Renaissance®-32 Supervisor
Whole-Body Counter Software for
Microsoft® Windows® 2000 Professional and XP® Professional

REN Plus-B32
Software User’s Manual

Software Version 4.1
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NOTE!

We assume that you are thoroughly familiar with 32-bit Microsoft Windows usage and terminology. If you are not fully acquainted with the Windows environment, including the use of the mouse, we strongly urge you to read the Microsoft documentation supplied with your Windows software and 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>. 
INSTALLATION

If you are installing a new multichannel buffer (MCB) in addition to RENAISSANCE, or if your MCB and/or new RENAISSANCE is accompanied by a CONNECTIONS-32 Driver Update Kit (Part No. 797230), follow the installation instructions that accompany the driver update kit.

For information on installation and configuration, hardware driver activation, network protocol configuration, and building the master list of instruments accessible within RENAISSANCE, see Chapter 2 (page 5) and the accompanying ORTEC MCB CONNECTIONS-32 Hardware Property Dialogs Manual.
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 1.3) 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 (Part No. 753800).
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, 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 personal 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.

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1In this manual, “Detector” 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.
1. INTRODUCTION

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 Detector hardware on which a spectrum was collected. Also, data can be analyzed directly in the Detector hardware memory, as well as stored directly from the Detector to disk.

Renaissance uses the network features of Windows so it can be used to control ORTEC CONNECTIONS-compliant 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 PC cannot access the Renaissance database on other PCs. In a facility where more than one PC 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.

1.2. Operating System Requirements

Renaissance operates on any PC running Microsoft Windows 2000 Professional or XP Professional. Renaissance requires 100 or more megabytes of disk space for the program, database, and spectrum files. For PCs with a memory-mapped MCB interface, no other interface can use memory mapped into page D of the PC memory map (see the accompanying ORTEC MCB CONNECTIONS Hardware Property Dialogs Manual, Part No. 931001, hereinafter called the “MCB Properties Manual”). Data can be saved or retrieved from any number of removable or fixed drives.

1.3. Detectors

Renaissance will control 1 to 250 NaI and HPGe Detectors at one time. These Detectors can be any of ORTEC’s CONNECTIONS-32-compliant MCBs — this manual describes two of our newest MCBs, the DSPEC Pro™ and the digiBASE™. The Detectors are configured by the supervisor and assigned unique identification numbers and names. The Detectors can be divided into groups for ease of use. The supervisor can display the data from any of these available Detectors, or can open spectra from disk into buffer windows. The operator can display the data from available Detectors.

Renaissance supports ORTEC MCBs interfaced to the computer via Ethernet, the serial port, USB port, an appropriate adapter card and cable, and the printer-port adapter.

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2However, the MCBs can be any mixture of CONNECTIONS-compliant the following types of units, properly installed and hardware-configured. See our catalog or visit our website at www.ortec-online.com for a complete listing of available instruments.
Renaissance correctly displays and stores a mixture of different sizes of spectra. Several Renaissance windows can be open in the program at one time, displaying Detectors, buffers, spectrum files from disk, and data analyses.
2. INSTALLATION

Installing Renaissance takes just a few minutes. If you received a *CONNECTIONS-32* Driver Update Kit (Part No. 797230) with your Renaissance installation CD, or if you purchased one or more new ORTEC MCBs in addition to Renaissance, software installation will be a two-step process.

**NOTE** ORTEC *CONNECTIONS-32* software products are designed to operate correctly only for users with full Administrator privileges. *Limiting user privileges could cause unexpected results.*

### 2.1. Installing Renaissance

1. Insert the Renaissance CD. If it does not autorun, go to the Windows Taskbar and click on **Start**, then **Run**... In the Run dialog, enter `D:\disk1\setup.exe` (use your CD-ROM drive designator), then click on **OK**. This will start the installation wizard. Click on **Next** and follow the wizard prompts.

2. If you also received a *CONNECTIONS-32* Driver Update Kit (with either Renaissance or a new ORTEC MCB), skip to Step 5 for now. You will be directed later to return to this section to select your instrument drivers. If you *did not receive a Driver Update Kit*, continue to Step 3.

3. On the Instrument Setup page, mark the checkbox(es) that corresponds to the instrument(s) physically attached to your PC; an example Instrument Setup dialog is shown in Fig. 1. To see more information on each instrument family, click on the family name and read the corresponding **Item Description** on the right side of the dialog.

   If you already have an ORTEC *CONNECTIONS-32* application installed on this PC, you probably already have ORTEC *CONNECTIONS-32* instruments attached to it. If so, they will be included on the **Local Instrument List** at the bottom of the dialog, along with any new instruments. Existing instruments (those previously configured before this installation) do not have to be powered on during this part of the installation procedure.

4. If you want other computers in a network to be able to use your MCBs, leave the **Allow other computers to use this computer’s instruments** marked so the MCB Server program will be installed. Most users will leave this box marked for maximum flexibility.

   **NOTE** If your PC uses Windows XP and you wish to use or share ORTEC MCBs across a network, *be sure to read Section 2.1.2.*

5. Click on **Done**. The installation wizard will resume copying files.
6. At the end of the wizard, restart the PC to complete software installation. Upon restart, remove the Renaissance CD from the drive.

7. After all processing for new plug-and-play devices has finished, you will be ready to configure the MCBs in your system. Connect and power on all local and network ORTEC instruments that you wish to use, as well as their associated PCs. Otherwise, the software will not detect them during installation. Any instruments not detected can be configured at a later time.

8. If any of the components on the network is a DSPEC Plus™, ORSIM™ II or III, MatchMaker, DSPEC®, 92X-II, 919E, 920E, 921E, or other module that uses an Ethernet connection, the network default protocol must be set to the **IPX/SPX Compatible Transport with NetBIOS** selection on all PCs that use **CONNECTIONS** hardware. For instructions on making this the default, see the network protocol setup discussion in the accompanying MCB Properties Manual.
9. To start the MCB Configuration program on your PC, click on Start, Programs, Renaissance, and MCB Configuration.

The MCB Configuration program will locate all of the (powered-on) ORTEC MCBs attached to the local PC and to (powered-on) network PCs, display the list of instruments found, allow you to enter customized instrument numbers and descriptions, and optionally write this configuration to those other network PCs. See Section 2.2 for more details on running this program, including customizing the instrument numbers and descriptions. If this is the first time you have installed ORTEC software on your system, be sure to read the information on initial system configuration in Section 2.2.

If you did not receive a CONNECTIONS-32 Driver Update Kit (Part No. 797230), your system is now ready to use. If you received the driver update kit, go to Section 2.1.1.

NOTE You can enable other device drivers later with the Windows Add/Remove Programs utility on the Control Panel. Select Connections 32 from the program list, choose Add/Remove, then elect to Modify the software setup. This will reopen the Instrument Setup dialog so you can mark or unmark the driver checkboxes as needed, after which you must re-run the MCB Configuration program as described above.

2.1.1. Installing the CONNECTIONS-32 Driver Update Kit

This section assumes that an ORTEC software application is already installed on your PC; if not, begin with Section 2.1. If you received more than one CONNECTIONS-32 Driver Update Kit, you need only install one of them.

1. Insert the CONNECTIONS-32 Driver Update CD, then go to the Windows Taskbar and click on Start, and Run... In the Run dialog, enter D:\ConnectionsSetup.exe (use your CD-ROM drive designator), then click on OK. This will start the installation wizard. Click on Next and follow the wizard prompts.

2. Return to Step 3 in Section 2.1 and follow the instrument setup and subsequent software installation steps.

After completion of the wizard, restart, and MCB configuration steps described in the preceding section, your system will be ready to use.
2.1.2. If You Have Windows XP Service Pack 2 and Wish to Share Your Local ORTEC MCBs Across a Network

**NOTE** If you do not have instruments connected directly to your PC or do not wish to share your instruments, this section does not apply to you.

If you have installed Windows XP Service Pack 2 and have fully enabled the Windows Firewall, as recommended by Microsoft, the default firewall settings will prevent other computers from accessing the **CONNECTIONS-32** MCBs connected directly to your PC. To share your locally connected ORTEC instruments across a network, you must enable **File and Printer Sharing** on the Windows Firewall Exceptions list. To do this:

1. From the Windows Control Panel, access the **Windows Firewall** entry. Depending on the appearance of your Control Panel, there are two ways to do this. Either open the **Windows Firewall** item (if displayed); or open the **Network Connections** item then choose **Change Windows Firewall Settings**, as illustrated in Fig. 2. This will open the Windows Firewall dialog.

2. Go to the Exceptions tab, then click to mark the **File and Printer Sharing** checkbox (Fig. 3).

**NOTE** This affects only the ability of other users on your network to access your MCBs. You are not required to turn on **File and Printer Sharing** in order to access networked MCBs on other PCs (as long as those PCs are configured to grant remote access).

3. To learn more about exceptions to the Windows Firewall, click on the **What are the risks of allowing exceptions** link at the bottom of the dialog.

4. Click on **OK** to close the dialog. No restart is required.
2. INSTALLATION

2.2. Configuring and Customizing the Master MCB List

The initial master list of MCBs available to the ORTEC programs on your PC is determined by the MCB Configuration program, which you run as part of software installation or update, or after installing a new MCB.

When MCB Configuration runs, it searches the PC and the network (if any) for MCBs, then displays a master list of the instruments found (Fig. 4).

Note that you can change the instrument numbers and descriptions at any time by double-clicking on an instrument entry in the Configure Instruments dialog. This will open the Change Description or ID dialog (Fig. 5). It shows the physical detector location (read-only) and allows you to change the ID and Description. Make the desired changes and click on Close.
If you or another user have already assigned a description to a particular instrument, you can restore the default description by deleting the entry in the Description field. Then, the next time you run MCB Configuration (see Section 2.3), the default description will be displayed.

When MCB Configuration runs, the resulting MCB configuration list is normally broadcast to all PCs on the network. If you do not want to broadcast the results, unmark the Update detector list on all systems checkbox under the instrument list (see Fig. 4) so the configuration will be saved only to the local PC.

The first time the system is configured, Fig. 6 will be displayed to remind you that all new instruments must be assigned a unique, non-zero ID number.
You can change all the instrument numbers by clicking on **Renumber All** to assign new numbers in sequence; or click on **Renumber New** to renumber just the new instruments. Figure 7 will be displayed if the list is a mixture of old and new numbers.

**NOTE** Remember that some applications use the instrument number to refer to a specific MCB or device (e.g., the `.JOB` file command SET_DETECTOR 5). Therefore, you might want to subsequently avoid changing its **number** so all defined processes will still operate.

Click on the **Help** button on the Configure Instruments dialog to display a detailed help screen.

When you have completed all changes to the instrument list, click on **Close** to close the Configure Instruments dialog. At this point, Renaissance and other **CONNECTIONS** applications can be run on any PC, and the MCB pick list for each program on each PC can be tailored to a specific list of instruments.
2.3. Re-Running the MCB Configuration Program to Update the Master Instrument List

When an MCB is added to the system, or if you change total memory size and number of segments for a multi-input MCB such as the Model 920 or a member of the OCTÊTE instrument family, you can’t communicate with the new input(s) until you have (1) enabled its CONNECTIONS-32 driver, if the appropriate driver is not already active; and (2) re-run the MCB Configuration program to add the new device to the Master Instrument List. To do this, open the Windows Add/Remove Programs utility on the Control Panel. Select Connections 32 from the program list, choose Add/Remove, then elect to Modify the software setup. This will reopen the Instrument Setup dialog (Fig. 1) so you can mark or unmark the driver checkboxes as needed then run the MCB Configuration program, according to the instructions beginning on page 5.

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 number and description assigned to a Detector by the MCB Configuration program. Instrument number and description are assigned when MCB Configuration polls the local PC 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 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 be careful to reassign each instrument its previous instrument number and description before making any more measurements. 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 PC. Doing so requires that you keep a separate record of the instrument numbers assigned to all Detectors in your system. Let us use the following example to illustrate the “manual editing” process:
2.4.1. Example: Restoring Instrument Identification Number and Description

Suppose Detector group **WBC 1** originally contains three NaI Detectors, **0014 WBC NaI 2**, **0015 WBC NaI 3**, and **0016 WBC NaI 4**.

Suppose we remove 2 detectors from the system and add a new one. We must manually run MCB Configuration to add the instrument to the Master Detector List. After running the MCB Configuration program from the Windows Taskbar, we find that the resulting Configure Instruments dialog looks similar to the one in Fig. 8. Note that our **WBC 1** detectors have been renumbered to **0010, 0011, and 0012**.

**Before** closing the Configure Instruments dialog, double-click on the first of the Detector entries that must be renumbered (and, in some cases, renamed). This will open the Change Description or ID dialog shown in Fig. 9. Enter the original instrument number in the **ID** field and, if necessary, restore the **Description**, then click on **OK**. Repeat for all Detectors that must be renumbered and renamed. Figure 10 shows the three Detectors restored to their specified instrument numbers and names.

When you are finished, click on **Close**.

To complete the operation, you must do the following:

1. Return to **Edit Ge Lists...** and **Edit NaI Lists...** and, if necessary, reassign the Detectors to the appropriate lists.

2. Use **Edit Detector Groups...** to ensure that the three Detectors are still assigned to group **WBC1**.

3. Go to **Operator Scan Type**, choose each scan type file that uses detector group **WBC1**, reselect this detector group from the droplist (even if it is already displayed as the current choice), and save the scan type file.

4. Confirm that the original QA **Settings...** are still in effect.
Fig. 9. Manually Re-Entering Original Detector ID Numbers and Descriptions.

5. Run background and sample QA measurements and check the results dialogs to confirm that the 3 Detectors are being properly tracked.

You are now ready to use detector group WBC1 again without having to redefine Ge or NaI detectors, detector groups, and scan types; and without affecting the integrity of your QA data.

Fig. 10. Original Instrument ID Numbers and Descriptions Restored.
3. GETTING STARTED IN RENAISSANCE

The first step in using Renaissance-32 is to run the Renaissance Supervisor program and 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 (on the Renaissance Start menu) and set up the parameters according to the instructions in Appendix B.

4. Identify the germanium detectors available to both the Supervisor and Operator (Services/Edit Detector Lists/Edit Ge Lists...; Section 5.7.6.1).

5. Identify the sodium iodide detectors available to both the Supervisor and Operator (Services/Edit Detector Lists/Edit NaI Lists...; Section 5.7.6.1).

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 190.

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 152.

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 5.5.1.6).

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 205 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 11 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. **Drop-down Detector List**, on the Toolbar, displays the list of currently available Detectors. Clicking on this field opens a list of all Detectors currently on the Renaissance Detector pick list. Selecting a Detector will open a new spectrum display and show the spectrum for this Detector. The name of the last Detector selected is shown.

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-32 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.
4. DISPLAY FEATURES

- **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. 12) 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. 18).

- **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. 13) 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. 18).

**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. 14). 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 livetime, realtime and presets for the spectrum selected.

Finally, when the mouse pointer is paused over the center of a Toolbar button, a pop-up **tool tip** (also **mouse over**) box opens, describing the button’s function (Fig. 15).
4. DISPLAY FEATURES

4.3. Using the Mouse

The mouse can be used to access the menus, Toolbar, and sidebars; adjust spectrum scaling; mark and unmark peaks and ROIs; select Detectors; work in the dialogs — every function in Renaissance except text entry. For most people, this might be more efficient than using the keyboard. The following sections describe 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 16 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. 16) 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. 17).
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.

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. 18 illustrates the process of marking a region with a rubber rectangle and zooming in using the right-mouse-button menu.
The rectangle can also be moved using the arrow keys. The \(<\text{Shift} + \rightarrow>\) and \(<\text{Shift} + \leftarrow>\) keys move the box left and right, while \(<\text{Shift} + \uparrow>\) and \(<\text{Shift} + \downarrow>\) 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. 19). 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. 19). Click and hold the left mouse button, drag the window to its new location, and release the mouse button.

### 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. 20) appear on many Renaissance dialogs, and allow the selection of only one of the choices.

**Checkboxes** (Fig. 21) are another common feature, allowing the selection of one or more of the options at the same time.

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. 22.

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.

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. Help

Renaissance provides two kinds of help: What’s This? help on the buttons and features of the main screen, and Question Mark help on features, fields, and procedures within the dialog boxes.

To use What’s This? help (Fig. 23), point the cursor at the desired screen feature and click the right mouse button. If help is available for
that feature, a small **What’s This?** box will open beside the cursor arrow. Left-click once on **What’s This?** to open the help message. Press `<Esc>` to close help.

To use **Question Mark** help (Fig. 24), locate the question mark ( ? ) box on the various dialogs and sidebars. Left-click on the ? (a ? appears beside the arrow pointer), point at the feature you want to know about, and left-click to open the help message. Press `<Esc>` to close help.

### 4.6. Drag and Drop

Several types of files can be selected and loaded into Renaissance using the Windows *drag-and-drop* feature. The file types are: spectra ( `.SPC, .AN1, .CHN` ), calibration ( `.CLB` ), library ( `.LIB` ), analysis results ( `.UFO` ), peak background correction ( `.PBC` ), and region of interest ( `.ROI` ).

The drag-and-drop file is handled the same as a read (recall) operation for that type of file. 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.

To drag and drop, open Renaissance and Windows Explorer, and display both together on the screen. Locate a file in Explorer such as `GVDEMO.ROI`. Now click and hold the left mouse button, move the mouse (along with the file “ghost”) to the Renaissance window, and release the mouse button. The `.ROI` file will be read and the regions set.

### 4.7. Associated Files

When Renaissance is installed, it registers the spectrum files in Windows so they can be opened from Windows Explorer by double-clicking on the filename. The spectrum files are displayed in WinPlots. These files are marked with a spectrum icon ( ) in the Explorer display. The `.JOB`, `.EFT`, and `.ENT` files are also registered, and have an ORTEC icon ( ). They open in Windows Notepad.

### 4.8. Editing

Many of the text entry fields in the Renaissance dialogs support the Windows editing functions on the right-mouse-button menu. Use these functions to copy text from field to field with ease,
as well as from program to program. Position the mouse pointer in the text field and click the right mouse button to open the menu shown in Fig. 25. Select a function from the menu with the left mouse button.
This chapter describes all of the Renaissance menu commands and their associated dialogs. As is customary for Windows menus, the shortcut key(s) (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 Recall... dialog under File 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**
- Settings...
- Recall...
- Save As...
- Export
- Import
- Print
- Compare...
- Exit
- About Renaissance...

**Acquire**
- Acquisition Settings...
  - Start Alt+1
  - Stop Alt+2
  - Clear Alt+3
  - Copy to Buffer Alt+5
  - QA ►
    - Settings...
    - Measure Background
    - Measure Sample
    - Status...
    - Control Chart...
  - Download Spectra

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ZDT Display Select F3
MCB Properties...
Gain Adjust

Calibrate
Energy...
Efficiency...
Lower Limit...
Description...
Recall Calibration...
Save Calibration...
Print Calibration...
Ge Calibration Wizard...
NaI Calibration Wizard...

Calculate
Settings...
Peak Info
Sum Channels
Smooth
Strip...
Sum Spectra...

Analyze
Settings ▶
Sample Type...
Reports...
Group Sample Type...
Attenuation...
Peak Background Correction ▶
Create PBC...
Select PBC...
Edit PBC...
Entire Spectrum in Memory...
Display Analysis Results...
Interactive in Viewed Area...

Library
Select Peak...
Select File...

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5. MENU COMMANDS

Edit ▶
  GammaVision Editor...
  Nuclide Navigator...
List...

Services
  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
  Off
  Mark
  UnMark
  Mark Peak
  Clear Delete
  Clear All
  Save File...
  Recall File...

Display
  Logarithmic
  Automatic
  Baseline Zoom
  Zoom In
  Zoom Out
  Center
  Full View
Preferences ▶
  Points
  Fill ROI
  Fill All
  Fill Singlets
  Fill Multiplet Peaks
  Fill Multiplet Composites
  Spectrum Colors...
  Peak Info Font/Color...

Window
  Cascade
  Tile Horizontally
  Tile Vertically
  Arrange Icons
  Close
  Close All
  [list of open spectrum windows]

Right-Mouse-Button Menu
  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

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5. MENU COMMANDS

5.1. File

The File menu contains the spectrum file save, recall, import/export, print, and compare commands as shown in Fig. 26.

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. 27. 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 which questions are 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.

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 save-file format in both the Supervisor and Operator programs. The formats for these and other Renaissance file types are described in the ORTEC Software File Structure Manual for DOS and Windows Systems (Part No. 753800).

The available file types are integer .CHN, integer .SPC, floating-point .SPC, and .SPE. 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. Both contain all of the analysis parameters (from analysis settings) and the complete calibration data. They are suitable for archiving, as the analysis can be reproduced from this file. 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 (e.g., 80387) and most languages for the PC. The .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. 28) is used to specify the program, arguments, and file directory to be used when the Export... function is selected.

Choose any program\(^3\) 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 directly entered character strings or the user can select from the list of “macros” shown in Fig. 29. 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.

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\(^3\)Any executable program that can be executed from the Windows Run command can be selected, including DOS batch commands.
**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., `$\{(FullBase)A\}.CHN$`).

**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. 30. The list is displayed by clicking on the arrow button to the right of the **Initial Directory:** field.

**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. 31. 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.

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. 32. 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., `$\{\text{FullBase}\}.CHN$`) 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., `$\{\text{FullBase}\}A.CHN$`).

**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 (`$\{\text{xxx}\}$`) 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. 33. The list is displayed by clicking on the arrow button to the right of the **Initial Directory:** field.

**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, Maximazed, 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. 34) to select the default file directories for spectrum files, calibrations, `.JOB` files, Operator scan type (.O PR) files, libraries, and other files. 4

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 on **Open** (see Section ? for instructions on changing drives and folders).

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.

**NOTE** Scan type (.O PR) 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).

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4Renaissance 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.
When all path changes have been completed, click on OK to use them or Cancel to retain the previous settings.

5.1.2. Recall...

This function opens a standard file-open dialog (Fig. 35) 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.\(^5\)

**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.

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.

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\(^5\)In addition, you can recall spectrum files generated by other ORTEC CONNECTIONS-32 programs, such as MAESTRO and GammaVision, that produce the .SPC, .CHN, and .SPE formats.
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.

If the MCB hardware supports State of Health (SOH), authentication or other status flags, the flags are checked when the spectrum is read. If any error flags are set, the message shown in Fig. 36 is displayed. Refer to the Properties dialog (Acquire/MCB Properties...) to display the errors, and to the MCB Properties Manual for the meanings of the status or error indicators.

5.1.3. Save As...

This command opens a standard file-save dialog (Fig. 37) so the current spectrum can be saved to disk. Enter any valid filename (consisting of an optional drive and directory, a filename, and an optional extension) in the File name field and click on 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.

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 supported digital spectrometers), both spectra are automatically 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. 38, is displayed. Choose the filename of the spectrum to be exported.

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, the WinPlots program will be executed. If the \texttt{-P} switch is specified on the command line (see Sections 5.1.1.2 and 13.1.3, page 368), the program will plot the spectrum and exit automatically.

5.1.5. Import...

The Import command (Fig. 39) is used to 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 or can be user-supplied. When the Import File dialog
opens, select the filename and click on **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. 40) 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.

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. 41.

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).

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 42 is a detailed view of a spectrum comparison similar to that in Fig. 41. 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 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 43 shows the About box for Renaissance. It provides software version information that will be useful should you need customer support.
If the PC is connected to the Internet, click on the **Visit ORTEC On-Line** button to browse our website, www.ortec-online.com, which, in addition to product catalogues, includes application notes, technical papers, information on training courses, and access to the Global Service Center.

## 5.2. Acquire

The **Acquire** menu is shown in Fig. 44. 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).

### 5.2.1. Acquisition Settings...

This command opens the Acquisition Settings dialog (Fig. 45), 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).

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 Detector, any subsequent ask-on-start prompts for that Detector will not be asked, and acquisition in that Detector 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 multidetector 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 shortcut `<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:
where

\[ \text{sss} \] is the sequence number of the spectrum. This is the index number shown on the digiDART spectrum list display.

\[ \text{iii} \] is the ID string entered when the spectrum was collected. It is shown on the digiDART spectrum list display.

\[ \text{ddd} \] is the date the spectrum was collected, as recorded in the MCB.

\[ \text{ttt} \] is the time the spectrum was collected, as recorded in the MCB.

\[ \text{ext} \] 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...

ORTEC CONNECTIONS-32 applications now use a uniform data-acquisition setup dialog called Properties. In Renaissance, the Properties dialog opens when you select the Acquire/MCB Properties... command. Two of our the Detectors most likely to be used with Renaissance — the DSPEC jr and digiBASE — are described here. Renaissance will operate with any ORTEC CONNECTIONS MCB. To see the Properties dialogs for our other CONNECTIONS-compliant MCBs, see the MCB Properties Manual.

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
access to 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. Find your Detector’s setup section here or in the MCB Properties Manual, move from tab to tab and set your hardware parameters, then click on 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 since a character was last entered. During the time the entry is underlined, no other program or PC on the network can modify this value.

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

5.2.9.1. DSPEC Pro

Amplifier

Figure 46 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.

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
The **Input Polarity** radio buttons select 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
The **Baseline Restore** is used to return 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**, **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 69).

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. 70). In the automatic mode, the current value is shown on the InSight sidebar (Fig. 64). For a low-count-rate system, the value will remain at about 90.

Preamplifier Type
Use the **Preamplifier Type** section to 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 logic\(^7\) and automatic flattop logic.\(^8\) 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.

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\(^6\)Patent number 5,912,825.

\(^7\)Patent number 5,872,363.

\(^8\)Patent number 5,821,533.
There should be a radioactive source near the detector so that the count rate causes a dead time of ~5%. Dead time is displayed on the DSPEC Pro front panel and on the Status Sidebar during data acquisition.

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.

**Amplifier 2**

Figure 47 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. The value of the rise time parameter in the DSPEC Pro is roughly equivalent to twice the integration time set on a conventional analog spectroscopy amplifier. Thus, a DSPEC Pro value of 12 µs corresponds to 6 µs in a conventional amplifier. Starting with the nominal value of 12.0, you should...
increase values of the rise time for better resolution for expected lower count rates, or when unusually high count rates are anticipated, reduce the rise time for higher throughput with somewhat worse resolution.

Use the up/down arrows to adjust the **Rise Time** within the range of 0.8 to 23.0 µs. After all the controls have been adjusted, return to the Amplifier tab and click on **Start Auto**. The most recent settings are saved in the DSPEC Pro firmware even when the power is turned off.

For the more advanced user, the InSight mode allows you to 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 on **Start**. The InSight mode is discussed in more detail in the following section.

Note that the Amplifier 2 tab graphically presents a *modeled shape*. This is *not* a sampled waveform of the actual pulse shape, only a model based on the current parameters. The modeled shape is nominally a quasi-trapezoid whose sides and top may be adjusted by the controls in this dialog. While a particular control is being adjusted, the model is updated to represent the changes made.

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 µs). 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, the optimize feature on the Amplifier tab can set the tilt value automatically. This automatic 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 feature also automatically adjusts the pole-zero setting.

The dead time per pulse is \((3 \times \text{Rise Time}) + (2 \times \text{Flattop Width})\).

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.

When you are satisfied with the settings, **Close** the Properties dialog and prepare to acquire data.
Once data acquisition is underway, the advanced user may wish to return to MCB Properties... and click on 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.

**Amplifier PRO**

This tab (Fig. 48) 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. 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 Section ?. You cannot optimize or pole-zero the DSPEC Pro while in LFR mode. The Optimize feature should be used with the LFR filter off. Subsequent measurements can then be taken with the LFR filter on. Also, 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, are:

- LFR mode off 1.1 µs to 48.4 µs
- LFR mode on 3.0 µs to 145.2 µs

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 alleviate the low-side peak tailing that results from increased charge trapping; see the discussion in the hardware manual. This function will not improve low resolution due to other causes (and might exacerbate the problem).

1. Set the bias, gain, rise time, flattop, and PZ as you would for data collection.

2. If you wish to use LFR Mode, turn it on.

3. If you wish to use Enhanced Throughput Mode, turn it on and either accept the automatically calculated, highest-throughput protection time, based on the current rise time and flattop; or enter the desired setting. (The latter might require one or more data acquisitions. When finished, proceed to Step 4).

4. Clear the MCB and acquire a well-isolated peak.

5. You will now use the gain stabilization section of the Stabilizer tab to configure the resolution enhancer. (The gain stabilizer and resolution are somewhat similar in function, and only one of these features can be used at a time.) Enter the Center channel and Width of the peak acquired in Step 4; the maximum Width is 255 channels. If you wish, use the Suggest button.

6. If you have already used the resolution enhancer, you can either use the previously established settings (which will go into effect when you turn on the enhancer in Step 7), or click on Initialize to clear all settings. Initialization does not change the current Center channel and Width.

7. Return to the PRO tab and turn on the resolution enhancer.

8. Clear the MCB, re-start acquisition, and monitor the FWHM of the target peak until it no longer changes. Typically, the more charge trapping exhibited by the detector, the longer the data collection time.

9. When you are satisfied that the FWHM has reached the best possible value, clear the MCB and collect another spectrum for confirmation.

10. At this point, the resolution enhancer is now “trained” for the current peak shape parameters and can be turned off. (You can leave it on, if you wish, but you might notice some peak broadening.)
11. If you change any parameters that affect peak position and/or shape, you must repeat this “training” procedure.

**ADC**

This tab (Fig. 49) 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**

The **Gate** control allows you to select a logic gating function. With this function **Off**, no gating is performed (that is, all detector signals are processed); with the function in **Coincidence**, 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).

**ZDT Mode**

Use this droplist to choose the **ZDT Mode** to be used for collecting the zero dead time (corrected) spectrum (see Section ?). The three modes are **Off** (LTC only), **NORM_CORR** (LTC and ZDT), and **CORR_ERR** (ERR and ZDT). If one of the ZDT modes 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 Renaissance, 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**

The **Conversion Gain** 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.
Upper- and Lower-Level Discriminators
In the DSPEC Pro, the lower- and upper-level discriminators are under computer control. 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. The Stabilizer tab (Fig. 50) 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 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 51 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 polarity is set in the DIM module.

The high voltage is overridden by the detector bias remote shutdown signal from the detector; high voltage cannot be enabled if the remote shutdown or overload signals prevent it. 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 shutdown can be ORTEC, TTL, 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.

The high voltage in the DSPEC Pro is supplied by the SMART-1 module or in a separate DIM. The recommended HV for SMART-1 is displayed on the dialog. For other detectors, see the detector manual or data sheet for the correct voltage. The polarity is determined by the DIM or SMART-1 module.

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. 52) 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.

![Fig. 52. DSPEC Pro About Tab.](image1)

Status

Figure 53 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**.

![Fig. 53. DSPEC Pro Status Tab.](image2)
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 54 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 Detector 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 Detector clock increments by 20 ms. Real time means elapsed time or clock time. Live time refers to the amount of time that the Detector 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 Detector is not available).

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

Enter the ROI Integral preset value in counts. With this preset condition, the Detector stops counting when the sum of all counts in all channels for this Detector marked with an ROI reaches this value. This has no function if no ROIs are marked in the Detector.
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. As the uncertainty is calculated approximately every 30 seconds, 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 $2^{31} - 1$ (over $2 \times 10^9$) counts.

**MDA Preset**

The MDA preset (Fig. 55) 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. The MDA preset is implemented in the hardware. The formulas for the MDA are given in various textbooks and in the “Analysis Methods” chapter in the GammaVision user manual and can be generally represented as follows:

$$MDA = \frac{a + \sqrt{b + c \times Counts}}{Live \ time \ * \ Eff \ * \ Yield}$$

The coefficients $a$, $b$, and $c$ are determined by the MDA formula to be used. The $Eff$ (detector efficiency) is determined from the calibration. The $Yield$ (branching ratio) is read from the working library using the nuclide and energy specified. The MDA value is the one you have entered in the dialog. $Counts$ is the gross counts in the specified region and $Live \ time$ is the live time. The MDA value is calculated in the MCB given the values $a$, $b$, $c$, $Live \ time$, $Eff$, and $Yield$. The calculated value is compared with the MDA value on the dialog and when it is lower, acquisition is stopped.
Coefficients A, B, and C can be entered as numbers. If the application, such as GammaVision, supports MDA calculations, you can click on the Suggest button to enter (from an internal table) the values for the MDA type selected. The MDA type should be chosen before the preset is selected here.

Select the Nuclide and Energy from the droplists. The Nuclide list contains all the nuclides in the working library. The Energy list shows all the gamma-ray energies for the selected nuclide in the library.

If the application supports efficiency calibration and the MCB is efficiency calibrated, the MDA is entered in the units selected in the application. If the unit is not efficiency calibrated, the MDA field is labeled Correction, the efficiency (Eff) is set to 1.0 and the preset operates as before. If the Correction factor is the actual MDA times the efficiency (known from other sources), the MDA preset will function normally.

5.2.9.2. digiBASE

Amplifier

Figure 56 shows the Amplifier tab. This tab contains the controls for Gain and Shaping Time.

The amplifier coarse gain is set to 1, 3, or 9 by changing a jumper setting (see the digiBASE user manual). Once the coarse gain is set, adjust the Fine gain with the horizontal slider bar or the edit box, in the range of 0.4 to 1.2. 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 0.4 to 10.8.
In almost all cases, the default **Shaping Time**, 0.75 µs, is the preferred setting. However, the digiBASE supports shaping times from 0.75 µs to 2 µs in steps of 0.25 µs.

### Amplifier 2

Figure 57 shows the Amplifier 2 tab, which accesses the InSight™ Virtual Oscilloscope mode. For the more advanced user, the InSight mode allows you to directly the digiBASE’s advanced shaping parameters and adjust them interactively while collecting live data. To access the InSight mode, click on **Start**, then refer to the discussion in Section 5.2.9.3.

When you are satisfied with the settings, **Close** the Properties dialog and prepare to acquire data. Once data acquisition is underway, the advanced user might wish to return to this tab and switch to the Insight mode to adjust the shaping parameters interactively with a “live” waveform showing the actual pulse shape, or just to verify that all is well.

### ADC

This tab (Fig. 58) contains the **Gate**, **Lower Level Discriminator**, and **Upper Level Discriminator** controls. In addition, the current real time and live time are monitored at the bottom of the dialog.

The **Gate** control allows you to select a logic gating function. With this function **Off**, no gating is performed (that is, all detector signals are processed).
When the **Gate** is set to **Enable**, if the ENABLE INPUT is low (<0.8V), real time, live time, and data acquisition are stopped. When the ENABLE INPUT is left open or forced high (>2.0V), real time, live time, and data acquisition are enabled.

If set to **Coincidence**, when the ENABLE INPUT is low, real time and live time operate normally, but no counts are stored in memory. If the ENABLE INPUT is high, normal acquisition occurs.

If set to **Event**, rising edges are counted by a 32-bit event counter. The contents of this counter can be monitored in the **Enable Counter** field on the Status tab (Section 5.2.9.2). The input impedance is 5 kΩ to +3.3V, protected to ±10 V.

The digiBASE operates at a **Conversion Gain** of 1024 only.

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 digiBASE has both a gain stabilizer and a zero stabilizer; their operation is discussed in more detail in the *ORTEC MCB CONNECTIONS-32 Hardware Property Dialogs Manual*.

The Stabilizer tab (Fig. 59) 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 cannot make further corrections in that direction. The **Center Channel** and **Width** fields show the peak currently used for stabilization.

![Properties](image)

**Fig. 59.** digiBASE Stabilizer Tab.
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 60 shows the High Voltage tab, which allows you to turn the high voltage on or off; and set and monitor the 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.

![Fig. 60. digiBASE High Voltage Tab.](image)

### About

This tab (Fig. 61) displays hardware and firmware information about the currently selected instrument 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.

![Fig. 61. digiBASE About Tab.](image)
Status

Figure 62 shows the Status tab. The Aux0 and Aux1 counters are reserved for future use. The Enable Counter functions when the Gate function on the ADC tab is set to Event and the digiBASE is actively acquiring data in a spectrum. Under these conditions, the Enable Counter accrues the number of events at the ENABLE INPUT since the Start command was issued. To clear this counter, click on the Clear Spectrum button on the toolbar or issue Acquire/Clear.

Presets

Figure 63 shows the Presets 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 either or both presets at one time. To disable a preset, enter a value of zero. If you disable both 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.

The values of all presets for the currently selected Detector 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 Detector clock
increments by 20 ms. Real time means elapsed time or clock time. Live time refers to the amount of time that the Detector 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 Detector is not available).

5.2.9.3. InSight Mode

The InSight display (Fig. 64) 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.

As none of the traditional analog signals are available in digital MCBs, 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 on the Stop button on the toolbar (or Acquire/Stop). The PHA mode is set to STOP when in the InSight mode.

The Status Sidebar changes from the PHA mode controls to the InSight controls for adjusting the peak display (Fig. 64). 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 is to 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 on 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 current MCB to another Detector or the buffer. The other Detector will be shown in its most recent mode (PHA or InSight). The buffer will always be shown in PHA mode. When you return to the current MCB, the display will return to the InSight mode. This also holds true if you exit Renaissance while in InSight mode; on next startup, this MCB will still be in InSight mode.

The display can include a Mark to indicate one of the other signals shown in Fig. 65. 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 it is necessary to get the best resolution at the highest throughput possible. By viewing the pulses and the pileup reject marker, the rise time can be increased or decreased to obtain a minimum of pileup reject pulses.

**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 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 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 flattop and stop after the end of the flattop) 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 µs 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 µs). 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.

5.2.9.4. Gain Stabilization

You can control the gain stabilizer on Detectors so equipped. 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 input pulse-height-to-channel-number relationship is:

\[
\text{Channel number} = \text{Intercept} + \text{Gain} \times \text{pulse height}
\]

where:
- \text{Intercept} = \text{The channel number of the zero-height input pulse}
- \text{Gain} = \text{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 in the MCB, 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. The ROI can be cleared after the Peak command so that peak count preset can be used on another peak.
The coarse and fine gains should be set to the desired values, both stabilizers initialized, and the pole zero triggered before setting either stabilization peak. For example, on the 92X this is done with the **Acquire/MCB Properties...** dialog; on the Model 919 it is done externally.

The **Initialize** dialog button sets the gain on the stabilization amplifier to its midpoint (that is, halfway between minimum gain and maximum gain). This should be done before selecting the ROI for the peak because the initialization might move the peak in the spectrum, and because it ensures that the maximum range is available for the stabilization process. If the peak is moved by this command, use the amplifier fine gain control (<Alt + -> or <Alt + +>) to move the peak to the desired channel.

When starting a new system, the zero-initialize command should also be given before starting the gain stabilization.

The **Suggest** button is used to set the peak center and peak width of the peak area used by the stabilizer. Before selecting this command, the ROI must be marked and the marker put in the region to be used. When operating, the peak will be centered in the ROI. After the region has been recorded, the stabilization is turned on. If the stabilization is turned on when this command is executed, the old stabilization region is replaced by the new peak defined by the marker, and stabilization continues using the new peak.

The **Gain Stabilizer Enabled** checkbox enables or disables the gain stabilization. It can only be turned on after the **Suggest** button has been used to select a working peak.

5.2.9.5. Zero Stabilization

The **Zero Stabilizer** function enables you to control the zero-level (or offset) stabilizer on Detectors so equipped. 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. The input pulse-height-to-channel-number relationship is:

\[
\text{Channel number} = \text{Intercept} + \text{Gain} \times \text{pulse height}
\]

where:

- \(\text{Intercept}\) = The channel number of the zero-height input pulse
- \(\text{Gain}\) = The relation between pulse height and channel number (slope of the curve)

Changes in either the zero intercept or gain can affect the positions of all the peaks in the spectrum. When used with the gain stabilizer, both the zero intercept and the gain (slope) are monitored to keep all the peaks in the spectrum stabilized. The zero stabilization and gain
stabilization are separate functions in the MCB 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 set symmetrically about the center of a peak with reasonably good count rate in the lower 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. The ROI can be cleared after the PEAK command so that peak count preset can be used on another peak.

The zero stabilization dialog **Initialize** button sets the zero offset to its midpoint (that is, halfway between minimum offset and maximum offset). This should be done before selecting the ROI for the peak because the initialization might move the peak in the spectrum, and because it ensures that the maximum range is available for the stabilization process.

The **Suggest** button is used to set the peak center and peak width of the peak area used by the stabilizer. Before selecting this command, the ROI must be marked and the marker put in the region to be used. When operating, the peak will be centered in the ROI. After the region has been recorded, the stabilization is turned on. If the stabilization is turned on when this command is executed, the old stabilization region is replaced by the new peak defined by the marker, and stabilization continues using the new peak.

The **Zero Stabilizer Enabled** checkbox enables or disables the zero stabilization. It can only be turned on after the **Suggest** button has been used to select a working peak.

5.2.9.6. Setting the Rise Time in Digital MCBs

To achieve the best results for your application, when using a digital spectrometer, such as the DSPEC Pro, DSPEC Jr, digiDART, DSPEC Plus, or DSPEC, 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-µs time constant; this setting is equivalent to 12-µs 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 66 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.

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>
<thead>
<tr>
<th>Input Count Rate Dynamic Range</th>
<th>Maximum Throughput</th>
<th>Rise Time (µs)</th>
</tr>
</thead>
<tbody>
<tr>
<td>0---&gt;20000</td>
<td>9000</td>
<td>12</td>
</tr>
<tr>
<td>0---&gt;50000</td>
<td>12500</td>
<td>8</td>
</tr>
<tr>
<td>0---&gt;75000</td>
<td>23500</td>
<td>4</td>
</tr>
<tr>
<td>0---&gt;100000</td>
<td>37000</td>
<td>2.4</td>
</tr>
<tr>
<td>0---&gt;150000</td>
<td>50000</td>
<td>1.6</td>
</tr>
<tr>
<td>0---&gt;200k</td>
<td>70000</td>
<td>0.8</td>
</tr>
<tr>
<td>0---&gt;220k</td>
<td>85000</td>
<td>0.6</td>
</tr>
<tr>
<td>0---&gt;250k</td>
<td>100000</td>
<td>0.4</td>
</tr>
<tr>
<td>0---&gt;300k</td>
<td>120000</td>
<td>0.2</td>
</tr>
</tbody>
</table>

The longest rise time shown in the table is 12 µs, even though some digital instruments can be set for rise times as long as 23 µs. If throughput is not an issue because all samples are low rate,
increasing the rise time beyond 12 µs 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.

### 5.2.10. Gain Adjust

The **Gain Adjust** wizard adjusts the Detector 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 Detectors in a group at one time or an individual Detector.

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

The first dialog for the wizard is shown in Fig. 67. Select the current detector or pick a Detector group from the droplist, then click **Next**.

![Select Detectors](image)

**Fig. 67. Set Up the Gain Adjust for the Current Detector or a Detector Group.**
The next wizard screen is shown in Fig 68. 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 Detector. You can enter a wide range to ensure that the peak will be located. The region must contain *only one peak*.

Click on **Next**.

Figure 69 shows the next wizard dialog. This screen displays the list of Detectors to be adjusted. The current fine gain for each Detector is displayed. Now click on the **Adjust Gain** button; this will open the reminder shown in Fig. 70.

Position the source(s) and click on **OK**. Renaissance Supervisor will acquire data and periodically attempt a peak fit.
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. 71.

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.

### 5.3. Calibrate

Figure 72 shows the full Calibrate menu. Renaissance includes a Calibration Wizard to assist in performing the energy and efficiency calibrations as well as a fully implemented true-coincidence correction (TCC) calibration for HPGe only. This menu continues to have 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 Detector are only available if the Detector is not acquiring data. If there is no energy calibration, all choices except Energy..., Recall Calibration..., and Calibration Wizard... are inactive (gray).

**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.
5. MENU COMMANDS

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 or TCC calibration data.

It is important that the energy, efficiency, and TCC 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.

A poorly done TCC calibration will cause incorrect activity reports due to a miscorrection for cascade summing.

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. The efficiency and TCC calibrations are linked because the TCC depends on the detector-source geometry. 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:
\[ E = a_1 + a_2 C + a_3 C^2 \]  \hspace{1cm} (1)

where:
- \( E \) = energy
- \( a_i \) = coefficients
- \( C \) = channel number

The formula for FWHM vs. channels is:
\[ F = b_1 + b_2 C + b_3 C^2 \]  \hspace{1cm} (2)

where:
- \( F \) = FWHM
- \( b_i \) = coefficients
- \( C \) = channel number

To calculate the FWHM in energy use the following:
\[ F(e) = F(c) (a_2 + 2a_3 * C) \]  \hspace{1cm} (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. 73) 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 Calibration

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.

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. 74). They can be moved around and sized if they obscure the spectrum.

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9Patent 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. 74) or FWHM vs. energy (Fig. 75).

![Energy Calibration Display](image)

**Fig. 74. 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
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.

Fig. 75. FWHM Calibration Display.
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. 76). Assign a filename and Renaissance will append the default energy-calibration extension, **.ENT**.

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. 77).

Select **Edit File**. Open the **.ENT** file to be edited; it will be displayed as shown in Fig. 78. Change energy values as needed and click on **Save**, or click on **Cancel** to retain the original values.
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. 79). 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.

![Recall Energy Table File]

**Fig. 79. 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. 80). 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.
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:

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

where:

- \(E\) = energy
- \(a_i\) = coefficients
- \(C\) = channel number
The formula for FWHM vs. channels is:

\[ F = b_1 + b_2 C + b_3 C^2 \]  \hspace{1cm} (5)

where:
- \( F \) = FWHM
- \( b_i \) = coefficients
- \( C \) = channel number

To calculate the FWHM in energy use the following:

\[ F(e) = F(c) (a_2 + 2a_3 * C) \]  \hspace{1cm} (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 152), and set the lower limit to the start channel of the Analysis Range on the Sample tab under Analyze/Settings/Sample Type... (see Fig. 150, page 157). 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. 81) 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. 82). 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.
Fig. 82. 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. 83; click the Title Bar icon on the Calibration Sidebar), or offline with an ASCII editor such as Windows Notepad.

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. 84). 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.
5. MENU COMMANDS

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. 85).

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. 86). 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.
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. 87). 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.\(^{10}\)

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.

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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:

\[
\varepsilon = e^{(a_1 + a_2 \ln(E))}
\]  

where:
- \(\varepsilon\) = 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:

\[
\varepsilon = e^{(a_1 + a_2 \cdot \ln(E) + a_3 (\ln(E))^2)}
\]  

where:
- \(\varepsilon\) = efficiency at energy \(E\)
- \(a_i\) = fitting coefficients
where:

\[ \varepsilon = \text{efficiency at energy } E \]
\[ a_i = \text{fitting coefficients} \]
\[ E = \text{energy} \]

### 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 grayed. 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:

\[
\varepsilon = e^{\left( \sum_{i=1}^{6} a_i E^{2-i} \right)}
\]  

(9)

where:

\[ \varepsilon = \text{efficiency at energy } E \]
\[ a_i = \text{fitting coefficients} \]
\[ E = \text{energy in MeV} \]

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.\(^{11,12,13}\) This fit can be

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used for p- or n-type detectors and is used in the Renaissance TCC correction method. Note that the TCC calibration requires a special calibration source, and the library must contain the daughter nuclides. See Section 5.3.11.3.

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. 88). 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. 89) 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. 90).

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.
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.

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. 91) 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 on **Apply**. 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. 92).

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.
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. 93). 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.
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. 94) 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.

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. 95.

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 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 96 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 97 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 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.

5.3.6.1. 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. 98).

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. 99.

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 the output filename for each of the different calibrations, which can subsequently be specified, for different sampling geometries, using Recall Calibration....
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.
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. 100). 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.¹⁴

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

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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:

\[ \varepsilon = e^{(a_1 + a_2 \ln(E))} \]  

(10)

where:
- \( \varepsilon \) = 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:

\[ \varepsilon = e^{(a_1 + a_2 \cdot \ln(E) + a_3 (\ln(E))^2)} \]  

(11)

where:
- \( \varepsilon \) = 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 grayed. 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:

\[ \varepsilon = e^{\left( \sum_{i=1}^{6} a_i E^{2-i} \right)} \]  

(12)

where:

- \( \varepsilon \) = 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.

Run Analyze/Interactive in viewed area... to automatically perform an efficiency calibration peak search. This must be done whenever you destroy the current efficiency calibration prior to attempting another 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. 101. (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.
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. 102).

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.

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 \texttt{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 \texttt{Save}... button in the \texttt{Table} section of the sidebar. This opens the \texttt{Save Efficiency Table} dialog shown in Fig. 103.

The table is saved as an ASCII file with the default extension \texttt{.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.

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 \texttt{Edit File}. This opens the dialog shown in Fig. 104. Select the \texttt{.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 \texttt{.EFT} files is the following line:

\begin{verbatim}
FitType = <iFit>
\end{verbatim}

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

\begin{verbatim}
0 no fit and no efficiency
1 interpolative fit
2 linear fit
\end{verbatim}
5. MENU COMMANDS

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. 105).
Fig. 105. 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. 106, 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 152), and set the **Lower Limit** to the start channel of the Analysis Range on the Sample tab under Analyze/Settings/Sample Type... (see Fig. 150, page 157).

![Fig. 106. Lower Limit for Calibrations.](image)

5.3.8. **Recall Calibration...**

This command (see Fig. 107) 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.

![Fig. 107. Recall Calibration.](image)

You can recall the energy calibration, the efficiency calibration, or both. The **Recall Energy Calibration** and **Recall Efficiency Calibration** checkboxes 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.
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. 108. 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.

Fig. 108. 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 109 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, efficiency, or TCC) will be replaced by the results of the subsequent steps. The TCC calibration is closely linked to the efficiency calibration, so when TCC Calibration is selected, Efficiency Calibration is also selected automatically.

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 8.8 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 110 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.

![Calibration files](image)

**Fig. 110. 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. When finished, click on **Next**.

True coincidence summing is not expected in whole-body counting, so the **TCC Library** field can be left blank. For TCC calculations, this library must be in the Nuclide-Navigator® III .MDB format (not .LIB). The daughter nuclides of the primary nuclides must also be in the TCC calibration library. This can be done automatically with NuclideNavigator III (see the NuclideNavigator III user manual for details). Under normal conditions, the daughter nuclides are not included in the analysis, so a library without daughters is used in the analysis.

Click on **Next** to continue.

### 5.3.11.4. Calibration Settings

The next dialog is shown in Fig. 111. 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 96 for details). The available fit types are **None, Interpolative, Linear, 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. 113).

### TCC Calibration Method

The **Single Point Source Method** uses a point source with all the nuclides needed in one source. The point source is normally a small area (1–2 mm diameter). Larger sources can be used if they are more than a few centimeters from the detector. An example of the nuclide mixture is given below.

The **Single Extended Source Method** uses bulk or large-volume sources such as Marinelli beakers or bottles with all the nuclides needed in one source.

The source must be a mixture of nuclides with gamma rays that do not have true coincidence summing and nuclides with gamma rays that do have summing. The energies of the gamma rays must extend over the range of interest for the unknown samples. A mixture of $^{109}$Cd, $^{113}$Sn, $^{139}$Ce, $^{203}$Hg, $^{134}$Cs, $^{137}$Cs, and $^{54}$Mn will be sufficient for most situations. $^{241}$Am can be added for lower energies.

**NOTE** $^{60}$Co should not be added because of the interference with gamma rays from $^{134}$Cs.

The selection of point or extended geometry changes the fitting process in the calibration calculation which gives different calibration coefficients for the different geometries. The TCC results depend on the source-detector geometry, so selecting the correct geometry is important.
Absorber

This section is active only when creating a new TCC calibration. The absorber present/not present selection determines the low-energy fitting function. The efficiency for low-energy gamma rays depends on the absorbing material between the detector and the source. The absorbing material and thickness are not important. Renaissance will automatically account for the loss in the fitting process if the absorber is present. The low-energy coefficients are listed as the last 2 (of 6) in the calibration records and are zero for absorber Not Present. When finished, click on Next.

Click on Next.

5.3.11.5. Sources and Spectrum Settings

Figure 112 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 that you save these spectra for QA purposes.

Click on Next to go to the Source Data Sheet (Fig. 113).
5.3.11.6. Source Data Sheet

Figure 113 shows the Source Data Sheet dialog. If you specified a new data source file (.
CAL file) name on the Calibration Files screen (see Section 5.3.11.3), this dialog will be empty. Otherwise, it will contain the source information from the selected .CAL file.

The source Label entered here is used in a later step that tells you which source to put on the detector.

If performing this calibration on the MCB, enter the live-time preset (Count Time) in seconds. The counting time must be long enough to accumulate well-formed peaks with low counting uncertainty.

.
CAL files contain calibration information tables that can be used for the calibration wizard but not the efficiency calibration (.EFT) files created in the Edit Efficiency step. The file contains all the data needed to perform an efficiency or efficiency-plus-TCC calibration using this standard source or sources. There is an entry in the file for each source used.

The table contains the following columns:

1. Isotope name (same as library).
2. Gamma-ray energy (keV).
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 114 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 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.

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

When finished, click on 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 on 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 on No.

At this point, the dialog shown in Fig. 115 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 PC’s resources.

In addition to the status dialog, the message shown in Fig. 116 is
displayed. Position the source and click on **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 on **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 on **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. 118), click on **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 on **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.

If you chose to use multiple sources, the wizard asks for the next source to be positioned (see Fig. 117). Click on **OK** to begin spectrum acquisition.

After all the spectra have been collected, the wizard merges the results and completes the calibration.
5.3.11.8. Reviewing the Calibration Wizard Results

The final screen in the calibration wizard is the review screen shown in Fig. 118. This shows the plots of the results of all the calibration steps. The TCC functions are not plotted, but indicated as Tcc Calibrated or Uncalibrated.

![Finish Calibration Wizard](image)

Fig. 118. Review the Calibration Results.

When the TCC calibration is performed, it includes recalculating the efficiency function, therefore, the efficiency curve (upper right) might not appear to be a good fit to the experimental points. This is because the total efficiency function is the combination of all the different functions.

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 80. If any changes are made, the efficiency (and TCC) calibration should be repeated. If new TCC was not selected, the efficiency calibration can be redone by clicking on Edit Efficiency. This will open up the complete efficiency calibration dialog as explained in Section 5.3.5, page 94. This does not redo the TCC calibration.

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.)

5.3.12. NaI Calibration Wizard...

The NaI Calibration Wizard guides you through the calibration process for one or more NaI detectors. The actual calculations are described in Sections 5.3.4 and 5.3.6.

- Do not use the NaI Calibration Wizard with mixed sources containing numerous and/or closely spaced or overlapping peaks. For the best results, spectra should be composed of well-defined singlet peaks.

- The first peak in the calibration file should be the highest-energy peak used for calibration. The second peak should be the lowest-energy good singlet. All other peaks are can be entered from lowest energy to highest. This method will allow the automatic calibration to proceed in a manner similar to the manual calibration methods, e.g., start at the maximum point, add the anchor point, then fill in the middle points.

- Note that NaI calibrations frequently require modifications for an optimal fit when using spectra generated from mixed gamma sources. This can be accomplished in the interactive mode on the last page of the calibration wizard.

- An analysis of the calibration spectrum should always be performed after the calibration is complete to ensure that the peaks were fit as expected. The peak fit can be viewed with Analyze/Display Analysis Results (Section 5.5.3).

- Unexpected peak fits are normally caused by a bad FWHM calibration and/or an inappropriate calibration Lower Limit value (see Section 5.3.7).

- If the Lower Limit is modified, the calibration should be adjusted.
• If adjustments are made to the energy/FHWM calibration then the efficiency calibration should be verified and adjusted as necessary.

5.3.12.1. Select Detectors

The first dialog is shown in Fig. 119. 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.

5.3.12.2. 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 from 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 120 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, the process can be repeated with new options.

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

5.3.12.3. Choose Calibration Files

Figure 121 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.

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. To view or change the contents of the library, click on Edit. This opens the Renaissance library editor, which is discussed in Section 5.6.4, page 191. When finished, click on Next.

5.3.12.4. Calibration Settings

The next dialog is shown in Fig. 122. The energy can be recalculated without changing the FWHM values. If you want to change the FWHM values, 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 108 for details). The available fit types are None, Interpolative, Linear, Quadratic, and Polynomial.

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. 124).

Click on Next.

5.3.12.5. Sources and Spectrum Settings

Figure 123 shows the next wizard screen. The Number of Sources is normally 2 or 3 for NaI detectors. The number refers to the number of different spectra (1 for each source) that are collected for a single calibration (see Section 5.3.4). 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 for the calibration will be saved to disk if the **Save Spectra** box is marked. The filename will be composed of the **Prefix** and an 8-character number that increments for each spectrum. We recommend that you save these spectra for QA purposes.

Click on **Next** to go to the Source Data Sheet.

### 5.3.12.6. Source Data Sheet

Figure 124 shows the Source Data Sheet dialog. If you specified a new **data source file** (.CAL file) name on the Calibration Files screen (see Section 5.3.12.3), this dialog will be empty. Otherwise, it will contain the source information from the selected .CAL file.

The source **Label** entered here is used in a later step that tells you which source to put on the detector.

If performing this calibration on the MCB, enter the live-time preset (**Count Time**) in seconds. The counting time must be long enough to accumulate well-formed peaks with low counting uncertainty.
.CAL files contain calibration information tables that can be used for the calibration wizard but not the efficiency calibration (.EFT) files created in the Edit Efficiency step. The file contains all the data needed to perform an efficiency calibration using this standard source or sources. There is an entry in the file for each source used.

The table contains the following columns:

1. Isotope name (same as library).
2. Gamma-ray energy (keV).
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 125 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 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.

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

When finished, click on Next. A Source Data Sheet (Fig. 125) 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 on 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 on No.

At this point, the dialog shown in Fig. 126 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 PC’s resources.

In addition to the status dialog, the message shown in Fig. 127 is displayed. Position the source and click on OK to begin spectrum acquisition.

If you chose to use multiple sources, the wizard asks for the next source to be positioned (see Fig. 128). Click on OK to begin spectrum acquisition.

After all the spectra have been collected, the wizard merges the results and completes the calibration.
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 on 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 on 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. 129), click on 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 on **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. Note that the FWHM and energy calibration will frequently require manual adjustments.

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

**5.3.12.7. 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.

**5.3.12.8. Reviewing the Calibration Wizard Results**

The final screen in the calibration wizard is the review screen shown in Fig. 129. This shows the plots of the results of all the calibration steps.

To review or change the energy or FWHM calibration, click on **Edit Energy**. This opens the complete energy calibration dialog as explained in Section 5.3.4. If any changes are made, the efficiency calibration should be repeated. To redo the efficiency calibration, click on **Edit Efficiency**. This will open up the complete efficiency calibration dialog as explained in Section 5.3.6. After adjusting the energy/FWHM, run **Analyze/Interactive in viewed area...** before changing the efficiency calibration.

Alternatively, calibrations 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**)
5.3.12.9. Error Messages

- **No close library match.** The counting statistics are inadequate for the analysis program to at the calibration source library energy. If this is the first peak in the library list for this source, the ROI peak-fit values will be used in the calibration. Either repeat the calibration for a longer count time or discard this peak.

- **No peaks found.** The counting statistics are inadequate for the analysis program to locate any peaks in the spectrum. If this is the first peak in the library list for this source, the ROI peak-fit values will be used in the calibration. Either repeat the calibration for a longer count time or discard this peak. Alternatively, the marked ROI might have fallen outside the peak or the cursor was not placed in the peak to be used for the calibration.

5.4. Calculate

Figure 130 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. 131) 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.

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. 132). 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. 133). 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:

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

where:

- $B$ = the background area
- $l$ = the ROI low limit
- $h$ = the ROI high limit
- $C_i$ = the contents of channel $i$
- $6$ = the number of data channels used (three on each end)
The gross area is the sum of all the channels marked by the ROI according to the following:

\[ A_{g} = \sum_{i = l}^{h} C_{i} \]  

(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:

\[ A_{ag} = \sum_{i = l+3}^{h-3} C_{i} \]  

(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:

\[ A_n = A_{ag} - \frac{B (h - l - 5)}{(h - l + 1)} \]  

(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:

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

(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:
\[ S_i = (O_{i-2} + 4O_{i-1} + 6O_i + 4O_{i+1} + O_{i+2})/16 \]  

(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. 134 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 Section 8, “Analysis Methods”) 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 (see Sections 5.3.11.1 [Ge] and 5.3.12.1 [NaI]). Use the standard file-open dialog (Fig. 135) to recall the first spectrum into a buffer window.
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 136 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.

### 5.5.1. Settings

Figure 137 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 151.

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

This opens the Ge Analysis Options dialog shown in Fig. 138. 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. 138) 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.)

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.

**Fig. 138. Sample Tab for Ge 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 8.8. 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. 139.

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.

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 \( \mu \text{Ci} \) 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 Seagate® 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. 140) 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 is applied by adding, changing, or removing the entry in the Operator program’s **Decay Date** field.

---

**Fig. 140. Decay Tab for Ge 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. 141) 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.

The **Print** option sends the `.RPT` file to the default Windows printer for this PC. 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).

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.

Choosing 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. 142) to select the Analysis Method, Additional Error, Analysis, and Peak Stripping 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 named RENWAN32. Renaissance also offers the RENGAM32, RENNPP32, and RENENV32 engines.
When RENGAM32 is selected, the Library Based Peak Stripping and Directed Fit methods are turned off and the selections disabled.

When RENNPP32 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 RENNPP32 to function in its intended mode. To perform the analysis without any library-based peak stripping, use the RENGAM32 engine. For manual library-based peak stripping, use RENWAN32.

When RENENV32 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 RENENV32 to function in its intended mode. To perform the analysis without any library-based peak stripping, use the RENGAM32 engine. For manual library-based peak stripping, use RENWAN32.

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.
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 8.9.

Peak Stripping

When **Peak Stripping** is enabled, the analysis will perform the library-based peak deconvolution or “peak interference correction” described in Section 8.3.5. 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. 143.

Peaked Background Correction

When the **Peaked Background Correction** (Section 8.6.2) 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 5.5.1.6).
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 multidetector 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 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 Attenuation” on page 209). 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 attenuation 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 8.6.4.

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. 150. 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. 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.

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. 144, 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. 145 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. 146 and 148 show, the linear background fit models the spectrum peaks very well. In Figs. 147 and 149, 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.
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.
Fig. 148. Linear Background Fit.

Fig. 149. Exponential Polynomial Background Fit.
In Figs. 146 and 147, 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. 148 and 149). 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. 150) 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.)

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. 151.

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 0.75 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.

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 Seagate® 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. 152) 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 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 a the current measurement.

Report Tab
This screen (Fig. 153) 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.

The Print option sends the .RPT file to the default Windows printer for this PC. 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.

Choosing 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. 154) 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 RENGSA. 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 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.

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) that 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, 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.

**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. 155.

**Peaked Background Correction**
When the **Peaked Background Correction** (Section 8.6.2) 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 5.5.1.6).

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 multidetector 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.
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 Attenuation” on page 209). 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 attenuation 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 8.6.4.

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.

5.5.1.3. **Reports**

This dialog (Fig. 156) 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.

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. 157, 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 that 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 on 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 on Apply.

NOTE Every parameter in the analysis options file will be applied to each spectrum in the list.
NOTE  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 on the Close (×) button.

### 5.5.1.5. Attenuation...

This starts the dialogs that allow you to view, change, add to, or delete from the attenuation database. The attenuation database is used for the calculations with collimators and material matrices. The initial dialog is shown in Fig. 158.

![Attenuation Materials Display](image)

The display shows the numerical table of Linear and Mass attenuation coefficients by energy on the left side and a graph of the selected coefficient for the selected material. The buttons at the top right corner of the graph select which set of coefficients are plotted. The buttons below these
are used to zoom and change the scale on the plot. To restore the graph to the default selections, click on **Refresh** at the top.

**Viewing Attenuation Materials in the Database**

To select a material, use the drop down list to show the available materials in the database. The display will update when a new material is selected.

**Editing Attenuation Materials**

To edit a material, select it, then click on the Edit button below the material field. This will open the dialog shown in Fig. 159, which is similar to Fig. 158, except the fields that can be changed are now white. Change any fields needed and click on **Update** to save these values in the database and exit the dialog. **Cancel** will exit this dialog without saving the new values. Click on **Clear** to erase all the energy and coefficient fields but leave the other fields unchanged. Use **Delete** on the main dialog to completely remove a material.

![Fig. 159. Edit Attenuation Material.](image)
Adding Materials to the Database with the Attenuation Coefficient Wizard

Click on Add in Fig 158 to start the Attenuation Coefficient Wizard. The first dialog is shown in Fig. 160. Click on Next to continue. At any time, click on Back to go back to a previous dialog to make corrections or review the entries. Click on Cancel to return to the main attenuation dialog without adding any material to the database. Mark the box to skip this dialog in the future.

Fig. 160. Start Matrix Material Add Wizard.

Click on Next to go to the Calculate Coefficients dialog (Fig. 161).
A new material can be defined as a combination of other materials already in the database or it can be defined directly in terms of the attenuation coefficients. Select **Calculate coefficients** to use materials already in the database. For example, to create sand from silicon and oxygen, use the Calculate method. The **Enter coefficients** method requires the actual values for the coefficients. These can be obtained from different reference sources. Care should be taken to use the correct values.

Click on **Next** to go to the New Material dialog (Fig. 162).
In this dialog, enter the name of the material. The name cannot duplicate the name of an existing material. You can either enter the chemical formula here or construct the material from the database materials on the next dialog. The chemical symbols must be entered exactly as stored in the database, including uppercase and lowercase letters.

Click on Next to continue. If the chemical symbol entered is not found in the database, the message shown in Fig. 163 is displayed. Before an element can be used, it must be entered into the database. Elements are entered in this dialog, but must be entered using the Enter Coefficients method.

If your entry is accepted, the wizard will move to the next page (Fig. 164).
On this dialog, the density and the atomic weight are entered. If a chemical formula was entered on the previous dialog, the atomic weight is entered as the default value here. For materials with no defined atomic formula, such as “combustibles”, there is no atomic weight value, so the density must be used. The density is entered in g/cc in all cases, that is, it does not depend on the units setting.

Click on Next to continue.

If you selected **Calculate coefficients** on the Calculate Coefficients dialog, the Composition dialog (Fig. 165) is displayed next. Otherwise, go to the **Enter coefficients** discussion on page 175. The chemical formula is used to calculate the total absorption coefficient from the individual coefficients in the database. These can be combined in one of two ways. On this dialog, select either combined by **Number of atoms** or by **Percent by atomic weight**. Both methods are a weighted average of the component coefficients, this selects the weighting factors.
In the example of sand, combining by number of atoms means that the total absorption coefficient is the sum of the silicon coefficient and twice the oxygen coefficient divided by the number of atoms (3). While the percent by weight method means that the total absorption coefficient is 0.4675 (weight percent silicon or 28.08 divided by 28.08 + 15.99 + 15.99) times the silicon coefficient and 0.5325 (weight percent oxygen or 31.98 divided by 28.08 + 15.99 + 15.99) times the oxygen coefficient. Click on **Next** to continue.

Figure 166 is shown next. This dialog is used to add materials or elements from the database (Master list) to the new material composition. If a chemical formula was entered previously, the elements and number are already entered. To add an element or material from the Master list, click on the element, enter the number of atoms, and click on **Add**. To remove an element from the new material, click on the element in the Composition list and click on **Remove**. To change the number of atoms, remove the element and add it, entering the correct number of atoms in the dialog.
When the composition of the new material is correct, click on **Finish**. This will return you to the Attenuation Materials dialog (Fig. 158), which will display the newly added new coefficients. To accept these values, click on **Close**.

**Entering Coefficients**

If you selected **Enter Coefficients** on the Calculate Coefficients dialog (Fig. 161, page 170), the Attenuation Materials dialog (Fig. 158, page 168) will open. The material name will now be displayed but its energy and coefficient table will be blank. Enter the first energy and the values for it in the columns in the table on the left. Press the down arrow `<↓>` to advance to the next energy. When completed, click **Update** to save them.

**Returning To and Exiting From the Attenuation Materials Dialog**

In both methods of entering new materials, clicking on **Update** displays the Attenuation Materials dialog (Fig. 158). Enter or remove as many materials as you wish.

Click on **Close** to return to the Supervisor display.
5.5.1.6. Peak Background Correction

The Peak Background Correction submenu is shown in Fig. 167. 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.

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. 168. 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.

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 filename 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 dialog will be shown when the file has been created, as shown in Fig. 169. The PBC filename will be the same as the spectrum filename.

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 (Fig. 170) 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. 171.

Figure 172 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. 173. 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. 174. 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. 175). If no peaks are shown, none were in the analysis file, possibly because they were all outside the energy analysis range.

![Fig. 174. Edit PBC Peak Values.](image)

![Fig. 175. The List of Analysis Nuclides (left) and the PBC Table (right).](image)
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 on 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. 173, then follow the manual nuclide and peak insertion instructions that begin on page 178.

The entire analysis nuclide list can be copied to the PBC list by opening the analysis list control menu (Fig. 176) and selecting Copy All to PBC.

To change the name of a nuclide on the PBC list, double-click on it to open the PBC Nuclide dialog (Fig. 173).

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. 177.

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. 174).

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 (the .UFO file selection dialog is shown in Fig. 178). 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**.

Figure 179 shows the display for a typical .UFO file, along with its spectrum file. Figure 180 shows the Analysis Results Sidebar. The buttons move the marker up and down through the results list, library, and spectrum simultaneously.

![Fig. 178. Open a .UFO File.](image-url)
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 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 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 **Library** buttons on the Status Sidebar.

The **Peak** buttons move the marker up and 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 and down through the unknown peaks that satisfy the sensitivity cutoff, in energy order, skipping over any library peaks.

The **Multiplet** buttons move up and 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.

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. 181.

Figure 179 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. 182 (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. 183. 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 (which is described in detail in the ORTEC Software File Structure Manual for DOS and Windows Systems):

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Energy</td>
<td>165.85 keV</td>
</tr>
<tr>
<td>Centroid</td>
<td>165.85 keV</td>
</tr>
<tr>
<td>Center</td>
<td>1003.88 keV</td>
</tr>
<tr>
<td>mlo, mhi</td>
<td>[0, 1022]</td>
</tr>
<tr>
<td>Fwhm</td>
<td>6.263 (0.477 keV)</td>
</tr>
<tr>
<td>Fw10%</td>
<td>12.01 (0.915 keV)</td>
</tr>
<tr>
<td>Fw04%</td>
<td>15.18 (1.16 keV)</td>
</tr>
<tr>
<td>Area</td>
<td>181118</td>
</tr>
<tr>
<td>Background</td>
<td>90107</td>
</tr>
<tr>
<td>Counts</td>
<td>181118</td>
</tr>
<tr>
<td>FirstNet</td>
<td>181118</td>
</tr>
<tr>
<td>FirstBackground</td>
<td>0</td>
</tr>
<tr>
<td>Uncertainty</td>
<td>0.0062793</td>
</tr>
<tr>
<td>Abundance</td>
<td>879.193</td>
</tr>
<tr>
<td>MDA</td>
<td>4.13299</td>
</tr>
<tr>
<td>twPeakFlag1.2.3</td>
<td>0x0000 0x0040 0x0000</td>
</tr>
<tr>
<td>Lo, HiWidth</td>
<td>3 3</td>
</tr>
<tr>
<td>BackLo, Hi</td>
<td>2647.33 2227.67</td>
</tr>
<tr>
<td>SlopeAbove</td>
<td>0</td>
</tr>
<tr>
<td>qfParaBack</td>
<td>0 0 0</td>
</tr>
<tr>
<td>irpNuclide</td>
<td>7 -754-7530 0 12</td>
</tr>
</tbody>
</table>

Fig. 183. UFO Peak Record Description.

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.
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 File Structures manual 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.
5. MENU COMMANDS

**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 File Structures Manual. 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. When the analysis is complete, the graphical results and peak area table are displayed as illustrated in Fig. 184. The table records can be sorted by such parameters as energy, area, FWHM, and background by clicking on the desired column header.

Figure 185 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 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.
Fig. 184. Results Interactive in Viewed Area.

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. 186). 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.

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. 181). 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. 180). 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 187. 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.

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. 188). This list shows the nuclide name, energy, gammas/100 disintegrations, and half life. Clicking on 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 on 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. If File name: contains the default entry, * .LIB, no library is currently selected. Select the desired disk and filename and click on Open. This library becomes the working library. The Renaissance analysis requires the .LIB format. Use the Edit command to write this 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 Nuclide Navigator III is installed). The GammaVision library editor is discussed here; the Nuclide-Navigator editor is described in the Nuclide Navigator III user manual.

Figure 189 shows the GammaVision library Editing dialog. The control menu is shown in Fig. 190 (click on the title bar icon to open it); it contains several of the commands necessary to create and edit the .LIB files.

<table>
<thead>
<tr>
<th>Nuclide</th>
<th>Energy</th>
<th>Percent</th>
<th>Half-Life</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cd-109</td>
<td>22.16</td>
<td>86.0000</td>
<td>436 Days</td>
</tr>
<tr>
<td>Cd-109</td>
<td>24.94</td>
<td>17.0000</td>
<td>436 Days</td>
</tr>
<tr>
<td>Am-241</td>
<td>59.54</td>
<td>36.3000</td>
<td>432 Yrs.</td>
</tr>
<tr>
<td>Hg-203</td>
<td>70.83</td>
<td>3.5200</td>
<td>46.59 Days</td>
</tr>
<tr>
<td>Hg-203</td>
<td>72.87</td>
<td>6.4000</td>
<td>46.59 Days</td>
</tr>
<tr>
<td>Cd-109</td>
<td>88.03</td>
<td>3.6100</td>
<td>436 Days</td>
</tr>
<tr>
<td>Co-57</td>
<td>122.07</td>
<td>85.6000</td>
<td>272.4 Days</td>
</tr>
<tr>
<td>Co-57</td>
<td>136.43</td>
<td>10.6000</td>
<td>272.4 Days</td>
</tr>
<tr>
<td>Ce-139</td>
<td>165.85</td>
<td>79.9500</td>
<td>137.7 Days</td>
</tr>
<tr>
<td>Hg-203</td>
<td>279.17</td>
<td>81.5000</td>
<td>46.59 Days</td>
</tr>
<tr>
<td>Sn-113</td>
<td>391.69</td>
<td>64.1600</td>
<td>115.1 Days</td>
</tr>
<tr>
<td>Cs-137</td>
<td>661.66</td>
<td>85.2100</td>
<td>30.17 Yrs.</td>
</tr>
<tr>
<td>Y-88</td>
<td>898.02</td>
<td>95.0000</td>
<td>106.7 Days</td>
</tr>
<tr>
<td>Co-60</td>
<td>1173.24</td>
<td>99.9000</td>
<td>1925 Days</td>
</tr>
<tr>
<td>Co-60</td>
<td>1332.50</td>
<td>99.9824</td>
<td>1925 Days</td>
</tr>
<tr>
<td>Y-88</td>
<td>1836.01</td>
<td>99.3500</td>
<td>106.7 Days</td>
</tr>
</tbody>
</table>

Fig. 188. Library List Dialog.

Fig. 189. Editing Library Dialog.
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. 191.

![Fig. 191. The Master Library (left) and Library Editing Dialog (right).](image)

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.
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. 192. 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. 196). Enter the energy of the gamma ray and the branching ratio of the peak.

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. 189) will change to **Edit** plus the name of the nuclide, as shown in Figure 193.

Click on **Edit [nuclide]...**. This will open the Edit Library Nuclide dialog (Fig. 194). 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.

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. 195.

**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. 196). 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.\(^\text{15}\)

Some old libraries could have these flags set in an unwanted manner. These libraries should be checked before use.

\(^{15}\)To duplicate the operation of older versions of Renaissance, mark either no lines or only the first line as a key line.
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 on 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 on Paste.

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. 197) will print a list of the library, ordered either by Nuclide or Energy, to either the printer or a disk file.

Fig. 197. Print Library to Printer or File.
5.7. Services

The Services menu contains several functions and utilities is shown in Fig. 198.

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.

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 filename extension of .JOB. To start a JOB or edit a .JOB file, select Services/Job Control... to display the dialog shown in Fig. 199.

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.

Once a JOB is started, most menu functions will be disabled (grayed) to prevent interference with the running JOB. The .JOB file name will 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. 200 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.

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 201 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.

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. 202. 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.

**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. 203) 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. 204. 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**.

**Fig. 204. 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. 205) 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).

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 PC 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 currently unlocked, selecting **Lock/Unlock** will open the dialog shown in Fig. 206. 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 on **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. 207. 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. 208) will ask for the password.
In addition, the owner of the Detector will be displayed on the Supplemental Information Line (see Fig. 209).

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.

5.7.6.  Edit Detector Lists

The Edit Detector Lists submenu is shown in Fig. 210. These command are used to select the Detectors on the system that will be used by Renaissance on this PC. Other applications (e.g., GammaVision, AlphaVision®, MAESTRO) on the same PC can have their own lists. In this way, the different Detectors on the network can be segregated by function or type.

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 211 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 the ORTEC MCB CONNECTIONS Hardware Property Dialogs Manual). 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 PCs connected to the workgroup.
To add a Detector to the Renaissance RGE [or RNAI] Pick List for this PC, 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.

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 212 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 212. 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. 213. These are the options that 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 is to ensure that 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.

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 208). 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. 214. 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 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 on Next to go to the Analysis Options page.
5.7.8.3. Analysis Options

Use this dialog (Fig. 215) 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.

To avoid the potential for duplicate entries, the Key field should be consistent for all scan types that use the same database.

Background Stripping

If the Detector Group contains only NaI detectors, you can choose channel-by-channel stripping. The methodology used retains negative channel counts for accurate peak determination and uncertainty reporting. This is in contrast to the Calculate/Strip... command in Supervisor (Section 5.4.5), which subtracts the channel-by-channel data to create a new derived spectrum which does not retain negative channel counts and, therefore, might not always generate the same results as the background stripping performed in the Operator program.

Marking the Strip spectra checkbox activates the Background Correction field on the Spectrum Settings page of the wizard (page 215), which allows you to 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.
NOTE  This background stripping method is only used in the Operator program, and the target spectrum stripped from the subject count cannot be changed. That is, once the scan is performed, it cannot be reanalyzed with a different background stripping spectrum. However, once a spectrum file has been stripped using the Operator program methodology, if you subsequently analyze it in the Supervisor program, Renaissance will permanently turn off that file’s spectrum-stripping capability, and it can no longer be used for stripping in Operator. If you wish to use a spectrum file from Operator with the Supervisor Calculate/Strip command, we recommend that you make a copy of the original spectrum and perform the Supervisor analysis on the copy.

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. 216). This will load the default constants for the selected formula into the CWT= fields (the formulas are explained in Section 8.7). If you wish to use a different correction, select User Defined and enter the values.

- 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:

```
[Spectrum File Prefix] [Subject Name] [Detector Desc] [File Prefix] [Seq No]
```

where:

- **Spectrum File Prefix** = defined on the Spectrum 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:

```
[Sample File Prefix] [Subject Name] [Detector Group] [File Prefix] [Seq No]
```

where:

- **Spectrum File Prefix** = defined on the Spectrum Settings page of the Scan Type Wizard.
- **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, as defined in Sections 5.3.11.1 [Ge] and 5.3.12.1 [NaI].

Print Spectra prints either the summed spectrum or the individual spectra as a standard WinPlots 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. 217) 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 210.

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.

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 PC. 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.3.2 and A.3.3, 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 on **Next** to go to the Detector Settings screen.

### 5.7.8.5. Detector Settings

This dialog (Fig. 218) 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.

**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 219 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.

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 on Next to go to the Save Scan screen.
5.7.8.7. Save Scan

The last dialog in the Operator Scan Type wizard is shown in Fig. 220. This screen displays the Operator Settings File and Scan Type description entered on the Scan Settings dialog (Fig. 214). 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.

5.7.9. Alarm Limits...

The Alarm Limits table (Fig. 221) 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 µCi/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.

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. 222) 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 or reset 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.
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<Del>**, 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. 223. 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.

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. 224, 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.

5.9. Display

The commands on the Display menu (Fig. 225) 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.

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. 226).

This command is duplicated by Keypad<++>, the Toolbar **Zoom In** button, and **Zoom In** on the right-mouse-button menu.

![Fig. 226. Vertical and Horizontal Full-Scale Setting on the Toolbar.](image)

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. 227). This selection is for the active spectrum display only.

**NOTE** The preferences selected here will also apply to the Operator program.

![Fig. 227. Display Preferences Submenu.](image)
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 228 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. 229) 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.
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. 230). 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).
5.10. **Window**

This menu contains standard Windows commands for controlling the display of the spectrum windows (Fig. 231). 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.

![Fig. 231. Windows Menu.](image)

5.11. **Right-Mouse-Button Menu**

Figure 232 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
types of Detectors when they are collecting data.) The data can also be cleared with \(<\text{Alt}+3>\), 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 \(<\text{Alt}+5>\) 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 modern digital spectrometers such as the DSPEC Pro, digiBASE, DSPEC jr 2.0, and DSPEC Plus. 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.
6. THE Ge REPORT

A typical Renaissance report for germanium spectra is shown in Figs. 233 through Fig. 237. The exact details of the report depend on the options selected, the spectrum, the calibration, and the libraries.

6.1. First Page

The beginning of the report (Fig. 233) shows all the bookkeeping data that are stored with the spectrum files along with other messages about the analysis.

Report Header

These top two lines are repeated on every page. The first line gives the program name, input/report code (in this example, 63), analysis version code (in this example, G52W2.01), analysis date, and page number.

The input/report code represents the user-entered requests and the status on the program’s ability to fulfill these requests. The number is decoded into binary with the following bit usage:

1. True if the spectrum is energy calibrated
2. True if the spectrum is efficiency calibrated
3. True if the library is a valid gamma-ray library
4. True if the isotopic abundance will be reported
5. True if the isotopic matrix will be reported
6. True if the peak/energy matrix will be reported
8. True if the PBC has been used
12. True if the directed fit has been enabled

These flags represent the analysis performed. This can be different than the analysis requested. For example, if the library could not be found, this bit would be turned off. Also, the isotopic abundance and isotopic matrix output bits would be off and the peak/energy matrix output bit would be turned on.

On this report, the code 63 (which is binary 0000 0011 1111, read digit numbers 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, and (6) peak/energy matrix is reported. 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.
Fig. 233. First Part of Ge Report.
The analysis version code changes as updates to the internal algorithms are made. This code is only useful when requesting assistance for a particular spectrum.

The second line gives the laboratory name as entered on the Sample tab under **Analyze/Settings/Sample Type...**, and spectrum name.

**Sample Description from File**
The sample description, if any, saved with the spectrum file. The `.SPC` file description is 128 characters (two lines) and the `.CHN` file description is 63 characters (one line).

**Spectrum Filename**
The user-entered name for a `.CHN` file or the original name of the `.SPC` file (from CONVERT) for `.SPC` files.

**Data Acquisition Parameters**
These include the date and time data acquisition started, the live time and real time values, and Detector ID as stored in the spectrum file.

**Calibration Information**
Includes the calibration filename, and information about each of the calibrations (energy, efficiency, TCC) performed. The filename and description are from the spectrum file if it is an `.SPC` file. Each set of calibration data shows the date the calibration calculation was performed (not the collection date of the calibration spectrum), so each calibration can have a different date. The offset and slope from the calibration data in the `.SPC` or `.CHN` file are presented; the quadratic factor is not printed.

**Analysis Library**
This section of the report prints the analysis library filename. If the library was not found, a “not found” message is printed here. If the manual library-based peak stripping is enabled, the two additional library filenames involved are printed here.

**Analysis Parameters**
Lists analysis-related factors including analysis engine, and analysis start and stop channels; peak rejection cutoff and peak search sensitivity; normalization factor, user-selected MDA, random and systematic error, fraction limit for nuclide identification, and background method; and half-lives decay limit.

The peak rejection level is the user-entered value for the 1-sigma error cutoff on peak utilization. Any peaks with 1-sigma counting error greater than this value are not used in the analysis. Library peaks that fail this test are still reported, but not used in the analysis. Peaks that are not in the library and fail are not reported in the unknown list.
The normalization factor is the factor for changing the output activities to the requested units from the internal units of becquerels. It is the quotient of the input multiplier and input divisor. A value of 1.0 leaves the activities in becquerels.

**User-Selected Corrections**

This lists all available corrections and whether or not they were performed in this analysis.

If the decay-during-acquisition correction was enabled, this entry is marked **YES**. The correction could be small due to the ratio of the half-life to the real time, so the effect might not be seen in the output activity.

**Quality Factor**

This value is a measure of how well the spectrum matched the centroid energies of the library peaks (see Section 8.2.6, page 263). It can range from 0.0 to 1.0, with 0.0 being the best. If this value approaches 1.0, the calibration should be checked. The value will also be large if there is large statistical variation in the library peaks in the spectrum. This can occur when screening low level samples for a few nuclides, because the centroid of a very small (or nonexistent) peak is not well-defined.

**Energy Recalibration Notice**

If the spectrum was recalibrated, this message is printed. The change could be small and the Quality Factor should be referenced for changes (see page 263 for more details). The new energy factors listed in this section are the offset and slope from the recalibration of the spectrum. These will not be very different from the previous values.

### 6.2. Unidentified Peak Summary

Figure 234 shows the peak/energy matrix of the unidentified peak summary. You can suppress this report. The first column is the peak channel as determined by the peak finder (see page 262). It is reported to two decimal places, but normal variation can be in the tenths of a channel.

The second column shows the 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.

The third column shows the background under the peak. This is the straight-line background.

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.
### Fig. 234. Unidentified Peak/Energy Matrix.

The next column shows either the net area divided by the live time to yield the counts/second for the peak or the net area times the efficiency at this energy. See page 376 (Ge) and page 383 (NaI).

The next column shows the counting uncertainty for this net peak area. The 1-sigma values are no higher than the peak cutoff.

The next column shows the full-width at half-maximum (FWHM) of the net peak area. This is in energy if the spectrum is calibrated, channels otherwise.

The next column shows the closest match from the suspected nuclide library if the spectrum is calibrated. If not calibrated or no match is found, a dash is printed. If a nuclide is listed in both the analysis library and the suspected nuclide library, it is possible for different peaks to be associated with the same nuclide in different libraries because the acceptance window is larger for the suspects than for the analysis. It could indicate that the energy calibration is incorrect or that the libraries need improving.

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<td>1.442E+03</td>
<td>0.84</td>
<td>Au-198M</td>
</tr>
<tr>
<td>5982.56</td>
<td>968.61</td>
<td>10110</td>
<td>158</td>
<td>2.64E+00</td>
<td>87.91</td>
<td>0.425E+00</td>
<td>0.84</td>
<td>1.442E+03</td>
<td>0.84</td>
<td>Pa-232</td>
</tr>
<tr>
<td>6962.73</td>
<td>1152.91</td>
<td>23750</td>
<td>766</td>
<td>1.405E+04</td>
<td>42.24</td>
<td>0.254E+00</td>
<td>0.84</td>
<td>1.442E+03</td>
<td>0.84</td>
<td>Co-60</td>
</tr>
<tr>
<td>6669.63</td>
<td>1332.40</td>
<td>20294</td>
<td>2192</td>
<td>4.790E+06</td>
<td>0.33</td>
<td>2.400E+00</td>
<td>0.84</td>
<td>1.442E+03</td>
<td>0.84</td>
<td>Co-60</td>
</tr>
<tr>
<td>6200.24</td>
<td>1530.60</td>
<td>5193</td>
<td>410</td>
<td>9.507E+03</td>
<td>34.89</td>
<td>0.219E+00</td>
<td>0.84</td>
<td>1.442E+03</td>
<td>0.84</td>
<td>Co-60</td>
</tr>
<tr>
<td>6726.24</td>
<td>1740.78</td>
<td>2966</td>
<td>412</td>
<td>1.000E+04</td>
<td>31.65</td>
<td>0.255E+00</td>
<td>0.84</td>
<td>1.442E+03</td>
<td>0.84</td>
<td>Co-60</td>
</tr>
<tr>
<td>9499.70</td>
<td>1566.49</td>
<td>2028</td>
<td>179</td>
<td>4.382E+03</td>
<td>52.40</td>
<td>0.313E+00</td>
<td>0.84</td>
<td>1.442E+03</td>
<td>0.84</td>
<td>Co-60</td>
</tr>
<tr>
<td>11738.55</td>
<td>1937.17</td>
<td>1940</td>
<td>429</td>
<td>1.102E+04</td>
<td>32.54</td>
<td>0.546E+00</td>
<td>0.84</td>
<td>1.442E+03</td>
<td>0.84</td>
<td>Co-60</td>
</tr>
<tr>
<td>15174.52</td>
<td>2505.48</td>
<td>308</td>
<td>190999</td>
<td>5.926E+05</td>
<td>0.84</td>
<td>2.974E-04</td>
<td>0.84</td>
<td>1.442E+03</td>
<td>0.84</td>
<td>Co-60</td>
</tr>
</tbody>
</table>

- s: Peak fails shape tests.
- D: Peak area deconvoluted.
- M: Peak is close to a library peak.

Gross minus background | Counting uncertainty
The next column shows a symbol if the peak is too wide or too narrow as compared to the shape calibration. For peaks, or if the spectrum is not calibrated, the column is blank.

The last column shows a symbol if the peak has been included in a deconvolution region. It can mean that the system is not correctly energy calibrated.

### 6.3. Peak/Energy Matrix

Figure 235 shows the peak/energy matrix for the library peaks. If the library-based peak stripping is enabled, there is a separate list for each library. The library name is printed at the beginning of the list. They are arranged in ascending energy order. The list can be suppressed. It is not printed if the library is not found or the spectrum is not calibrated.

<table>
<thead>
<tr>
<th>Nuclide</th>
<th>Peak Channel</th>
<th>Energy</th>
<th>Background</th>
<th>Net Area</th>
<th>Intensity</th>
<th>Uncert</th>
<th>FWHM</th>
</tr>
</thead>
<tbody>
<tr>
<td>AM-241</td>
<td>360.97</td>
<td>59.56</td>
<td>212820.</td>
<td>136020.</td>
<td>68.410</td>
<td>0.82</td>
<td>1.429</td>
</tr>
<tr>
<td>CS-134</td>
<td>1408.26</td>
<td>515.50</td>
<td>69474.</td>
<td>1112.</td>
<td>0.555</td>
<td>45.75</td>
<td>0.159s</td>
</tr>
<tr>
<td>K-40</td>
<td>5091.05</td>
<td>89474.</td>
<td>1112.</td>
<td>0.555</td>
<td>45.75</td>
<td>0.159s</td>
<td></td>
</tr>
<tr>
<td>CS-134</td>
<td>3411.48</td>
<td>563.23</td>
<td>123511.</td>
<td>281345.</td>
<td>140.572</td>
<td>0.26</td>
<td>1.815b</td>
</tr>
<tr>
<td>Cs-137</td>
<td>3480.22</td>
<td>569.31</td>
<td>139684.</td>
<td>510466.</td>
<td>255.233</td>
<td>0.17</td>
<td>1.619b</td>
</tr>
</tbody>
</table>

<s>Peak fails shape tests.</s>  
<s>DPeak area deconvoluted.</s>

**Fig. 235. Identified Peak Summary.**

The first column shows the nuclide name as listed in the library.

The second column is the peak channel as determined by the peak finder (see Section 8.2.5). If the peak centroid cannot be found, then 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.

The third column shows the 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.

The fourth column shows the background under the peak. In most cases this is the straight-line background, but can be the stepped background in a deconvoluted region.
The fifth 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.

The next column shows the net area divided by the live time to yield the counts/second for the peak.

The next column shows the counting uncertainty for this net peak area. All library peaks are reported, even if their error exceeds the input sensitivity cutoff.

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.

### 6.4. Library Peak Usage

Figure 236 shows the isotope/peak matrix or summary of library peak usage. You can suppress this part of the report. It is also not available if the library is not found or the spectrum is not efficiency-calibrated. If the library-based peak stripping is enabled, there is a separate list for the two analysis libraries. The library name is printed at the beginning of the list.

The first column shows the nuclide name. These are arranged in library order. The nuclides are separated by a blank line. The second column shows the average activity in becquerels or other units. This number has been normalized by the scaling factors, the decay-during-acquisition correction, the decay during sample collection, and random summing.

The third column shows the peak energies for each nuclide, in the library order. This is the library energy.

The next column shows the activity based only on this peak. For a nuclide with only one peak, this is the same as the entry in column 2, except for the normalization and correction factors.

The next column can contain a symbol ( *, !, ?, @, %, $, +, -, =, & , or } ) 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.
**Fig. 236. Summary of Library Peak Usage.**

The symbols have the following meanings:

* The peak FW10M and FW25M were wider than the calibrated shape by more than 20% which would indicate that this could be a multiplet. Deconvolution was not possible, however, because only one peak was in the library.
! This peak was in an area that was deconvoluted and the area of this component was zero or minus. The peak was then removed as a component and the deconvolution redone. This usually indicates this peak was not present or the energy calibration needs adjusting.

? The peak FW25M is less than 80% of the calibration FW25M. This usually indicates that this peak is not present.

@ 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 that there might be a small peak near the main peak that should be included in the library.

% The 1-sigma counting error was greater than the user-set sensitivity cutoff value.

$ This peak was identified as belonging to this nuclide, but the first peak in the library was not present or was disqualified. Normally, the first peak in the library is the main peak for the nuclide, and this would indicate that this peak does not belong to this nuclide. The library should be changed to reflect the actual peaks.

+ The abundance for this peak was higher than the running average of those included so far (starting at the first energy for this nuclide in the library and going down the peaks for this nuclide).

- The abundance for this peak was lower than the running average of those included so far (starting at the first energy for this nuclide in the library and going down the peaks for this nuclide).

= 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. This means the peak could not be attributed to this nuclide.

The library should be changed to include the actual peaks or the calibration checked. This also occurs for very small peaks where the peak shape is ill-defined.

} The peak area for this peak was derived using other peaks for this nuclide. This is enabled by the library-based peak stripping option.

The next column can contain a symbol, ( ), that indicates which peaks were used in the average activity calculation for this nuclide. There might 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.
6.5. Nuclides in Sample

Figure 237 shows the activity in the sample. 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. You enter the column label. If decay correction is requested, the decay-corrected activity is also printed. If the nuclide is not found, the MDA value is printed with a < symbol after the nuclide name, and no uncertainty.

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.

![Table of Nuclides in Sample]

**Fig. 237. Summary of Nuclides in Sample.**
# THE NaI REPORT

A typical Renaissance report for NaI spectra is shown in Figs. 238 through 243. 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. 238) shows all the bookkeeping data that are stored with the spectrum files along with other messages about the analysis.

![First Page of NaI Report](image)

**Program name**

This is the name of the program that produced this report; it does not change.

**Laboratory name**

This is the name of the laboratory as entered under **Analyze/Settings/Sample Type**.

**Input/Report code**

This number 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.
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. The second line of the header is specified on the System tab under Analyze/Settings/Sample Type.... The top two lines are repeated on each page of the report.

ANALYSIS DATE
The date the analysis was performed.

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 operator input name for the original name of the .SPC file.

SPECTRUM COLLECTION DATE
This is the date the spectrum was collected as recorded in the spectrum file.

SPECTRUM COLLECTION LIVE TIME, REAL TIME
The live time and real time values as stored in the spectrum file.

DETECTOR DESCRIPTION
The detector description are from the spectrum file. The .SPC file descriptions are 128 characters each (two lines) and 63 characters each (one line) for the .CHN files.

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.

CALIBRATION DATE FOR ENERGY AND EFFICIENCY
This is the date the calibration calculation was performed. It is not the collection date of the calibration spectrum.

ENERGY CALIBRATION FACTORS
The energy factors are the offset and slope from the calibration data in the .SPC or .CHN file. The quadratic factor is not printed.

The rest of page 1 is shown in Fig. 239.
7. THE NaI REPORT

Fig. 239. NaI Report Page 1, continued.

**LIBRARY FILENAME**

The analysis library filename is printed. If the library was not found, then a “not found” message is printed here.

**MDA FACTOR**

This is the factor used in the MDA calculation, as set on the System tab under Analyze/Settings/Sample Type....

**ANALYSIS REGION**

This is the start/stop channels as input by the operator. The analysis region in energy is printed at the end of the report.

**NORMALIZATION FACTOR**

This is the factor to change the output activities to the requested units from the internal units of becquerels. It is the quotient of the input multiplier and input divisor. A value of 1.0 leaves the activities in becquerels.

**FRACTION LIMIT**

This is the value used in the analysis to reject isotopes, as set on the System tab under Analyze/Settings/Sample Type....
HALF-LIFE DECAY LIMIT
This is the decay limit for rejecting isotopes, as set on the System tab under Analyze/Settings/Sample Type.

BACKGROUND METHOD
The background method selected by the operator is shown here.

LIBRARY MATCH WIDTH
This is the peak acceptance width set by the operator in the Analysis Settings dialog.

CORRECTIONS
All of the available corrections are listed along with the on/off status.

DECAY DATE
The decay-corrected activity is corrected to this date. If the decay correction is off, this is blank.

DECAY DURING ACQUISITION
If the decay during acquisition was enabled, then this is on. The correction could be small due to the ratio of the half-life to the real time, so the effect might not be seen in the output activity.

7.2. Unidentified Peak Summary

Figure 240 shows the second page of the report. The first section of this page provides the peak/energy matrix of the unidentified peak summary. This report can be suppressed by the user.

PEAK CHANNEL
The first column is the peak channel as determined by the peak finder (see page 262). It is reported to two decimal places, but normal variation can be in the tenths of a channel.

CENTROID ENERGY
The second column shows the 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.

LIST OF PEAK FLAGS
This is a list of the flags that are printed at the far right of this page.
### Background Counts
The third column shows 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.

### Intensity CTS/SEC
The next column shows 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.3.2.1).

### Uncertainty
The next column shows 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.

### Peak Width
The next column shows the FWHM of the net peak area. This is in energy if the spectrum is calibrated, otherwise it is in channels.

The next column shows a symbol if the peak is too wide or too narrow as compared to the shape calibration. For acceptable peaks, or if the spectrum is not calibrated, the column is blank.

---

<table>
<thead>
<tr>
<th>Channel</th>
<th>Energy</th>
<th>Counts</th>
<th>Counts * Area</th>
<th>Efficiency</th>
<th>Uncert</th>
<th>1 Sigma</th>
<th>5 keV</th>
</tr>
</thead>
<tbody>
<tr>
<td>31.14</td>
<td>69.07</td>
<td>633650</td>
<td>126666.2997E+05</td>
<td>0.93</td>
<td>31.113</td>
<td>3.8D</td>
<td></td>
</tr>
<tr>
<td>283.49</td>
<td>913.49</td>
<td>72774</td>
<td>3950.6.249E+04</td>
<td>9.79</td>
<td>63.007</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Legend for peak flags
- S: Peak fails shape tests.
- D: Peak area deconvoluted.

Peak intensity or peak area efficiency
Peak width
Peak flags

Fig. 240. Unidentified Peak Summary on Page 2.
The last column shows a symbol 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. 241) 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.

**LIBRARY USED**
- This shows the name of the library used for the peak list shown below.

**NUCLIDE**
- The first column shows the nuclide name as listed in the library.

**PEAK CHANNEL**
- The second column is the peak channel as determined by the peak finder (see page 262). If the peak centroid cannot be found, then 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**
- The third column shows the 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 fourth column shows 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 fifth 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.
7. THE NaI REPORT

**Fig. 241. Identified (Library) Peak List.**

<table>
<thead>
<tr>
<th>NUCLIDE</th>
<th>PEAK CENTROID</th>
<th>BACKGROUND</th>
<th>NET AREA</th>
<th>INTENSITY</th>
<th>UNCERT</th>
<th>FWHM</th>
</tr>
</thead>
<tbody>
<tr>
<td>C0-57</td>
<td>41.85</td>
<td>122.07</td>
<td>10408.6</td>
<td>467239.1</td>
<td>1557.463</td>
<td>0.18</td>
</tr>
<tr>
<td>C0-57</td>
<td>0.00</td>
<td>136.43</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
</tr>
<tr>
<td>C2-137</td>
<td>209.42</td>
<td>661.30</td>
<td>6726.0</td>
<td>250136.1</td>
<td>757.127</td>
<td>0.26</td>
</tr>
<tr>
<td>C0-60</td>
<td>357.34</td>
<td>1173.24</td>
<td>44672.7</td>
<td>74122.7</td>
<td>247.074</td>
<td>0.55</td>
</tr>
<tr>
<td>C0-60</td>
<td>401.49</td>
<td>1332.50</td>
<td>35493.1</td>
<td>71386.7</td>
<td>237.953</td>
<td>0.53</td>
</tr>
</tbody>
</table>

Legend for peak flags:
- S Peak fails shape tests.
- D Peak area deconvoluted.

- **INTENSITY CTS/SEC**
The next column shows either the net area divided by the live time to yield the counts/second for the peak, or the efficiency at this energy times the peak area. See Section B.5.2. for instructions on selecting one or the other.

- **UNCERTAINTY**
The next column shows 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 242 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.
Fig. 242. Library Peak Use Summary.

NUCLIDE
The first column shows the nuclide name. These are arranged in library order. The nuclides are separated by a blank line.

AVERAGE ACTIVITY
The second column shows the 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.

ENERGY keV
The third column shows the peak energies for each nuclide, in the library order. This is the library energy.

ACTIVITY
The next column shows the activity based only on this peak. For a nuclide with only one peak, this is the same as the entry in column 2.

MDA FOR THIS PEAK
This is the MDA for this nuclide based on this peak only.
HALF LIFE IN DAYS
This is the half-life for this nuclide in days. This and the next column can be suppressed by modifying G30WINDS.INI.

BRANCHING RATIO
This is the branching ratio for this energy for this isotope. See HALF LIFE IN DAYS.

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.

COMMENTS
This column contains the half-life in days, followed by the branching ratio. This could be overwritten by other messages.

7.5. Summary of Nuclides in Sample

Figure 243 shows the last page of the report, which lists the activity in the sample. 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. 243). 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.
### Summary of Nuclides in Sample

<table>
<thead>
<tr>
<th>Nuclide</th>
<th>Activity (Bq/Kg)</th>
<th>Uncertainty (1 Sigma)</th>
<th>Total Uncertainty</th>
</tr>
</thead>
<tbody>
<tr>
<td>C0-57</td>
<td>4.9015E+03</td>
<td>0.13%</td>
<td>5.56%</td>
</tr>
<tr>
<td>C0-60</td>
<td>5.8754E+03</td>
<td>0.54%</td>
<td>5.40%</td>
</tr>
<tr>
<td>Cs-137</td>
<td>9.6778E+03</td>
<td>0.25%</td>
<td>5.57%</td>
</tr>
</tbody>
</table>

**Summary**

Total Activity (9.0 to 1696.7 keV) 2.0453044E+04 Bq/Kg

---

**Sign-off**

- **Analyzed by:** Callie Kitts
- **Reviewed by:** Supervisor
- **Laboratory:** ORTEC

---

**Fig. 243. Final Analysis Summary.**
8. ANALYSIS METHODS — Ge

The Renaissance software incorporates four analysis engines from GammaVision and a new ROI analysis engine, ROI32. 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 result 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.

8.1. General

The Renaissance programs analyze spectrum files and produce a list of the background, net area, counting uncertainty FWHM, and net count rate for all peaks in the spectrum. If possible, it will also give 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, operator inputs and the list of peaks and nuclides found in the spectrum.

8.1.1. RENWAN32

The general flow or sequence of operation of the program is shown on the flow chart (Figs. 244 and 245). The remainder of the chapter explains the calculations performed, how the inputs are used, and how the output is produced. The explanation follows the flow chart.

8.1.2. RENGAM32

The RENGAM32 analysis engine is an alternate analysis engine for Renaissance. It operates in much the same way as RENWAN32 to produce a text report (.RPT) file and a binary output (.UFO) file. This method reports only on nuclides that are in the spectrum. A large list of possible candidate nuclides can be in the library, but only those nuclides with gamma-ray energies that match the gamma-ray energies in the spectrum are analyzed further. This method 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.
Fig. 244. Analysis Flow Chart.
8. ANALYSIS METHODS — Ge

Fig. 245. Analysis Flow Chart (continued).
RENGAM32 adds the following to the analysis:

The first step in the analysis of a spectrum is to search the spectrum for any peaks (see Sections 8.2.7). The sensitivity factor you entered on the System tab under Analyze/Settings/Sample Type... is used as a lower limit on peak size. Next, the spectrum peak list is compared with the library peaks. Any library peak within 2 times the detector FWHM of a spectrum peak is marked as a candidate. Now, any nuclide in the library that does not have at least one candidate is discarded. Next, if the first peak in the library is not marked as a candidate, the nuclide is discarded. At this point, the nuclide list (library) contains only nuclides with at least their most intense gamma ray located in the spectrum.

Next, all remaining nuclides are checked against their multiple line signature. For each nuclide, any other peaks of that nuclide (up to 4) must also be marked as candidates if the yield times the efficiency for this peak is greater than 10% of the yield times the efficiency of the first peak. The nuclide is discarded if any of the associated peaks are not candidates (i.e., are not found in the spectrum).

At the end of this process, the library only contains nuclides that have passed the test of having multiple peaks (or one, for single-gamma-ray nuclides) in the spectrum. The analysis continues as described for RENWAN32 with this reduced library.

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.

8.1.3. RENNPP32

The RENNPP32 analysis engine is an alternate analysis engine for Renaissance. It has been optimized to meet the requirements of gamma spectrum analysis in nuclear power plants. It operates similarly to RENWAN32, and produces a report file (.RPT) and a binary output (.UFO) file. These files are compatible with the files produced by RENWAN32 and RENGAM32.

RENNPP32 operates in the same way as RENGAM32 to reject library nuclides not found in the spectrum. Operation continues as described for RENWAN32 for the initial peak area, recalibration, deconvolution, and activity calculation. However, after the completion of the activity calculation, the library is modified to remove any nuclides not identified to be present in the spectrum. The spectrum is then re-analyzed completely with the modified library. Any peak previously associated with library nuclides that have been removed are now in the unknown list.

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.)

8.1.4. RENENV32

Renaissance also offers the RENENV32 analysis engine. Much of the operation is the same as RENWAN32, and it produces a report file (.RPT) and a binary output (.UFO) file. RENENV32 operates like RENNPP32 to reduce the library to located nuclides, energy-shift the multiplet deconvolutions, and report activities for the located nuclides. At this point, RENENV32 calculates the MDA of all the rejected nuclides in the library. This gives a full report for the library.

8.1.5. ROI32

This analysis engine reads an .ROI file, then performs a singlet fit to the ROI peaks using a linear background and without adjusting the peak limits. It then performs a peak search and deconvolution to find any peaks not in ROI regions. Library and .UFO files can be used instead of .ROI files. If no .ROI, library, or .UFO file is specified, the ROI records in the .SPC file will be used.

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). The steps are to calculate the background, then the net area, then the centroid.

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.

8.2.1.1. Automatic

For the first pass, the peak centroid is the library energy (Fig. 246).

To calculate the 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 three 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 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.

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. 247). 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. 248, 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 about which method should be used, use the Auto selection.
8.2.1.5. Example Background

An example is shown in Fig. 248, with the spectrum printout in Table 2. The report section for this peak is shown in Fig. 249.

Fig. 248. Background of a Small Peak Near Large Peak.
### Table 2. Spectrum and Five-Point Smooth.

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</tr>
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</table>
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.

Figure 250 shows an example of the differences among the four methods for determining the background.

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:

\[ A_g = \sum_{i=1}^{h} c_i \]  

(20)
where:

\[ A_g = \text{the gross area} \]
\[ C_i = \text{the data value of channel } i \]
\[ l = \text{the center channel of the background calculation width at the low energy side of the spectrum} \]
\[ h = \text{the center channel of the background calculation width at the high energy side of the spectrum} \]

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. 248, Fig. 249, 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. 251).

\[ A_b = \frac{B_i + B_h}{2} \times W \]  \hspace{1cm} (21)

where:

\[ A_b = \text{the background area} \]
\[ B_i = \text{the background on low side of peak} \]
\[ B_h = \text{the background on high side of peak} \]
\[ W = \text{the peak width} \]

**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” 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 was rejected for any shape test by the total summation method.
4. The peak is a singlet.
If all these conditions are met, the spectrum region for 3 times the calibration FWHM, centered on the peak energy, is fit with a grid-search, least-squares fit with nonlinear coefficients. 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 up 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. 248, Fig. 249, and Table 2 to calculate the background for this peak. Substituting in the above formulas yields:
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8.2.3.2. Directed Fit Method

A section of a spectrum with a negative peak is shown in Fig. 252. 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.

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.

\[
\text{bkg error} = \left( \frac{(\text{background area}) (\text{peakwidth})}{(\text{width of low average} + \text{width of high average})} \right)^{1/2}
\]

\[
\text{gross area error} = \sqrt{\text{gross area}}
\]

\[
\text{net area error} = \sqrt{(\text{gross area error})^2 + (\text{background error})^2}
\]

Referring back to Fig. 246, Fig. 249, and Table 2, the background uncertainty is:

\[
\text{Background error} = \sqrt{(432)(2311 - 2276 + 1)} \div 5 + 5
\]

\[
= 39.4
\]

\[
\text{Net area error} = \sqrt{(18143 + 1552.4)}
\]

\[
= 140.4 \text{ or } 0.8\% \text{ of net peak area}
\]

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 extrapolated between the two channels that bracket the respective height value.

**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 on the data in the measured full-width at one twenty-fifth (1/25) maximum (FW0.4M) for the peak.
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\[ \text{Peak centroid} = \frac{\sum_{i=l}^{h} i \cdot C_i}{\sum_{i=l}^{h} C_i} \]  

(26)

where:

\[ i = \text{the channel number} \]
\[ C_i = \text{net contents of channel } i \]

For the directed fit method, the centroid comes 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 re-analyzed.

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 0.5 times the FWHM, or one channel (whichever is greater), that centroid is associated with that library energy. The FWHM multiplier can be changed on the System tab under Analyze/Settings/Sample Type.... 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 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 10 keV and the number of peaks is 0 below and 10 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 Calibration menu can be used to print the new coefficients from the .UFO file. They are printed on the output report.
Table 3. Example Net Spectrum.

<table>
<thead>
<tr>
<th>Channel</th>
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<th>Net Spectrum</th>
<th>Channel</th>
<th>Background</th>
<th>Net Spectrum</th>
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<td>2391.034</td>
<td>2317</td>
<td>12.2510</td>
<td>-2.251</td>
</tr>
<tr>
<td>2293</td>
<td>11.9774</td>
<td>2393.023</td>
<td>2318</td>
<td>12.2624</td>
<td>1.737</td>
</tr>
<tr>
<td>2294</td>
<td>11.9888</td>
<td>1972.011</td>
<td>2319</td>
<td>12.2738</td>
<td>-0.273</td>
</tr>
</tbody>
</table>

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 8.3.

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
峰将略微改变。这种变化通常很小，但在一个计数很少的谱中可以是一个很高的百分比。在给定的谱中，有些峰面积可能会改变，有些可能会保持不变。有些峰可能会从已知列表移动到未知列表（或相反），因为未校正的中心位置太远，不能通过库能量验证。

另外，所有良好库峰的能量差也被计算。这是表征能量差的绝对值与库能量的和的分数之和，平均到峰数。这在点数为2-3个（或更多）的校正中会得到一个介于0和1之间的数，0表示最好的校正。对于2-3点校正，这个数可以大于1.0，因为计算的FWHM（是一个线性函数）不匹配谱的FWHM在谱的两端。如果高值被报告，那么分析结果不可接受时，应该进行更好的校正。校正部分可以用于产生多点校正，这将减少能量差。

\[
QUALITY \ FACTOR = \frac{\sum_{i=1}^{n} |E_{pi} - E_{Li}|}{FWHM_{Li}}
\]  (27)

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

这个“能量-归一化差”被印在报告上。对于复杂的谱，这个数将从0.1到0.3的范围。一个大的值表示需要进行新校正或库不匹配的谱。较小的值通常与较少的峰或较好的校正有关。

如果能量校正已发生，库峰列表将重新分析与新的能量校正。这结果是更准确的峰值，用于计算峰值背景和确定峰中心，以非库峰多峰的的分解。

8.2.7. Peak Search

在库峰确定后，谱被搜索以确定其他峰。即使未请求未知峰值列表，也需要这一步，以便正确计算靠近峰的背景及对峰中心的确定，以非库峰多峰的的分解。阶梯背景测试将高于峰区域的背景与峰区域的背景进行比较（见“多峰背景”）。

8.2.7. Peak Search

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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 independent of 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. 253).

\begin{equation}
C''(n) = \sum_{i=0}^{2j} k_i C(n - j + i) \tag{28}
\end{equation}

where:

- \( k_i \) = the smoothed second difference weighting functions,
- \( 2j + 1 \) = the smoothing width

The peaks are located where the second derivative varies significantly from zero.

A typical gamma-ray spectrum is shown in Fig. 254. 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.

![Typical Gamma-Ray Spectrum](image)

**Fig. 254. A Typical Gamma-Ray Spectrum.**

Not all of these will appear in a given spectrum. For example, escape peaks cannot occur for photons less than about 1 MeV.

The shape of the second derivative can be used to reject Compton edges and other non-peak structure in the data (Fig. 255).

### 8.2.7.1. Peak Acceptance Tests

The second difference must pass the following tests to be considered a peak.

\[
C''(n) < -2 \sqrt{C(n) \sum_{i=1}^{2j} (k_i)^2}
\]  

(29)
In addition, the spectrum data at the channel indicated by the second derivative must pass these tests.

\[ C''(n) < G \cdot C''(n \pm 1) \]  

(30)

where:
- \( G \) = a constant proportional to the resolution of the detector
- \( k_i \) = the second difference coefficients
- \( C(n) \) = the channel data of the \( n \)th channel
- \( C'' \) = the second difference at the \( n \)th channel

The peak centroid is calculated using the weighted channel sum method as follows:

\[ P = \frac{\sum_{i=1}^{h} i \cdot C_i}{\sum_{i=1}^{h} i} \]  

(31)

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 two channels later.

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 entered by the operator, 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” switch is turned on. 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. Locating Multiplets

Any region that contains more than one peak, including library and non-library peaks, passing the sensitivity test in a region that is 3.3 times the FWHM width will be deconvoluted. If a peak in the region is a library peak and is not the first peak in the library for this nuclide, the first (in library order) peak in the energy analysis range for this nuclide must have a positive net area and a defined centroid for this peak to be included in the deconvolution unless the first library peak is also in this multiplet region. If, however, the peak was located by the peak finder, it might be included in the deconvolution as an unknown peak. The areas of disqualified peaks are set to zero.

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 is printed on the report and the individual peaks are labeled in the comment field of the nuclide/peak matrix.

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.
8.3.1. Background for Multiplets

The background for peak multiplets is calculated in an analogous manner to singlets with the exception that the width of the region is from 1.5 times the FWHM below the lowest peak to 1.5 times the FWHM above the highest peak (Fig. 256).

![Fig. 256. Background for Multiplets.](image)

8.3.2. Stepped Background

If the slope of the background across the peak area is less than the slope of the background above (higher in energy) the peak area (that is, if the background under the peaks is declining faster than the background above the peak area is declining), a step is inserted in the background for each positive area peak (Fig. 257). The total height of the steps is equal to the difference between the background below the peak area and the value of the background above the peak region projected backward to the background point at the low end of the multiplet. The size of the step inserted at each peak centroid is proportional to the height of the peak. The result is then smoothed with a smoothing function equal to the resolution of the detector at this energy. This background is calculated after the deconvolution and if the stepped background is needed, the net spectrum is recalculated and the deconvolution is repeated.
A real spectrum with stepped background is shown in Fig. 258. The two components of the doublet are of equal size.

### 8.3.3. Parabolic Background

In some cases, like that shown in Fig. 259, the straight-line background can be significantly above the actual spectrum. This can occur if the peaks are on the low energy side of a rapidly rising background. In this case, if these two conditions are met, the parabolic background is calculated:

1. The background on the low-energy side of the multiplet is less than the background on the high-energy side.
2. At least 3 contiguous points in the lower 75% of the multiplet region are less than the straight line background.
3. For energies above 200 keV, the peak search sensitivity is 2 or higher.

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.
Fig. 258. Stepped Background.

Figure 259 shows this case for an actual spectrum.

Fig. 259. Parabolic Background.
8. ANALYSIS METHODS — Ge

8.3.4. 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. 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. 260). 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.

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.
8.3.5. 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. When enabled, the program will now automatically identify the isotopes in the library that are too close together and calculate their activities indirectly. This method is also referred to as peak-interference correction.

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 Ra-226 is at 185.99 keV. The peak overlaps the 185.72 keV peak of U-235. If these two isotopes are both in the library, Ra-226 and the 185.72 keV U-235 peak are flagged when the library is read. Table 4 shows some common examples. These energies are from Erdmann and Soyka. Other references might have different energies, but the overlaps will still occur.
### 8. ANALYSIS METHODS — Ge

#### Table 4. Gamma Peak Overlap Examples.

<table>
<thead>
<tr>
<th>Isotope</th>
<th>Energy (keV)</th>
<th>Probability</th>
<th>Isotope with close energy</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tc-99m</td>
<td>140.99</td>
<td>89.3</td>
<td>Mo-99</td>
</tr>
<tr>
<td>Ra-224</td>
<td>241.00</td>
<td>3.90</td>
<td>Sr-92</td>
</tr>
<tr>
<td>Ra-226</td>
<td>185.99</td>
<td>3.28</td>
<td>U-235</td>
</tr>
<tr>
<td>Am-241</td>
<td>26.35</td>
<td>2.5</td>
<td>U-237</td>
</tr>
<tr>
<td>Am-241</td>
<td>33.20</td>
<td>0.11</td>
<td>Ce-144</td>
</tr>
<tr>
<td>Am-241</td>
<td>59.54</td>
<td>36.3</td>
<td>U-237</td>
</tr>
</tbody>
</table>

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 U-235 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 U-235 peak is calculated using the branching ratio of that gamma-ray, the efficiency and the activity. The U-235 area is subtracted from the area of the peak at 185 keV, to give the area that is due to Ra-226. From this, the activity of Ra-226 in the sample is calculated.

### 8.4. Nuclide Activity

The nuclide activity is calculated for all peaks in the library whose energy is between the energy limits selected by the operator for the analysis (in-range). There are several methods of determining if a nuclide is present or not, and if MDA should be reported.

The nuclide is reported as present if one of the following is true:

1. The first in-range peak of the nuclide in the library is present in the spectrum, and the counting uncertainty is below the peak cutoff.
2. All of the peaks marked as key lines are present.
3. The fraction limit test is passed.

To duplicate the method in GammaVision V4.12 and older, no key lines are marked and the fraction limit is zero.
If the nuclide is not present, the MDA is reported unless the “No MDA” flag is turned on. MDA Method 3 suppresses all MDA output.

The nuclide activity (in becquerels or curies), based on the peak at energy, $E$, is given by:

$$ A_{Ei} = \frac{N_{Ei}}{\varepsilon_E \cdot t \cdot \gamma_d} $$ \hspace{1cm} (32)

where:

- $A_{Ei}$ = the activity of nuclide $i$ based on energy $E$
- $N_{Ei}$ = the net peak area for peak at energy $E$
- $\varepsilon_E$ = the detector efficiency at energy $E$
- $t$ = the livetime
- $\gamma_d$ = the gammas/disintegration for energy $E$ of this nuclide

The gammas/disintegration value is in the library and the efficiency factor is stored in the .CLB record of the .SPC spectrum file.

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.

8.4.1. Average Activity

The average activity for the nuclide is calculated by first doing a gammas/disintegration weighted average of the first and second library peak activity, if the activity of the second peak is within two times the error of the first peak activity. Only peaks that do not have the “Not in Average” flag set are included. The error in the first peak activity includes counting error of the first peak, error in the library entries, and error in the calibration. Subsequent peaks are likewise included in a running average if their activity is within two times the error of the current average activity. That is:

$$ A_{AVE} = \frac{\sum_{i=1}^{n} I_i}{\sum_{i=1}^{n} G_i} $$ \hspace{1cm} (33)
where:

\[ A_{\text{AVE}} = \text{the average activity} \]
\[ I_i = \text{the corrected (for all factors) intensity of the } i\text{th peak} \]
\[ G_i = \text{the gamma/disintegration of the } i\text{th peak} \]
\[ n = \text{the number of peaks included in the activity} \]

8.5. MDA

The Minimum Detectable Activity (MDA) is a measure of how small an 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. Except for the MDA formula chosen and the sensitivity threshold, the MDA is not affected by the analysis software.

For all peaks, 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.

The MDA reported might be any one of the following MDA formalisms. The type used is printed on the report. In the following definitions, the peak count and peak count rate are calculated according to the various formulas. These are then converted to an MDA with all the corrections performed for the relevant library peak.

8.5.1. Method 1 — Traditional ORTEC

The peak count is equal to the square root of the sum of twice the uncertainty in the background and 2500 over the sensitivity squared plus 50 over the sensitivity, all multiplied by 100 over the sensitivity. The peak count rate is the peak count divided by the live time.

\[
\text{Peak Area Rate} = \frac{100}{\text{SENS}} \times \sqrt{\frac{2 \times BKG + \frac{2500}{\text{SENS}^2}}{\text{SENS}}} + \frac{50}{\text{SENS}} \times \frac{1}{\text{LIVETIME}}
\]
where:

\[ \text{SENS} = \text{the user-set sensitivity in percent (peak cutoff)} \]
\[ \text{BKG} = \text{the peak background (see text)} \]
\[ \text{LIVETIME} = \text{the spectrum live time} \]

### 8.5.2. Method 2 — ORTEC Critical Level

The critical level is 2.33 times the square root of the background. If the peak area exceeds this level, bit 2 of the nuclide flag is set to 1.

### 8.5.3. Method 3 — Suppress MDA Output

The MDA is not calculated and is set to 0.0. For nuclides not present, there is no printout on the nuclide report. The individual peaks are included in the other parts of the report.

### 8.5.4. Method 4 — KTA Rule

The peak count is equal to the square root of average channel contents in a region equal to 2.5 times the calculated FWHM times the number of channels in the FWHM. This value is scaled by the sigma value of 1, 2, or 3 and divided by the live time to give the peak count-rate sigma for the selected value.

\[
P = \frac{\sqrt{B \times W}}{\text{LT}} \times \sigma
\]  
where:

\[ P = \text{peak count rate} \]
\[ B = \text{average background/channel at peak energy} \]
\[ W = \text{FWHM in channels} \]
\[ \sigma = \text{confidence level (1, 2, or 3)} \]

### 8.5.5. Method 5 — Detection Limit, 2 Sigma

The peak count is equal to twice the sum of 1 plus the square root of the sum of 1 plus twice the background. The peak count rate is this divided by the live time.

\[
P = 2 \times \frac{1 + \sqrt{1 + 2 \times B}}{\text{LT}}
\]  
(36)
where:

\[ P = \text{peak count rate} \]
\[ B = \text{background} \]
\[ LT = \text{live time} \]

**8.5.6. Method 6 — Detection Limit, 3 Sigma**

The peak count is equal to 4.5 times the sum of 1 plus the square root of the sum of 1 plus 0.8888 times the background. The peak count rate is this divided by the live time.

\[
P = 4.5 \times \left( 1 + \sqrt{1 + 0.8888 \times B} \right) \frac{1}{LT}
\]  
(37)

where:

\[ P = \text{peak count rate} \]
\[ B = \text{background} \]
\[ LT = \text{live time} \]

**8.5.7. Method 7 — Currie Limit**

The Currie limit is 1.645 times the square root of the background divided by the live time.

\[
P = 1.645 \times \frac{\sqrt{B}}{LT}
\]  
(38)

**8.5.8. Method 8 — RISO**

The MDA is 4.65 times the square root of the background divided by the live time.

\[
P = 4.65 \times \frac{\sqrt{B}}{LT}
\]  
(39)
8.5.9. Method 9 — ORTEC LLD

The LLD value is 4.66 times the error in the peak area divided by the live time.

\[ P = 4.66 \times \frac{\sigma_p}{LT} \]  

(40)

8.5.10. Method 10 — Peak Area

The peak count rate is the net peak area divided by the live time. This peak area could be negative, so the MDA can be negative.

\[ P = \frac{A}{LT} \]  

(41)

8.5.11. Method 11 — DIN 25 482 Method

The peak count is equal to the square root of average channel contents in a region equal to 2.5 times the calculated FWHM times the number of channels in the FWHM. The peak area count rate is 1.35 times the sum of 1.0 and the square root of the sum of 1.0 plus 2.96 times the peak area, divided by the live time.

\[ P = \frac{1.35 \times \left( 1.0 + \sqrt{1.0 + 2.96 \times \text{area}} \right)}{LT} \]  

(42)

8.5.12. Method 12 — NUREG 4.16

This is the method defined in NUREG 4.16.

\[ P = \frac{2.71 + 4.66 \times \sigma_b}{LT} \]  

(43)

where:

\[ P = \text{peak count rate} \]

\[ \sigma_b = \text{error in background} \]
8.5.13. Method 13 — Counting Lab USA

The background is calculated as the straight line between the average of the three points centered at 1.25 times the FWHM below the peak energy and the average of the three points centered at 1.25 times the FWHM above the peak energy. The total counts is the integration of all the channels between these same endpoints. The peak count rate is the total counts minus the background counts divided by the live time. Negative values are allowed and will be used to generate negative activities.

\[ P = \frac{a - b}{LT} \]  

where:
- \( a \) = total area
- \( b \) = calculated background
- \( LT \) = live time


This is the method of Erkennungsgrenze described in the German DIN 25 482 teil 5. Further details can be obtained from this document. The formula is as follows:

\[ R_{*n} = \frac{k_{1,a}^2}{2t} \cdot \frac{b}{2l} \left( 1 + \sqrt{1 + \frac{4R_o t}{k_{1,a}^2}} \cdot \frac{2l}{b} \left( 1 + \frac{2l}{b} \right) \right) \]  

where:
- \( k_{1,a} \) = 1.96
- \( b \) = number of channels in the peak region
- \( l \) = number of channels in the background regions above and below the peak region
- \( t \) = counting time
- \( R_o \) = the count rate in the peak region (total counts divided by the live time)
- \( R_{*n} \) = the Erkennungsgrenze for the peak region \( n \)
8.5.15. Method 15 — Nachweisgrenze DIN 25 482

This is the method of Nachweisgrenze described in the German DIN 25 482 teil 5. The formula is as follows:

\[
\rho^{*}_n = \left( k_{1,\alpha} + k_{1,\beta} \right) \sqrt{\frac{\rho_o}{t} \left( 1 + \frac{b}{2l} \right)} + \frac{1}{4t} \left( k_{1,\alpha} + k_{1,\beta} \right)^2 \left( 1 + \frac{b}{2l} \right)
\]  

(46)

where:
\( k_{1,\alpha} = 1.96 \)
\( k_{1,\beta} = 1.96 \)
\( b \) = number of channels in the peak region
\( l \) = number of channels in the background regions above and below the peak region
\( t \) = counting time
\( \rho_o \) = expectation value of the peak region background
\( \rho^{*}_n \) = the Nachweisgrenze for the peak region \( n \)

8.5.16. Method 16 — EDF and CEA (France)

This is the method defined for the EDF and CEA in Rapport CEA-R-5506, “Determination du Seuil et de la Limite de Detection en Spectrometrie Gamma.” In the implementation here, the \( K_\alpha \) is set to 2.75 for 99.7% confidence level.

The peak area rate is 6.2 times the square root of the background divided by the live time.

\[ P = 6.2 \times \frac{\sqrt{B}}{LT} \]  

(47)

8.5.17. Method 17 — NUREG 0472

This method is defined as the LLD in NUREG 0475 (1985), with the exception of the fractional radiochemical yield, which is omitted. The NUREG formula is defined in microcuries, but Renaissance uses becquerels for all internal calculations. The peak count rate (corresponding to becquerels) is 4.66 times the square root of the background divided by the live time, corrected back to the sample collection time. This is shown in the formula:
\[ P = 4.66 \times \frac{\sqrt{B}}{LT \times e^{-\lambda \Delta t_s}} \]  

where  
\[ \lambda = \text{the decay constant for the nuclide} \]  
\[ \Delta t_s = \text{the time between the midpoint of the sample collection and the start of acquisition of the spectrum} \]

The **Sample Collection** start and end dates and times are entered on the Decay tab under **Analyze/Settings/Sample Type**.... The correction does not have to be enabled in order for you to use the MDA type. However, to enter the times you must enable the correction, enter the two dates and times, then disable the correction if you do not wish to use it. If no dates and times are entered, the date and time of the acquisition are used, meaning that no decay correction is made. Note that the MDA values are always corrected for decay, but if the decay-to-date correction is not enabled, the activities will be reported without decay correction.

The background is the peak background determined in the normal peak calculation. This background region can be wide compared to the FWHM of a spectrum peak at this energy. The width can be reduced by using the width factor in the initialization file. See Appendix C.4.2 for details.

The peak count rate is converted to activity (see below) including the branching ratio for the gamma-ray energy. The branching ratio is not included in the NUREG formula.

**8.5.18. Peak Area Rate**

In all cases, the reported MDA is this peak area rate converted to activity. The MDA activity will include the efficiency correction and any other corrections being used.

**8.6. Corrections**

If enabled, the following corrections are made on a nuclide-by-nuclide or peak-by-peak basis.

**8.6.1. 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:

\[
DDA = \frac{\ln 2 \times \frac{\text{Real time}}{\text{half-life}}}{1 - e^{-\left(\ln 2 \times \frac{\text{Real time}}{\text{half-life}}\right)}}
\]  

where:
- \(DDA\) = the decay correction factor
- \(\text{Real time}\) = the spectrum real time
- \(\text{half-life}\) = the half-life of the nuclide of interest
- \(\ln 2\) = the natural log of 2

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 doesn’t change during the count time, so the live time correction will correctly account for the lost counts during the count time.

### 8.6.2. 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.

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.

8.6.3. Decay Correction

If enabled, the decay 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 menu. 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.

8.6.4. 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. 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 absorption correction is made. One of two types of absorption correction (as defined in ASTM E181-82)\(^\text{16}\) 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.

8.6.4.1. 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:

\[ A_c = A \times e^{\mu} \times x \]  

(50)

where:
- \( A \) = the peak area at energy \( E \)
- \( \mu \) = 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 \( \mu \) (Length, entered on the Corrections tab, Fig. 143, page 150).

For values between the table values, the \( \mu \) are linearly interpolated between the table values. The correction value is always 1 or greater.

### 8.6.4.2. 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.

\[ A_c = A \times \frac{\mu x}{1 - e^{-\mu x}} \]  

(51)

where:
- \( A \) = the peak area at energy \( E \)
- \( \mu \) = 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 \( \mu \) (Length, entered on the Corrections tab; see Fig. 143, page 150).

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.

In all cases the correction factor is constrained to be between 1.0 (no correction) and 1000.

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 ($\text{Length}$, entered on the Corrections tab; see Fig. 143, page 150), so that the factor you have entered is the sample thickness.

8.6.4.3. 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. 261. The $^{154}$Eu peaks are used because they are distributed over the range of interest.
The results with an absorber are shown in Fig. 262. The intensity columns from both figures have been transferred to Table 5, which also shows the ratio of the two sets of intensities and the logarithm of the ratio.

<table>
<thead>
<tr>
<th>NUCLIDE</th>
<th>PEAK CENTROID</th>
<th>BACKGROUND NET AREA</th>
<th>INTENSITY</th>
<th>UNCERT</th>
<th>FWHM</th>
</tr>
</thead>
<tbody>
<tr>
<td>EU-154</td>
<td>205.11 42.74</td>
<td>13258.27358.27.36</td>
<td>1.12</td>
<td>1.407s</td>
<td></td>
</tr>
<tr>
<td>EU-154</td>
<td>600.85 123.06</td>
<td>4562.40707.40.71</td>
<td>0.68</td>
<td>1.090s</td>
<td></td>
</tr>
<tr>
<td>EU-154</td>
<td>1215.85 247.88</td>
<td>2402.5359.5.36</td>
<td>2.56</td>
<td>1.230s</td>
<td></td>
</tr>
<tr>
<td>EU-154</td>
<td>1244.33 253.66</td>
<td>1757.208.21</td>
<td>43.82</td>
<td>0.317s</td>
<td></td>
</tr>
<tr>
<td>EU-154</td>
<td>2910.12 591.73</td>
<td>1334.2679.2.68</td>
<td>4.42</td>
<td>1.569s</td>
<td></td>
</tr>
<tr>
<td>EU-154</td>
<td>3517.08 714.92</td>
<td>1205.278.28</td>
<td>38.89</td>
<td>0.354s</td>
<td></td>
</tr>
<tr>
<td>EU-154</td>
<td>3558.02 723.23</td>
<td>1185.8792.8.79</td>
<td>1.47</td>
<td>1.628s</td>
<td></td>
</tr>
<tr>
<td>EU-154</td>
<td>4296.72 873.15</td>
<td>602.4686.4.69</td>
<td>2.01</td>
<td>1.697s</td>
<td></td>
</tr>
<tr>
<td>EU-154</td>
<td>4903.03 996.20</td>
<td>718.3682.3.68</td>
<td>2.62</td>
<td>1.690s</td>
<td></td>
</tr>
<tr>
<td>EU-154</td>
<td>4944.84 1004.69</td>
<td>799.6249.6.25</td>
<td>2.00</td>
<td>1.824s</td>
<td></td>
</tr>
<tr>
<td>EU-154</td>
<td>6273.41 1274.33</td>
<td>85.8654.8.65</td>
<td>1.13</td>
<td>2.100s</td>
<td></td>
</tr>
<tr>
<td>EU-154</td>
<td>7860.54 1596.44</td>
<td>0.256.26</td>
<td>6.25</td>
<td>1.780s</td>
<td></td>
</tr>
</tbody>
</table>

s Peak fails shape tests.
D Peak area deconvoluted.
Table 5. Absorption.

<table>
<thead>
<tr>
<th>Energy</th>
<th>Without</th>
<th>With</th>
<th>Ratio</th>
<th>Log(ratio)</th>
</tr>
</thead>
<tbody>
<tr>
<td>123.14</td>
<td>63.23</td>
<td>40.71</td>
<td>1.553</td>
<td>0.440</td>
</tr>
<tr>
<td>248.04</td>
<td>7.80</td>
<td>5.36</td>
<td>1.455</td>
<td>0.275</td>
</tr>
<tr>
<td>591.74</td>
<td>3.31</td>
<td>2.68</td>
<td>1.235</td>
<td>0.211</td>
</tr>
<tr>
<td>723.3</td>
<td>11.50</td>
<td>8.79</td>
<td>1.308</td>
<td>0.269</td>
</tr>
<tr>
<td>873.20</td>
<td>5.75</td>
<td>4.69</td>
<td>1.226</td>
<td>0.204</td>
</tr>
<tr>
<td>1004.76</td>
<td>7.71</td>
<td>6.25</td>
<td>1.234</td>
<td>0.210</td>
</tr>
<tr>
<td>1274.45</td>
<td>10.29</td>
<td>8.65</td>
<td>1.190</td>
<td>0.174</td>
</tr>
</tbody>
</table>

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 6.

Table 6. Results — Measured Correction.

<table>
<thead>
<tr>
<th>Nuclide</th>
<th>No absorber</th>
<th>Uncorrected absorber</th>
<th>Corrected absorber</th>
</tr>
</thead>
<tbody>
<tr>
<td>$^{154}$Eu</td>
<td>12750 Bq</td>
<td>10900 Bq</td>
<td>12750 Bq</td>
</tr>
<tr>
<td>$^{155}$Eu</td>
<td>8020</td>
<td>4813</td>
<td>7621</td>
</tr>
<tr>
<td>$^{125}$Sb</td>
<td>2900</td>
<td>2190</td>
<td>2890</td>
</tr>
</tbody>
</table>

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.
8.6.4.4. Example — Table Values

The same spectrum example can be used to show the calculated coefficients. Using the mass attenuation coefficients table\(^{17}\) 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 7 shows the mass attenuation coefficients for oxygen, silicon and sand (SiO\(_2\)).

The sand value can be calculated using the mass ratios. In this case it is also given in the handbook tables. The density of the sand was measured to be 1.67 g/cm\(^3\). 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 8. Note that the calculated correction is more accurate below 100 keV than the measured correction so \(^{155}\)Eu is more accurately corrected. Figure 263 shows the two correction files. The vertical scales have been adjusted to account for the difference in the input factor of 1.6.

\[\text{Table 7. Calculated Coefficients.}\]

<table>
<thead>
<tr>
<th>Energy</th>
<th>mu/rho Oxygen</th>
<th>mu/rho Silicon</th>
<th>mu/rho Sand</th>
<th>mu Sand</th>
</tr>
</thead>
<tbody>
<tr>
<td>30</td>
<td>.372</td>
<td>1.41</td>
<td>.859</td>
<td>1.43</td>
</tr>
<tr>
<td>40</td>
<td>.257</td>
<td>.696</td>
<td>.463</td>
<td>.773</td>
</tr>
<tr>
<td>50</td>
<td>.213</td>
<td>.437</td>
<td>.318</td>
<td>.531</td>
</tr>
<tr>
<td>60</td>
<td>.191</td>
<td>.322</td>
<td>.252</td>
<td>.421</td>
</tr>
<tr>
<td>80</td>
<td>.168</td>
<td>.224</td>
<td>.194</td>
<td>.324</td>
</tr>
<tr>
<td>100</td>
<td>.156</td>
<td>.184</td>
<td>.169</td>
<td>.282</td>
</tr>
<tr>
<td>150</td>
<td>.136</td>
<td>.145</td>
<td>.140</td>
<td>.234</td>
</tr>
<tr>
<td>200</td>
<td>.124</td>
<td>.128</td>
<td>.126</td>
<td>.210</td>
</tr>
<tr>
<td>300</td>
<td>.107</td>
<td>.108</td>
<td>.108</td>
<td>.180</td>
</tr>
<tr>
<td>400</td>
<td>.0957</td>
<td>.0962</td>
<td>.0959</td>
<td>.160</td>
</tr>
<tr>
<td>500</td>
<td>.0873</td>
<td>.0875</td>
<td>.0874</td>
<td>.146</td>
</tr>
<tr>
<td>600</td>
<td>.0808</td>
<td>.0808</td>
<td>.0808</td>
<td>.135</td>
</tr>
<tr>
<td>800</td>
<td>.0708</td>
<td>.0707</td>
<td>.0707</td>
<td>.118</td>
</tr>
<tr>
<td>1000</td>
<td>.0637</td>
<td>.0635</td>
<td>.0636</td>
<td>.106</td>
</tr>
<tr>
<td>1500</td>
<td>.0518</td>
<td>.0518</td>
<td>.0518</td>
<td>.0865</td>
</tr>
<tr>
<td>2000</td>
<td>.0446</td>
<td>.0448</td>
<td>.0447</td>
<td>.0746</td>
</tr>
</tbody>
</table>

Table 8. Results — Calculated Correction.

<table>
<thead>
<tr>
<th>Nuclide</th>
<th>No absorber</th>
<th>Uncorrected absorber</th>
<th>Corrected absorber</th>
</tr>
</thead>
<tbody>
<tr>
<td>$^{154}$Eu</td>
<td>12750 Bq</td>
<td>10900 Bq</td>
<td>12450 Bq</td>
</tr>
<tr>
<td>$^{155}$Eu</td>
<td>8020</td>
<td>4813</td>
<td>7965</td>
</tr>
<tr>
<td>$^{125}$Sb</td>
<td>2900</td>
<td>2190</td>
<td>2776</td>
</tr>
</tbody>
</table>

8.7. 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.,\textsuperscript{18} 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

\textsuperscript{18}J.R. Watts, J.M. Barber, G.R. Rao, and M.C. McFee, “Chest-wall Thickness Predictions for Actinide Lung Counting.” 42\textsuperscript{nd} Annual Conference on Bioassay, Analytical, and Environmental Radiochemistry, 1996.
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) 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.

8.7.1. 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:

\[ A_c = A e^{\mu x} \]  

(52)

where:
- \( A \) = the peak area at energy \( E \)
- \( \mu \) = 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 \( \mu \). This is entered by the operator.

For values between the table values, the \( \mu \) are linearly interpolated between the table values. The correction value is always 1 or greater.

8.7.1.1. 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:

\[ A_c = A \frac{\mu x}{1 - e^{-\mu x}} \]  

(53)

---

8. ANALYSIS METHODS — Ge

where:

\[ A = \text{the peak area at energy } E \]
\[ \mu = \text{the table value at energy } E \text{ and is normally the mass attenuation coefficient} \]
\[ x = \text{the absorption factor and is a function of the sample weight, density or thickness such that it is in inverse units of } \mu. \text{ This is entered by the operator.} \]

In these formulas, the “\(x\)” is the chest wall thickness CWT. The CWT is given by:

\[ CWT = 0.4657 + 4.731 \cdot \left( \frac{wt}{ht} \right) \] (54)

where:

\[ wt = \text{the weight in kg} \]
\[ ht = \text{the height in cm} \]

The weight and height are converted to kg if entered in lbs/inches.

8.8. 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. 264). 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.

The random summing correction factor is:

\[ RSF = \frac{1}{1 - \frac{\sum Ct}{F \times T_l}} \] (55)

where:

\[ RSF = \text{the random summing factor (multiplier)} \]
\[ \sum Ct = \text{the sum of the contents of all channels} \]
\[ F = \text{the operator input slope of the correction curve} \]
\[ T_l = \text{the live time} \]
8.8.1. 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 (Calculate menu items). 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 9.
Table 9. Random Summing Data.

<table>
<thead>
<tr>
<th>Position</th>
<th>Count Rate (Cr)</th>
<th>Peak Area</th>
<th>Ratio (R)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>200</td>
<td>100000</td>
<td>1.00</td>
</tr>
<tr>
<td>2</td>
<td>2000</td>
<td>98850</td>
<td>0.98</td>
</tr>
<tr>
<td>3</td>
<td>4000</td>
<td>97200</td>
<td>0.97</td>
</tr>
<tr>
<td>4</td>
<td>6200</td>
<td>95900</td>
<td>0.95</td>
</tr>
<tr>
<td>5</td>
<td>8000</td>
<td>94800</td>
<td>0.94</td>
</tr>
<tr>
<td>6</td>
<td>9500</td>
<td>93700</td>
<td>0.937</td>
</tr>
</tbody>
</table>

Using the lowest and highest count rate values, the slope is calculated as:

\[
SLOPE = \left( \frac{Cr_{\text{init}} - Cr_{\text{final}}}{R_{\text{init}} - R_{\text{final}}} \right) = \frac{200 - 9500}{1.0 - 0.937}
\]

\[
= -147619
\]  

The negative of this slope is the factor entered by the operator as the random summing factor.

8.9. 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.

The total uncertainty value is composed of the random and systematic errors in all of the factors involved in producing the final nuclide concentration result. The error is given by:

\[
\sigma_t = \sqrt{\sum \sigma_{ri}^2 + \frac{1}{3} \sum \sigma_{si}^2}
\]  

where:

- \( \sigma_t \) = total uncertainty
- \( \sigma_{ri} \) = the individual random error
- \( \sigma_{si} \) = the individual systematic error
The random uncertainties are:

- Counting
- Additional
- Random summing
- Absorption correction

The systematic uncertainties are:

- Nuclide uncertainty from library
- Efficiency fitting uncertainty from calibration
- Calibration source uncertainty
- Geometry correction
- Additional

All the random uncertainties are evaluated at 1 sigma. The counting uncertainty was discussed previously. The random summing uncertainty is estimated to be 10% of the square root of the correction.

The additional random error is input by the operator.

The efficiency uncertainty, both above and below the knee is calculated in the calibration section program. These values are printed on the calibration report.

The calibration source uncertainty entered by the operator is the 1-sigma uncertainty in the source values used in the efficiency calibration. This value is usually supplied with the calibration standard. It is the uncertainty calculated by the supplier for the values given for the standard. The additional systematic error is input by the operator.
The Renaissance analysis engine, RENGSA, uses \texttt{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 new ROI analysis engine, ROI32, is discussed in Section 8.1.5.

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. \texttt{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:

$$Area = \text{Fit Height} \times FWHM \times \frac{\sqrt{2\pi}}{2.35} \quad (59)$$

where:

$$\begin{align*}
\text{Fit Height} & = F(i_1) - F(i_2) \\
i_1 & = \text{channel where } F \text{ is maximum} \\
i_2 & = \text{channel where } F \text{ is minimum}
\end{align*}$$
9.1.3. Peak Statistics

The uncertainty (1 sigma) in the net area of the peak is computed as follows:

\[
\text{Net Uncertainty} = \sqrt{\text{Background Variance} + \text{Gross Area}}
\]

where the Background Variance was computed as follows:

\[
\text{Background Variance} = \left( \frac{\text{Background}^2}{(\text{Channels})(\text{BackLo} + \text{BackHi})} \right)
\]

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:
Critical Level = 2.33 \sqrt{\text{Background Variance}} \quad (62)

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 FWHM’s 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 $\chi^2$.

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:

\[
\text{Background} = B_L + \frac{(B_H - B_L) \times (C_H - C_L)}{C_H - C_L}
\]  

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. 266).

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.

**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 \( \chi^2 \) 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:

\[
B = (169.242 - 1.87175 \times (C - C_{\text{Start}})) + (0.002288748 \times (C - C_{\text{Start}})^2)
\]  (64)

where:
- \( B \) = background in channel \( C \)
- \( C \) = channel
- \( C_{\text{Start}} \) = 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:

\[
\chi^2 = \sum_{i=\text{Min}}^{\text{Max}} \frac{(F_i p(i) - b(i))^2}{w_i}
\]  (65)

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

\[
p(i) = \sum_{j=1}^{N} c_j e^{-\frac{(x-x_j)^2}{2\sigma_j^2}}
\]  (66)

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 \( \chi^2 \). 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, $\chi^2$ is calculated. If the new fit has not changed $\chi^2$ 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 A.3.2).

### 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 10 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 10. Gamma Peak Overlap Examples.

<table>
<thead>
<tr>
<th>Isotope</th>
<th>Energy (keV)</th>
<th>Probability</th>
<th>Isotope with close energy</th>
</tr>
</thead>
<tbody>
<tr>
<td>$^{99m}$Tc</td>
<td>140.99</td>
<td>89.3</td>
<td>$^{99}$Mo</td>
</tr>
<tr>
<td>$^{224}$Ra</td>
<td>241.00</td>
<td>3.90</td>
<td>$^{92}$Sr</td>
</tr>
<tr>
<td>$^{226}$Ra</td>
<td>185.99</td>
<td>3.28</td>
<td>$^{233}$U</td>
</tr>
<tr>
<td>$^{241}$Am</td>
<td>26.35</td>
<td>2.5</td>
<td>$^{237}$U</td>
</tr>
<tr>
<td>$^{241}$Am</td>
<td>33.20</td>
<td>0.11</td>
<td>$^{144}$Ce</td>
</tr>
<tr>
<td>$^{241}$Am</td>
<td>59.54</td>
<td>36.3</td>
<td>$^{237}$U</td>
</tr>
</tbody>
</table>

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:

\[
Fraction = \frac{\sum_{l=1}^{n} BranchingRatio_l}{\sum_{p=1}^{n} BranchingRatio_p}
\]  

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... (page 158).

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... (page 163).

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:

\[
\text{Nuclide Activity} = \frac{\sum (\text{Peak Activity} \times \text{Branching Ratio})}{\sum \text{Branching Ratio}}
\]  

(68)

The *uncertainty* in this value is computed by adding the peak uncertainties in quadrature as follows:

\[
\text{Uncertainty} = \sqrt{\frac{\sum (\text{PeakUncertainty})^2}{\text{Number of Peaks}}}
\]

(69)

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.\textsuperscript{20,21}

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:

\[
\text{MPA} = 2.71 + 3.29 \sqrt{2(\text{Bkg Variance})}
\]

(70)

where \(\text{Bkg Variance}\) is calculated in Eq. (61) if the peak is located; or is calculated in Eq. (71) when the peak is too small for Poisson statistics (not located).

---


\[ Bkg \ Variance = \sum_{i=l}^{h} C_i \]  

(71)

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 \( \times \) FWHM) above and below the centroid energy, for a total width of (MDA factor \( \times \) FWHM). The **MDA Factor** is entered on the Analysis tab under Analyze/Settings/Sample Type... (page 164). The FWHM is calculated from the calibration FWHM formula.

The MDA is then given as the following formula:

\[ MDA = \frac{MPA}{\varepsilon \times T \times \gamma_d} \]  

(72)

where:

- \( \varepsilon \) = the efficiency at the peak energy
- \( T \) = the live time of the acquisition
- \( \gamma_d \) = 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 8.7.
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** (FWHM_{Spectrum}/FWHM_{Calibration}) for a list of peaks in a library from a calibration source.

- **Average FWTM** (full width at tenth maximum) ratio (FWTM_{Spectrum}/FWTM_{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 267 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.
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. 268) 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.

![Quality Assurance Settings Dialog](image)

**Fig. 268. 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 Renaissance QA database, RenpQA32.Mdb, is installed as part of the standard Renaissance installation, and should be located in the \User directory on the drive where Renaissance was installed. 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 on OK to start the QA database setup wizard and go to Section 10.3, page 319, 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. 269, 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 on OK.

**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. 270 is displayed.

### 10.2.3. Measure Sample

This command opens the Sample QA Measurement dialog (Fig. 271). It contains a reminder to place the QA source on the Detector. Click on **Overwrite** to replace the last measurement. Click on **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. 272. Click on **OK** to close the dialog.
10. QUALITY ASSURANCE

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. 273. The short dashed lines represent the warning limits and the long dashed lines represent the acceptance threshold limits.

Figure 274 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.
Choose the chart time period (Week, Month, or Quarter) from the Scale menu (Fig. 275).

The Plot Variable menu (Fig. 276) contains functions for selecting Activity, Peak Energy, Peak Width @ Half Max, Peak Width @ Tenth Max, or Background.

The Detector menu item opens the list of Detectors for which background and sample measurements have been made (Fig. 277). 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.

The Options menu (Fig. 278) 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.

- 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 279 through 282 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. 279 and 280 to the location of the question marks in Figs. 281 and 282.
Fig. 280. Printout of Control Chart with Fixed Vertical Scale On.

Fig. 281. Control Chart On Screen with Fixed Vertical Scale Off.
10. QUALITY ASSURANCE

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 283 shows the first wizard screen. Mark the *second* radio button, **User Data Source (Applies to this machine only)**. Click on Next.

Fig. 282. Printout of Control Chart with Fixed Vertical Scale Off.

Fig. 283. First QA Database Wizard Screen.
The second wizard screen is shown in Fig. 284. Scroll down the list and highlight **Microsoft Access Driver (*.mdb)**, then click on **Next**.

![Fig. 284. Second QA Database Wizard Screen.](image1)

Figure 285 shows the setup summary on the final wizard screen. Click on **Finish**.

![Fig. 285. Final Wizard Screen.](image2)
When the wizard closes, an ODBC setup dialog (Fig. 286) 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. 287) 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.
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. 288.

In the **Database Name** field, enter `RenpQA32.Mdb`, then click on **OK**. to return to the ODBC setup dialog. Click again on **OK**.

The Quality Assurance Settings dialog (Fig. 268) will now open. At this point, the database is ready and QA setup and measurements can proceed.
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 11 provides a quick reference to all of the Renaissance keyboard and keypad functions. These accelerators are also illustrated in Fig. 289, 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 File 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 11. Quick Reference to GammaVision Keyboard Commands.

<table>
<thead>
<tr>
<th>Key or Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;1&gt; or &lt;F5&gt;</td>
<td>Change vertical scale so spectrum peaks are smaller.</td>
</tr>
<tr>
<td>&lt;↑&gt; or &lt;F6&gt;</td>
<td>Change vertical scale so spectrum peaks are larger.</td>
</tr>
<tr>
<td>&lt;↓&gt;</td>
<td>In rubber rectangle mode, shift rectangle down (toward baseline) one pixel.</td>
</tr>
<tr>
<td>&lt;↑&gt;</td>
<td>In rubber rectangle mode, shift rectangle up (away from baseline) one pixel.</td>
</tr>
<tr>
<td>←</td>
<td>Move marker to higher channel. In rubber rectangle mode, shift rectangle right one pixel.</td>
</tr>
<tr>
<td>→</td>
<td>Move marker to lower channel. In rubber rectangle mode, shift rectangle left one pixel.</td>
</tr>
<tr>
<td>&lt;→ or &lt;F7&gt;</td>
<td>Narrow the horizontal scale.</td>
</tr>
<tr>
<td>↔ or &lt;F8&gt;</td>
<td>Widen the horizontal scale.</td>
</tr>
<tr>
<td>Ctrl + →</td>
<td>Jump to next higher peak.</td>
</tr>
<tr>
<td>Ctrl + ←</td>
<td>Jump to next lower peak.</td>
</tr>
<tr>
<td>Shift + →</td>
<td>Jump to next higher ROI.</td>
</tr>
<tr>
<td>Shift + ←</td>
<td>Jump to next lower ROI.</td>
</tr>
<tr>
<td>Alt + →</td>
<td>Advance to next library entry.</td>
</tr>
<tr>
<td>Alt + ←</td>
<td>Recede to previous library entry.</td>
</tr>
<tr>
<td>PageUp</td>
<td>Jump to higher channel number in 1/16th-screen-width increments.</td>
</tr>
<tr>
<td>PageDown</td>
<td>Jump to lower channel number in 1/16th-screen-width increments.</td>
</tr>
<tr>
<td>Home</td>
<td>Jump to first channel of the full spectrum.</td>
</tr>
<tr>
<td>End</td>
<td>Jump to last channel of the full spectrum.</td>
</tr>
<tr>
<td>Ctrl + F9</td>
<td>Select Detector i (i = 1 to 12, in pick list order).</td>
</tr>
<tr>
<td>F2</td>
<td>Switch ROI bit control from OFF to SET to CLEAR.</td>
</tr>
<tr>
<td>F3</td>
<td>In supported digital spectrometers, switch between the two spectra stored in ZDT mode.</td>
</tr>
<tr>
<td>Shift + F3</td>
<td>In supported digital spectrometers, switch the disk spectrum to compare normal to disk ZDT spectrum or ZDT spectrum to disk normal spectrum.</td>
</tr>
<tr>
<td>F4 or Alt + 6</td>
<td>Switch between displaying selected Detector and buffer.</td>
</tr>
<tr>
<td>F5 or 1</td>
<td>Change vertical scale so that spectrum peaks are smaller.</td>
</tr>
<tr>
<td>F6 or ▼</td>
<td>Change vertical scale so that spectrum peaks are larger.</td>
</tr>
<tr>
<td>F7 or ←</td>
<td>Narrow the horizontal scale.</td>
</tr>
<tr>
<td>F8 or +</td>
<td>Widen the horizontal scale.</td>
</tr>
<tr>
<td>Alt + F7</td>
<td>Reset both horizontal and vertical scaling to view complete spectrum.</td>
</tr>
<tr>
<td>Keypad&lt;</td>
<td>Zoom out.</td>
</tr>
<tr>
<td>Keypad&lt;</td>
<td>Zoom in.</td>
</tr>
<tr>
<td>Keypad&lt;5</td>
<td>Center expanded display on cursor.</td>
</tr>
<tr>
<td>Keypad&lt;</td>
<td>Switch to logarithmic vertical scale.</td>
</tr>
<tr>
<td>Keypad&lt;</td>
<td>Switch to auto vertical scale.</td>
</tr>
<tr>
<td>Insert&lt;Ins</td>
<td>Mark the peak region around the cursor as an ROI.</td>
</tr>
<tr>
<td>Delete&lt;Del</td>
<td>Clear the ROI.</td>
</tr>
<tr>
<td>Shift + ↑</td>
<td>Shift the compare spectrum upwards.</td>
</tr>
<tr>
<td>Shift + ↓</td>
<td>Shift the compare spectrum downwards.</td>
</tr>
<tr>
<td>Alt + 1</td>
<td>Start acquisition in selected Detector.</td>
</tr>
<tr>
<td>Alt + 2</td>
<td>Stop acquisition in selected Detector.</td>
</tr>
<tr>
<td>Alt + 3</td>
<td>Clear data in selected Detector.</td>
</tr>
<tr>
<td>Alt + 5</td>
<td>Copy data in the selected Detector to the buffer.</td>
</tr>
<tr>
<td>Alt + 6 or F4</td>
<td>Switch between displaying selected Detector and buffer.</td>
</tr>
<tr>
<td>Alt + →</td>
<td>Decrease amplifier fine gain by smallest increment (where supported).</td>
</tr>
<tr>
<td>Shift + Alt + →</td>
<td>Decrease amplifier fine gain by several increments.</td>
</tr>
<tr>
<td>Alt + +</td>
<td>Increase amplifier fine gain by smallest increment.</td>
</tr>
<tr>
<td>Shift + Alt + +</td>
<td>Increase amplifier fine gain by several increments.</td>
</tr>
<tr>
<td>PrintScreen</td>
<td>Capture screen to Windows Clipboard.</td>
</tr>
</tbody>
</table>
11. KEYBOARD ACCELERATORS

Fig. 289. 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) \(<\text{PageDown}>/\text{PageUp}>\)

\(<\text{PageDown}>\) and \(<\text{PageUp}>\) 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 \(<\text{Insert}>\) 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**  \(<\text{Insert}>\) and Keypad<Ins> work conveniently in combination with \(<\text{Ctrl} + ←>\) and \(<\text{Ctrl} + →>\) to rapidly set peak ROIs.

11.2.8. Clear ROI \(<\text{Delete}>\) or Keypad<Del>

\(<\text{Delete}>\) and Keypad<Del> 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  
$<\uparrow>/<\downarrow>/<\leftarrow>/<\rightarrow>$

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+$\uparrow>$/<$Shift+$\downarrow>$

In Compare mode, the $<$Shift+$\uparrow>$ or $<$Shift+$\downarrow>$ 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+$+->.
11.2.15. Screen Capture

The \texttt{<PrintScreen>} key captures the entire monitor display to the Windows Clipboard, where it is available for use in other applications such as word processors, Windows Paint, etc. Some older keyboards require \texttt{<Alt + PrintScreen>} or \texttt{<Shift + PrintScreen>}. A typical usage would be to set up the display as desired for the snapshot, then press \texttt{<PrintScreen>}. Start the desired graphics or word processing application. Copy the image from the Clipboard with \texttt{<Ctrl + V>} or \texttt{Edit/Paste} (refer to the documentation for the graphics or word processing program). See the FullShot manual for other screen-capture and screen-printing methods.

11.3. Keyboard Number Combinations

\textbf{NOTE} Only the keyboard numbers will function in the following combinations. The keypad number keys will \textit{not} perform these functions.

11.3.1. Start \texttt{<Alt + 1>}

\texttt{<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 \texttt{<Alt + 2>}

\texttt{<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 \texttt{<Alt + 3>}

\texttt{<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 \texttt{<Alt + 5>}

\texttt{<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> 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

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

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

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

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

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

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

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. 14). 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

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/> 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<*> 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> 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<+> and Keypad<-G04> 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

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 GammaVision or MAESTRO. 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.
12. JOB FILES

**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**
Smoothes 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:

$(FullPath) = D:\USER\SOIL\SAM001
$(FileExt) = SPC
$(FileDir) = D:\USER\SOIL
$(ShortPath) = SAM001.SPC
$(ShortBase) = SAM001
The following variables are expanded in `.JOB` file strings:

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>$(FullPath)</code></td>
<td>Full pathname of the spectrum file</td>
</tr>
<tr>
<td><code>$(FullBase)</code></td>
<td>Full pathname of the spectrum without the “.” and extension</td>
</tr>
<tr>
<td><code>$(FileExt)</code></td>
<td>File extension of the spectrum file without the “.”</td>
</tr>
<tr>
<td><code>$(FileDir)</code></td>
<td>Directory of the spectrum file without the last backslash ()</td>
</tr>
<tr>
<td><code>$(McaDir)</code></td>
<td>Renaissance directory without the last backslash</td>
</tr>
<tr>
<td><code>$(CurDir)</code></td>
<td>Starting (current) directory of Renaissance</td>
</tr>
<tr>
<td><code>$(Loop)</code></td>
<td>Current value of the loop counter (zero based)</td>
</tr>
<tr>
<td><code>$(Loop1)</code></td>
<td>Loop counter plus 1</td>
</tr>
<tr>
<td><code>$(Bel)</code></td>
<td>ASCII bell character</td>
</tr>
<tr>
<td><code>$(CR)</code></td>
<td>ASCII carriage return character</td>
</tr>
<tr>
<td><code>$(FF)</code></td>
<td>ASCII form feed character</td>
</tr>
<tr>
<td><code>$(LF)</code></td>
<td>ASCII line feed character</td>
</tr>
<tr>
<td><code>$(ESC)</code></td>
<td>ASCII escape character</td>
</tr>
<tr>
<td><code>$(AutoFile)</code></td>
<td>Create an automatic filename based on the Start/Save/Report settings</td>
</tr>
<tr>
<td><code>$(ShortPath)</code></td>
<td>Relative pathname of the spectrum file</td>
</tr>
<tr>
<td><code>$(ShortBase)</code></td>
<td>Relative pathname of the spectrum without the “.” and extension</td>
</tr>
<tr>
<td><code>$(Password)</code></td>
<td>Value entered in ASK_PASSWORD command</td>
</tr>
<tr>
<td><code>$(Owner)</code></td>
<td>Value entered in ASK_PASSWORD command</td>
</tr>
</tbody>
</table>

The filename variables are updated each time a READ operation is performed. The READ operations are:

- ANALYZE "file"
- ASK_CALIBRATION
- ASK_LIBRARY
- ASK_OPTIONS
- ASK_PBC
- ASK_SPECTRUM
- CALIBRATE_EFFICIENCY
- CALIBRATE_ENERGY
- LOAD
- RECALL
- RECALL_CALIBRATION
- RECALL_EFFICIENCY
- RECALL_ENERGY
- RECALL_OPTIONS
- RECALL_ROI
- 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.
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:

```plaintext
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.

```plaintext
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>
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.”

This command is disabled by Windows if any “sound” software is used. It should be used with caution if other sound-producing software is running.

BEEP ID
A numerical ID is given based on a desired system event. For example, BEEP 7 will exit Windows.

<table>
<thead>
<tr>
<th>ID</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>Beep Speaker</td>
</tr>
<tr>
<td>1</td>
<td>Default Beep</td>
</tr>
<tr>
<td>2</td>
<td>Start Windows</td>
</tr>
<tr>
<td>3</td>
<td>Asterisk</td>
</tr>
<tr>
<td>4</td>
<td>Exclamation</td>
</tr>
<tr>
<td>5</td>
<td>Critical Stop</td>
</tr>
<tr>
<td>6</td>
<td>Question</td>
</tr>
<tr>
<td>7</td>
<td>Exit Windows</td>
</tr>
</tbody>
</table>

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:

```plaintext
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 8.2.7) 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:

```
MARK_PEAKS
REPORT "TESTDAT.RPT"
```

The above procedure does a peak-search-directed report of nuclides found.

**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, including 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.
13. UTILITIES

13.1. WinPlots

This program makes a hardcopy output of any type of ORTEC spectrum file in a fixed format with many user-set optional variations (such as grid lines) available. The plotting output devices include the full range of graphics-capable printing devices supported by Windows (i.e., hardcopy is not limited only to plotters). WinPlots allows any printer to be selected and set up. 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, click on Start on the Windows Taskbar, then Programs, Renaissance, and WinPlots (see Fig. 290). WinPlots can also be run in command-line mode for use in .JOB files, or directly from other Windows programs (see Section 13.1.3).

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. 291.
13.1.1. **File**

Figure 292 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. 293), 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.

The sample description, format, and number of channels are shown at the bottom of the dialog to aid in selecting the correct file.
Figure 293 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.

![Fig. 293. The Recall Spectrum File for Plotting Dialog.](image)

The **Print Plot**... dialog (Fig.294) 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 on **Properties** to change print options such as paper size, orientation, and output resolution.

![Fig. 294. The Print Plot Dialog.](image)

### 13.1.2. Options

The **Options** menu is shown in Fig. 295. These menu items control the plot settings and WinPlots operation.

![Fig. 295. The Options Menu.](image)
13.1.2.1. **Plot...**

The **Plot Options** dialog is shown in Fig. 296. 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.

![Fig. 296. The Plot Options Dialog.](image)

If the printer supports color printing, the **Colors...** button will be enabled. Clicking on it will display Fig. 297. 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.

![Fig. 297. The Color Options Dialog.](image)
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. 298 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.

**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. 299. 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.

13.2. TRANSLT

The TRANSLT program (TRANSLT.EXE, located in `c:\Program Files\Renaissance`) translates several different text files to and from `.SPC` or `.CHN` files. All operation is controlled from the command line. The command line is:

```
```

where:

- `type`  
  - chn: The inname file is in CHN format.
  - spc: The inname file is in SPC format.
  - txt: The inname file is in ASCII text format.

The default is based on the filename extension and the `-i` switch. Both chn and spc cannot be used together.
The input spectrum file, no default; default extension is SPC. If the input file is a .TXT file, it must contain the following:

**ACQUISITION INFORMATION**

- Real Time: 4219.799805
- Live Time: 3600.000000
- Acquisition start date: 07-Jun-1991
- Acquisition start time: 10:37:33

**SPECTRUM**

<table>
<thead>
<tr>
<th>Channel</th>
<th>Data 1</th>
<th>Data 2</th>
<th>Data 3</th>
<th>Data 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>0.0000E+000</td>
<td>0.0000E+000</td>
<td>0.0000E+000</td>
<td>0.0000E+000</td>
</tr>
<tr>
<td>4</td>
<td>0.0000E+000</td>
<td>0.0000E+000</td>
<td>0.0000E+000</td>
<td>0.0000E+000</td>
</tr>
<tr>
<td>8</td>
<td>0.0000E+000</td>
<td>0.0000E+000</td>
<td>0.0000E+000</td>
<td>0.0000E+000</td>
</tr>
<tr>
<td>12</td>
<td>0.0000E+000</td>
<td>0.0000E+000</td>
<td>0.0000E+000</td>
<td>0.0000E+000</td>
</tr>
</tbody>
</table>

If the file contains channel numbers at the beginning of the line, the channel number must end in a colon (:). The spectrum data can be integer or real numbers and can be any number of columns.

The header information in the .TXT file will be converted and stored in the .SPC file if it is in the correct format. The correct format for the .TXT input file is the same as the .TXT format created as the output file.

**type**

- chn  The outname file is in CHN format.
- spc  The outname file is in SPC format.
- txt  The outname file is in ASCII text format.

**outname**

The output spectrum file. The default is the inname with the extension changed. If the outname is not given, the spectrum file will not be overwritten by the default name. The length of the spectrum file converted from text will be the next higher power of two with the surplus channels set to 0.

**w**

Set the format output to 128 characters per line; default is 70 characters per line.

**nc**

Do not print channel as first number in line; default is to print the channel number. The channel number is followed by a colon (:) to separate it from the data.

**col n**

Number of data columns is n; default is 5. Error returned if line width will exceed available space.
ni  Do not write acquisition or analysis information in output file; default is to write this information.

nh  Do not write header information in output file; default is to write this information.

i  Import a text file and save as .SPC (or .CHN) file. If one filename is given, default is to convert that file to the other format, i.e., for AAA.SPC; the output will be AAA.TXT. If two filenames are given, the default is to convert the spectrum to text. The .TXT file will be overwritten even if the .SPC file is not located.

An example is:

    TRANSLT -SPC GOODSPEC -TXT TEXTSPEC -ni -nh -col1

This will make a text file of one column with no header, no analysis information, and one channel per line.
APPENDIX A. STARTUP AND CONFIGURATION

To start Renaissance, click on Start on the Windows Taskbar, then on Programs, Renaissance, and Renaissance Supervisor (see Fig. 300). It can also be run from Start, Run..., and entering a command line in the Run dialog, with or without arguments as described below.

A.1. Command Line Options

Renaissance is run with the following command line properties:

```
```

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, **M32MCA** is used by default. 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 362) 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 362) 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 M32MCA.CFG. The nuclide library is the last library used. And no JOB is automatically executed unless the file.job argument is included.

A.2. Program Files

RENSUPR.EXE The Renaissance Supervisor program.

RENOPER.EXE The Renaissance Operator program.

RENPQA32.EXE The program for displaying the data stored in the database as a control chart display.

ISOCTL.DLL
MCBCIO32.DLL
MCBLOC32.DLL Windows dynamic link libraries used by Renaissance for access to the MCB hardware and display support.

CAN32.DLL The Windows dynamic link library containing the analysis engine used in the interactive analysis and calibration sections of Renaissance.

RENGAM32.EXE The Windows analysis program that performs the auto-isotope analysis of the .SPC files. It can only be run under Windows.

RENGSA.EXE The NaI analysis engine.

RENWAN32.EXE The Windows analysis program that performs the analysis of the .SPC files. It can only be run under Windows.

RENNPP32.EXE Analysis engine for analyzing samples in nuclear power plants.

RENEV32.EXE Analysis engine for analyzing complex environmental samples and includes directed-fit capabilities for singlets and multiplets.

MCBCON32.EXE The Detector configuration program for the local PC and the entire network. It should be run manually whenever MCBs are added to the network configuration. All machines to be included in a network configuration should have MCBSER32 running. See the ORTEC MCB CONNECTIONS Hardware Property Dialogs Manual for more information.
MCBSER32.EXE The communications link between the network and the local Detectors. To use Renaissance to access Detectors attached to a PC elsewhere on the network, make sure MCBSER32 is running on that remote PC, see the ORTEC MCB CONNECTIONS Hardware Property Dialogs Manual for more information.

FULLSHOT.EXE is a screen-capture program by Inbit™ for sending images directly from the monitor screen to the FullShot™ window, a disk file, the Windows clipboard, or a printer. It supports any Windows printer. The FullShot™ manual is included.

A.3. Analysis Setup

All of the analysis engines have several options that can be specified in a disk file (B3OWINDS.INI) and the report output text can be specified in a disk file (B3OWIN.TXT). 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.3.1. RENWAN32, RENGAM32, RENNPP32, and RENENV32

The RENWAN32, RENGAM32, RENNPP32, and RENENV32 analysis engines perform the analysis of a complete 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 RENWAN32 only) is:

```
RENWAN32 file.SPC [DEBUG] [file.INI]
```

file.SPC 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 .UFO for the binary output and the extension of .RPT for the text output.

DEBUG This optional parameter controls the output of debugging information on the RENWAN32 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.
This optional file is the .INI file (such as B30WINDS.INI) 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 .INI files for different spectra, different analyses can be produced.

### A.3.2. B30WINDS.INI (Germanium Spectrum Analysis)

The B30WINDS.INI file contains initial or default values for the analysis engine for germanium. 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 or cannot be read, then the internal values are used. Some of these values can only be set in this file.

#### A.3.2.1. Contents

**B30WIN.TXT**  
Message file name

Report Definition Filename. The name of the file that defines the standard analysis report format.

**YES NO**  
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
Filename for the average energy table. The Sample Default File (SDF) setting overwrites this parameter in most cases. (Included for backward compatibility with older spectrum formats. When analyzing .chn spectra using the Analyze/Spectrum on Disk... command or when the analysis is done external to Renaissance, this setting will be used.)

D:\A27\IEQT.TBL  IEq table filename
Filename for the iodine equivalence table. The Sample Default File (SDF) setting overwrites this parameter in most cases. (Included for backward compatibility with older spectrum formats. When analyzing .chn spectra using the Analyze/Spectrum on Disk... command or when the analysis is done external to Renaissance, this setting will be used.)

**F**
Average Energy Flag
T = Do average energy calculation.
F = Do not do average energy calculation.

The Sample Default File (SDF) setting overwrites this parameter in most cases. (Included for backward compatibility with older spectrum formats. When analyzing .chn spectra using the Analyze/Spectrum on disk... command or when the analysis is done external to Renaissance, this setting will be used.)

**F**
Iodine Equivalence Flag
T = Do Iodine Equivalence calculation
F = Do not do Iodine Equivalence calculation

The SDF setting overwrites this parameter in most cases. (Included for backward compatibility with older spectrum formats. When analyzing .chn spectra using the Analyze/Spectrum on disk... command or when the analysis is done external to Renaissance, this setting will be used.)

**F**
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.
APPENDIX A. STARTUP AND CONFIGURATION

1000 # 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.

1000 # 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 = 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 not available because these functions rely on information stored in the .UFO file.

1 T MDA type, T=Allow change

MDA Type
T = Allow change and use the MDA Type specified in the SDF.
F = Do not allow change and always use the MDA number specified on this line, regardless of the analysis options setting.
The MDA number is based on the order in which MDA methods are listed on the System tab under Analyze/Settings/Sample Type....

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
MPC/DAC Flag
T = Use the specified MPC/DAC file unless a different MPC/DAC file is given in the analysis options.
F = Do not use an MPC/DAC file unless one is specified in the analysis options.

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 Accept Small Peaks Flag
T = Small peaks with bad shape that meet the uncertainty cutoff are kept.
F = Peaks flagged as too narrow with <200 counts are rejected. If all peaks for a nuclide fall into this category then the isotope activity is reported as less than the MDA.

A Derived peak area char
 Derived Peak Area Character. Character displayed in the unidentified and identified peak summaries.

F Print discarded peak table Discarded Peak Table Flag
T = The Summary of Discarded Isotope Peaks table shows discarded peaks with background, net counts, intensity, uncertainty, similar to the identified peak summary in addition to calculating nuclide peak activity. A discarded peak is a peak with non-zero area identified with an isotope that has been determined to have zero activity.
F = If the library peak matrix table is not displayed, the Summary of Discarded Peaks table is displayed after the Summary of Nuclides in Sample table and includes only peak energies with the associated nuclide and flags.

12 Half-life decay cutoff
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.

2. Activity range factor
A peak is used in the nuclide activity average if:
- Peak Activity * (1 - A) < activity of first peak in isotope and
- Peak Activity * (1 + A) > activity of first peak in isotope

where

\[ A = Activity\ Range\ Factor \times \sqrt{\text{count uncert}^2 + \left(\frac{\text{half-life uncert}}{100}\right)^2 + \left(\frac{\text{calib source uncert}}{196}\right)^2} \]

T = Perform activity range test
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.

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 = 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.

0.0

Min. step background energy

Stepped Background Minimum Energy. 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.

T

Fraction Limit Test Flag (used 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.

F

Narrow Peak for Activity Calculation flag (used only in Env32 with Directed Fit turned on)

T = Use all small peaks with bad shape that meet the uncertainty cutoff in calculating the average nuclide activity regardless of the Accept Small Peaks Flag setting listed above.

F = Omit small peaks with bad shape that meet the uncertainty cutoff from the average nuclide activity calculation unless the Accept Small Peaks Flag listed above is set to True.

T

Print 0 act. peaks in nuclide table

Zero Area Library Peak flag (used only in Npp32 and Env32)

T = Show peaks with no area in Library Usage Summary. This would include all library peaks that were not found in the spectrum.

F = Only show peaks in the Library Usage Summary that have greater than zero activity and summarize how many library peaks were found as compared to the number listed in the library for that nuclide.

T

Use peak cutoff

Use Peak Cutoff Flag

T = Use Peak Cutoff specified in the analysis options (analysis options) 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 options (analysis options) file and use all peaks found regardless of uncertainty in the analysis.
APPENDIX A. STARTUP AND CONFIGURATION

2 F
Second MDA type, T = Calculate
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.

F
Sort isotope peaks by energy
 Sort Nuclide Peaks by Energy Flag (Wan32 and Gam32 only)
 T = Sort peaks in the Library Usage Summary by energy
 F = Sort peaks in the Library Usage Summary by library ranking order (old method).

2.0
Multiplet channel shift limit
The maximum number of channels that multiplet peaks can be shifted in the peak-fit optimization.

0.0
Background width / FWHM for MDAs
MDA Background Width. Use this value times the peak FWHM to determine the background area for calculating the MDA. If set to zero, then use the entire background area for the peak to calculate the MDA. (Use zero for old method.)

F
Print MDA Flag (WAN32, NPP32, AND ENV32 only)
 T = Print MDA in Nuclide Summary
 T = Print nuclide MDA in Nuclide Summary along with activity.
 F = Print the MDA only when the nuclide is not found in the spectrum (old method).

F
 Maximum Half-life to Unknowns Flag
 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.

MDA
Nuclide summary MDA text
MDA column header in “Summary of Nuclides in Sample” section of report. This column header is displayed only if the Print MDA Flag discussed above is set to True.

A.3.3. G30WINDS.INI (Sodium Iodide Spectrum Analysis)
The G30WINDS.INI file contains initial or default values for the analysis engine for sodium iodide. 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 or cannot be read, then the internal values are used. Some of these values can only be set in this file.
A.3.3.1. Contents

G30WIN.TXT

Report Definition Filename. The name of the file that defines the standard analysis report format.

YES  NO

Spelling of Yes and No displayed on analysis report under the Corrections - Status column. Alternates to English can be substituted.

JANFEBMARAPRMAJOUMJULAUGSEPCTNOVDEC

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  
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 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 (in lines) of analysis report.

T  
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 not available because these functions rely on information stored in the .UFO file.
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 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 Flag
Not used in Renaissance.

**F**
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**
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.*
Library based peak stripping
Not used in Renaissance.

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 = 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. 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 301 shows the Motor Selection tab.

![Renaissance motor setup](image)

**Fig. 301.** 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. 302).

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.
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.
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 ORTEC Software File Structures Manual for DOS and Windows Systems 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

.FC --- “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

.CH --- “CHaNnels”; MAESTRO-style spectral data file; binary format.

.SPC --- “SPeCtrum”; spectrum with full analysis settings, calibration, descriptions, etc; “Inform” type binary format.

.AN --- 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.)

<table>
<thead>
<tr>
<th>Field Name</th>
<th>SQL Data Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Detector</td>
<td>SQL_LONG</td>
<td>Detector ID number. (Primary Key)</td>
</tr>
<tr>
<td>DetName</td>
<td>SQL_CHAR (64)</td>
<td>Detector Pick List Name</td>
</tr>
<tr>
<td>DetDesc</td>
<td>SQL_CHAR (64)</td>
<td>Detector Description</td>
</tr>
<tr>
<td>Creation</td>
<td>SQL_TIMESTAMP</td>
<td>Date/Time this record created</td>
</tr>
<tr>
<td>NumMeas</td>
<td>SQL_LONG</td>
<td>Measurement counter (all types) for this detector</td>
</tr>
<tr>
<td>NumBack</td>
<td>SQL_INTEGER</td>
<td>Background type only Measurement counter for this detector</td>
</tr>
<tr>
<td>SamFile</td>
<td>SQL_CHAR (128)</td>
<td>Sample Type File Name</td>
</tr>
<tr>
<td>SamType</td>
<td>SQL_CHAR (80)</td>
<td>Sample Type Description</td>
</tr>
<tr>
<td>LibFile</td>
<td>SQL_CHAR (128)</td>
<td>Nuclide Library File Name</td>
</tr>
<tr>
<td>Field Name</td>
<td>SQL Data Type</td>
<td>Description</td>
</tr>
<tr>
<td>------------</td>
<td>---------------------</td>
<td>----------------------------------------------------------</td>
</tr>
<tr>
<td>Setup</td>
<td>SQL_SMALLINT</td>
<td>Setup Flagword</td>
</tr>
<tr>
<td>Limits</td>
<td>SQL_SMALLINT</td>
<td>Limit Settings Flagword</td>
</tr>
<tr>
<td>MinBack</td>
<td>SQL_REAL</td>
<td>Min. Background CPS Acceptance Limit</td>
</tr>
<tr>
<td>LowBack</td>
<td>SQL_REAL</td>
<td>Low Background CPS Excursion Warning Level</td>
</tr>
<tr>
<td>BigBack</td>
<td>SQL_REAL</td>
<td>High Background CPS Excursion Warning Level</td>
</tr>
<tr>
<td>MaxBack</td>
<td>SQL_REAL</td>
<td>Max. Background CPS Acceptance Limit</td>
</tr>
<tr>
<td>MinActivity</td>
<td>SQL_REAL</td>
<td>Min. Total Activity Acceptance Limit</td>
</tr>
<tr>
<td>LowActivity</td>
<td>SQL_REAL</td>
<td>Low Total Activity Excursion Warning Level</td>
</tr>
<tr>
<td>BigActivity</td>
<td>SQL_REAL</td>
<td>High Total Activity Excursion Warning Level</td>
</tr>
<tr>
<td>MaxActivity</td>
<td>SQL_REAL</td>
<td>Max. Total Activity Acceptance Limit</td>
</tr>
<tr>
<td>MinShift</td>
<td>SQL_REAL</td>
<td>Min. Average Peak Shift Acceptance Limit</td>
</tr>
<tr>
<td>LowShift</td>
<td>SQL_REAL</td>
<td>Low Average Peak Shift Warning Level</td>
</tr>
<tr>
<td>BigShift</td>
<td>SQL_REAL</td>
<td>High Average Peak Shift Warning Level</td>
</tr>
<tr>
<td>MaxShift</td>
<td>SQL_REAL</td>
<td>Max. Average Peak Shift Acceptance Limit</td>
</tr>
<tr>
<td>MinFWHM</td>
<td>SQL_REAL</td>
<td>Min. Average FWHM Ratio Acceptance Limit</td>
</tr>
<tr>
<td>LowFWHM</td>
<td>SQL_REAL</td>
<td>Low Average FWHM Ratio Warning Level</td>
</tr>
<tr>
<td>BigFWHM</td>
<td>SQL_REAL</td>
<td>High Average FWHM Ratio Warning Level</td>
</tr>
<tr>
<td>MaxFWHM</td>
<td>SQL_REAL</td>
<td>Max. Average FWHM Ratio Acceptance Limit</td>
</tr>
<tr>
<td>MinFWTM</td>
<td>SQL_REAL</td>
<td>Min. Average FWTM Ratio Acceptance Limit</td>
</tr>
<tr>
<td>LowFWTM</td>
<td>SQL_REAL</td>
<td>Low Average FWTM Ratio Warning Level</td>
</tr>
<tr>
<td>BigFWTM</td>
<td>SQL_REAL</td>
<td>High Average FWTM Ratio Warning Level</td>
</tr>
<tr>
<td>MaxFWTM</td>
<td>SQL_REAL</td>
<td>Max. Average FWTM Ratio Acceptance Limit</td>
</tr>
<tr>
<td>Operator</td>
<td>SQL_CHAR(64)</td>
<td>User name last entered on the System tab under Analyze/Settings/Sample Type... at start of latest measurement</td>
</tr>
</tbody>
</table>
C.2.2. Application Information Table

(One of these tables for entire database; one record for Renaissance.)

<table>
<thead>
<tr>
<th>Field Name</th>
<th>SQL Data Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ModelNumber</td>
<td>SQL_LONG</td>
<td>Product model number (i.e., 66)</td>
</tr>
<tr>
<td>SerialNumber</td>
<td>SQL_CHAR(32)</td>
<td>Product serial number</td>
</tr>
<tr>
<td>AppName</td>
<td>SQL_CHAR(16)</td>
<td>Application Name (i.e., “Renaissance”)</td>
</tr>
<tr>
<td>AppVersion</td>
<td>SQL_CHAR(8)</td>
<td>Version/Revision (i.e., “4.0” or greater)</td>
</tr>
<tr>
<td>Laboratory</td>
<td>SQL_CHAR(64)</td>
<td>Laboratory name entered under Renaissance system dialog</td>
</tr>
</tbody>
</table>

C.2.3. 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.)

<table>
<thead>
<tr>
<th>Field Name</th>
<th>SQL Data Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Measurement</td>
<td>SQL_LONG</td>
<td>Measurement number (primary key)</td>
</tr>
<tr>
<td>MeasTime</td>
<td>SQL_TIMESTAMP</td>
<td>Date/Time for this measurement</td>
</tr>
<tr>
<td>MeasType</td>
<td>SQL_SMALLINT</td>
<td>Activity analysis (1) or Background (0)</td>
</tr>
<tr>
<td>LiveTime</td>
<td>SQL_REAL</td>
<td>Acquisition live time in seconds</td>
</tr>
<tr>
<td>CountRate</td>
<td>SQL_REAL</td>
<td>Background CPS (only for Background measurement)</td>
</tr>
<tr>
<td>Activity</td>
<td>SQL_REAL</td>
<td>Total activity</td>
</tr>
<tr>
<td>PeakShift</td>
<td>SQL_REAL</td>
<td>Average peak shift</td>
</tr>
<tr>
<td>FWHMRatio</td>
<td>SQL_REAL</td>
<td>Average FWHM ratio</td>
</tr>
<tr>
<td>FWTMRatio</td>
<td>SQL_REAL</td>
<td>Average FWTM ratio</td>
</tr>
</tbody>
</table>

C.2.4. Peaks Table(s)

(Where “...d” is the detector number in decimal, “mmmm” 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.)
### Field Names, SQL Data Types, and Descriptions

<table>
<thead>
<tr>
<th>Field Name</th>
<th>SQL Data Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>PeakNumber</td>
<td>SQL_LONG</td>
<td>Peak number counter (primary key)</td>
</tr>
<tr>
<td>PeakFlags</td>
<td>SQL_LONG</td>
<td>Analysis results flags</td>
</tr>
<tr>
<td>Nuclide</td>
<td>SQL_CHAR(8)</td>
<td>Library nuclide name this peak belongs to</td>
</tr>
<tr>
<td>Energy</td>
<td>SQL_REAL</td>
<td>Library energy</td>
</tr>
<tr>
<td>Centroid</td>
<td>SQL_REAL</td>
<td>Actual centroid energy</td>
</tr>
<tr>
<td>CalFWHM</td>
<td>SQL_REAL</td>
<td>Expected (calibrated) FWHM at this energy</td>
</tr>
<tr>
<td>FWHM</td>
<td>SQL_REAL</td>
<td>Actual FWHM</td>
</tr>
<tr>
<td>FWTM</td>
<td>SQL_REAL</td>
<td>Actual FWTM (Ge only)</td>
</tr>
<tr>
<td>Area</td>
<td>SQL_REAL</td>
<td>Net counts in peak</td>
</tr>
<tr>
<td>Background</td>
<td>SQL_REAL</td>
<td>Background counts</td>
</tr>
</tbody>
</table>

### C.3. The Renaissance v4.1 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>
<thead>
<tr>
<th>Table</th>
<th>Comment</th>
<th>Key</th>
<th>Keys to Other Tables in this Table</th>
</tr>
</thead>
<tbody>
<tr>
<td>ActivityLimits</td>
<td>Alarm and warning limits by peak and nuclide</td>
<td>LimitID</td>
<td></td>
</tr>
<tr>
<td>AnalysisGroup</td>
<td></td>
<td>AnalysisGroupID</td>
<td>AnalysisResultsID</td>
</tr>
<tr>
<td>AnalysisParams</td>
<td>Analysis parameters</td>
<td>AnalysisID</td>
<td>AbsorptionID</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>GeoID</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>IEQID (IodineEQID)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>EBARID (AverageEnergyID)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>DACID</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>ReportParamsID</td>
</tr>
<tr>
<td>AnalysisResults</td>
<td>Standard analysis results</td>
<td>AnalysisResultsID</td>
<td>SpectrumID</td>
</tr>
<tr>
<td>Table</td>
<td>Comment</td>
<td>Key</td>
<td>Keys to Other Tables in this Table</td>
</tr>
<tr>
<td>--------------------</td>
<td>----------------------------------------------</td>
<td>--------------------------------</td>
<td>----------------------------------------------------------------------------------------------------</td>
</tr>
<tr>
<td>Attenuation</td>
<td>Attenuation calculated with two spectra</td>
<td>AttenuationID</td>
<td>AnalysisID, EnergyCalID, EffCalID, DetrctorID, RefAnalysisID (an AnalysisResultsID value), CurAnalysisID (an AnalysisResultsID value)</td>
</tr>
<tr>
<td>AttenuationCoefficients</td>
<td>Energy, Linear and Mass coefficients</td>
<td></td>
<td>AttenuationMaterialID</td>
</tr>
<tr>
<td>AttenuationMaterials</td>
<td>Material name, formula, density, and weight</td>
<td>AttenuationMaterialID</td>
<td></td>
</tr>
<tr>
<td>AverageEnergy</td>
<td>EBAR values</td>
<td>AverageEnergyID</td>
<td></td>
</tr>
<tr>
<td>ChestWallThickness</td>
<td>Chest wall thickness parameters</td>
<td>CWTID</td>
<td></td>
</tr>
<tr>
<td>DAC</td>
<td>DAC values</td>
<td>DACID</td>
<td></td>
</tr>
<tr>
<td>Detectors</td>
<td>Detector information</td>
<td>DetectorID</td>
<td></td>
</tr>
<tr>
<td>EffCal</td>
<td>Efficiency calibration</td>
<td>EfficiencyID</td>
<td>DetectorID, CertificateID</td>
</tr>
<tr>
<td>EffCalPeaks</td>
<td>Efficiency calibration peaks</td>
<td>EfficiencyID and Energy</td>
<td>EfficiencyID</td>
</tr>
<tr>
<td>EffCertificate</td>
<td>Efficiency Certificate values</td>
<td>CertificateID and Peak Energy</td>
<td></td>
</tr>
<tr>
<td>EnergyCal</td>
<td>Energy calibration</td>
<td>EnergyID</td>
<td>DetectorID</td>
</tr>
<tr>
<td>EnergyCalPeaks</td>
<td>Energy calibration peaks</td>
<td>EnergyID and Peak Energy</td>
<td>EnergyID</td>
</tr>
<tr>
<td>Geometry</td>
<td>Geometry correction calculated from two spectra</td>
<td>GeometryID</td>
<td>DetectorID, RefAnalysisID (an AnalysisResultsID value), CurAnalysisID (an AnalysisResultsID value)</td>
</tr>
<tr>
<td>IodineEquivalence</td>
<td>IEQ values</td>
<td>IodineEQID</td>
<td></td>
</tr>
<tr>
<td>Nuclides</td>
<td>Standard analysis results</td>
<td>NuclideID</td>
<td>AnalysisResultsID</td>
</tr>
<tr>
<td>Peaks</td>
<td>Standard analysis results</td>
<td>PeaksID</td>
<td>AnalysisResultsID, ShapeID</td>
</tr>
<tr>
<td>PkShapeCal</td>
<td>Peak shape calibration</td>
<td>PkShapeID</td>
<td>DetectorID, ECalID</td>
</tr>
<tr>
<td>RenLimits</td>
<td>Renaissance weighted activity, warning and alarm</td>
<td>RenLimitID</td>
<td>AnalysisGroupID, AnalysisResultsID</td>
</tr>
</tbody>
</table>
### C.3.3. Renaissance Database Table Descriptions

#### C.3.3.1. Table: ActivityLimits

**Properties**

- **Date Created:** 5/7/03 3:43:36 PM
- **Last Updated:** 5/7/03 3:43:36 PM
- **Orientation:** 0

- **Def. Updatable:** True
- **OrderByOn:** False
- **RecordCount:** 1

**Columns**

<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Size</th>
<th>Description/Attributes</th>
</tr>
</thead>
<tbody>
<tr>
<td>LimitID</td>
<td>Number (Long)</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td>Nuclide</td>
<td>Text</td>
<td>8</td>
<td>Nuclide name</td>
</tr>
<tr>
<td>Energy</td>
<td>Number (Double)</td>
<td>8</td>
<td>Peak energy (keV)</td>
</tr>
<tr>
<td>AlarmLimit</td>
<td>Number (Double)</td>
<td>8</td>
<td>Alarm limit on activity (Bq)</td>
</tr>
<tr>
<td>WarningLimit</td>
<td>Number (Double)</td>
<td>8</td>
<td>Warning limit on activity (Bq)</td>
</tr>
</tbody>
</table>
C.3.3.2. Table: AnalysisGroup

Properties

<table>
<thead>
<tr>
<th>Property</th>
<th>Value</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Date Created</td>
<td>5/7/03 3:43:36 PM</td>
<td></td>
</tr>
<tr>
<td>Last Updated</td>
<td>5/7/03 3:43:36 PM</td>
<td></td>
</tr>
<tr>
<td>Orientation</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>Def. Updatable</td>
<td>True</td>
<td></td>
</tr>
<tr>
<td>OrderByOn</td>
<td>False</td>
<td></td>
</tr>
<tr>
<td>RecordCount</td>
<td>65</td>
<td></td>
</tr>
</tbody>
</table>

Columns

<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Size</th>
<th>Description/Attributes</th>
</tr>
</thead>
<tbody>
<tr>
<td>AnalysisGroupID</td>
<td>Number (Long)</td>
<td>4</td>
<td>Fixed Size, Auto-Increment</td>
</tr>
<tr>
<td>AnalysisResultsID</td>
<td>Number (Long)</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td>IsWarning</td>
<td>Yes/No</td>
<td>1</td>
<td>At least one nuclide exceeded the warning limit</td>
</tr>
<tr>
<td>IsAlarm</td>
<td>Yes/No</td>
<td>1</td>
<td>At least one nuclide exceeded the alarm limit</td>
</tr>
<tr>
<td>TotalActivity</td>
<td>Number (Double)</td>
<td>8</td>
<td>Total in individual spectrum</td>
</tr>
<tr>
<td>TotalCounts</td>
<td>Number (Double)</td>
<td>8</td>
<td>Total in individual spectrum</td>
</tr>
<tr>
<td>Spectrum</td>
<td>Text</td>
<td>255</td>
<td>Spc file name</td>
</tr>
<tr>
<td>Weight</td>
<td>Number (Double)</td>
<td>8</td>
<td>Weighting factor in average</td>
</tr>
</tbody>
</table>
### C.3.3.3. Table: AnalysisParams

#### Properties

<table>
<thead>
<tr>
<th>Property</th>
<th>Value</th>
<th>Def. Updatable</th>
<th>OrderByOn</th>
<th>RecordCount</th>
</tr>
</thead>
<tbody>
<tr>
<td>Date Created</td>
<td>5/7/03 3:43:36 PM</td>
<td>True</td>
<td>False</td>
<td>48</td>
</tr>
<tr>
<td>Last Updated</td>
<td>5/7/03 3:43:36 PM</td>
<td>True</td>
<td>False</td>
<td>48</td>
</tr>
<tr>
<td>Orientation</td>
<td>0</td>
<td>True</td>
<td>False</td>
<td>48</td>
</tr>
</tbody>
</table>

#### Columns

<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Size</th>
<th>Description/Attribute</th>
</tr>
</thead>
<tbody>
<tr>
<td>AnalysisID</td>
<td>Number (Long)</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td>Description</td>
<td>Text</td>
<td>255</td>
<td></td>
</tr>
<tr>
<td>Date</td>
<td>Date/Time</td>
<td>8</td>
<td>Date of analysis</td>
</tr>
<tr>
<td>AbsorptionID</td>
<td>Number (Long)</td>
<td>4</td>
<td>Attenuation data index</td>
</tr>
<tr>
<td>GeoID</td>
<td>Number (Long)</td>
<td>4</td>
<td>Geometry data index</td>
</tr>
<tr>
<td>IEQID</td>
<td>Number (Long)</td>
<td>4</td>
<td>Iodine equivalence data index</td>
</tr>
<tr>
<td>EBARID</td>
<td>Number (Long)</td>
<td>4</td>
<td>Average energy data index</td>
</tr>
<tr>
<td>DACID</td>
<td>Number (Long)</td>
<td>4</td>
<td>Derived air concentration data index</td>
</tr>
<tr>
<td>ReportParamsID</td>
<td>Number (Long)</td>
<td>4</td>
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<td>microCuries if Yes, Bq if no</td>
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<td>fDirectedFit</td>
<td>Yes/No</td>
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<td>Decay correct to date specified if Yes</td>
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<td>fDecayAcq</td>
<td>Yes/No</td>
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<td>Decay during sample collection</td>
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<td>Yes/No</td>
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<td>Yes/No</td>
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<td>Analyze with high priority if Yes (recommended)</td>
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<td>TCC correction. Should not be needed in Renaissance.</td>
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<td>------</td>
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<td>Library 2 for manual peak stripping</td>
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<td>255</td>
<td>Library 3 for manual peak stripping</td>
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<td>Library used for unknown peak list</td>
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**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**

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<td>Analysis Results ID number</td>
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<tr>
<td>Date</td>
<td>Date/Time</td>
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<td>Date analysis performed</td>
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<td>Energy calibration used in the analysis</td>
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<td>Description: Efficiency calibration used in the analysis</td>
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<td>Energy calibration used in analysis</td>
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Attributes: Unique, Enforced
Attributes: One-To-One
C.3.3.5. Table: Application

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Def. Updatable: True  
Last Updated: 5/7/03 3:43:36 PM  
OrderByOn: False  
Orientation: 0  
RecordCount: 1

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<td>AppVersion</td>
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C.3.3.6. Table: Attenuation

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<td>255</td>
<td>Name of absorber</td>
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<tr>
<td>Date</td>
<td>Date/Time</td>
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<td>Name of absorber</td>
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<td>Reference analysis ID</td>
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<td>CurAnalysisID</td>
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<td>Yes if external absorber</td>
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<td>Density of absorber (g/cm^3)</td>
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<td>Correction</td>
<td>Number (Long)</td>
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<td>Linear attenuation coefficient at this energy</td>
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C.3.3.7. Table: Attenuation Coefficients

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Relationships

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C.3.3.8. Table: AttenuationMaterials

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- Last Updated: 5/7/03 3:43:36 PM
- Orientation: 0
- RecordCount: 3
- Def. Updatable: True
- OrderByOn: False

Columns

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<td>Date</td>
<td>Date/Time</td>
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<td>Date material entered</td>
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<td>AtomicWeight</td>
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<td>Formula</td>
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Relationships

- AttenuationMaterials AttenuationCoefficients
- AttenuationMaterialID AttenuationMaterialID

Attributes:
- Enforced
- 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

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<td>Date EBAR values entered</td>
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C.3.3.10. Table: ChestWallThickness

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<td>Text</td>
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<td>CWT = Param1 + Param2 * Weight / Height</td>
</tr>
<tr>
<td>Param1</td>
<td>Number (Double)</td>
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<td>cm</td>
</tr>
<tr>
<td>Param2</td>
<td>Number (Double)</td>
<td>8</td>
<td>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)</td>
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C.3.3.11. Table: DAC

### Properties

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<tr>
<td>Description</td>
<td>Text</td>
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</tr>
<tr>
<td>Date</td>
<td>Date/Time</td>
<td>8</td>
<td>Date DAC values entered or edited</td>
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<tr>
<td>Units</td>
<td>Text</td>
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<td></td>
</tr>
<tr>
<td>Isotope</td>
<td>Text</td>
<td>50</td>
<td></td>
</tr>
<tr>
<td>DAC</td>
<td>Number (Double)</td>
<td>8</td>
<td>Derived air concentration (formerly Maximum Permissible Concentration)</td>
</tr>
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C.3.3.12. Table: Detectors

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- Def. Updatable: True
- Last Updated: 5/7/03 3:43:36 PM
- OrderByOn: False
- Orientation: 0
- RecordCount: 8

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<td>Date/Time</td>
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<td>Date record created</td>
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<td>Detector serial number (SMART-1™ detectors only. 0 if not a SMART-1 detector)</td>
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<td>nMCB</td>
<td>Number (Integer)</td>
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<tr>
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<td>Detector device/segment number</td>
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<td>Host</td>
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<td>Host computer</td>
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<td>DetectorType</td>
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<td>0 or 1 = HPGe, 2=NaI, 3=CZT</td>
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C.3.3.13. Table: EffCal

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<td>5/7/03 3:43:36 PM</td>
<td>OrderByOn:</td>
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<th>Size</th>
<th>Description/Attributes</th>
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<tr>
<td>EfficiencyID</td>
<td>Number (Long)</td>
<td>4</td>
<td>Efficiency calibration ID</td>
</tr>
<tr>
<td>Description</td>
<td>Text</td>
<td>255</td>
<td>Efficiency Calibration description</td>
</tr>
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<td>Date</td>
<td>Date/Time</td>
<td>8</td>
<td>Efficiency Calibration creation date</td>
</tr>
<tr>
<td>DetectorID</td>
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<td>4</td>
<td></td>
</tr>
<tr>
<td>CertificateID</td>
<td>Number (Long)</td>
<td>4</td>
<td>Efficiency calibration certificate ID</td>
</tr>
<tr>
<td>SourceToDetectorDistance</td>
<td>Number (Double)</td>
<td>8</td>
<td>Distance for efficiency calibration (cm)</td>
</tr>
<tr>
<td>NPairs</td>
<td>Number (Integer)</td>
<td>2</td>
<td>Number peaks used in calibration</td>
</tr>
<tr>
<td>EKnee</td>
<td>Number (Double)</td>
<td>8</td>
<td>Knee energy</td>
</tr>
<tr>
<td>FitAbove</td>
<td>Number (Integer)</td>
<td>2</td>
<td>1=interpolate, 2=linear, 3–5=quadratic, 6=polynomial, 7=TCC</td>
</tr>
<tr>
<td>ASigma</td>
<td>Number (Double)</td>
<td>8</td>
<td>Reduced chisq of efficiency fit above knee</td>
</tr>
<tr>
<td>ACoef0</td>
<td>Number (Double)</td>
<td>8</td>
<td>Efficiency coefficients</td>
</tr>
<tr>
<td>ACoef1</td>
<td>Number (Double)</td>
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<td></td>
</tr>
<tr>
<td>ACoef2</td>
<td>Number (Double)</td>
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</tr>
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<td>ACoef3</td>
<td>Number (Double)</td>
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</tr>
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<td>Number (Double)</td>
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<td>ACoef5</td>
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<td>ACoef6</td>
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<td>FitBelow</td>
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<td>1=interpolate, 2=linear, 3–5=quadratic</td>
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<tr>
<td>BSigma</td>
<td>Number (Double)</td>
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<td>Reduced chisq of efficiency fit below knee</td>
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<tr>
<td>BCoef0</td>
<td>Number (Double)</td>
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<td>Efficiency coefficients below the knee</td>
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<td>BCoef1</td>
<td>Number (Double)</td>
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</tr>
<tr>
<td>BCoef2</td>
<td>Number (Double)</td>
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<td></td>
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<tr>
<td>Name</td>
<td>Type</td>
<td>Size</td>
<td>Description/Attributes</td>
</tr>
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<td>------------</td>
<td>------</td>
<td>------------------------------------------------</td>
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<td>Yes/No</td>
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<td>Absorber present during TCC calibration</td>
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<tr>
<td>IsAbsorber</td>
<td>Yes/No</td>
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<td>Absorber present during TCC calibration</td>
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<tr>
<td>IsPointSource</td>
<td>Yes/No</td>
<td>1</td>
<td>Point source used for tcc calibration</td>
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<tr>
<td>LTS0</td>
<td>Number (Double)</td>
<td>8</td>
<td>Linear-to-Square coefficients</td>
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<tr>
<td>LTS1</td>
<td>Number (Double)</td>
<td>8</td>
<td>Linear-to-Square coefficients</td>
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<td>LTS2</td>
<td>Number (Double)</td>
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<td>Linear-to-Square coefficients</td>
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<td>PTT0</td>
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<td>Peak to Total coefficients</td>
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<td>Peak to Total coefficients</td>
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**Relationships**

**EffCal**  **Spectra**

EfficiencyID  EfficiencyID

Attributes: Enforced
Attributes: One-To-Many
C.3.3.14. Table: EffCalPeaks

Properties

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<td>5/7/03 3:43:36 PM</td>
</tr>
<tr>
<td>Last Updated</td>
<td>5/7/03 3:43:36 PM</td>
</tr>
<tr>
<td>Orientation</td>
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</tr>
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<td>Def. Updatable</td>
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<td>OrderByOn</td>
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Columns

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<th>Type</th>
<th>Size</th>
<th>Description/Attributes</th>
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<tbody>
<tr>
<td>EfficiencyID</td>
<td>Number (Long)</td>
<td>4</td>
<td>Efficiency calibration ID</td>
</tr>
<tr>
<td>Energy</td>
<td>Number (Double)</td>
<td>8</td>
<td>Library peak energy</td>
</tr>
<tr>
<td>Efficiency</td>
<td>Number (Double)</td>
<td>8</td>
<td>Efficiency value calculated from peak area</td>
</tr>
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C.3.3.15. Table: EffCertificate

**Properties**

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<td>Date Created</td>
<td>5/7/03 3:43:36 PM</td>
<td>Efficiency calibration certificate ID</td>
</tr>
<tr>
<td>Last Updated</td>
<td>5/7/03 3:43:36 PM</td>
<td>Certificate description</td>
</tr>
<tr>
<td>Orientation</td>
<td>0</td>
<td>Isotope name</td>
</tr>
<tr>
<td>RecordCount</td>
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<td>Library half life</td>
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</table>

**Columns**

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<td>Description</td>
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<td>Date</td>
<td>Date/Time</td>
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<td>Certificate date and time</td>
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<td>Nuclide</td>
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<td>Halflife</td>
<td>Number (Double)</td>
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<td>Library half life</td>
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<td>Energy</td>
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<td>Percent</td>
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<td>Library branching ratio</td>
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<td>Certificate Uncertainty in activity</td>
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<td>Display units for the activity 0=GPS, 1=Bq, &gt;1=μCi</td>
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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

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<tr>
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<td>Date/Time</td>
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<td>Calibration date</td>
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<td>Library</td>
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<td>Full path name of library</td>
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<td>nValues</td>
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<td>Number energy/channel pairs used in calibration</td>
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<td>Energy calibration</td>
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<td>ESlope</td>
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</tr>
<tr>
<td>EQuadratic</td>
<td>Number (Double)</td>
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<td></td>
</tr>
<tr>
<td>EChisq</td>
<td>Number (Double)</td>
<td>8</td>
<td>Reduced chisq for energy calibration</td>
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<td>FWHM calibration</td>
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Relationships

- **EnergyCal** to **Spectra**
  - EnergyID to EnergyID
    - Attributes: Enforced
    - Attributes: One-To-Many
C.3.3.17. Table: EnergyCalPeaks

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**Columns**

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<th>Description/Attributes</th>
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<td>EnergyCal EnergyID value</td>
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<td>Number (Double)</td>
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<td>Channel</td>
<td>Number (Double)</td>
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C.3.3.18. Table: Geometry

**Properties**

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<tr>
<td>Last Updated:</td>
<td>5/7/03 3:43:36 PM</td>
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<td>RecordCount:</td>
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**Columns**

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</tr>
<tr>
<td>Description</td>
<td>Text</td>
<td>50</td>
<td>Description</td>
</tr>
<tr>
<td>Date</td>
<td>Date/Time</td>
<td>8</td>
<td>Date geometry correction created</td>
</tr>
<tr>
<td>DetectorID</td>
<td>Number (Long)</td>
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<td></td>
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<td>RefAnalysisID</td>
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<td>Reference analysis ID</td>
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<td>CurAnalysisID</td>
<td>Number (Long)</td>
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<td>Current analysis ID</td>
</tr>
<tr>
<td>Energy</td>
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<td>Peak energy</td>
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<td>RefArea</td>
<td>Number (Double)</td>
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<td>Reference analysis peak area</td>
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<td>CurArea</td>
<td>Number (Double)</td>
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<td>Current analysis peak area</td>
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<td>Correction</td>
<td>Number (Double)</td>
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<td>Geometry correction at this energy</td>
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C.3.3.19. Table: IodineEquivalence

Properties

Date Created: 5/7/03 3:43:36 PM
Last Updated: 5/7/03 3:43:36 PM
Orientation: 0

Def. Updatable: True
OrderByOn: False
RecordCount: 0

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</tr>
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<td>Date</td>
<td>Date/Time</td>
<td>8</td>
<td>Date IEQ data entered</td>
</tr>
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<td>Isotope</td>
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</tr>
<tr>
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C.3.3.20. Table: Nuclides

Properties

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- **Def. Updatable:** True
- **Last Updated:** 5/7/03 3:43:36 PM
- **OrderByOn:** True
- **Orientation:** 0
- **RecordCount:** 480

Columns

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<td>Nuclide name</td>
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<td>Calculated abundance in Bq</td>
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<td>Isotope counting error</td>
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<td>Uncertainty</td>
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C.3.3.21. Table: Peaks

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- Last Updated: 5/7/03 3:43:36 PM
- Def. Updatable: True
- OrderByOn: True
- Orientation: 0
- RecordCount: 1353

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C.3.3.22. Table: PkShapeCal

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<td>Short-term tail energy, amplitude, and slope at energy 2</td>
</tr>
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<td></td>
</tr>
<tr>
<td>STTSlope2</td>
<td>Number (Double)</td>
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<td></td>
</tr>
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<td>Long-term tail energy, amplitude, and slope at energy 1</td>
</tr>
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<td>Chisq</td>
<td>Number (Double)</td>
<td>8</td>
<td>Reduced chisq of fit</td>
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<td></td>
</tr>
<tr>
<td>maxChan</td>
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<tr>
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<td>8</td>
<td>Cubic spline coefficients</td>
</tr>
<tr>
<td>Coeff1</td>
<td>Number (Double)</td>
<td>8</td>
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</tr>
<tr>
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<td>Type</td>
<td>Size</td>
<td>Description/Attributes</td>
</tr>
<tr>
<td>----------</td>
<td>--------------------</td>
<td>------</td>
<td>------------------------</td>
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<tr>
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<td>Number (Double)</td>
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</tr>
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<td></td>
</tr>
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<tr>
<td>Weight3</td>
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<td></td>
</tr>
<tr>
<td>Energy4</td>
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</tr>
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<tr>
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</tr>
<tr>
<td>Energy5</td>
<td>Number (Double)</td>
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</tr>
<tr>
<td>Coeff5</td>
<td>Number (Double)</td>
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</tr>
<tr>
<td>Weight5</td>
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C.3.3.23. Table: RenLimits

Properties

- Date Created: 5/7/03 3:43:36 PM
- Last Updated: 5/7/03 3:43:36 PM
- Orientation: 0

Order By On: False
Def. Updatable: True
Record Count: 1243

Columns

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<td></td>
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<td>AnalysisGroupID</td>
<td>Number (Long)</td>
<td>4</td>
<td>Key to analysis group table</td>
</tr>
<tr>
<td>AnalysisResultsID</td>
<td>Number (Long)</td>
<td>4</td>
<td>Key to analysis results table. Zero if this is an average</td>
</tr>
<tr>
<td>Nuclide</td>
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<td>50</td>
<td></td>
</tr>
<tr>
<td>LibEnergy</td>
<td>Number (Double)</td>
<td>8</td>
<td>Library energy (keV)</td>
</tr>
<tr>
<td>Energy</td>
<td>Number (Double)</td>
<td>8</td>
<td>Centroid energy (keV)</td>
</tr>
<tr>
<td>Activity</td>
<td>Number (Double)</td>
<td>8</td>
<td>Bq</td>
</tr>
<tr>
<td>MDA</td>
<td>Number (Double)</td>
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<tr>
<td>Uncertainty</td>
<td>Number (Double)</td>
<td>8</td>
<td>Relative total uncertainty</td>
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<td>AlarmLimit</td>
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<td>Bq</td>
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<tr>
<td>WarningLimit</td>
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<td>Bq</td>
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<td>Area</td>
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<td>Peak area</td>
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C.3.3.24. Table: RenResults

Properties

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<th>Value</th>
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<th>OrderByOn</th>
<th>RecordCount</th>
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<td>False</td>
<td>30</td>
</tr>
<tr>
<td>Last Updated</td>
<td>5/7/03 3:43:36 PM</td>
<td>False</td>
<td>True</td>
<td></td>
</tr>
<tr>
<td>Orientation</td>
<td>0</td>
<td></td>
<td>True</td>
<td></td>
</tr>
</tbody>
</table>

Columns

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<th>Type</th>
<th>Size</th>
<th>Description/Attributes</th>
</tr>
</thead>
<tbody>
<tr>
<td>RenResultsID</td>
<td>Number (Long)</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td>Date</td>
<td>Date/Time</td>
<td>8</td>
<td>Analysis date</td>
</tr>
<tr>
<td>HistoryID</td>
<td>Number (Long)</td>
<td>4</td>
<td>SubjectHistory table</td>
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<tr>
<td>AnalysisGroupID</td>
<td>Number (Long)</td>
<td>4</td>
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</tr>
<tr>
<td>TotalActivity</td>
<td>Number (Double)</td>
<td>8</td>
<td>Total activity in spectrum, or average total activity</td>
</tr>
<tr>
<td>IsAverage</td>
<td>Yes/No</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>IsSum</td>
<td>Yes/No</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>TotalCounts</td>
<td>Number (Double)</td>
<td>8</td>
<td>Total counts in spectrum (or average total counts)</td>
</tr>
<tr>
<td>Subject</td>
<td>Text</td>
<td>100</td>
<td>Based on key being used (Name, Badge, or SSN)</td>
</tr>
<tr>
<td>PrintSpc</td>
<td>Yes/No</td>
<td>1</td>
<td>Print spectrum</td>
</tr>
<tr>
<td>PrintMCS</td>
<td>Yes/No</td>
<td>1</td>
<td>Print MCS plots</td>
</tr>
<tr>
<td>RptZAPeaks</td>
<td>Yes/No</td>
<td>1</td>
<td>Report zero-area peaks</td>
</tr>
<tr>
<td>RptZANucls</td>
<td>Yes/No</td>
<td>1</td>
<td>Report zero-area nuclides</td>
</tr>
<tr>
<td>IndividualRpt</td>
<td>Yes/No</td>
<td>1</td>
<td>Save individual reports?</td>
</tr>
<tr>
<td>CombinedRpt</td>
<td>Yes/No</td>
<td>1</td>
<td>Save combined reports?</td>
</tr>
<tr>
<td>CatRpt</td>
<td>Yes/No</td>
<td>1</td>
<td>Concatenate reports?</td>
</tr>
<tr>
<td>CombinedDB</td>
<td>Yes/No</td>
<td>1</td>
<td>Save combined results to database?</td>
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<td>Number (Long)</td>
<td>4</td>
<td>Key field (Name, Badge, or SSN)</td>
</tr>
<tr>
<td>OprPath</td>
<td>Text</td>
<td>255</td>
<td>Pathname of .OPR file</td>
</tr>
<tr>
<td>DivWeight</td>
<td>Yes/No</td>
<td>1</td>
<td>Divide activity by weight?</td>
</tr>
</tbody>
</table>
### Relationships

<table>
<thead>
<tr>
<th>SubjectHistory</th>
<th>RenResults</th>
</tr>
</thead>
<tbody>
<tr>
<td>HistoryID</td>
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</tr>
<tr>
<td></td>
<td>HistoryID</td>
</tr>
</tbody>
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Attributes:
- SubjectHistory: Enforced
- RenResults: One-To-Many
C.3.3.25. Table: ReportParams

Properties

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<td>5/7/03 3:43:36 PM</td>
</tr>
<tr>
<td>Last Updated</td>
<td>5/7/03 3:43:36 PM</td>
</tr>
<tr>
<td>Orientation</td>
<td>0</td>
</tr>
<tr>
<td>Def. Updatable</td>
<td>True</td>
</tr>
<tr>
<td>OrderByOn</td>
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<tr>
<td>RecordCount</td>
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</table>

Columns

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<th>Type</th>
<th>Size</th>
<th>Description/Attributes</th>
</tr>
</thead>
<tbody>
<tr>
<td>ReportParamsID</td>
<td>Number (Long)</td>
<td>4</td>
<td>Report parameters ID number</td>
</tr>
<tr>
<td>Date</td>
<td>Date/Time</td>
<td>8</td>
<td>Date record created</td>
</tr>
<tr>
<td>wSigma</td>
<td>Number (Integer)</td>
<td>2</td>
<td>Number standard deviations for uncertainty</td>
</tr>
<tr>
<td>Units</td>
<td>Text</td>
<td>12</td>
<td></td>
</tr>
<tr>
<td>Weight</td>
<td>Number (Double)</td>
<td>8</td>
<td>Sample weight or volume</td>
</tr>
<tr>
<td>fUncertaintyPercent</td>
<td>Yes/No</td>
<td>1</td>
<td>Report uncertainty in percent</td>
</tr>
<tr>
<td>fUncertaintyTotal</td>
<td>Yes/No</td>
<td>1</td>
<td>Report total and counting uncertainty</td>
</tr>
<tr>
<td>fuC</td>
<td>Yes/No</td>
<td>1</td>
<td>Yes: Report activity in µCi * Numerator / Denominator. No: activity in Bq * Numerator / Denominator</td>
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<td>Numerator</td>
<td>Number (Double)</td>
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<tr>
<td>Denominator</td>
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<td>Activity units factor denominator</td>
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<td>List library peaks</td>
</tr>
<tr>
<td>fListIso</td>
<td>Yes/No</td>
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<td>List isotope activity</td>
</tr>
<tr>
<td>fListUnknowns</td>
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<td>fListIsoMatrix</td>
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<td>List peaks by isotope</td>
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<td>fPrint</td>
<td>Yes/No</td>
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<td>Print report</td>
</tr>
<tr>
<td>fProgram</td>
<td>Yes/No</td>
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<td>Send report to the program</td>
</tr>
<tr>
<td>fGenerator</td>
<td>Yes/No</td>
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<td>Run report generator</td>
</tr>
<tr>
<td>File</td>
<td>Text</td>
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<td>Report file name</td>
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<td>Program</td>
<td>Text</td>
<td>255</td>
<td>Report display program</td>
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<td>Template</td>
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Relationships

ReportParams  AnalysisParams
ReportParamsID  ReportParamsID

Attributes: Enforced
Attributes: One-To-Many
C.3.3.26. Table: Spectra

Properties

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</tr>
<tr>
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<td>5/7/03 3:43:36 PM</td>
</tr>
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<td>Def. Updatable</td>
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<tr>
<td>OrderByOn</td>
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Columns

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<tr>
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<td>Original efficiency calibration</td>
</tr>
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<td>AcquisitionDate</td>
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<td>Spectrum acquisition date (local time)</td>
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<tr>
<td>TimeBias</td>
<td>Number (Long)</td>
<td>4</td>
<td>Difference in minutes between UTC and local time</td>
</tr>
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<td>LiveTime</td>
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<td>Live time (seconds)</td>
</tr>
<tr>
<td>RealTime</td>
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<td>Real time (seconds)</td>
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Relationships

**EnergyCal**  
EnergyID: EnergyID  
Attributes: Enforced  
Attributes: One-To-Many

**EffCal**  
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

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</tr>
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<td>Text</td>
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<td>Last name</td>
</tr>
<tr>
<td>First</td>
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<td>MiddleInitial</td>
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</tr>
<tr>
<td>Badge</td>
<td>Text</td>
<td>50</td>
<td>Badge number (not necessarily unique)</td>
</tr>
<tr>
<td>SSN</td>
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<td>Social Security Number</td>
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Relationships

Subject   SubjectHistory
SubjectID  SubjectID

Attributes: Enforced
Attributes: One-To-Many
C.3.3.28. Table: SubjectHistory

Properties

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<tr>
<td>Last Updated</td>
<td>5/7/03 3:43:36 PM</td>
</tr>
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Columns

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</tr>
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<td>Number (Long)</td>
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<td>Key from Subject table</td>
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<tr>
<td>CWTID</td>
<td>Number (Long)</td>
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<td>Key from ChestWallThickness table</td>
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<tr>
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<td>Date/Time</td>
<td>8</td>
<td>Date comment added</td>
</tr>
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<td>Comment</td>
<td>Text</td>
<td>128</td>
<td></td>
</tr>
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<td>Company</td>
<td>Text</td>
<td>50</td>
<td>Company or division</td>
</tr>
<tr>
<td>IntakeDate</td>
<td>Date/Time</td>
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<td></td>
</tr>
<tr>
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<td>Number (Double)</td>
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<td>kg</td>
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<td>Height</td>
<td>Number (Double)</td>
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<td>cm</td>
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<tr>
<td>Option2</td>
<td>Text</td>
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<td></td>
</tr>
<tr>
<td>Option3</td>
<td>Text</td>
<td>128</td>
<td></td>
</tr>
<tr>
<td>Option4</td>
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<td>Option 1 description entered by the operator</td>
</tr>
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<td>Option 3 description entered by the operator</td>
</tr>
<tr>
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## Relationships

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<th>Table</th>
</tr>
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<td>HistoryID</td>
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Attributes:  
- Enforced  
- One-To-Many

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<th>Table</th>
</tr>
</thead>
<tbody>
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<td>SubjectID</td>
</tr>
</tbody>
</table>

Attributes:  
- Enforced  
- One-To-Many
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 ...**
`.RENWAN32.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:

<table>
<thead>
<tr>
<th>Error #</th>
<th>Warning #</th>
<th>Reason</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>Read error in UFO peak record</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>Read error in UFO nuclide record</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>Write error in UFO peak record</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>Write error in UFO nuclide record</td>
</tr>
<tr>
<td>3</td>
<td>1</td>
<td>Invalid acquisition date and time</td>
</tr>
<tr>
<td>4</td>
<td>0</td>
<td>Illegal absorption correction</td>
</tr>
<tr>
<td>5</td>
<td>1</td>
<td>Read error in spectrum file</td>
</tr>
</tbody>
</table>

**Analysis Failed!**
`.RENWAN32.EXE` has finished executing, but an error was encountered. Refer to the “RENWAN32 completion codes...” message.

**Analysis Failed (Job Error 18)**
The ANALYZE command failed (look for the RENWAN32 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 RENWAN32.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 RENWAN32.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 RENWAN32 . 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 RENWAN32 . 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 RENWAN32.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 `RENWAN32.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 `RENWAN32.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 `RENWAN32 . 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 `RENWAN32 . 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 RENWAN32.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 <Del> 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 RENWAN32.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 \texttt{RENWAN32.EXE} or some other application program.

Out of Memory! (WinExec error 0)
Error encountered trying to spawn \texttt{RENWAN32.EXE} or some other application program.

Path Not Found! (WinExec error 3)
Error encountered trying to spawn \texttt{RENWAN32.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 \texttt{RENWAN32.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 RENWAN32 .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.

RENWAN32 Error Messages (i = 1):

<table>
<thead>
<tr>
<th>Error #</th>
<th>Warning #</th>
<th>Reason</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>?</td>
<td>Invalid spectrum filename</td>
</tr>
<tr>
<td>1</td>
<td>1</td>
<td>Read error in UFO peak record</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>Read error in UFO nuclide record</td>
</tr>
<tr>
<td>1</td>
<td>3</td>
<td>Read error in spectrum non-data record</td>
</tr>
<tr>
<td>1</td>
<td>4</td>
<td>Read error in UFO file</td>
</tr>
<tr>
<td>1</td>
<td>200</td>
<td>Attempt to read start channel after stop channel</td>
</tr>
<tr>
<td>1</td>
<td>201</td>
<td>Read error on disk for .CHN files</td>
</tr>
<tr>
<td>1</td>
<td>202</td>
<td>Read error on disk for .SPC files</td>
</tr>
<tr>
<td>1</td>
<td>203</td>
<td>Attempt to read invalid spectrum file type</td>
</tr>
<tr>
<td>2</td>
<td>0</td>
<td>Illegal filename</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>Write error in UFO peak record</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>Write error in UFO nuclide record</td>
</tr>
<tr>
<td>2</td>
<td>3</td>
<td>Write error in other UFO records</td>
</tr>
<tr>
<td>2</td>
<td>4</td>
<td>Invalid record for UFO file</td>
</tr>
<tr>
<td>2</td>
<td>7</td>
<td>Write error on report file</td>
</tr>
<tr>
<td>2</td>
<td>8</td>
<td>Invalid record request for table file</td>
</tr>
<tr>
<td>3</td>
<td>0</td>
<td>Invalid acquisition date and time</td>
</tr>
<tr>
<td>4</td>
<td>0</td>
<td>Illegal absorption correction</td>
</tr>
<tr>
<td>4</td>
<td>3</td>
<td>Spectrum not found</td>
</tr>
<tr>
<td>5</td>
<td>0</td>
<td>Read error in spectrum file</td>
</tr>
<tr>
<td>5</td>
<td>3</td>
<td>Spectrum wrong file type</td>
</tr>
</tbody>
</table>
### Error # | Warning # | Reason
--- | --- | ---
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):

<table>
<thead>
<tr>
<th>Error #</th>
<th>Warning #</th>
<th>Reason</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>Warning, not an error</td>
<td></td>
</tr>
<tr>
<td>0</td>
<td>1</td>
<td>More than 500 peaks in the library. First 500 used</td>
</tr>
<tr>
<td>1</td>
<td>Library error</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>1</td>
<td>Library File error</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>Invalid library file header</td>
</tr>
<tr>
<td>1</td>
<td>3</td>
<td>Corrupt or missing library file</td>
</tr>
<tr>
<td>1</td>
<td>4</td>
<td>No peaks in library</td>
</tr>
<tr>
<td>1</td>
<td>5</td>
<td>ASCII library file might be corrupted.</td>
</tr>
<tr>
<td>1</td>
<td>13</td>
<td>Data type mismatch</td>
</tr>
<tr>
<td>1</td>
<td>53, 75, 76</td>
<td>Library file not found</td>
</tr>
<tr>
<td>1</td>
<td>71</td>
<td>The disk drive containing the library is not ready</td>
</tr>
<tr>
<td>2</td>
<td>Invalid configuration entry</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>No matrix</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>Gross Weight = 0</td>
</tr>
<tr>
<td>2</td>
<td>3</td>
<td>Tare Weight &gt; Gross Weight</td>
</tr>
<tr>
<td>2</td>
<td>3</td>
<td>Gross Weight = 0 And GeometryMode &gt; 1</td>
</tr>
<tr>
<td>2</td>
<td>4</td>
<td>MatrixDensity too small</td>
</tr>
<tr>
<td>2</td>
<td>5</td>
<td>Matrix not found</td>
</tr>
<tr>
<td>2</td>
<td>10</td>
<td>Container thickness too small</td>
</tr>
<tr>
<td>2</td>
<td>11</td>
<td>Container density = 0</td>
</tr>
<tr>
<td>2</td>
<td>12</td>
<td>Invalid U or Pu weight</td>
</tr>
<tr>
<td>2</td>
<td>13</td>
<td>Container not found in database</td>
</tr>
<tr>
<td>2</td>
<td>20</td>
<td>Detector standoff = 0</td>
</tr>
<tr>
<td>2</td>
<td>21</td>
<td>Detector height = 0</td>
</tr>
<tr>
<td>2</td>
<td>22</td>
<td>Detector not found in database</td>
</tr>
<tr>
<td>2</td>
<td>23</td>
<td>Collimator not found in database</td>
</tr>
<tr>
<td>2</td>
<td>30</td>
<td>Invalid container values</td>
</tr>
<tr>
<td>2</td>
<td>31</td>
<td>Invalid matrix values</td>
</tr>
<tr>
<td>3</td>
<td>1</td>
<td>Attenuation coefficients not found</td>
</tr>
</tbody>
</table>
APPENDIX D. ERROR MESSAGES

<table>
<thead>
<tr>
<th>Error #</th>
<th>Warning #</th>
<th>Reason</th>
</tr>
</thead>
<tbody>
<tr>
<td>4</td>
<td></td>
<td>Analysis errors</td>
</tr>
<tr>
<td>4 1</td>
<td></td>
<td>Could not read analysis engine out of spc file</td>
</tr>
<tr>
<td>4 2</td>
<td></td>
<td>No peaks found</td>
</tr>
<tr>
<td>4 3</td>
<td></td>
<td>Error reading peaks from database</td>
</tr>
<tr>
<td>4 4</td>
<td></td>
<td>Invalid input report format</td>
</tr>
<tr>
<td>4 5</td>
<td></td>
<td>Invalid analysis engine</td>
</tr>
</tbody>
</table>

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 `RENWAN32.EXE` or some other application program; refer to Windows SDK documentation for meaning of code <n>. 
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.
APPENDIX E. ERROR MESSAGES

**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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