False
Orientation:	0	RecordCount:	65

Columns

Name	Type	Size	Description/Attributes
AnalysisGroupID	Number (Long)	4	Fixed Size, Auto-Increment
AnalysisResultsID	Number (Long)	4	
IsWarning	Yes/No	1	At least one nuclide exceeded the warning limit
IsAlarm	Yes/No	1	At least one nuclide exceeded the alarm limit
TotalActivity	Number (Double)	8	Total in individual spectrum
TotalCounts	Number (Double)	8	Total in individual spectrum
Spectrum	Text	255	Spc file name
Weight	Number (Double)	8	Weighting factor in average

C.3.3.3. Table: AnalysisParams**Properties**

Date Created:	5/7/03 3:43:36 PM	Def. Updatable:	True
Last Updated:	5/7/03 3:43:36 PM	OrderByOn:	False
Orientation:	0	RecordCount:	48

Columns

Name	Type	Size	Description/Attribute
AnalysisID	Number (Long)	4	
Description	Text	255	
Date	Date/Time	8	Date of analysis
AbsorptionID	Number (Long)	4	Attenuation data index
GeoID	Number (Long)	4	Geometry data index

Name	Type	Size	Description/Attribute
IEQID	Number (Long)	4	Iodine equivalence data index
EBARID	Number (Long)	4	Average energy data index
DACID	Number (Long)	4	Derived air concentration data index
ReportParamsID	Number (Long)	4	Report parameters index
Operator	Text	64	Operator name
Laboratory	Text	64	Laboratory name
StartChan	Number (Long)	4	Start channel for analysis
EndChan	Number (Long)	4	End channel for analysis
Faccor	Number (Double)	8	Should be between 0.5 and 1.0. Used for library/spectrum peak matching.
Cutoff	Number (Double)	8	Peak error cutoff
UnkCutoff	Number (Double)	8	Unknown peak error cutoff
Sensitivity	Number (Double)	8	Peak search sensitivity
RanSumFact	Number (Double)	8	Random summing factor
Multiplier	Number (Double)	8	Dimension multiplier
Divisor	Number (Double)	8	Dimension divisor
Weight	Number (Double)	8	Sample weight or volume
Activity	Text	50	Activity units
Size	Text	50	Size units
RandomError	Number (Double)	8	Additional random error
SystematicError	Number (Double)	8	Additional systematic error
FracLimit	Number (Double)	8	Fraction Limit test in percent
HalfLivesLimit	Number (Double)	8	Half-lives decay limit
ActRange	Number (Double)	8	Activity range factor
StepEnergy	Number (Double)	8	Minimum step background energy
wMDA	Number (Integer)	2	First MDA type
wMDA2	Number (Integer)	2	Second MDA type
DecayDate	Date/Time	8	Decay date
DecayCollStart	Date/Time	8	Decay during collection start time
DecayCollEnd	Date/Time	8	Decay during collection end time

Name	Type	Size	Description/Attribute
wBackType	Number (Integer)	2	Background fit type
wPeakStripping	Number (Integer)	2	0=no,1=library based, 2=manual
AttenuationFactor	Number (Double)	8	Attenuator thickness
fuCi	Yes/No	1	microCuries if Yes, Bq if no
fDirectedFit	Yes/No	1	Do directed fit if Yes
fRandSum	Yes/No	1	Use random summing factor if Yes
fDecay	Yes/No	1	Decay correct to date specified if Yes
fDecayAcq	Yes/No	1	Decay during acquisition
fDecayColl	Yes/No	1	Decay during sample collection
fIEQ	Yes/No	1	IEQ calculation if Yes
fEBR	Yes/No	1	Average energy calculation if Yes
fDAC	Yes/No	1	DAC calculation if Yes
fPBC	Yes/No	1	PBC correction if Yes
fGeometry	Yes/No	1	Geometry correction if Yes
fAttenuation	Yes/No	1	Attenuation correction if Yes
fPriorityHigh	Yes/No	1	Analyze with high priority if Yes (recommended)
fTcc	Yes/No	1	TCC correction. Should not be needed in Renaissance.
Library1	Text	255	Main library
Library2	Text	255	Library 2 for manual peak stripping
Library3	Text	255	Library 3 for manual peak stripping
SuspectLibrary	Text	255	Library used for unknown peak list
PBCFile	Text	255	
AnalysisProgram	Text	255	

Relationships

AnalysisParams AnalysisResults

AnalysisID

AnalysisID

Attributes: Unique, Enforced

Attributes: One-To-One

ReportParams AnalysisParams

ReportParamsID ReportParamsID

Attributes: Enforced

Attributes: One-To-Many

C.3.3.4. Table: AnalysisResults

Properties

Date Created: 5/7/03 3:43:36 PM

Def. Updatable: True

Last Updated: 5/7/03 3:43:36 PM

OrderByOn: False

Orientation: 0

RecordCount: 48

Columns

Name	Type	Size	Description/Attribute
AnalysisResultsID	Number (Long)	4	Analysis Results ID number
Date	Date/Time	8	Date analysis performed
SpectrumID	Number (Long)	4	
AnalysisID	Number (Long)	4	Analysis ID number
EnergyCalID	Number (Long)	4	Energy calibration used in the analysis
EffCalID	Number (Long)	4	Description: Efficiency calibration used in the analysis
AnalysisVersion	Text	50	Analysis program version
RecalEIntercept	Number (Double)	8	Energy calibration used in analysis
RecalESlope	Number (Double)	8	Energy calibration used in analysis
RecalEQuadratic	Number (Double)	8	Energy calibration used in analysis
TotalActivity	Number (Double)	8	Total activity in spectrum (Bq)

Name	Type	Size	Description/Attribute
IEQValue	Number (Double)	8	Iodine equivalence (Bq)
IEQDecayed	Number (Double)	8	Time decayed iodine equivalence (Bq)
EBRValue	Number (Double)	8	EBR value in spectrum
EBRDecayed	Number (Double)	8	Time decayed EBR value
NumberNuclidePeaks	Number (Integer)	2	Number of nuclide peaks in library
NumberUnknowns	Number (Integer)	2	Number of unknown peaks in spectrum
NumberNuclides	Number (Integer)	2	Number of nuclids in library
Errnum	Number (Long)	4	Analysis results error code
Warnum	Number (Long)	4	Analysis results warning code

Relationships

AnalysisParams AnalysisResults

AnalysisID AnalysisID

Attributes: Unique, Enforced

Attributes: One-To-One

C.3.3.5. Table: Application

Properties

Date Created:	5/7/03 3:43:36 PM	Def. Updatable:	True
Last Updated:	5/7/03 3:43:36 PM	OrderByOn:	False
Orientation:	0	RecordCount:	1

Columns

Name	Type	Size	Description/Attributes
ModelNumber	Text	50	
SerialNumber	Text	32	
AppName	Text	50	
AppVersion	Text	50	

Name	Type	Size	Description/Attributes
Laboratory	Text	64	

C.3.3.6. Table: Attenuation

Properties

Date Created: 5/7/03 3:43:36 PM Def. Updatable: True
 Last Updated: 5/7/03 3:43:36 PM OrderByOn: False
 Orientation: 0 RecordCount: 0

Columns

Name	Type	Size	Description/Attributes
AttenuationID	Number (Long)	4	
Description	Text	255	
Date	Date/Time	8	Date correction calculated
DetectorID	Number (Long)	4	
AbsorberName	Text	50	Name of absorber
RefAnalysisID	Number (Long)	4	Reference analysis ID
CurAnalysisID	Number (Long)	4	Current analysis ID
fExternal	Yes/No	1	Yes if external absorber
Density	Number (Double)	8	Density of absorber (g/cm ³)
Energy	Number (Long)	4	Peak energy
RefArea	Number (Long)	4	Reference analysis peak area
CurArea	Number (Long)	4	Current analysis peak area
Correction	Number (Long)	4	Linear attenuation coefficient at this energy

C.3.3.7. Table: Attenuation Coefficients**Properties**

Date Created: 5/7/03 3:43:36 PM Def. Updatable: True
 Last Updated: 5/7/03 3:43:36 PM OrderByOn: False
 Orientation: 0 RecordCount: 43

Columns

Name	Type	Size	Description/Attribute
AttenuationMaterialID	Number (Long)	4	
Energy	Number (Double)	8	
LinearCoefficient	Number (Double)	8	
MassCoefficient	Number (Double)	8	

Relationships

AttenuationMaterials **AttenuationCoefficients**
 AttenuationMaterialID AttenuationMaterialID

Attributes: Enforced
 Attributes: One-To-Many

C.3.3.8. Table: AttenuationMaterials**Properties**

Date Created: 5/7/03 3:43:36 PM Def. Updatable: True
 Last Updated: 5/7/03 3:43:36 PM OrderByOn: False
 Orientation: 0 RecordCount: 3

Columns

Name	Type	Size	Description/Attributes
AttenuationMaterialID	Number (Long)	4	
Date	Date/Time	8	Date material entered

Name	Type	Size	Description/Attributes
Name	Text	50	
Density	Number (Double)	8	
AtomicWeight	Number (Double)	8	
Formula	Text	50	Chemical formula (Optional)

Relationships

AttenuationMaterials **AttenuationCoefficients**
AttenuationMaterialID AttenuationMaterialID

Attributes: Enforced
Attributes: One-To-Many

C.3.3.9. Table: AverageEnergy

Properties

Date Created: 5/7/03 3:43:36 PM Def. Updatable: True
Last Updated: 5/7/03 3:43:36 PM OrderByOn: False
Orientation: 0 RecordCount: 0

Columns

Name	Type	Size	Description/Attributes
AverageEnergyID	Number (Long)	4	
Description	Text	255	
Date	Date/Time	8	Date EBAR values entered
Isotope	Text	50	
AverageEnergy	Number (Double)	8	

C.3.3.10. Table: ChestWallThickness**Properties**

Date Created:	5/7/03 3:43:36 PM	Def. Updatable:	True
Last Updated:	5/7/03 3:43:36 PM	OrderByOn:	False
Orientation:	0	RecordCount:	5

Columns

Name	Type	Size	Description/Attributes
CWTID	Number (Long)	4	
Description	Text	50	CWT = Param1 + Param2 * Weight / Height
Param1	Number (Double)	8	cm
Param2	Number (Double)	8	cm ² / kg (if the desired units are in/lb, Param2 is converted to cm-in/lb before the CWT is calculated. CWT is always in cm)

C.3.3.11. Table: DAC**Properties**

Date Created:	5/7/03 3:43:36 PM	Def. Updatable:	True
Last Updated:	5/7/03 3:43:36 PM	OrderByOn:	False
Orientation:	0	RecordCount:	0

Columns

Name	Type	Size	Description/Attributes
DACID	Number (Long)	4	
Description	Text	255	
Date	Date/Time	8	Date DAC values entered or edited
Units	Text	50	
Isotope	Text	50	
DAC	Number (Double)	8	Derived air concentration (formerly Maximum Permissible Concentration)

C.3.3.12. Table: Detectors**Properties**

Date Created:	5/7/03 3:43:36 PM	Def. Updatable:	True
Last Updated:	5/7/03 3:43:36 PM	OrderByOn:	False
Orientation:	0	RecordCount:	8

Columns

Name	Type	Size	Description/Attributes
DetectorID	Number (Long)	4	
Date	Date/Time	8	Date record created
SerialNumber	Text	50	Detector serial number (SMART-1™ detectors only. 0 if not a SMART-1 detector)
nMCB	Number (Integer)	2	
nDevSeg	Number (Integer)	2	Detector device/segment number
Host	Text	50	Host computer
DetectorType	Number (Integer)	2	0 or 1 = HPGe, 2=NaI, 3=CZT
DetectorName	Text	255	Detector pick list name

C.3.3.13. Table: EffCal**Properties**

Date Created:	5/7/03 3:43:36 PM	Def. Updatable:	True
Last Updated:	5/7/03 3:43:36 PM	OrderByOn:	False
Orientation:	0	RecordCount:	2

Columns

Name	Type	Size	Description/Attributes
EfficiencyID	Number (Long)	4	Efficiency calibration ID
Description	Text	255	Efficiency Calibration description
Date	Date/Time	8	Efficiency Calibration creation date
DetectorID	Number (Long)	4	

Name	Type	Size	Description/Attributes
CertificateID	Number (Long)	4	Efficiency calibration certificate ID
SourceToDetectorDistance	Number (Double)	8	Distance for efficiency calibration (cm)
NPairs	Number (Integer)	2	Number peaks used in calibration
EKnee	Number (Double)	8	Knee energy
FitAbove	Number (Integer)	2	1=interpolate, 2=linear, 3-5=quadratic, 6=polynomial, 7=TCC
ASigma	Number (Double)	8	Reduced chisq of efficiency fit above knee
ACoef0	Number (Double)	8	Efficiency coefficients
ACoef1	Number (Double)	8	
ACoef2	Number (Double)	8	
ACoef3	Number (Double)	8	
ACoef4	Number (Double)	8	
ACoef5	Number (Double)	8	
ACoef6	Number (Double)	8	
FitBelow	Number (Integer)	2	1=interpolate, 2=linear, 3-5=quadratic
BSigma	Number (Double)	8	Reduced chisq of efficiency fit below knee
BCoef0	Number (Double)	8	Efficiency coefficients below the knee
BCoef1	Number (Double)	8	
BCoef2	Number (Double)	8	
IsTcc	Yes/No	1	
IsAbsorber	Yes/No	1	Absorber present during TCC calibration 1
IsPointSource	Yes/No	1	Point source used for tcc calibration
LTS0	Number (Double)	8	Linear-to-Square coefficients
LTS1	Number (Double)	8	
LTS2	Number (Double)	8	
PTT0	Number (Double)	8	Peak to Total coefficients
PTT1	Number (Double)	8	Peak to Total coefficients
FileName	Text	255	Calibration file name

Relationships

EffCal **Spectra**
EfficiencyID EfficiencyID

Attributes: Enforced
Attributes: One-To-Many

C.3.3.14. Table: EffCalPeaks**Properties**

Date Created: 5/7/03 3:43:36 PM Def. Updatable: True
Last Updated: 5/7/03 3:43:36 PM OrderByOn: False
Orientation: 0 RecordCount: 28

Columns

Name	Type	Size	Description/Attributes
EfficiencyID	Number (Long)	4	Efficiency calibration ID
Energy	Number (Double)	8	Library peak energy
Efficiency	Number (Double)	8	Efficiency value calculated from peak area

C.3.3.15. Table: EffCertificate**Properties**

Date Created: 5/7/03 3:43:36 PM Def. Updatable: True
Last Updated: 5/7/03 3:43:36 PM OrderByOn: False
Orientation: 0 RecordCount: 0

Columns

Name	Type	Size	Description/Attributes
CertificateID	Number (Long)	4	Efficiency calibration certificate ID
Description	Text	255	Certificate description
Date	Date/Time	8	Certificate date and time

Name	Type	Size	Description/Attributes
Nuclide	Text	50	Isotope name
Halflife	Number (Double)	8	Library half life
Energy	Number (Double)	8	Library peak energy
Percent	Number (Double)	8	Library branching ratio
ActivityBq	Number (Double)	8	Certificate Activity (Bq)
Uncertainty	Number (Double)	8	Certificate Uncertainty in activity
Units	Number (Integer)	2	Display units for the activity 0=GPS, 1=Bq, >1= μ Ci

C.3.3.16. Table: EnergyCal

Properties

Date Created:	5/7/03 3:43:36 PM	Def. Updatable:	True
Last Updated:	5/7/03 3:43:36 PM	OrderByOn:	False
Orientation:	0	RecordCount:	2

Columns

Name	Type	Size	Description/Attributes
EnergyID	Number (Long)	4	Energy calibration ID
Description	Text	255	Calibration description
Date	Date/Time	8	Calibration date
DetectorID	Number (Long)	4	
Library	Text	255	Full path name of library
nValues	Number (Long)	4	Number energy/channel pairs used in calibration
EIntercept	Number (Double)	8	Energy calibration
ESlope	Number (Double)	8	
EQuadratic	Number (Double)	8	
EChisq	Number (Double)	8	Reduced chisq for energy calibration
FIntercept	Number (Double)	8	FWHM calibration
FSlope	Number (Double)	8	
FQuadratic	Number (Double)	8	

Name	Type	Size	Description/Attributes
FSqrt	Number (Double)	8	Not yet implemented.
FChisq	Number (Double)	8	Reduced chisq for FWHM calibration
FileName	Text	255	Energy calibration file name

Relationships

EnergyCal **Spectra**
 EnergyID EnergyID

Attributes: Enforced
 Attributes: One-To-Many

C.3.3.17. Table: EnergyCalPeaks

Properties

Date Created: 5/7/03 3:43:36 PM Def. Updatable: True
 Last Updated: 5/7/03 3:43:36 PM OrderByOn: False
 Orientation: 0 RecordCount: 0

Columns

Name	Type	Size	Description/Attributes
EnergyID	Number (Long)	4	EnergyCal EnergyID value
Energy	Number (Double)	8	
Channel	Number (Double)	8	
Fwhm	Number (Double)	8	

C.3.3.18. Table: Geometry**Properties**

Date Created:	5/7/03 3:43:36 PM	Def. Updatable:	True
Last Updated:	5/7/03 3:43:36 PM	OrderByOn:	False
Orientation:	0	RecordCount:	0

Columns

Name	Type	Size	Description/Attributes
GeometryID	Number (Long)	4	
Description	Text	50	Description
Date	Date/Time	8	Date geometry correction created
DetectorID	Number (Long)	4	
RefAnalysisID	Number (Long)	4	Reference analysis ID
CurAnalysisID	Number (Long)	4	Current analysis ID
Energy	Number (Double)	8	Peak energy
RefArea	Number (Double)	8	Reference analysis peak area
CurArea	Number (Double)	8	Current analysis peak area
Correction	Number (Double)	8	Geometry correction at this energy

C.3.3.19. Table: IodineEquivalence**Properties**

Date Created:	5/7/03 3:43:36 PM	Def. Updatable:	True
Last Updated:	5/7/03 3:43:36 PM	OrderByOn:	False
Orientation:	0	RecordCount:	0

Columns

Name	Type	Size	Description/Attributes
IodineEQID	Number (Long)	4	
Description	Text	255	
Date	Date/Time	8	Date IEQ data entered

Name	Type	Size	Description/Attributes
Isotope	Text	50	
Value	Number (Double)	8	

C.3.3.20. Table: Nuclides

Properties

Date Created:	5/7/03 3:43:36 PM	Def. Updatable:	True
Last Updated:	5/7/03 3:43:36 PM	OrderByOn:	True
Orientation:	0	RecordCount:	480

Columns

Name	Type	Size	Description/Attributes
NuclideID	Number (Long)	4	
AnalysisResultsID	Number (Long)	4	Analysis Results ID number
Library	Number (Integer)	2	
Nuclide	Text	16	Nuclide name
Abundance	Number (Double)	8	Calculated abundance in Bq
CountingError	Number (Double)	8	Isotope counting error
TotalError	Number (Double)	8	Total error
MDA	Number (Double)	8	MDA
MDA2	Number (Double)	8	Second MDA
HalfLife	Number (Double)	8	Halflife in days
Uncertainty	Number (Double)	8	Uncertainty in halflife
PBCValue	Number (Double)	8	Peak Background Correction value
DecayCorr	Number (Double)	8	Decay time correction factor
DecayAcq	Number (Double)	8	Decay during acquisition factor
DecayCol	Number (Double)	8	Decay during collection factor
DACValue	Number (Double)	8	DAC value
fMDAAct	Yes/No	1	MDA value used for activity
fBelowCritical	Yes/No	1	Area is below critical level for first peak

Name	Type	Size	Description/Attributes
fNucReport	Yes/No	1	
fNoPeaks	Yes/No	1	No peaks in energy range being analyzed
fBelowSens	Yes/No	1	Area is between sensitivity and critical level
fCorrection	Yes/No	1	Decay correction time > specified number of half-lives
fAcquisition	Yes/No	1	Decay during acquisition > specified number of half-lives
fFoundNuc	Yes/No	1	Nuclide present
fTableNuc	Yes/No	1	Nuclide in table
fAbGood	Yes/No	1	All peaks used in abundance calc. were good
fConflict	Yes/No	1	Library energy conflict
fPBCSub	Yes/No	1	PBC subtracted
fTstFailed	Yes/No	1	Failed key line or fraction test
Parent1	Text	50	Parent isotope name
Parent2	Text	50	Parent isotope name
Parent3	Text	50	Parent isotope name
Daughter1	Text	50	Daughter isotope name
Daughter1BR	Number (Double)	8	Branching ratio
Daughter2	Text	50	Daughter isotope name
Daughter2BR	Number (Double)	8	Branching ratio
Daughter3	Text	50	Daughter isotope name
Daughter3BR	Number (Double)	8	Branching ratio
fThermal	Yes/No	1	Thermal neutron activation
fFNAct	Yes/No	1	Fast neutron activation
fThFis	Yes/No	1	Thermal neutron fission
fNatural	Yes/No	1	Natural
fPhoton	Yes/No	1	Photon reaction
fCharged	Yes/No	1	Charged particle reaction
fNoMDA	Yes/No	1	No MDA
fNoTotal	Yes/No	1	Activity not in total

C.3.3.21. Table: Peaks**Properties**

Date Created:	5/7/03 3:43:36 PM	Def. Updatable:	True
Last Updated:	5/7/03 3:43:36 PM	OrderByOn:	True
Orientation:	0	RecordCount:	1353

Columns

Name	Type	Size	Description/Attributes
PeaksID	Number (Long)	4	
AnalysisResultsID	Number (Long)	4	AnalysisResults Table ID
ShapeID	Number (Long)	4	Peak shape ID number
Library	Number (Integer)	2	
Nuclide	Text	50	Nuclide name
SuspectNuclide	Text	50	
Energy	Number (Double)	8	Energy (keV) (library energy if this is a library peak)
EnergyErr	Number (Double)	8	Energy uncertainty
BranchingRatio	Number (Double)	8	Branching ratio (%)
BRErr	Number (Double)	8	Branching ratio uncertainty
TCCCorr	Number (Double)	8	TCC correction to branching ratio
Abundance	Number (Double)	8	Peak activity (Bq)
AbundErr	Number (Double)	8	Error in activity (Bq)
MDA	Number (Double)	8	MDA (Bq)
MDA2	Number (Double)	8	Second MDA (Bq)
Area	Number (Double)	8	Peak area
AreaErr	Number (Double)	8	Error in area (absolute counting uncertainty)
Background	Number (Double)	8	Background
CentroidC	Number (Double)	8	Centroid (channels)
CentroidCErr	Number (Double)	8	Error in Centroid (channels)
CentroidE	Number (Double)	8	Centroid (keV)
FWHM	Number (Double)	8	FWHM (channels)
FWHMErr	Number (Double)	8	Error in FWHM

Name	Type	Size	Description/Attributes
FW10M	Number (Double)	8	FW 1/10th max (channels)
FW25M	Number (Double)	8	FW 1/25th max (channels)
Counts	Number (Double)	8	Net counts
PeakLo	Number (Long)	4	Peak low channel limit
PeakHi	Number (Long)	4	Peak high channel limit
MultiLo	Number (Long)	4	Multiplet low channel limit
MultiHi	Number (Long)	4	Multiplet high channel limit
Multiplet	Number (Integer)	2	Multiplet index
BackLoWidth	Number (Integer)	2	Background width below peak
BackHiWidth	Number (Integer)	2	Background width above peak
BackLo	Number (Double)	8	Background value below peak
BackHi	Number (Double)	8	Background value above peak
BackType	Number (Integer)	2	1=linear, 2=stepped, 4=parabolic
BackIntercept	Number (Double)	8	Parabolic background coefficients
BackSlope	Number (Double)	8	
BackQuad	Number (Double)	8	
BackSlopeAbove	Number (Double)	8	Slope of background above peak (for stepped background)
fPeakOutOfRange	Yes/No	1	Out of energy range being analyzed
fBeta	Yes/No	1	Beta peak
fNoNuclide	Yes/No	1	Nuclide not in the spectrum (Env32 only)
fNoPeak	Yes/No	1	Peak not found during peak search (Env32 only)
fMultiplet	Yes/No	1	Result of deconvolution
fMisshapen	Yes/No	1	Peak grossly out of shape
fFw25mLow	Yes/No	1	$FW25M/2.2 < 0.8 * FWHM$
fFw25mHigh	Yes/No	1	$FW25M/2.2 > 1.2 * FWHM$
fFw10mHigh	Yes/No	1	$FW10M/1.83 > 1.2 * FWHM$
fFwhm1	Yes/No	1	Only one entry in library < FWHM
fFwhm2	Yes/No	1	Two or more entries in library < FWHM
fFwhm3	Yes/No	1	$FWHM(actual) \text{ not in range } (.8FWHM_{calc} < FWHM_{actual} < 1.2FWHM_{calc})$

Name	Type	Size	Description/Attributes
fTooNarrow	Yes/No	1	$HI \leq LO + 0.8 * FWHM$
fNetAreaNeg	Yes/No	1	Area negative
fBadCentroid	Yes/No	1	
fNoCentroid	Yes/No	1	Centroid not found
fSensError	Yes/No	1	Error > sensitivity for peak itself
fSensError1	Yes/No	1	Error > sensitivity for first in-range peak
fDirfitpk	Yes/No	1	Directed fit peak
fTooClose	Yes/No	1	Too close for deconvolution
fInterference	Yes/No	1	Interference corrected — all peaks in this isotope
fHalfLives	Yes/No	1	Too many half-lives for MDA type 17 to be calculated
fActHigh	Yes/No	1	Activity above average
fActLow	Yes/No	1	Activity below average
fStripped	Yes/No	1	Library based peak stripping peak
fMDA	Yes/No	1	MDA used
fRejected	Yes/No	1	This peak not used in activity
fUsed	Yes/No	1	
fIndirCalc	Yes/No	1	Area calculated indirectly
fRejected1	Yes/No	1	First peak in isotope rejected
fDuplicate	Yes/No	1	Duplicate library energies
fUnkMultiplet	Yes/No	1	Unknown in a multiplet
fPBC	Yes/No	1	PBC corrected
fParabolic	Yes/No	1	Parabolic background
fStepped	Yes/No	1	Stepped background used
fTccIso	Yes/No	1	TCC isotope
fTccPeak	Yes/No	1	TCC peak
fUnknown	Yes/No	1	
fGammaRay	Yes/No	1	Gamma ray
fXRay	Yes/No	1	X-ray
fPositron	Yes/No	1	Positron decay
fSingleEsc	Yes/No	1	Single escape

Name	Type	Size	Description/Attributes
fDoubleEsc	Yes/No	1	Double escape
fKeyLine	Yes/No	1	Key line
fNotInAverage	Yes/No	1	Not in isotope activity average
fFirstKey	Yes/No	1	First key line in isotope (by library order)

C.3.3.22. Table: PkShapeCal

Properties

Date Created: 5/7/03 3:43:36 PM Def. Updatable: True
 Last Updated: 5/7/03 3:43:36 PM OrderByOn: False
 Orientation: 0 RecordCount: 0

Columns

Name	Type	Size	Description/Attributes
PkShapeID	Number (Long)	4	Shape calibration ID
Description	Text	255	
Date	Date/Time	8	Calibration date
DetectorID	Number (Long)	4	
ECalID	Number (Long)	4	Energy calibration ID
PkShapeDesc	Text	255	Peak shape description
PkShapeDate	Date/Time	8	Calibration date
PkShapeType	Number (Long)	4	0=Gaussian, 1=Lorentzian, 2=Voigt, 3=Splines, 4=Tails
Eta	Number (Double)	8	Voigt fit eta
STTEnergy1	Number (Double)	8	Short-term tail energy, amplitude, and slope at energy 1
STTAmp1	Number (Double)	8	
STTSlope1	Number (Double)	8	
STTEnergy2	Number (Double)	8	Short-term tail energy, amplitude, and slope at energy 2
STTAmp2	Number (Double)	8	
STTSlope2	Number (Double)	8	
LTTEnergy1	Number (Double)	8	Long-term tail energy, amplitude, and slope at energy 1

Name	Type	Size	Description/Attributes
LTTAmp1	Number (Double)	8	
LTTSlope1	Number (Double)	8	
Chisq	Number (Double)	8	Reduced chisq of fit
minChan	Number (Long)	4	
maxChan	Number (Long)	4	
Energy1	Number (Double)	8	Cubic spline coefficients
Coeff1	Number (Double)	8	
Weight1	Number (Double)	8	
Energy2	Number (Double)	8	
Coeff2	Number (Double)	8	
Weight2	Number (Double)	8	
Energy3	Number (Double)	8	
Coeff3	Number (Double)	8	
Weight3	Number (Double)	8	
Energy4	Number (Double)	8	
Coeff4	Number (Double)	8	
Weight4	Number (Double)	8	
Energy5	Number (Double)	8	
Coeff5	Number (Double)	8	
Weight5	Number (Double)	8	

C.3.3.23. Table: RenLimits**Properties**

Date Created:	5/7/03 3:43:36 PM	Def. Updatable:	True
Last Updated:	5/7/03 3:43:36 PM	OrderByOn:	False
Orientation:	0	RecordCount:	1243

Columns

Name	Type	Size	Description/Attributes
RenLimitID	Number (Long)	4	
AnalysisGroupID	Number (Long)	4	Key to analysis group table
AnalysisResultsID	Number (Long)	4	Key to analysis results table. Zero if this is an average
Nuclide	Text	50	
LibEnergy	Number (Double)	8	Library energy (keV)
Energy	Number (Double)	8	Centroid energy (keV)
Activity	Number (Double)	8	Bq
MDA	Number (Double)	8	
Uncertainty	Number (Double)	8	Relative total uncertainty
AlarmLimit	Number (Double)	8	Bq
WarningLimit	Number (Double)	8	Bq
Area	Number (Double)	8	Peak area

C.3.3.24. Table: RenResults**Properties**

Date Created:	5/7/03 3:43:36 PM	Def. Updatable:	True
Last Updated:	5/7/03 3:43:36 PM	OrderByOn:	False
Orientation:	0	RecordCount:	30

Columns

Name	Type	Size	Description/Attributes
RenResultsID	Number (Long)	4	
Date	Date/Time	8	Analysis date
HistoryID	Number (Long)	4	SubjectHistory table
AnalysisGroupID	Number (Long)	4	
TotalActivity	Number (Double)	8	Total activity in spectrum, or average total activity
IsAverage	Yes/No	1	
IsSum	Yes/No	1	
TotalCounts	Number (Double)	8	Total counts in spectrum (or average total counts)
Subject	Text	100	Based on key being used (Name, Badge, or SSN)
PrintSpc	Yes/No	1	Print spectrum
PrintMCS	Yes/No	1	Print MCS plots
RptZAPeaks	Yes/No	1	Report zero-area peaks
RptZANucls	Yes/No	1	Report zero-area nuclides
IndividualRpt	Yes/No	1	Save individual reports?
CombinedRpt	Yes/No	1	Save combined reports?
CatRpt	Yes/No	1	Concatenate reports?
CombinedDB	Yes/No	1	Save combined results to database?
KeyOn	Number (Long)	4	Key field (Name, Badge, or SSN)
OprPath	Text	255	Pathname of .OPR file
DivWeight	Yes/No	1	Divide activity by weight?

Relationships**SubjectHistory RenResults**

HistoryID 1
HistoryID

Attributes: Enforced
Attributes: One-To-Many

C.3.3.25. Table: ReportParams**Properties**

Date Created: 5/7/03 3:43:36 PM Def. Updatable: True
Last Updated: 5/7/03 3:43:36 PM OrderByOn: False
Orientation: 0 RecordCount: 48

Columns

Name	Type	Size	Description/Attributes
ReportParamsID	Number (Long)	4	Report parameters ID number
Date	Date/Time	8	Date record created
wSigma	Number (Integer)	2	Number standard deviations for uncertainty
Units	Text	12	
Weight	Number (Double)	8	Sample weight or volume
fUncertaintyPercent	Yes/No	1	Report uncertainty in percent
fUncertaintyTotal	Yes/No	1	Report total and counting uncertainty
fuC	Yes/No	1	Yes: Report activity in μCi * Numerator / Denominator. No: activity in Bq * Numerator / Denominator
Numerator	Number (Double)	8	Activity units factor numerator
Denominator	Number (Double)	8	Activity units factor denominator
fListLibPeaks	Yes/No	1	List library peaks
fListIso	Yes/No	1	List isotope activity
fListUnknowns	Yes/No	1	
fListIsoMatrix	Yes/No	1	List peaks by isotope
fPrint	Yes/No	1	Print report

Name	Type	Size	Description/Attributes
fProgram	Yes/No	1	Send report to the program
fGenerator	Yes/No	1	Run report generator
File	Text	255	Report file name
Program	Text	255	Report display program
Template	Text	255	Report generator template name

Relationships

ReportParams **AnalysisParams**
 ReportParamsID ReportParamsID

Attributes: Enforced
 Attributes: One-To-Many

C.3.3.26. Table: Spectra

Properties

Date Created: 5/7/03 3:43:36 PM Def. Updatable: True
 Last Updated: 5/7/03 3:43:36 PM OrderByOn: False
 Orientation: 0 RecordCount: 48

Columns

Name	Type	Size	Description/Attributes
SpectrumID	Number (Long)	4	
DetectorID	Number (Long)	4	
EnergyID	Number (Long)	4	Original energy calibration
EfficiencyID	Number (Long)	4	Original efficiency calibration
SampleDesc	Text	255	Sample description
AcquisitionDate	Date/Time	8	Spectrum acquisition date (local time)
TimeBias	Number (Long)	4	Difference in minutes between UTC and local time
LiveTime	Number (Double)	8	Live time (seconds)

Name	Type	Size	Description/Attributes
RealTime	Number (Double)	8	Real time (seconds)
SpcFile	Text	255	

Relationships

EnergyCal **Spectra**
 EnergyID EnergyID

Attributes: Enforced
 Attributes: One-To-Many

EffCal **Spectra**
 EfficiencyID EfficiencyID

Attributes: Enforced
 Attributes: One-To-Many

C.3.3.27. Table: Subject

Properties

Date Created: 5/7/03 3:43:36 PM Def. Updatable: True
 Last Updated: 5/7/03 3:43:36 PM OrderByOn: False
 RecordCount: 4

Columns

Name	Type	Size	Description/Attributes
SubjectID	Number (Long)	4	
Name	Text	64	Last name
First	Text	64	First name
MiddleInitial	Text	2	Middle initial
Badge	Text	50	Badge number (not necessarily unique)
SSN	Text	50	Social Security Number

Relationships

Subject **SubjectHistory**
SubjectID SubjectID

Attributes: Enforced
Attributes: One-To-Many

C.3.3.28. Table: SubjectHistory

Properties

Date Created:	5/7/03 3:43:36 PM	Def. Updatable:	True
Last Updated:	5/7/03 3:43:36 PM	OrderByOn:	False
Orientation:	0	RecordCount:	30

Columns

Name	Type	Size	Description/Attributes
HistoryID	Number (Long)	4	Subject history
SubjectID	Number (Long)	4	Key from Subject table
CWTID	Number (Long)	4	Key from ChestWallThickness table
Date	Date/Time	8	Date comment added
Comment	Text	128	
Company	Text	50	Company or division
IntakeDate	Date/Time	8	
Weight	Number (Double)	8	kg
Height	Number (Double)	8	cm
ChestWallThickness	Number (Double)	8	cm
Option1	Text	128	
Option2	Text	128	
Option3	Text	128	
Option4	Text	128	
Opt1Text	Text	50	Option 1 description entered by the operator
Opt2Text	Text	50	Option 2 description entered by the operator

Name	Type	Size	Description/Attributes
Opt3Text	Text	50	Option 3 description entered by the operator
Opt4Text	Text	50	Option 4 description entered by the operator

Relationships

SubjectHistory **RenResults**
 HistoryID HistoryID

Attributes: Enforced
 Attributes: One-To-Many

Subject **SubjectHistory**
 SubjectID SubjectID

Attributes: Enforced
 Attributes: One-To-Many

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APPENDIX D. SYSTEM AND JOB ERROR MESSAGES

Errors are displayed in warning boxes, or in some cases in the information line at the bottom of the window.

Acquisition Failure (JOB Error 11)

For some reason an acquisition function failed from a .JOB file.

Already started.

Detector already active when a Start Acquisition command was issued.

Altering Detector data.

Restoring data to a Detector would destroy the data already there.

Amplifier not pole-zeroed.

Warning from an MCB with automatic pole zero, indicating that the Detector should be pole-zeroed.

Analysis Completed for ...

RENWAN.EXE has finished executing.

Analysis Error <n>

A call to CLAN1.DLL has been completed, but an error was encountered. The error code <n> has the following meaning:

<u>Error #</u>	<u>Warning #</u>	<u>Reason</u>
1	1	Read error in UFO peak record
1	2	Read error in UFO nuclide record
2	1	Write error in UFO peak record
2	2	Write error in UFO nuclide record
3	1	Invalid acquisition date and time
4	0	Illegal absorption correction
5	1	Read error in spectrum file

Analysis Failed!

RENWAN.EXE has finished executing, but an error was encountered. Refer to the "RENWAN completion codes..." message.

Analysis Failed (Job Error 18)

The ANALYZE command failed (look for the RENWAN error code for specifics).

Analyzing (Please Wait) ...

Analysis via `DLAN1.DLL` is being executed.

Attempt to dynamically link to a task! (WinExec error 5)

Error encountered trying to spawn `RENWAN.EXE` or some other application program.

Auto Calibration failed (Job Error 21)

An error occurred when the `CALIBRATE_AUTO` command was executed.

Auto PZ aborted.

The MCB Auto PZ function was aborted (by `<Esc>`).

Buffer and Detector not same size or segments.

Error when trying to restore data which does not match the Detector configuration.

Calibration per channel wrong.

Error when trying to calibrate spectrum, arising whenever the calibration slope would be 0, negative or greater than 100 units per channel.

Can't allocate memory for library.

Attempting to load a library for which there is not enough room in memory. Best dealt with by trying again or removing some other applications from memory.

Can't find any more peaks!

A peak could not be found in the direction indicated by the function button pressed.

Can't Find Any More ROIs.

Attempting to index to the next ROI in a direction for which no more ROIs can be located.

Can't read library file.

Attempting to open or read the library file resulting in some kind of file I/O error, usually because the file doesn't exist, but also possibly because the disk is defective.

Can't RESTORE to acquiring Detector.

Error preventing the Restore function from altering data in a Detector in which one or more segment(s) are actively acquiring data.

**Can't Run Protected Mode Application in Real Mode!
(WinExec error 18)**

Error encountered trying to spawn `RENWAN.EXE` or some other application program.

Can't Run Second Instance of this .EXE (multiple writeable data segments)! (WinExec error 16)

Error encountered trying to spawn [RENWAN.EXE](#) or some other application program.

Can't Run Second Instance of this .EXE (Non-shareable DLL in use)! (WinExec error 17)

Error encountered trying to spawn [RENWAN.EXE](#) or some other application program.

Cannot get valid Spectral Data!

The File/Save function was not presented with valid spectral data; usually the result of problems obtaining data from a Detector.

Comm. Failure!

Detector communication failure, most likely resulting from a timeout (the Detector failed to respond within a reasonable period of time).

Configuration failed!

Attempted reconfiguration failed, most likely because of some conflict with Detectors physically installed.

Could not properly fit the peak.

Function requiring a fitted peak could not obtain an acceptable peak, probably because of too few counts, too narrow, or non-Gaussian peak shape, or bad statistics such as calculated sigma-squared less than zero.

Couldn't get background subtracted ROI.

A function requiring a background subtracted ROI couldn't obtain such, probably because there was no ROI at the point specified, or maybe because there weren't statistically significant counts above background.

Default Printer Failed! Undefined at Control Panel?

The REPORT or PRINT function was aborted because the default system printer has not been properly set up. Go to the Printers function in Windows Control Panel, install the appropriate printer, and select it as outlined in the Microsoft Windows documentation.

Detector #.. ; ; Error ... (Macro) ... (Micro)

An unresolved error originating in the Detector. The offending Detector command is shown, together with the macro and micro error codes. If the error persists, the error codes should be recorded and the factory should be contacted. These error codes are explained in the hardware manual for the Detector.

Detector busy or Segment not responding.

This indicates the Detector was unable to respond within a certain time limit, due to other activities, such as multiple instances of Renaissance accessing the Detector at the same time, or otherwise heavy use of the Detector interface.

Detector does not support Field Mode (Job Error 19)

An attempt was made to execute the LOOP_SPECTRA or VIEW command on a Detector that does not support Field Mode.

Detector Error!

The selected Detector could not be STARTed or STOPped due to some unresolved error condition.

Detector Not Located.

A Detector could not be located at the configured address.

Do you want to save buffer?

A function that would destroy the buffer (such as COPY or EXIT) queries the user unless the buffer has not been modified since last being saved.

Do you want to save Library?

The nuclide library has been modified by the library editor, but the user has not yet saved the changes.

DOS 4.0 Application! (WinExec error 13)

Error encountered trying to spawn RENWAN.EXE or some other application program.

Error opening file.

If trying to write a file, this would indicate a disk controller problem such as a full disk. If trying to read a file, this would indicate that the filename specified could not be found.

Error reading file -- STRIP aborted.

Could not read the file requested for stripping.

Error reading file.

File read error is usually a result of damaged media.

Error writing file.

File write error is usually a result of damaged media or full disk.

.EXE for earlier version of Windows! (WinExec error 15)

Error encountered trying to spawn `RENWAN.EXE` or some other application program.

Failure obtaining ROI (or Peak).

A function that requires a defined ROI (or Peak, in the case of the Calibrate function) when the marker is not placed in a channel with an ROI bit set (and if a Peak is not very close by).

Failure of Detector function (JOB Error 12)

This error arises from a JOB that encounters an error when trying to access a Detector.

File already exists!

If the file output function requested would write a file with the same name as another file that already exists, the user is prompted for confirmation of the operation by this warning. See also "OK To Overwrite Existing File?"

File is wrong size Can't STRIP.

The STRIP function requires a compatible file for stripping from the spectrum in memory; i.e., must contain the same number of channels.

File Not Found! (WinExec error 2)

Error encountered trying to spawn `RENWAN.EXE` or some other application program.

Fine gain is at limit of ...

This message appears in the Information Line when an attempt is made to change the MCB gain setting with the keyboard function, but while the MCB cannot be decreased or increased any further.

FWHM Fit Error Exceeds 25%.

The peaks entered in an energy calibration produced a FWHM fit with an error on at least one peak greater than 25%.

Hardware failure!

This message appears as the result of a Detector execution error with micro code 137, indicating a hardware failure.

High voltage not enabled.

START was attempted on a 92X while the high voltage was not enabled.

Illegal Entry!

Certain values are not permitted in manual dialog entries or tables.

Illegal Detector.

The Detector number for the requested function was not identifiable as part of the active configuration.

Incorrect Windows Version! (WinExec error 10)

Error encountered trying to spawn [RENWAN.EXE](#) or some other application program.

Insufficient memory.

System memory has been exhausted. Usually, this error arises when the buffer cannot be created due to insufficient available memory in the system. Sometimes this error can be eliminated by attempting the buffer operation again, but this is not recommended due to the marginal state of the system, which might result in other errors.

Invalid Argument (Job Error 17)

The ROI limits in SET_PRESET_UNCERTAINTY command were invalid. The VIEW command specified a spectrum that was not stored in the Detector. The ZOOM command did not specify valid integers.

Invalid Command or Missing Argument. (JOB Error 4)

A syntax error in a JOB, meaning that a command could not be interpreted; usually the result of misspelling.

Invalid Device or Segment!

This message arises as a result of a Detector execution error with micro code 134, indicating that an invalid device or Segment was selected.

Invalid .EXE file! (WinExec error 11)

Error encountered trying to spawn [RENWAN.EXE](#) or some other application program.

Invalid File Format!

A function to recall a file could not obtain data in the proper format.

Invalid library format!

An attempt was made to load a nuclide library from a file which was not in the proper format.

Invalid LOOP count. (JOB Error 7)

The LOOP statement could not be executed properly in a JOB.

Invalid Start Date/Time -- Battery Backup Lost??

A 919 or 92X Detector contained an unrecognizable start date. This is usually an indication that the backup power was lost.

Invalid Start Record.

No valid Start Record file could be found to provide the start date/time for an installed 917 or 918 Detector.

JOB Aborted or Premature EOF (JOB Error 1)

A JOB was aborted by the user, or an End-of-File was encountered while trying to obtain a command from the executing .JOB file.

JOB Error.

A generic error message indicating that an error was encountered while executing a .JOB file. Usually some explanatory phrase is given.

**Library requires separate data segments for each task!
(WinExec error 6)**

Error encountered trying to spawn RENWAN.EXE or some other application program.

Library too large to load.

Library files larger than 65,000 bytes are not admissible as internally resident libraries. (However, any size library can be used for Master Library.)

Multiple-device Detector added.

While performing the CONFIGURATION dialog function ADD, a 919 device type was specified, and there is room to add up to four Detectors for each 919 device added; the ADD function is automatically repeated for each possible Detector number.

Must have a value greater than zero!

Certain analysis or library table entries require values greater than 0.0.

Must have valid calibration!

Certain analysis functions cannot be performed if the calibration is invalid.

Must select 92X type Detector!

This error results from an attempt to perform a function available for only 92X-type Detectors.

Need an ROI at the desired peak location.

The Stabilizer function requires a valid ROI at the desired peak.

No Buffer to RESTORE from!

The RESTORE function requires a valid spectrum in buffer.

No close library match.

The REPORT function could not obtain a library entry close enough to the located peak.

No File Name.

A file function was requested without specifying the filename adequately.

No more library peak energies!

A peak search was attempted in a direction where no more can be found.

No more multiplets!

The multiplet finding sidebar function in Analysis Results display mode cannot find any more multiplets in the direction indicated.

No more peaks for this nuclide!

The “peaks within nuclide” sidebar function in Analysis Results mode cannot find any more peaks within the selected nuclide.

No more unknown peaks!

The unknown peak finding sidebar function in Analysis Results display mode cannot find any more unknown peaks in the direction indicated.

No peaks found!

The peak search function could not find any valid peaks in the spectrum.

No ROI found to report!

The REPORT function could not find any ROIs in range.

No ROI There To Clear.

The **Clear ROI** function (the or <Delete> key) requires at least one channel at the marker with the ROI bit set.

No segment selected.

The Detector function could not be performed because no Segment was selected.

Not Allowed During Acquisition!

An execution error (micro 135) arising from the Detector, indicating that the Detector command is not allowed while acquisition is in progress.

Not Allowed During Current Mode!

An execution error arising from the Detector (micro 136), indicating that the Detector command attempted is not allowed in the current mode of operation.

Not enough data points for fit.

Efficiency calibration fit for specified type requires a minimum number of table entries for that type; e.g., for a polynomial fit, six or more points are required.

Not enough memory STRIP aborted.

The STRIP function temporarily allocates enough memory to read the file, but the allocation failed in this case, probably due to insufficient available memory in the system. The STRIP function is discontinued.

Not enough memory for COMPARE.

The COMPARE mode could not be executed due to insufficient memory for the second spectrum.

NOTE: Settings for SEGMENT <n>

Renaissance is informing the user in the case of multi-segment Detector that he is performing settings (e.g., through an ASK function) on a specific segment only.

OK to add another device?

When a 919 device is being added in the CONFIGURATION dialog, the user is prompted for confirmation before automatically proceeding with the addition of up to four Detector numbers.

OK to attempt another instance?

Attempt to start an analysis (via [RENWAN.EXE](#)) while a previous analysis has not yet finished, or had been aborted abnormally. Renaissance is asking the user to allow it to continue with this operation in case it is not properly sensing the state of the previous analysis. If the user permits this to continue (by answering Yes), but if the previous instance was actually still running, then another “WinExec()...” error will occur.

OK to destroy contents of Detector?

The RESTORE function prompts the user for confirmation before writing the contents of the buffer into the Detector.

OK to overwrite ‘...’ ?

A file output function discovered that the specified filename already exists, and will only overwrite the file after the user confirms his intentions. See also “File already exists!”

OK to save changes?

The user is being prompted to allow the system to save a modified file such as a library file, table file, or sample-type defaults file.

OK to use it anyway?

A new configuration was applied but failed due to some conflict with the Detectors physically present; it is possible to use the configuration anyway by answering Yes to this query.

OS/2 Application! (WinExec error 12)

Error encountered trying to spawn RENWAN.EXE or some other application program.

Out of Memory! (WinExec error 0)

Error encountered trying to spawn RENWAN.EXE or some other application program.

Path Not Found! (WinExec error 3)

Error encountered trying to spawn RENWAN.EXE or some other application program.

Peak rejected for asymmetry.

Peak statistics could not be obtained for the function due the calculated non-Gaussian asymmetry of the obtained peak.

Preset already reached.

Acquisition START was attempted on a Detector or Segment which had already satisfied the preset condition(s) in some way.

Presets can't be changed during acquisition.

Changes in the preset condition(s) are not allowed while the Detector is actively acquiring.

Presets not programmed to Detector correctly!

Usually a failure of the selected Detector to accept the commands from Renaissance to program presets. Often the result of improper configuration or faulty interface.

Previous analysis did not run to completion!

Attempt to start an analysis (via RENWAN.EXE) while a previous analysis has not yet finished, or had been aborted abnormally. See "OK to attempt another instance?"

Problem with Buffer. (JOB Error 2)

A JOB error resulting from some problem with the buffer, usually indicating insufficient memory to create or enlarge the buffer as needed.

Problem with Calculation. (JOB Error 13)

A JOB error resulting from a problem with a calculation.

Problem with RECALL. (JOB Error 10)

The RECALL statement could not be executed in a JOB.

Problem with REPORT. (JOB Error 14)

The REPORT function could not be exercised in a JOB.

Problem with SAVE. (JOB Error 9)

The SAVE function could not be executed in a JOB.

QA failed (Job Error 22)

An error occurred when the QASAMPLE or QABACKGROUND command was executed.

Sample Changer Hardware Failure. (JOB Error 16)

The Sample Changer hardware handshake failed in some way; usually the result of too much time before SAMPLE READY is obtained.

Start/Save/Report sequence aborted!

Start/Save/Report sequence aborted (usually by manual intervention, but also resulting from certain errors.)

Start/Save/Report waiting for completion of previous analysis...

A status message indicating that the **Start/Save/Report** sequence has been suspended while waiting for completion of an ongoing analysis.

Table is Full!

A limit of 96 entries is allowed in the calibration table.

There are no stored spectra to view (Job Error 20)

An attempt was made to execute the LOOP_SPECTRA or VIEW command on a Detector that does not have any stored spectra.

The Serial I/O Command timed out (Job Error 24)

The WAIT_SERIAL command timed out before receiving a response from the selected Detector.

The Serial I/O Response did not match (Job Error 25)

The WAIT_SERIAL command did not time out, however, the actual and expected responses did not match.

The WAIT program was not started by Renaissance (Job Error 23)

All programs “WAITed for” have to be started by Renaissance.

Token Error.

A token error in a JOB, meaning that some argument to the command was invalid or out of context.

Unable to CALL -- Invalid file name. (JOB Error 8)

A JOB error resulting from a problem with the CALL function (usually because the file does not exist).

Unable to COMPARE files of different sizes.

The COMPARE function requires compatible files.

Unable to cut peak or peak not selected!

The library editor **Cut** function or Analysis Results **Delete** library peak function is complaining that it cannot cut or delete a peak from the library for some reason, usually because a peak is not selected.

Unable to open file -- STRIP aborted.

The STRIP function is aborted if the file cannot be read.

Unable to open file for COMPARE.

The COMPARE function is aborted if the second spectrum cannot be read.

Unable to Read Specified File. (JOB Error 3)

A file input/output error encountered while executing a JOB.

Unable to RUN non-executable program. (JOB Error 6)

The specified program could not be RUN from a JOB.

Unable to strip Detector memory.

The stripping function must be performed in the buffer.

Unknown .EXE type! (WinExec error 14)

Error encountered trying to spawn RENWAN.EXE or some other application program.

Unknown (misspelled) Command. (JOB Error 5)

A command in a .JOB file could not be executed because it could not be interpreted as a valid command (usually a result of misspelling).

WAIT program was not started by Renaissance (JOB Error 23)

All programs "WAITed for" have to be started by Renaissance. In Windows 95/98/NT, the 32-bit programs are completely independent.

WAN32 completion codes: i=<i> errnum=<e> warnum=<w>

The following numbers are returned by the analysis routines and displayed on the information line. Renaissance analysis engine returns values from either the analysis engine or the Renaissance engine.

If i is 0, there was no error. If i is 1, then the error came from WAN32 and the error is in the first table. If i is 2, then the error came from Renaissance and the error is in the second table.

RENWAN Error Messages (i = 1):

<u>Error #</u>	<u>Warning #</u>	<u>Reason</u>
1	?	Invalid spectrum filename
1	1	Read error in UFO peak record
1	2	Read error in UFO nuclide record
1	3	Read error in spectrum non-data record
1	4	Read error in UFO file
1	200	Attempt to read start channel after stop channel
1	201	Read error on disk for .CHN files
1	202	Read error on disk for .SPC files
1	203	Attempt to read invalid spectrum file type
2	0	Illegal filename
2	1	Write error in UFO peak record
2	2	Write error in UFO nuclide record
2	3	Write error in other UFO records
2	4	Invalid record for UFO file
2	7	Write error on report file
2	8	Invalid record request for table file
3	0	Invalid acquisition date and time
4	0	Illegal absorption correction
4	3	Spectrum not found
5	0	Read error in spectrum file
5	3	Spectrum wrong file type

<u>Error #</u>	<u>Warning #</u>	<u>Reason</u>
6	1	Library not sorted
6	2	Read error on library
6	3	Invalid record request for library
6	4	Library not found
10	Error #	System error (e.g., math overflow)

Renaissance analysis error and warning numbers (i = 2):

<u>Error #</u>	<u>Warning #</u>	<u>Reason</u>
0		Warning, not an error
0	1	More than 500 peaks in the library. First 500 used
1		Library error
1	1	Library File error
1	2	Invalid library file header
1	3	Corrupt or missing library file
1	4	No peaks in library
1	5	ASCII library file might be corrupted.
1	13	Data type mismatch
1	53, 75, 76	Library file not found
1	71	The disk drive containing the library is not ready
2		Invalid configuration entry
2	1	No matrix
2	2	Gross Weight = 0
2	3	Tare Weight > Gross Weight
2	3	Gross Weight = 0 And GeometryMode > 1
2	4	MatrixDensity too small
2	5	Matrix not found
2	10	Container thickness too small
2	11	Container density = 0
2	12	Invalid U or Pu weight
2	13	Container not found in database
2	20	Detector standoff = 0
2	21	Detector height = 0
2	22	Detector not found in database
2	23	Collimator not found in database
2	30	Invalid container values
2	31	Invalid matrix values
3	1	Attenuation coefficients not found

Error #	Warning #	Reason
4		Analysis errors
4	1	Could not read analysis engine out of spc file
4	2	No peaks found
4	3	Error reading peaks from database
4	4	Invalid input report format
4	5	Invalid analysis engine

Warning 128.**Warning 64.****Warning 8.**

All three of the above messages are the result of Detector Start or Stop warnings and are hardware dependent.

Warning: Buffer was modified.

When the program is being closed, this message will appear if the buffer spectrum had been modified but not yet saved to disk. Thus the user is prompted for confirmation of possibly saving the buffer before proceeding to terminate the application.

Warning: File Changes.

The table editor sensed that modifications were made, but the user had not saved the file. See "OK to save changes?"

Warning: Library was modified.

The library was edited or modified for analysis but not yet written to a file. See "OK to save changes?"

Warning: Sample Type Defaults changed

Analysis options have been modified but not yet written to selected file. See "OK to save changes?"

WinExec() Error <n>!

Error encountered trying to spawn [RENWAN.EXE](#) or some other application program; refer to Windows SDK documentation for meaning of code <n>.

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APPENDIX E. RENAISSANCE ERROR MESSAGES

There are two types of Renaissance errors: Group I errors are displayed in warning boxes. Group II errors appear in the Supplementary Information Line at the bottom left of the window.

E.1. Group I

Activity Alarm

This error message appears on the Operator screen when the activity equals the alarm limit.

Activity Warning

This error message appears on the Operator screen when the activity equals the warning limit.

Acquisition Failure

An acquisition function failed from a .JOB file.

Cannot get valid Spectral Data!

The **File/Save** function was not presented with valid spectral data; usually the result of problems obtaining data from a Detector.

Can't read library file.

Attempt to open or read the library file resulted in some kind of file I/O error; usually because the file doesn't exist, but also possibly because the disk is defective.

Date must be of form dd-Mon-yy. Year must be > 1980

The date entered must be in this form: 12-Apr-1994, with the month abbreviated to three letters. The year must be after 1980.

Detector busy or not responding.

This indicates the Detector was unable to respond within a certain time limit, due to other activities, such as heavy use of the Detector interface.

Exceeded Activity ALARM Limit for Nuclide

The activity has exceeded the alarm limit. This error only appears in the Operator program.

Exceeded Activity WARNING Limit for Nuclide

The activity has exceeded the warning limit. This error only appears in the Operator program.

Error During Print - Print Aborted.

An error occurred while printing, so printing has discontinued. Check the printer for problems such as paper jams, no paper, low toner, loose cable, etc.

Error Opening File

If trying to write a file, this indicates a disk controller problem such as a full disk. If trying to read a file, this indicates that the filename specified could not be found.

Error Reading File

File read error is usually a result of damaged media.

Error Writing File

File write error is usually a result of damaged media or full disk.

Failure of MCB function

This error arises from a JOB that encounters an error when trying to access a Detector.

Illegal Entry!

Certain values are not permitted in manual dialog entries or tables.

Illegal MCB!

The Detector number for the requested function was not identifiable as part of the active configuration.

Illegal Time

The time entered must be in the form hh:mm:ss. For example, 08:12:55 is 8:12 o'clock and 55 seconds.

Illegal Value for Count Time

Count Time for source must be > 0 .

Incorrect Password Verification

The password given is incorrect. Enter the correct password.

Insufficient memory.

System memory has been exhausted. Usually, this error arises when the buffer cannot be created due to insufficient available memory in the system. Sometimes this error can be eliminated by attempting the buffer operation again, but this is not recommended because of the marginal state of the system, which might result in other errors.

Invalid Command or Missing Argument

A syntax error in a JOB, meaning that a command could not be interpreted; usually the result of misspelling.

Invalid File Format!

A function to recall a file could not obtain data in the proper format.

Invalid LOOP count

The LOOP statement could not be executed properly in a JOB.

Invalid Path Specification

The path given is not valid. Enter the valid path.

Invalid Source Name

Source Name must contain at least one printing, non-blank character.

Job aborted or Premature EOF

A JOB was aborted by the user, or an end-of-file was encountered while trying to obtain a command from the executing .JOB file.

Job Error # at line number #

An error was encountered while executing a .JOB file at the line number specified.

Illegal Segment

A JOB tried to specify a Segment number that was invalid for the selected Detector or buffer.

Invalid library format!

An attempt was made to load a nuclide library from a file which was not in the proper format.

Library too large to load.

Library files larger than 65,000 bytes are not admissible as internally resident libraries. (However, any size library can be used as the Master Library.)

Mark Peak for Calibration

Make sure the marker is in the ROI.

Must be in Buffer to RECALL file

The **Recall** option under the **File** menu is grayed (disabled) unless the buffer is selected.

No peaks found!

The peak search function could not find any valid peaks in the spectrum. Error during analysis (library or calibration error).

Not enough memory for COMPARE

The Compare mode could not be executed due to insufficient memory for the second spectrum.

Password File Not Found -- OK to Create?

The password file name specified could not be found. Click on **OK** to create a new password file.

Problem with Buffer

A JOB error resulting from some problem with a buffer, usually indicating insufficient memory to create or enlarge a buffer as needed.

Problem with Calculation

A JOB error resulting from a problem with a calculation.

Problem with RECALL

The RECALL statement could not be executed in a JOB.

Problem with REPORT

The REPORT function could not be exercised in a JOB.

Problem with SAVE

The SAVE function could not be executed in a JOB.

QA Background Alarm

The QA background has exceeded the alarm limits.

QA Data spans less than 1 hour -- Unable to plot

The quality assurance data must span at least 1 hour in order to be used for a plot.

QA Peak Energy Alarm for peak at keV

The QA peak energy has exceeded the alarm limits.

QA Peak Shape Alarm for peak at keV

The QA peak shape has exceeded the alarm limits.

QA Total Activity Alarm

The QA total activity has exceeded the alarm limits.

Table is Full!

A limit of 96 entries is allowed in the calibration table.

Top or Bottom Detector:**No Peak found at specified keV in Source****Perform Calibration in Learn Mode.**

While running a calibration sequence, an error was found. The calibration sequence needs to be redone from **Calibrate/Learn Calibration Sequence**.

Unable to CALL -- Invalid file name

A JOB error resulting from a problem with the CALL function (usually because the file does not exist).

Unable to COMPARE files of different sizes.

The Compare function requires compatible files.

Unable to Read Specified File

A file input/output error encountered while executing a JOB.

Unable to RUN non-executable program

The specified program could not be RUN from a JOB.

Unknown (misspelled) Command

A command in a .JOB file could not be executed because it could not be interpreted as a valid command (usually a result of misspelling).

WinExec() Error 1!

Error encountered trying to spawn WAN1.EXE or some other application program.

E.2. Group II

Background Acquisition Complete

The background count is finished.

Can't find any more ROIs.

Attempting to index to the next ROI in a direction for which no more ROIs can be located.

Couldn't get background subtracted ROI.

A function requiring a background-subtracted ROI couldn't obtain such, probably because there was no ROI at the point specified, or perhaps because there were no statistically significant counts above background.

Could not properly fit the peaks.

Function requiring a fitted peak could not obtain an acceptable peak, probably because of too few counts, too narrow or non-Gaussian peak shape, or bad statistics such as calculated sigma-squared less than zero.

Failure obtaining ROI (or Peak).

A function that requires a defined ROI (or Peak, in the case of the Calibrate function) when the marker is not placed in a channel with an ROI bit set (and if a Peak is not very close by).

FWHM Fit Error Exceeds 25%

The peaks entered in an energy calibration produced a FWHM fit with an error on at least one peak greater than 25 percent.

Must have a value greater than zero!

Certain analysis or library table entries require values greater than 0.0.

Must select MicroACE-type MCB!

Detector Control. This error results from an attempt to perform a function available for only MicroACE-type Detectors.

No ROI There To Clear.

The ROI Clear function (<Delete>) requires at least one channel at the marker with the ROI bit set.

Presets can't be changed during acquisition.

Changes in the preset condition(s) are not allowed while the Detector is actively acquiring.

Presets not programmed to Detector correctly!

Usually a failure of the selected Detector to accept the commands from Renaissance-Ge to program presets. Often the result of improper configuration or faulty interface.

ROI was not BEGUN (no start channel defined)

The ROI could not be BEGUN since no start channel was defined. Define the start channel and try again to mark the ROI.

Unable to Fit Peak Please Mark Again.

Peak marked for calibration could not be fit to Gaussian curve. Please try marking it again.

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zoom	23		
WINPLOTS	375		
command line	380		