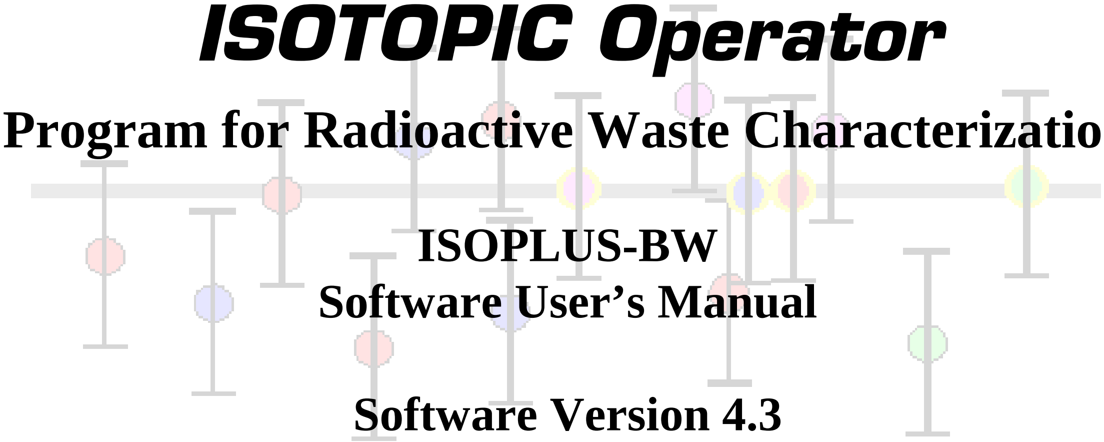
ORTEC®

ISOTOPIC Operator



Program for Radioactive Waste Characterization

ISOPLUS-BW
Software User’s Manual

Software Version 4.3

Printed in U.S.A.
ORTEC Part No. 796090
Manual Revision N
0714

Advanced Measurement Technology, Inc.
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TABLE OF CONTENTS

NOTE!

We assume that you are familiar with Microsoft® Windows® usage and terminology. If not, be sure to familiarize yourself with a few simple Windows applications before proceeding.

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

1. INTRODUCTION

Welcome to the Operator component of ISOTOPIC version 4.3. This ISOTOPIC Operator *Software User's Manual* is intended to be used in conjunction with the accompanying ISOTOPIC Supervisor program's user manual (P/N 783630), after the software and hardware have been installed according to the accompanying *Getting Started* guide (P/N 931065). The *Getting Started* guide also includes a detailed, step-by-step walkthrough of ISOPLUS-BW from configuration in the ISOTOPIC Supervisor program through field use with ISOTOPIC Operator. See the *Supervisor User's Manual* for a thorough introduction to ISOTOPIC v4.3, its capabilities, analysis engines, and analysis methods.

Most ISOTOPIC users work with our portable, USB multichannel buffers (MCBs), such as the digiDART® or IDM-200-V. Hardware setup for the digiDART is discussed in Section 8.2.2, **Acquire/MCB Properties...**.

Note that, as of v4.2, ISOTOPIC began taking side detector efficiency into account. As a result, detector efficiency is greater than in previous versions of ISOTOPIC, and activity values using the same configuration parameters are usually concomitantly lower in v4.x. For large standoff distances the results should be about the same between the versions.

1.1. Using This Manual

This manual contains all the information you will need to run ISOTOPIC Operator after setup has been performed in the ISOTOPIC Supervisor program.

- Chapter 2 discusses the Operator display features.
- Chapter 3 describes the setup and startup activities common to ISOTOPIC Operator's Container/Surface Mode and Soil Mode.
- Chapter 4 tells how to perform Container/Surface Mode scans and interpret the report.
- Chapter 5 tells how to perform Soil Mode scans and interpret the report.
- Chapter 6 introduces the features of the Crystal Reports window.
- Chapter 7 provides in-depth information on performing in situ measurements.
- Chapter 8 is a reference guide to the Operator menu commands.
- Chapter 9 tells how to perform quality assurance measurements.
- Chapter 10 discusses the accelerator (shortcut) key functions in Operator.

1.2. Before Using ISOTOPIC Operator

Before you can begin making measurements in ISOTOPIC Operator, the following tasks must be performed:

- The MCB and detector hardware must be properly connected, powered on, and adjusted.
- The correct library for the nuclides of interest must be created in ISOTOPIC Supervisor or the accompanying Nuclide Library Editor program.
- In Supervisor, the detectors must be energy and efficiency calibrated with the appropriate source(s). If the detectors are not efficiency calibrated, all nuclide activities will be reported as zero.
- The *operator permissions*, which determine the parameters operators can adjust, must be set. If all permissions are enabled, operators can perform all ISOTOPIC functions except calibration, attenuation database entry, selection of SAP BusinessObjects® Crystal Reports™ templates, QA setup, and choosing the spectrum display preferences.
- The Container/Surface and Soil mode *configurations*, which govern data acquisition and analysis in the Operator program, must be created. If the **Allow modification of configuration settings** operator permission is set in the Supervisor program, operators can create and/or modify configurations within the Operator program.
- If your organization uses ISOTOPIC's onboard quality assurance tools, QA settings must be established for each detector to be used.

If the Supervisor setup steps have not been satisfactorily completed, when you start the Operator program, a dialog or Status Bar message will indicate that one or more values could not be read from the database. Follow the instructions in Chapters 4 and 5 to adjust the configuration as necessary to clear the error message.

1.3. What's New in v4.3

- ISOTOPIC operates on computers running 32- and 64-bit Microsoft® Windows® 7 Professional and Windows XP SP3 (32-bit).
- Reports for both the Container/Surface Mode and Soil Mode are in HTML and SAP® BusinessObjects Crystal Reports™ v11.5.

- Close geometry algorithm added in v4.2 has now been validated to include bottle counting mode for 1-liter bottles or other small cylinders placed on the endcap.

- Soil mode L:D ratios now include a calibration for D/L>2.8 to accommodate the IDM-200-V used in our ISO-CART-85.

- A new applications chapter (Chapter 7) discusses the ins and outs of using ISOTOPIC and the ISO-CART-85 to perform in situ measurements.

- To assist systems integrators, Appendix A in the *Supervisor Manual* expands the discussion of the ISOTOPIC analysis engines and how to start them from the command line. In addition, Appendix B documents the structure of the ISOTOPIC database.

1.4. Operation/Release Notes for v4.2

1.4.1. Regional Settings

Except for Icelandic Windows, your Windows **Regional Settings** *must be configured to use a period (**.**) as the* ***Decimal Symbol*** to avoid errors when setting up or using container configurations.

1.4.2. USB-Interface MCBs: "UNKNOWN MODE" Error After Power Loss

If your MCB has a USB interface (e.g., digiDART, DSPEC Pro®) and the computer-to-MCB connection is lost while running either the Supervisor or Operator program, the software will immediately close the window for the missing MCB, post the **Detector busy or not responding** message on the status bar at the bottom of the screen, and open a buffer window (Fig. 1). To reopen communication with the MCB in the Operator program:

1) Make sure all cable connections are secure.

2) Reselect the **Configuration** type from the droplist.

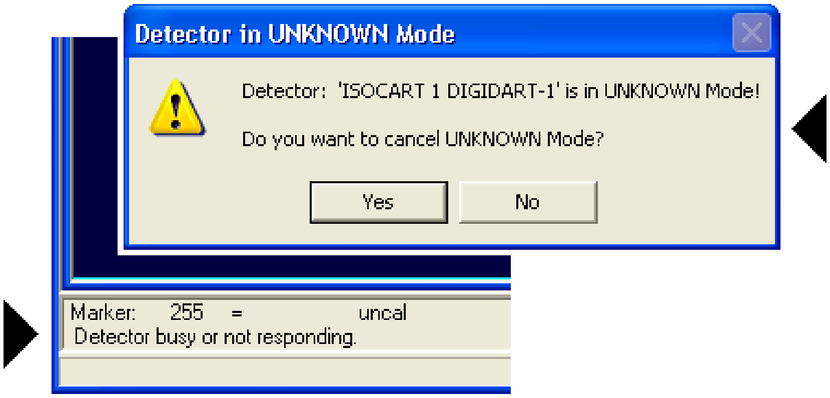
3) The UNKNOWN Mode dialog will open, asking if you wish to cancel the unknown mode (see Fig. 1).

- Clicking **Yes** will clear the MCB memory, reset the unit to data acquisition mode, and open a corresponding spectrum window.

- Clicking **No** will reset the MCB to the proper mode, but might retain the instrument memory *unless the MCB is powered exclusively by the USB bus, for instance, the digiDART*. If your MCB is line- or battery-powered and has a spectrum in memory, click **No**.

If the corresponding spectrum window does not open at this point, re-select the desired **Configuration**. If the spectrum has been retained in MCB memory, it will be displayed onscreen. It can then be analyzed with the **Configuration in memory...** command on the **Analyze** menu.

4) Before resuming data collection, make sure the detector high voltage is on.



Detector in UNKNOWN Mode

Detector: 'ISOCART 1 DIGIDART-1' is in UNKNOWN Mode!

Do you want to cancel UNKNOWN Mode?

Marker: 255 = uncal

Detector busy or not responding.

Figure 1. USB-Connected Detector in Unknown Mode.

1.5. Caution: The MCB Configuration Program Can Affect QA and Other Functions

Detectors are identified in ISOTOPIC based on the *instrument number and description* assigned to the MCBs by the MCB Configuration program. The MCB Configuration polls the local computer and network for attached ORTEC MCBs and builds a Master Detector List of the MCBs found, each with an instrument number and description. This instrument identification is then used for all QA measurements. ***Be sure to thoroughly read the Connections Driver Update Kit instructions as well as all MCB Configuration-related instructions in the ISOTOPIC Getting Started Guide (P/N 931065) before re-running MCB Configuration.***

1.6. Sample Measurement Files and Filename Conventions

Beginning with ISOTOPIC v4, all sample measurement, analysis, reanalysis, and reporting is performed in the Operator program, including the reanalysis of archived data. Detector QA measurements can be made in both the Supervisor and Operator programs. The type and number of files generated during sample measurement differs slightly between Container/Surface Mode and Soil Mode.

NOTE When you archive a particular ISOTOPIC database (the instructions are in the *Supervisor Manual*), we strongly recommend you move *not only the* `.MDB` *database file, but all of the analysis, spectrum, bitmap, and reporting files related to the records in that database. Subsequently, these should all be stored in the same folder or in the same relationship (relative folder structure) as when they were originally acquired.* Otherwise, the **Recall File** and **Recall Configuration and File(s)** commands might not be able to correctly recall all the necessary information, and existing Container/Surface Mode HTML reports might not show the embedded spectrum and fine-tuning plot images.

1.6.1. Container/Surface Mode

As noted in the introduction, the Container/Surface Mode configuration wizard combines analysis and report setup, detector selection and position information, collimator description, and container characterization in one convenient wizard. The resulting analysis setup, called a *configuration*, is stored in the ISOTOPIC database. The files generated for each sample include `.SPC`, `.An1`, `.UFO`, `.BMP`, and `.HTML` files. Additional information is captured in the database for each measurement.

Filenames for `.SPC`, `.An1`, `.UFO`, and `.HTML` files are structured as follows:

`[Container ID] [Iso] [nnnnn]`

where `Container ID` is entered on the upper section of the ISOTOPIC Operator screen, `Iso` identifies these as files generated in ISOTOPIC, and `nnnnn` is a numerical suffix that reflects the number of acquisitions performed to date with the corresponding detector for the current database. Example:

`Drum 1234 Iso00567.Spc`

For each sample, ISOTOPIC creates an activity plot bitmap and a spectrum histogram bitmap, which are incorporated into the HTML-format report. The filenames for these respectively end in `Activity` and `Spectrum`.

For multi-detector configurations, ISOTOPIC Operator generates an `.HTML` report for each individual detector and a report in which the results from all detectors are averaged or weighted as specified for the configuration. The filename for this averaged report ends in `_Ave`.

1.6.1.1. Reanalysis

When you reanalyze a Container/Surface Mode scan data set, a new suite of spectrum, analysis, and report files are created; the original files are not overwritten. Filenames are structured as follows:

[Container ID] [Buf] [nnnnn]

where Container ID is entered on the upper section of the ISOTOPIC Operator screen, Buf identifies these as files generated using a buffer window, and nnnnn is a numerical suffix reflecting the number of reanalyses performed in a buffer window for the current database.

1.6.2. Soil Mode

The Soil Mode setup dialog includes analysis, acquisition, detector, calibration, and report settings, which can be saved as standalone.M1 files (rather than configurations saved in a database) for later reuse. The files generated for each sample include .SPC, .An1, .UFO, and .RPT files. Additional information is captured in the database for each measurement.

The filenames are structured as follows:

[Field ID] [Iso] [nnnnn]

where Field ID is entered at the top of the Soil Mode setup dialog, Iso identifies these as files generated in ISOTOPIC, and nnnnn is a numerical suffix that reflects the number of acquisitions performed to date with the corresponding detector for the current database. Example:

D&D Site XYZ Iso00200.Spc

For each sample, ISOTOPIC creates a results plot bitmap and a spectrum histogram bitmap, which are incorporated into the HTML report. Note that Soil Mode measurements are made with only a single detector so there is no averaged report.

1.6.2.1. Reanalysis

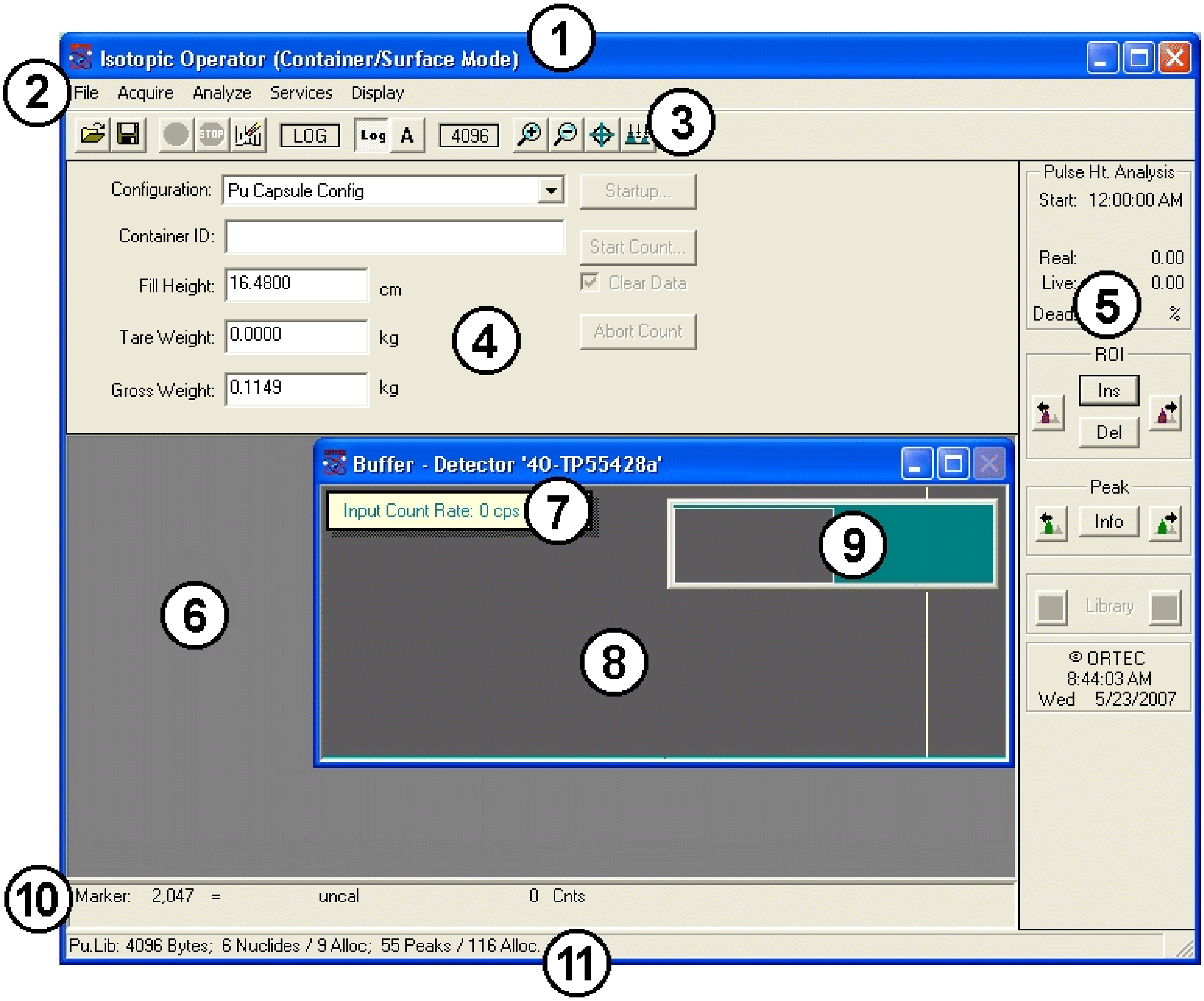
When you reanalyze a Soil Mode scan data set, a new suite of spectrum, analysis, and report files are created; the original files are not overwritten. Filenames are structured as follows:

[Field ID] [Buf] [nnnnn]

where Field ID is entered at the top of the Soil Mode setup dialog, Buf identifies these as files generated using a buffer window, and nnnnn is a numerical suffix reflecting the number of reanalyses performed in a buffer window for the current database.

2. DISPLAY FEATURES

This chapter addresses the ISOTOPIC Operator display features, discusses the role of the mouse and keyboard, and covers the use of the toolbar and sidebars. To start the Operator program, either double-click the **Isotopic Operator** desktop icon; or go to the Windows Start menu, enter the letters oper in the "*Search programs and files*" box, and select the **Isotopic Operator** result. The password dialog (see Fig. 12 , page 17) will open. If user accounts and passwords have been assigned in the Supervisor program, enter your password and click **OK**. If no password has been assigned, simply click **OK**. The main Operator screen will be displayed. Figure 2 shows the principal screen features.



Configuration: Pu Capsule Config

Container ID:

Fill Height: 16.4800 cm

Tare Weight: 0.0000 kg

Gross Weight: 0.1149 kg

☑ Clear Data

Pulse Ht. Analysis
Start: 12:00:00 AM
Real: 0.00
Live: 0.00
Dead: %

Input Count Rate: 0 cps

© ORTEC
8:44:03 AM
Wed 5/23/2007

Marker: 2,047 = uncal 0 Cnts

Pu.Lib: 4096 Bytes; 6 Nuclides / 9 Alloc; 55 Peaks / 116 Alloc.

Figure 2. Main ISOTOPIC Screen Features.

1) **Title bar**, shows 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 source of the data, either the MCB name or "Buffer" and the spectrum name.

2) **Menu Bar**, shows the available menu commands, which can be selected with either the mouse or keyboard; these functions are discussed in detail in Chapter 8.

3) **Toolbar**, beneath the menu bar, contains icons for recalling scans, saving them to disk, starting and stopping data acquisition, and adjusting the vertical and horizontal scales for the active spectrum.

4) **Scan Control Area** displays the selections for the current assay. Data collection is defined by these entries and the scan is started here. The *scan control buttons* are discussed in Section 3.1.1.

5) **Status Sidebar**, on the right side of the screen, provides information on the current MCB presets and counting times, the time and date, and a set of buttons that allow you to move easily between peaks, ROIs, and library entries (see Section 2.4).

6) **Spectrum Area** displays one window for each MCB defined in the configuration. The title bar will contain the MCB name for the MCBs. To switch windows, click the window to be activated, or cycle between windows by pressing **<Ctrl + Tab>**. The status sidebar shows the values for the active window. Each spectrum window contains an **Expanded Spectrum View** and a **Full Spectrum View** (see items 8 and 9 below).

7) **Input Count Rate** indicator; see Section 8.6.7.

8) The **Expanded Spectrum View** shows all or part of the full histogram. A particular part of the spectrum can be expanded for more detail. The expanded view can have any vertical and horizontal scaling. 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).

9) The **Full Spectrum View** shows the full histogram of the MCB memory. The vertical scale is always logarithmic, and the window can be moved and sized (see Section 2.3.4). 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 that area in the Full Spectrum View and the expanded display updates immediately at the new position.

10) **Marker Information Line**, beneath the spectrum, shows the marker channel, marker energy, and channel contents.

11) **Supplementary Information Line**, below the Marker Information Line, is used to show warning messages or instructions.

2.1. Spectrum Display, Scaling, and Zooming

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. The Full Spectrum View shows the entire data memory of the MCB 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 2.3.1, 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 2.3.3). 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 may 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.

Note that the color and fill properties of the spectrum windows are controlled by the **Display/ Preferences** settings in ISOTOPIC Supervisor.

2.2. The Toolbar

The row of buttons below the menu bar provides convenient shortcuts to some of the most common ISOTOPIC menu commands.

The **Recall** button retrieves a scan data set. This is the equivalent of selecting **File/Recall Scan Data Set...** from the menu.

Save copies the currently displayed spectrum to disk. It duplicates the menu function **File/Save As...**.

Start Acquisition starts data collection in the active MCB. This duplicates **Acquire/ Start** and **<Alt + 1>**.

Stop Acquisition stops data collection in the active MCB. This duplicates **Acquire/Stop** and **<Alt + 2>**.

Clear Spectrum clears the MCB or file spectrum in the active window. This duplicates **Acquire/Clear** and **<Alt + 3>**.

The next section of the toolbar (Fig. 3) contains the buttons that control the spectrum vertical scale. These commands are also on the **Display** menu. In addition, the vertical and horizontal scales can be adjusted by zooming in with the mouse (see Fig. 7).

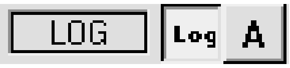


Figure 3. Vertical Scaling Section of Toolbar.

Vertical Log/Lin Scale switches between logarithmic and linear scaling. When switching from logarithmic to linear, it uses the previous linear scale setting. The keyboard equivalent is **Keypad</>**.

Vertical Auto Scale turns on the *autoscale* mode, a linear scale that automatically adjusts until the largest peak shown is at its maximum height without overflowing the display. The keyboard equivalent is **Keypad<*>**.

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

The horizontal scaling section (Fig. 4) 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. 7).

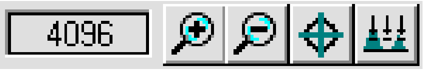


Figure 4. Horizontal Scaling Section of Toolbar.

Zoom In decreases the horizontal full scale of the Expanded Spectrum View according to the discussion in Section 8.5.4, 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 8.5.5, 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.

Finally, when you pause the mouse pointer over the center of a toolbar button, a pop-up *tool tip* opens, describing the button’s function (Fig. 5).

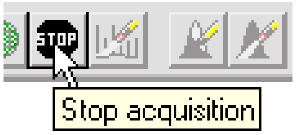


Figure 5. Tool Tip.

2.3. Using the Mouse

The mouse can be used for every function in ISOTOPIC except text entry. The following sections describe specialized mouse functions.

2.3.1. 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.

2.3.2. The Right-Mouse-Button Menu

Figure 6 shows the right-mouse-button menu, which is available only in the Expanded Spectrum View. The available commands will depend on the spectrum displayed and whether the rubber rectangle is active.

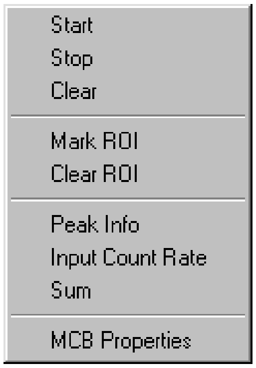


Figure 6. Right-Mouse-Button Menu for Spectra.

2.3.3. Using the "Rubber Rectangle"

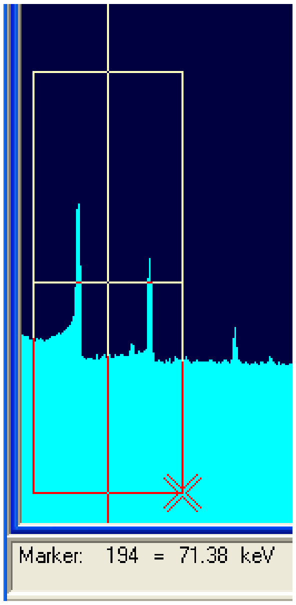
The *rubber rectangle* is used for selecting a particular area of interest within a spectrum. It can be used in conjunction with the right-mouse-button menu (see Fig. 6) for many functions. To draw a rubber rectangle:

- Click and hold the left mouse button; this anchors the starting corner of the rectangle.
- Drag the mouse diagonally across the area of interest. As you drag, the mouse will be drawing a reverse-color rectangle bisected by the marker line to form a "crosshair" (Fig. 7). This makes it easy to select the center channel in the area of interest — for instance, the center of an ROI you wish to mark or unmark, a portion of the spectrum to be summed, or a peak for which you want detailed information.
- Release the mouse button to anchor the ending corner of the rectangle.
- Once the area of interest is marked, select the applicable command from the toolbar, menus, right-mouse-button menu, Status Sidebar, or keyboard.

2.3.4. Sizing and Moving the Full Spectrum View

- **Resizing** — Roll the mouse pointer over the side edge, bottom edge, or corner of the window until the pointer changes to a double-sided arrow (see Fig. 8). Click and drag the edge of the window until it is the size you want, then release the mouse button.

- **Moving** — Roll the mouse pointer onto the top edge of the window until the pointer changes to a four-sided arrow (see Fig. 8). Click and drag the window to its new location, and release the mouse button.



Marker: 194 = 71.38 keV

Figure 7.

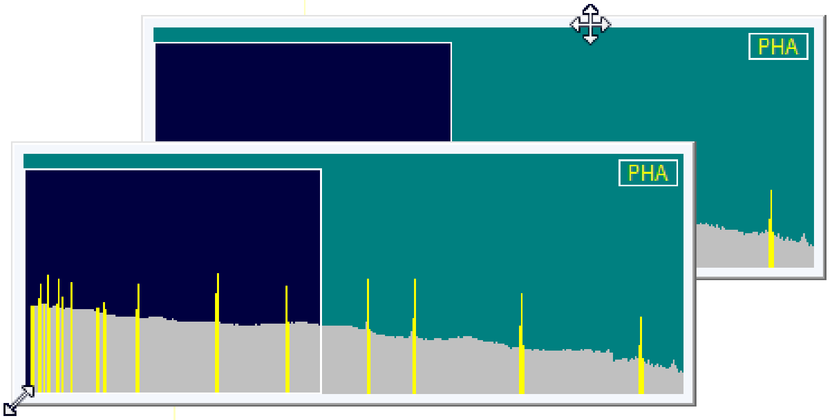


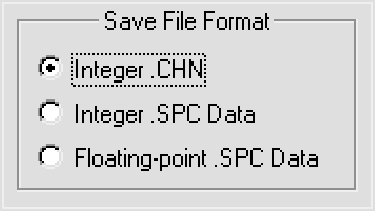
Figure 8. Two-Sided Pointer for Sizing Full Spectrum View, and Four-Sided Pointer for Moving Window.

2.4. Buttons and Boxes

This section describes ISOTOPIC's radio buttons, indexing buttons, and checkboxes.

- **Radio buttons** (Fig. 9) appear on many ISOTOPIC dialogs, and allow only one of the choices to be selected.

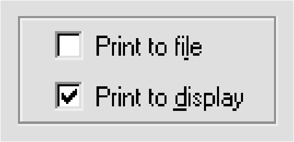
- **Checkboxes** (Fig. 10) are another common feature, allowing one or more of the options to be selected at the same time.



Save File Format

● Integer .CHN
○ Integer .SPC Data
○ Floating-point .SPC Data

Figure 9. Radio Buttons.



☐ Print to file
☑ Print to display

Figure 10. Checkboxes.

- The **ROI**, **Peak**, and **Library** 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 ISOTOPIC posts a `no more entries` message on the Supplementary Information Line.

- The indexing buttons are displayed in two different ways, depending on whether ISOTOPIC is in MCB or buffer mode, as shown in Fig. 11. However, they function the same way in both modes. In buffer mode, 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 move forward or backward through the library to the next closest library entry. Each button press advances to the next library entry and moves the marker to the corresponding energy. If a library file has not been loaded or the Detector is not calibrated, these buttons are disabled.

HINT Instead of using the **Peak** buttons to move from a previously identified peak, click the marker anywhere in the spectrum then click 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, peak data are displayed on the Marker Information Line at the bottom of the screen.

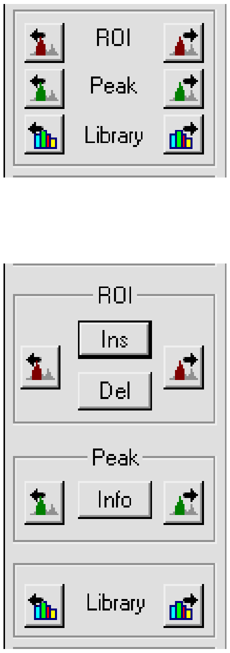


Figure 11. MCB mode, top; buffer mode, bottom).

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

2.5. Opening Files with Drag-and-Drop

ISOTOPIC Supervisor lets you open ORTEC spectrum (`.SPC`, `.AN1`, `.CHN`), library (`.LIB`), and region of interest (`.ROI`) files by dragging and dropping them from Windows Explorer into the ISOTOPIC window. A spectrum file opens in a buffer window, a library file is loaded as the working library, and the ROIs saved in an `.ROI` file are set in the currently active spectrum window.

2.6. Associated Files

Installing ISOTOPIC registers the spectrum files in Windows so they can be opened from Windows Explorer by double-clicking the filename. The spectrum files are displayed in GVPlot. These files are marked with a spectrum icon () in the Explorer display. The `.EFT` and `.ENT` files are also registered, and have an ORTEC icon (). They open in Windows Notepad.

[Intentionally blank]

3. PREPARING TO SCAN — BOTH MODES

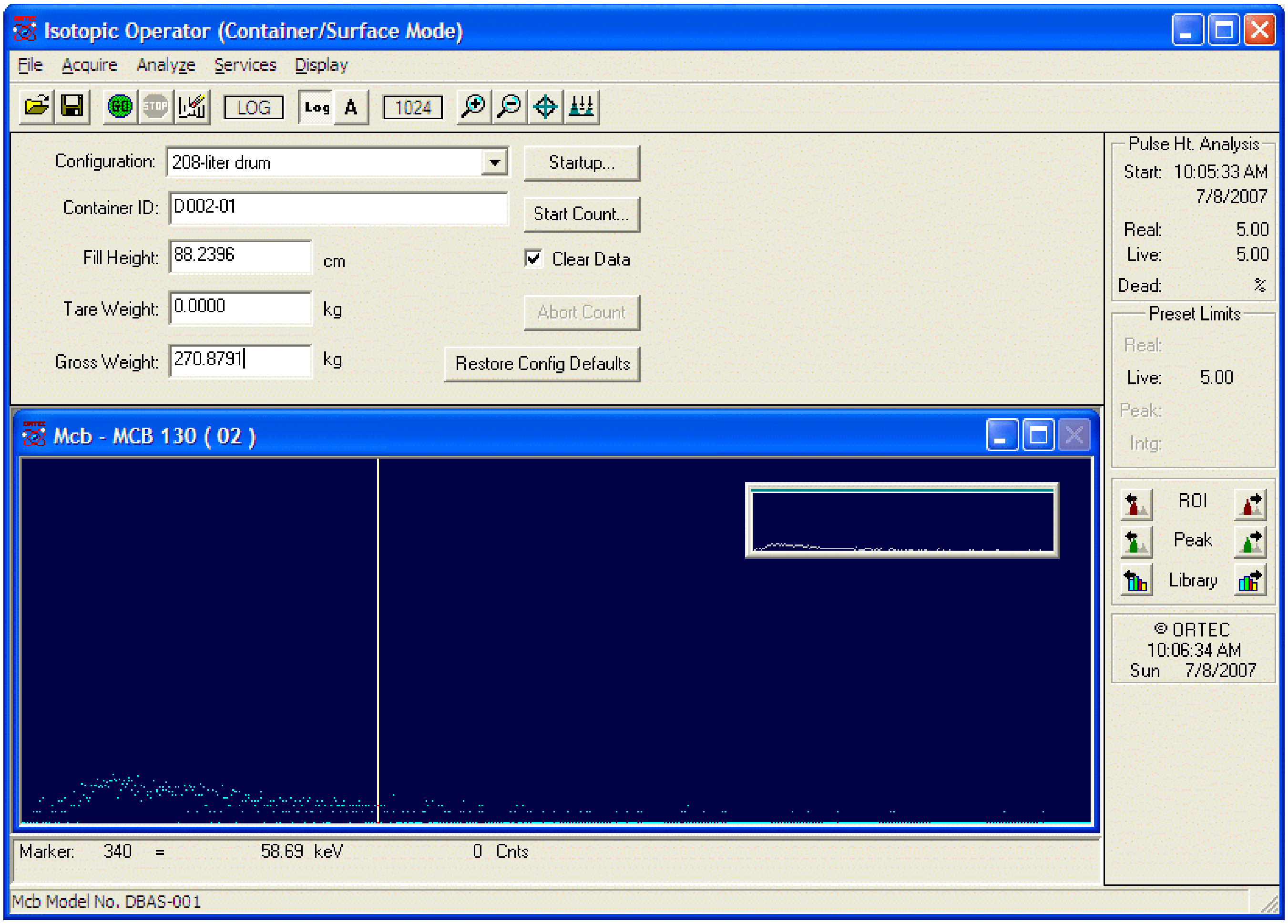
3.1. Starting ISOTOPIC Operator

Little, B

Figure 12. Log-in to ISOTOPIC Operator.

Before starting ISOTOPIC Operator, make sure that the Supervisor program is closed so all of the setup options will go into effect. Then double-click the **Isotopic Operator** desktop icon or go to the Windows Start menu, enter the letters `oper` in the "*Search programs and files*" box, and select the **Isotopic Operator** entry. The Operator login dialog (Fig. 12) will be displayed. The name you enter here will be saved in the database and printed on reports generated during this work session.

Figures 13 and 14 show the ISOTOPIC Operator display for Container/Surface Mode and Soil Mode, respectively (as reflected by the title bar). ***The mode is selected in the Supervisor program and cannot be changed in the Operator program.***



Configuration: 208-liter drum

Container ID: D002-01

Fill Height: 88.2396 cm

Tare Weight: 0.0000 kg

Gross Weight: 270.8791 kg

☑ Clear Data

Pulse Ht. Analysis
Start: 10:05:33 AM 7/8/2007
Real: 5.00
Live: 5.00
Dead: %

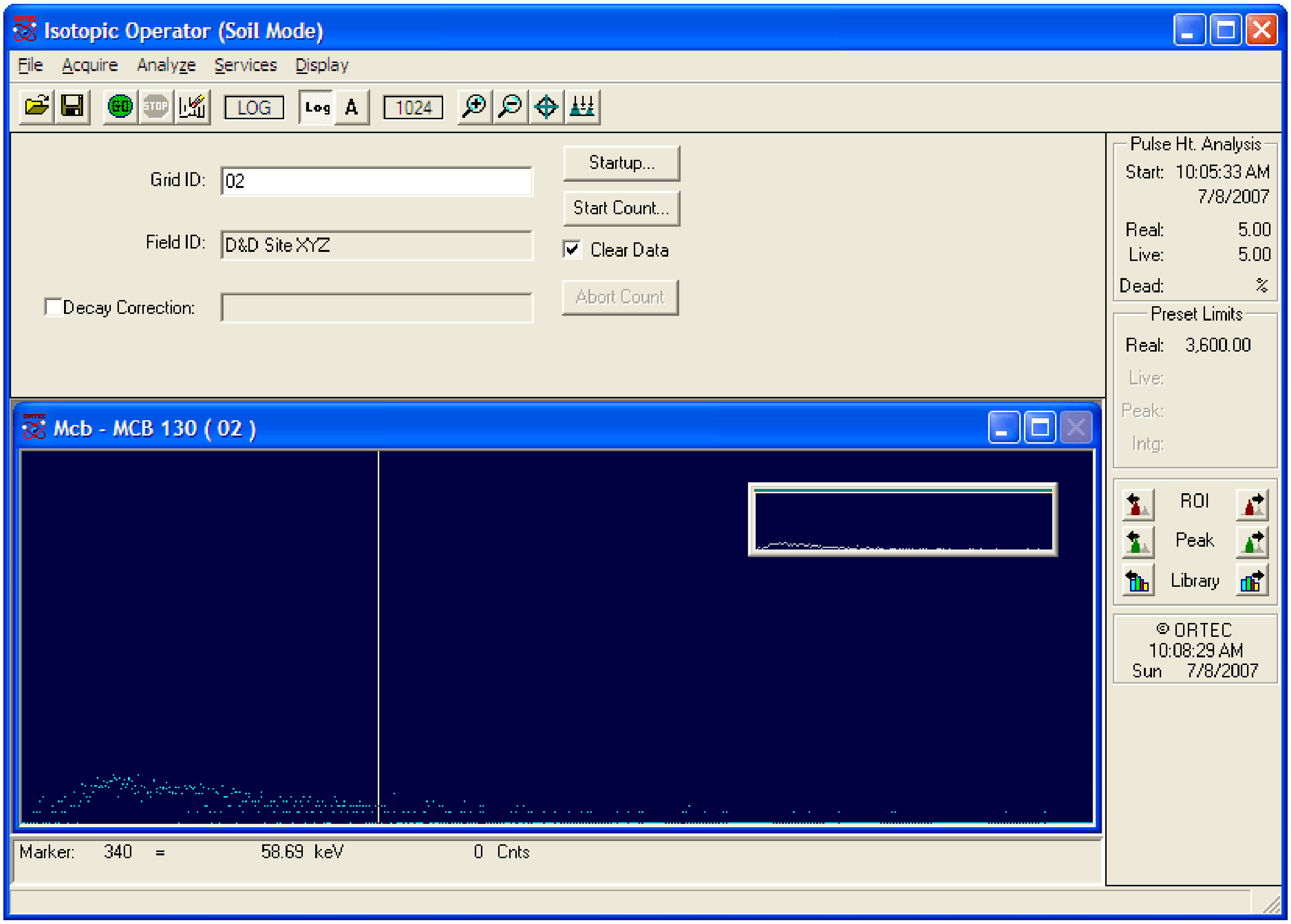
Preset Limits
Real:
Live: 5.00
Peak:
Intg:

© ORTEC
10:06:34 AM
Sun 7/8/2007

Marker: 340 = 58.69 keV 0 Cnts

Mcb Model No. DBAS-001

Figure 13. Main Screen for Analyzing Containers.



Grid ID: 02

Field ID: D&D Site XYZ

☐ Decay Correction:

☑ Clear Data

Pulse Ht. Analysis
Start: 10:05:33 AM 7/8/2007
Real: 5.00
Live: 5.00
Dead: %

Preset Limits
Real: 3,600.00
Live:
Peak:
Intg:

Marker: 340 = 58.69 keV 0 Cnts

© ORTEC
10:08:29 AM
Sun 7/8/2007

Figure 14. Main Screen for Analyzing Soils.

Note the **Startup** button to the right of the **Name** field. This opens the Startup Wizard, which allows you to efficiently perform a number of setup steps and performance checks at the beginning of each series of measurements; see Section 3.3.

The Container/Surface and Soil mode screens are very much alike and operate in the same manner. The differences are due to the different counting situations of the two modes.

- The Container/Surface Mode can operate with multiple detectors, and up to eight MCB windows can be displayed at once.

- The Soil Mode operates with only one detector.

3.1.1. Scan Control Buttons

These buttons are displayed on the right side of Scan Control Area.

This opens the Startup Wizard, discussed in Section 3.3, which allows you to perform a number of setup steps and performance checks at the beginning of each series of measurements. If you are using a **No detector** configuration to reanalyze an existing data set, this button is inactive (gray).

Click to begin the measurement using the MCB group governed by the current **Configuration**. Before starting the count, be sure that all subject fields have been filled in and the subject is ready to be counted.

This button becomes active once the count has begun. Clicking it opens the Count Suspended dialog (Fig. 15). Click on **Resume** to continue the count with the data and settings unmodified. Click **Restart** to erase the spectrum and start the count over. This is used when an error is discovered during the count. The error should be corrected before you click on **Restart**. **Abort** will terminate the scan.

The Current Acquisition has been Suspended.

Select an Option Below:

Figure 15. Abort Count.

(Container/Surface Mode only.) This button resets all entries in the Scan Control Area to the defaults for the currently selected configuration.

3.1.2. Operator Warning Messages

On MCBs with state-of-health monitoring, such as the digiDART, a warning message similar to Fig. 16 may be displayed in a dialog or on the Status Bar at the bottom of the program window when you start the Operator program or try to start data acquisition. This is a normal condition when the MCB has been improperly shut down. Fortunately, data loss is unlikely in these cases. Click **Yes** to ignore the message.

The instrument reported a bad state-of-health and should be checked

Do you wish to ignore this message?

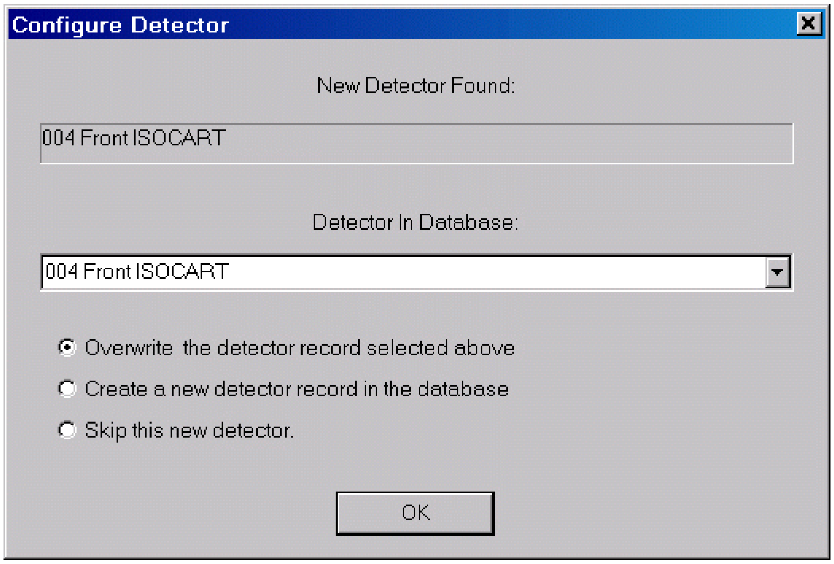
Figure 16. State-of-Health Warning from digiDART.

(To view the state-of-health status for the MCB, select **Acquire/MCB Properties...**, and click the Status tab.)

If the **Start Count** button is gray (inactive), one or more setup parameters are not set to valid values. If the Operator program opens showing a buffer window, the current configuration has no assigned valid detector(s).

If the analysis parameters have not been set in the Supervisor program, a "Could not load analysis record from database" message will be displayed in a warning dialog or on the Status Bar at the bottom of the Operator window. If you have access to the **Analyze/Configuration Settings...** command, use it to set up the configuration parameters correctly.

After an MCB is added to or removed from the system, or has been moved from one computer or port to another, if list of available MCBs has not been correctly reconfigured, the Configure Detector dialog (Fig. 17) will be displayed on startup. *The recommended option in response to this dialog is to select the* ***Skip*** *option*, exit from Operator, re-run the MCB Configuration program and correctly restore the **Description** text string, then return to the Operator program. See the "Container Configuration" discussion in the QA chapter of the *Supervisor Manual*.



004 Front ISOCART

004 Front ISOCART

● Overwrite the detector record selected above
○ Create a new detector record in the database
○ Skip this new detector.

Figure 17. Reconfigure MCBs or Overwrite Detector Name in Database?

3.2. Sample Measurement vs. Reanalysis of Existing Data Sets

ISOTOPIC Operator has two analytical modes:

- **Sample Measurement** in Container/Surface or Soil Mode; this is discussed in Chapters 3.3 through 5.
- **Analysis** and reanalysis of current and archived (stored) data. Analysis of stored spectrum files is discussed in Section 8.1.1; analysis of scan data sets from an ISOTOPIC database is discussed in Section 8.1.2. In both cases, analysis is performed with the **Analyze/ Configuration in Memory** command (Section 8.3.4).

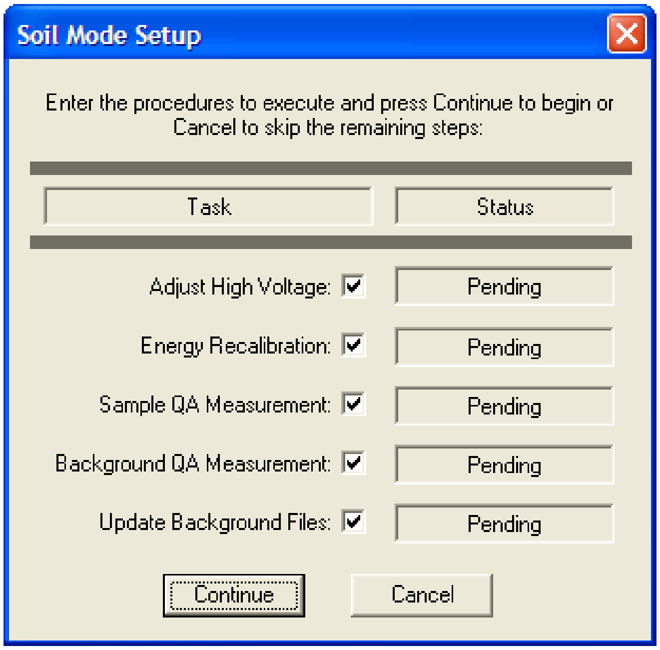
3.3. Using the Startup Wizard

The **Startup** button opens the Startup Wizard (Fig. 18), which guides you through a number of setup steps and performance checks at the beginning of each series of measurements. It operates only on the detector(s) in the currently selected configuration. If you are using a **No detector** configuration in order to reanalyze existing data scans, the **Startup** button is disabled. As soon as you select a configuration associated with a detector(s), the button activates. The Startup Wizard is especially useful for measurement stations where you select the configuration tailored to the particular station's detector(s).

The tasks on this list are enabled or disabled in the Supervisor program with the **Services/Operator Permissions...** feature. The available tasks have an active (white) checkbox that might or might not be marked, depending on the tasks last requested during startup. In the first Startup Wizard screen, marked tasks have a **Pending** status. Tasks that have not been enabled in Supervisor are gray (inactive) with a **Skipped** status.

NOTE The counting presets are defined in the Container/Surface or Soil mode configuration dialogs (Sections 8.3.1 and 8.3.2, respectively). You can access these with the **Analyze/Configuration Settings...** command if the **Allow Modification of Configuration Parameters** permission has been set in Supervisor.

You can perform all or part of the activated tasks at any time during the work session. To perform all of them, make sure each has a checkmark beside it, then click **Continue**. To perform a subset of the available tasks, unmark the unwanted ones before clicking **Continue**. After each task is completed, the Startup Wizard dialog is displayed again with the **Status** updated to show the completion. (Each time this dialog is presented, you can mark or unmark any of the remaining tasks.) Click **Continue** to perform the next checkmarked task. To stop the process at any time, click **Cancel**. Any tasks that have not been completed will not be performed.



Enter the procedures to execute and press Continue to begin or Cancel to skip the remaining steps:

Task	Status
Adjust High Voltage: ☑	Pending
Energy Recalibration: ☑	Pending
Sample QA Measurement: ☑	Pending
Background QA Measurement: ☑	Pending
Update Background Files: ☑	Pending

Figure 18. Startup Tasks.

At the end of the procedure, the Startup Wizard opens one last time showing the final disposition of each task. Click **Continue** to close the wizard and return to the main Operator screen.

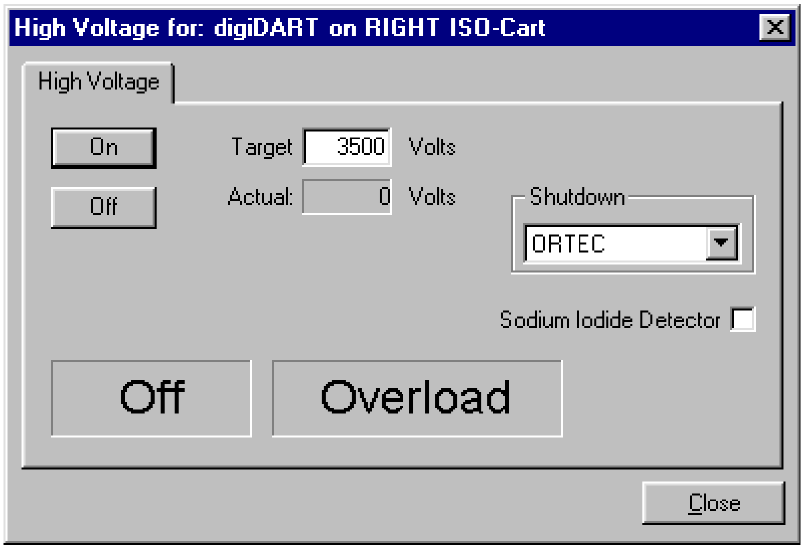
3.3.1. Adjust High Voltage

This command opens the High Voltage dialog for the MCBs (Fig. 19). The details of the dialog depend on the MCB type; for an example, see the discussion for the digiDART HV tab on page 94.

Note that the Overload indicator means there is a bad connection in your system. The Shutdown indicator means either the detector is warm or the wrong **Shutdown** mode has been chosen.

Click **Close** to continue the Startup. In a multi-detector system, this dialog is displayed for each detector in sequence.

After the HV setup is completed, the list (Fig. 18) is shown again with the Status changed to show the completion. Click **Continue** to perform the next test. Click **Cancel** to stop the startup at this point and the remaining steps will not be performed.


High Voltage for: digiDART on RIGHT ISO-Cart

Target: 3500 Volts

Actual: 0 Volts

Shutdown: ORTEC

Sodium Iodide Detector ☐

Figure 19. The High Voltage Properties.

3.3.2. Energy Recalibration

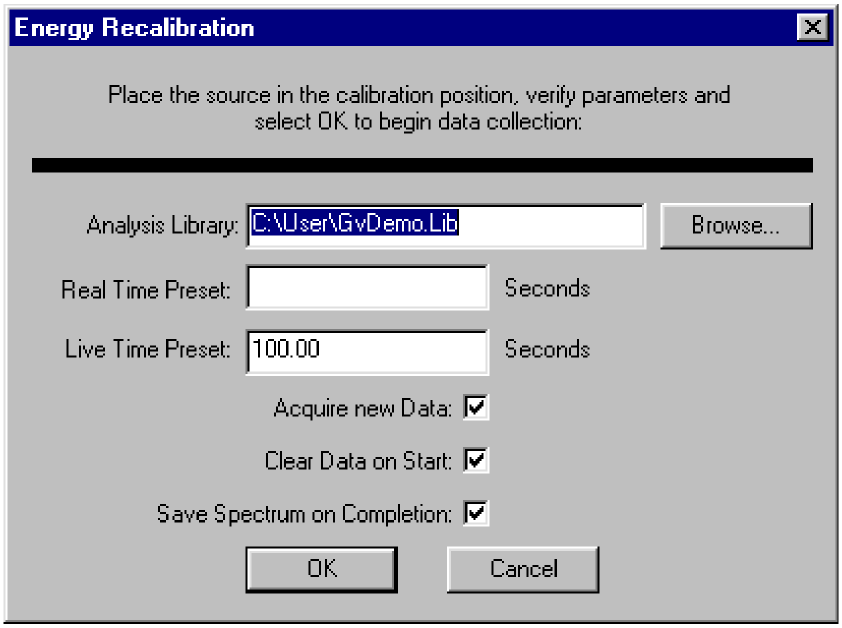
The Energy Recalibration dialog is shown in Fig. 20. When you click **OK**, the spectrum is collected as selected in the checkboxes, the calibration performed, and the results stored without any further operator input. See Section 8.4.1 for more detailed information on the recalibration process.

NOTES If the current configuration has a calibration file associated with the detector(s), the calibration file overrides the results of this recalibration. To remove the calibration file from the configuration, use **Analyze/Configuration Settings...** (Sections 8.3.1.4 and 8.3.2.1). Detective®-series instruments with fixed calibrations are not affected by this procedure (refer to the identifier's hardware manual for more information on this).

This step requires a calibration source and sufficient count time for a good spectrum. In a multi-detector system, this dialog is only displayed once and all the data are collected at the same time. In such cases, multiple sources are required or the detectors must be arranged so they all "see" the calibration source during spectrum acquisition.

If the resulting peak shift is >1%, a message box asks if you wish to apply or discard the new calibration. If the calibration has shifted significantly you might wish to associate a new calibration file with the currently selected configuration using **Analyze/Configuration Settings...**.

After the calibration is completed, the list (Fig. 18) is shown again with the Status changed to show the completion. Click **Continue** to perform the next test. Click **Cancel** to stop the startup at this point and the remaining steps will not be performed.


Energy Recalibration

Place the source in the calibration position, verify parameters and select OK to begin data collection:

Analysis Library: C:\User\GvDemo.Lib

Real Time Preset: Seconds

Live Time Preset: 100.00 Seconds

Acquire new Data: ☑

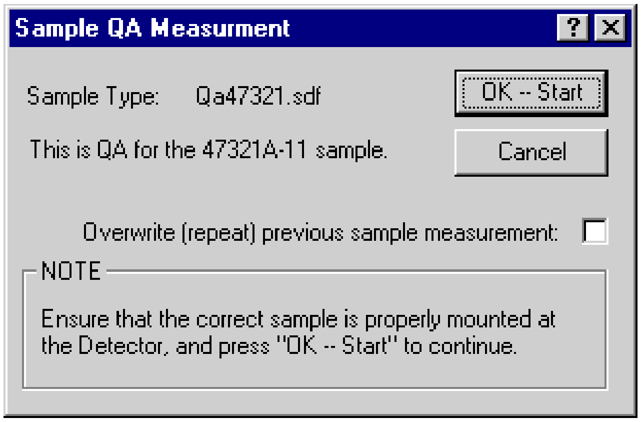
Clear Data on Start: ☑

Save Spectrum on Completion: ☑

Figure 20. Start the Energy Recalibration.

3.3.3. Sample QA Measurement

This performs the Sample QA measurement as described in Section 9.2 to verify the system is operating properly.[1] The results are stored in the database. The dialog is shown in Fig. 21. This step requires the QA source. In a multi-detector system, this dialog is only displayed once and all the data are collected at the same time. Therefore, multiple sources are required or the detectors to be arranged so they all “see” the QA source during spectrum acquisition.


Sample QA Measurment

Sample Type: Qa47321.sdf

This is QA for the 47321A-11 sample.

Overwrite (repeat) previous sample measurement: ☐

NOTE

Ensure that the correct sample is properly mounted at the Detector, and press "OK -- Start" to continue.

Figure 21. Starting Sample Type QA Measurement.

---

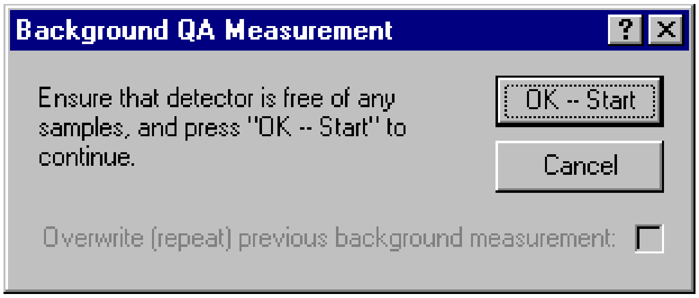
[1] Before using this command, the QA settings for each detector in the system must be established individually; see the “Quality Assurance” chapter in the *Supervisor Manual*.

If a bad measurement is made and can easily be corrected, repeat the measurement and click the **Overwrite** box to replace the bad data point with the correct result.

Acquisition starts when you click **OK-Start**. After the measurement is completed, the list (Fig. 18) is displayed again with the Status changed to show the completion. Click **Continue** to perform the next test. Click **Cancel** to stop the startup at this point and the remaining steps are not performed.

3.3.4. Background QA Measurement

This performs the Background QA measurement as described in Section 9.1 to verify the background. The dialog is shown in Fig. 22. This is not the PBC background as collected in Step 3.3.5. In a multi-detector system, this dialog is only displayed once and all the data are collected at the same time.



Ensure that detector is free of any samples, and press "OK -- Start" to continue.

Overwrite (repeat) previous background measurement: ☐

Figure 22. Begin Count for Background QA.

If a bad measurement is made and can easily be corrected, repeat the measurement and click the **Overwrite** box to replace the bad data point with the correct result.

Acquisition starts when you click **OK-Start**. After the measurement is completed, the list (Fig. 18) is displayed again with the Status changed to show the completion. Click **Continue** to perform the next test. Click **Cancel** to stop the startup at this point and the remaining steps will not be performed.

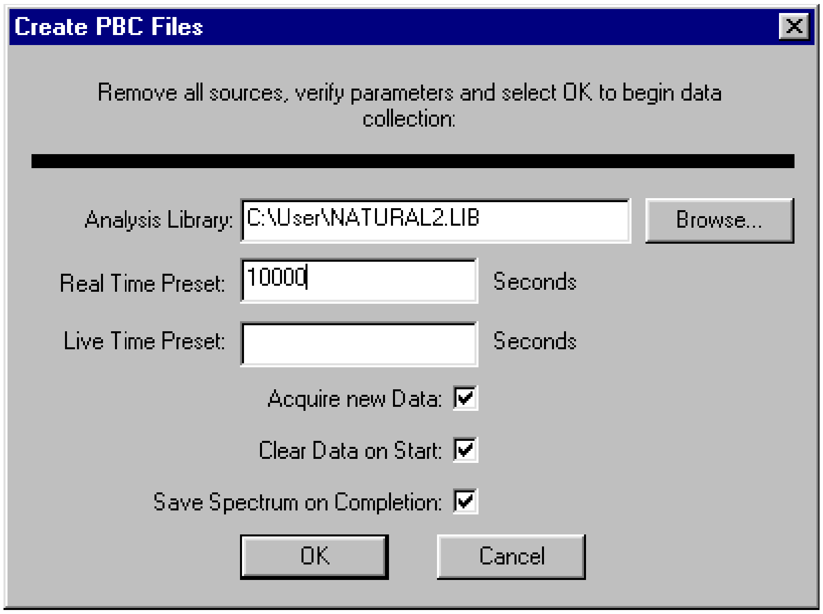
3.3.5. Update Background File

This command affects Container/ Surface Mode only. It starts the PBC Wizard (Fig. 23), which automatically collects the background spectrum, analyzes it, and creates the .PBC file. The currently selected configuration parameters, except library, count time, and PBC file (if any), are used in the analysis. The peak background correction is turned off for the analysis.

NOTES This procedure *changes your configuration* as follows: If the current configuration does not specify a .PBC file, this function creates a .PBC file and automatically enters it in the **PBC File** field on the Detectors page of the Configuration Wizard. If the current configuration specifies a .PBC file, this update function creates a new background file and automatically substitutes it in the configuration.

In a multi-detector system, this dialog is only displayed once and all the data are collected at the same time.

Acquisition starts when you click **OK**. After the measurement is completed, the list (Fig. 18) is displayed again with the Status changed to show the completion. Click **Continue** to perform the next test. Click **Cancel** *to stop the startup at this point and not perform the remaining steps.*



Create PBC Files

Remove all sources, verify parameters and select OK to begin data collection:

Analysis Library: C:\User\NATURAL2.LIB

Real Time Preset: 10000 Seconds

Live Time Preset: Seconds

Acquire new Data: ☑

Clear Data on Start: ☑

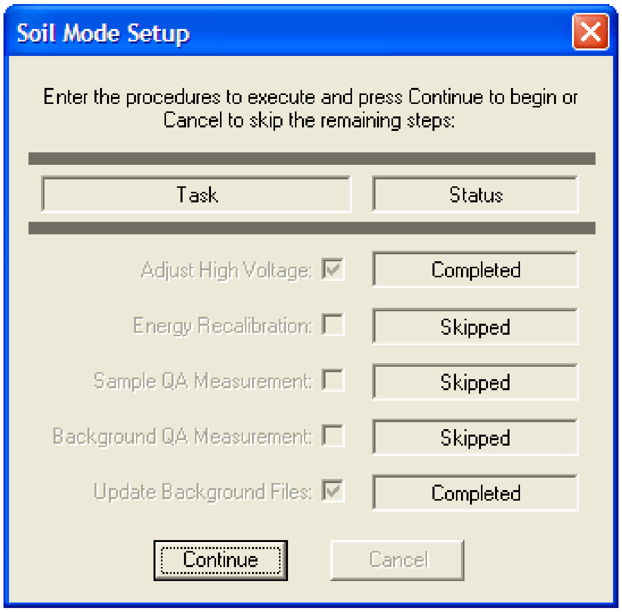
Save Spectrum on Completion: ☑

Figure 23. PBC Wizard.

3.3.6. Ending the Startup Procedure

Click **Continue** to complete the startup procedure. In a multi-detector system, this dialog (Fig. 24) is displayed for each detector in sequence.

After the final setup step is completed, the list is displayed with the Status changed to **Completed** or **Skipped** for all the steps. Click **Done** to end the startup phase.



Soil Mode Setup

Enter the procedures to execute and press Continue to begin or Cancel to skip the remaining steps:

Task	Status
Adjust High Voltage: ☑	Completed
Energy Recalibration: ☐	Skipped
Sample QA Measurement: ☐	Skipped
Background QA Measurement: ☐	Skipped
Update Background Files: ☑	Completed

Figure 24. The Final Startup Dialog.

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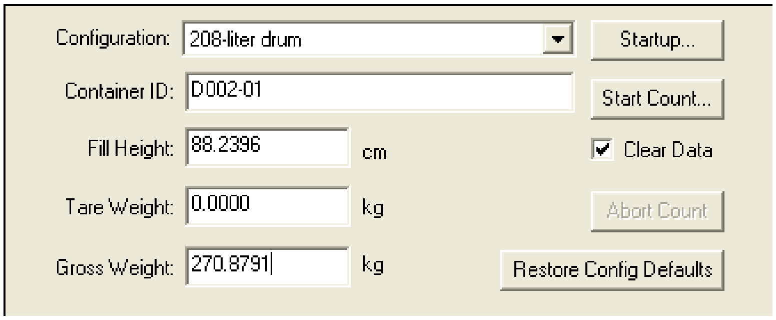
4. USING CONTAINER/SURFACE MODE

This chapter describes how to use the Container/Surface Mode, and presumes you have completed all of the startup activities in Chapter 3.

Figure 25 shows the Scan Control Area for this mode.



Configuration: 208-liter drum

Container ID: D002-01

Fill Height: 88.2396 cm

Tare Weight: 0.0000 kg

Gross Weight: 270.8791 kg

☑ Clear Data

Figure 25. Scan Control Area — Container/Surface Mode.

First, choose a **Configuration** (formerly called a *scan type*) from the droplist. This list contains all the configurations in the current database.

The database will automatically retrieve the **Fill Height**, **Tare Weight**, and **Gross Weight**. To ensure your analysis results are accurate, enter the correct **Fill Height** and **Gross Weight** for each container before counting. To reset these values to the defaults in the configuration, click **Restore Config Defaults**.

To easily distinguish among sample results, be sure to assign a unique **Container ID** to each sample (e.g., *Container 1*, *Container 2*), and to each reanalysis of an existing sample spectrum (e.g., *Container 1*, *Container 1 Reanalysis 1*). All results for the original analysis and any reanalyses are stored in the ISOTOPIC database. In addition, a suite of spectrum, analysis, and report files are created as described in Section 1.6.

IMPORTANT Do not use the characters **/ | \ ? * <** or **>** in your **Container ID** because Windows cannot use them in filenames. As a result, the data will be written only to the database. The corresponding suite of spectrum, analysis, and report files will not be created; instead, an "Error opening file" message will displayed on the Status Bar and the Isotopic fine-tuning plot will not open. In this situation, however, you can generate the spectrum and other files. Use the **File/Recall scan data set** command to retrieve this analysis record from the database, then **Analyze/Configuration in memory...** to generate the files.

If you discover an error after the analysis, correct the values then use **Analyze/Configuration in Memory...** to repeat the analysis.

If the **Clear Data** box is marked, the data memory in the MCB automatically clears when you click **Start Count**.

When the detectors are arranged properly around the container, click **Start Count** to begin data collection.

If the **Ask for Detector Position Adjustments on Start** checkbox is marked for this configuration, the Detector page from the Configuration Wizard opens, for each detector in the system, so the actual detector position(s) can be entered.

Once acquisition starts, the live spectrum for each detector is shown in the spectrum display window. The Status Sidebar on the right of the screen shows the counting values for the selected detector. To select a detector, put the mouse in the window and click.

Spectrum acquisition continues until the preset conditions are met. To stop the count at any time before that, click the **Abort Count** button. This opens the Count Suspended dialog (Fig. 26). Click on **Resume** to continue the count with the data and settings unmodified. Click **Restart** to erase the spectrum and start the counting over. This is used when an error is discovered in the count. The error should be corrected before you click **Restart**. **Abort** terminates the scan.

The Current Acquisition has been Suspended.

Select an Option Below:

Figure 26. Abort or Resume Count.

When data collection ends for each detector, the Sample Description dialog displays the current Container ID for this measurement, allowing you to add additional information as desired. Click **OK**.

IMPORTANT If you cancel the Sample Description dialog or close it by pressing the **<Esc>** key, ***data acquisition will be aborted without further notice!*** Be sure to click **OK**.

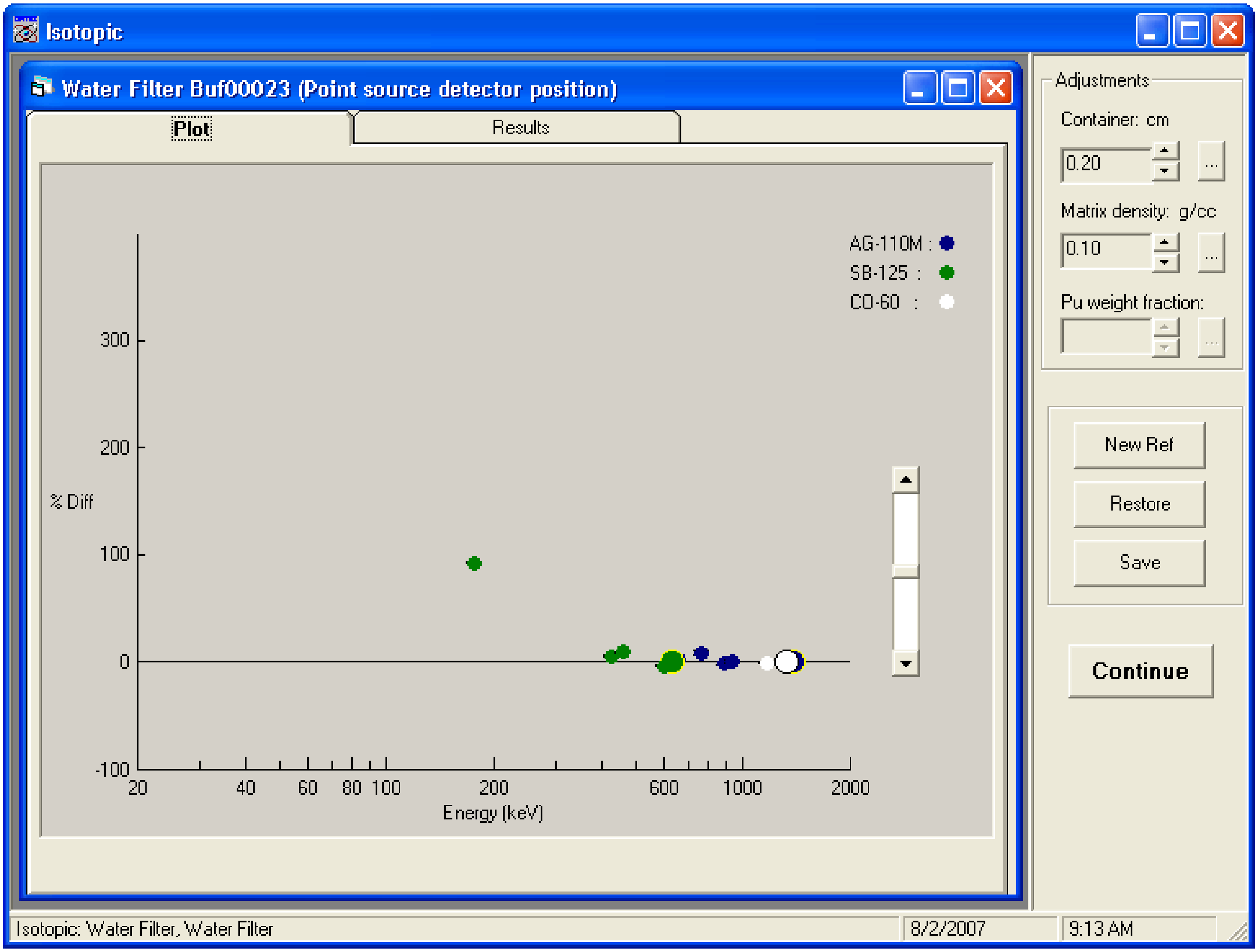
If **Allow Isotope Plot** has been marked under **Services/Operator Permissions...** in the Supervisor program, the Results plot is displayed, as discussed in the following section.

The report generated according to the settings on the Report tab under **Analyze/Configuration Settings...** (see page 116 and Fig. 95). The Container/Surface report is discussed in Section 4.2.

If the **Allow Modification of Configuration Parameters** permission is enabled under **Services/ Operator Permissions...** in the Supervisor program, you can use **Analyze/Configuration Settings...** to change the report settings as needed.

4.1. Results Plot

After the analysis is complete, the results are displayed graphically in the Isotopic window (Fig. 27).



Water Filter Buf00023 (Point source detector position)

Container: cm 0.20

Matrix density: g/cc 0.10

Pu weight fraction:

Isotopic: Water Filter, Water Filter | 8/2/2007 | 9:13 AM

Figure 27. Interactive Analysis Plot Window.

The fine-tuning plot allows you to adjust the attenuation properties of the item being measured to simulate the material with which the gamma ray actually interacts. After correcting for attenuation, detector efficiency, and yield, if the activities computed from several gamma rays emitted by a particular nuclide are the same (% diff is small for all points), you have additional assurance the model is correct.

Both the plot and the numerical results are displayed. The plot shows how well the analysis performed, and displays up to six nuclides as determined by the library order. The analysis can be adjusted to improve the fit, saved to the database, then displayed and/or printed. The results are not displayed or printed until you close the Isotopic window by clicking the upper-right Close box.

One plot screen is shown for each detector in the configuration. In addition to the instructions in the remainder of this section and Chapter 7, the *Getting Started* guide includes an example interactive analysis.

4.1.1. The Plot Window

If the attenuation, geometry and efficiency have been correctly calculated, the activity calculated for each gamma ray from the isotope will yield the same activity. The plot shows the difference between the activity calculated for the reference peak and the activity calculated for the other peaks. In the ideal case, the difference (% diff) is 0 (zero) for all energies. The reference peak has a black or yellow band around the colored center. If the matrix or container assumptions are not correct, then the absorption correction will not be calculated correctly. This is shown in the plot by the % diff being different for all the energies. To correct the calculation, the container thickness and the matrix density are adjusted until the plot of the different energy points are as close to 0 in the % diff plot as possible.

4.1.1.1. Adjustments

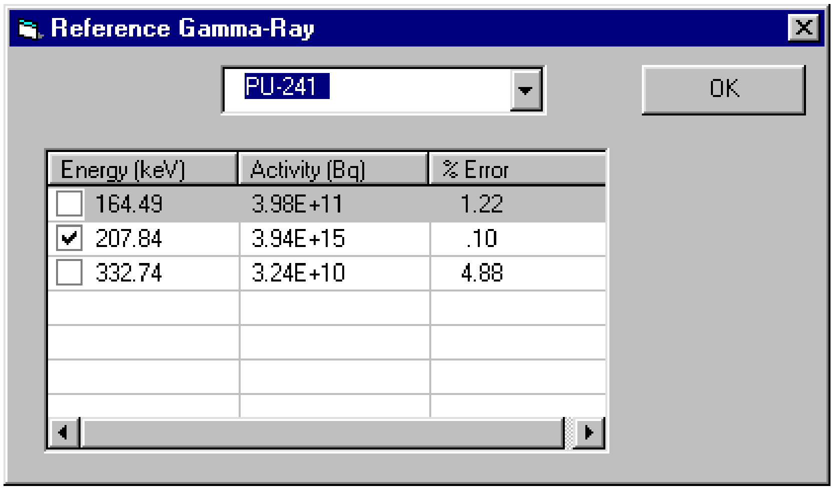
After viewing the plot for each detector, first adjust the **Matrix density** either by clicking the up/down buttons or clicking the (**...**) button and entering a value. This will change the points displayed as the point-by-point activity calculation is redone for the new setting. The different nuclides will be affected differently because they are likely to be distributed differently in the container and thus attenuated differently by the matrix. After the best alignment is obtained, adjust the **Container** thickness to improve the % diff. Readjust the matrix once more to make the fit better.

If the sample contains a significant amount of uranium or plutonium, then the self-attenuation will affect the results. Based on the peaks in the spectrum, ISOTOPIC automatically determines whether the **weight fraction** control should be for uranium or plutonium. Use it to adjust the amount of uranium or plutonium in the sample. The fine-tuning plot automatically updates the fit as it changes the self-attenuation.

4.1.1.2. New Ref

Clicking the **New Ref** button (Fig. 28) displays the current reference peak for the nuclides and allows you to change it. The reference peak should be high-yield (both branching ratio and efficiency) and not close to other peaks.

Select the isotope from the droplist to show its list of gamma rays. The currently selected peak has a checkmark beside it. To change to another peak, click the box next to the new peak.



Energy (keV)	Activity (Bq)	% Error
☐ 164.49	3.98E+11	1.22
☑ 207.84	3.94E+15	.10
☐ 332.74	3.24E+10	4.88

Figure 28. View or Change Reference Peak.

Note the **% Error** column. This shows the peak error, and is supplied to help you select the proper reference peak.

When a new reference peak is selected, the plot graph is automatically updated with the new results.

4.1.1.3. Restore

Click on **Restore** to change all the values to the conditions when the plot was first displayed.

4.1.1.4. Save

After the adjustments have been made and the plot is satisfactory, you are ready to **Save** the adjustments, then view the numerical results on the Results tab.

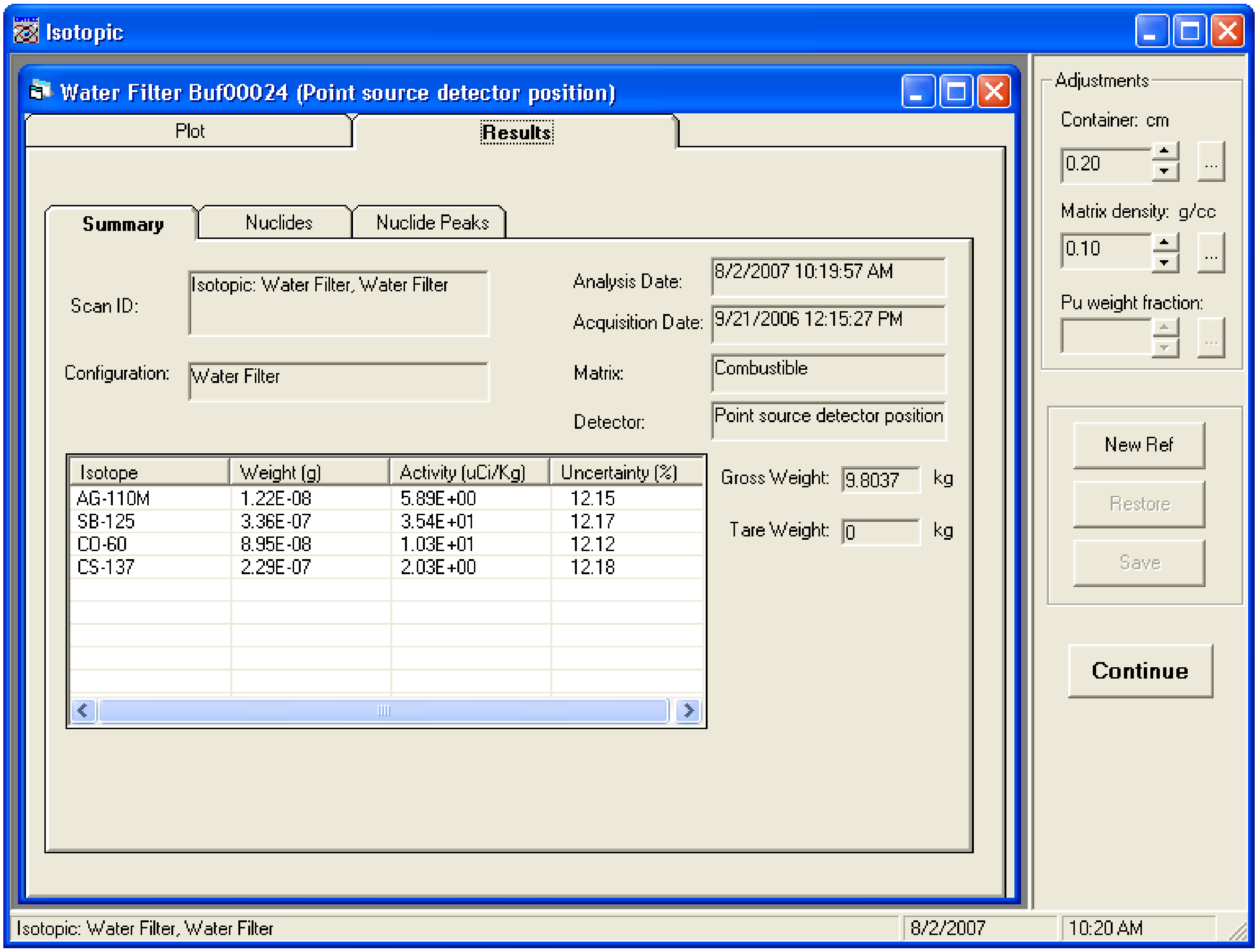
IMPORTANT	If you have made adjustments, be sure to click **Save** (which will overwrite the original settings) so that the report reflects these new settings. There will be a momentary delay as the adjustments are stored in the ISOTOPIC database and a new suite of spectrum, analysis, and report files are created. You can use the **File/Recall Reports...** command to view both the original and adjusted reports as Crystal Reports (see Chapter 6) or access the `.HTML` reports with Windows Explorer.

4.1.2. The Results Window

Values on these tabs can only be modified with the **Adjustments** or by changing the reference gamma ray. When finished viewing the results and fine-tuning windows, click **Continue** to return to the main Operator interface.

4.1.2.1. Summary Tab

The Summary tab (Fig. 29) displays the sample information and the results of the container analysis for this detector spectrum only. Both the grams and specific activity are listed.



Scan ID: Isotopic: Water Filter, Water Filter

Configuration: Water Filter

Analysis Date: 8/2/2007 10:19:57 AM

Acquisition Date: 9/21/2006 12:15:27 PM

Matrix: Combustible

Detector: Point source detector position

Isotope	Weight (g)	Activity (uCi/Kg)	Uncertainty (%)
AG-110M	1.22E-08	5.89E+00	12.15
SB-125	3.36E-07	3.54E+01	12.17
CO-60	8.95E-08	1.03E+01	12.12
CS-137	2.29E-07	2.03E+00	12.18

Gross Weight: 9.8037 kg

Tare Weight: 0 kg

Container: cm 0.20

Matrix density: g/cc 0.10

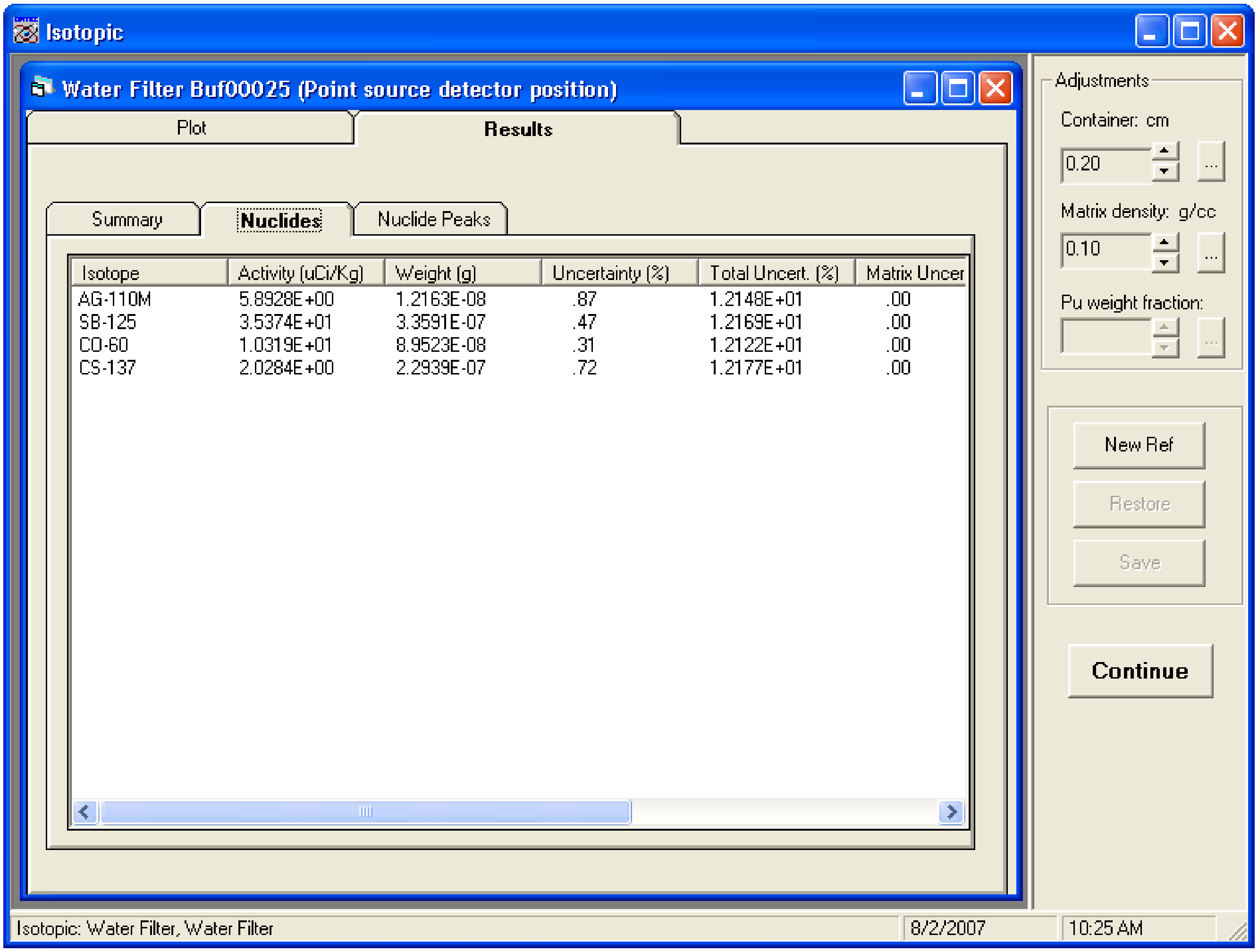
Pu weight fraction:

Isotopic: Water Filter, Water Filter 8/2/2007 10:20 AM

Figure 29. The Results Summary Dialog for this Spectrum.

4.1.2.2. Nuclides Tab

The Nuclides tab (Fig. 30) shows several values based on the inputs and analysis options. They are: **Isotope**, **Activity**, **Weight**, **Error** (in the weight), **Total Error** (in the Activity), **Matrix Error** (contribution to the activity error due to the uncertainty in the matrix absorption), **Geo Error** (contribution to the activity error due to the uncertainty in the geometry correction), **Nuclide Norm** (normalization factor for the individual isotope), **Geo Norm** (normalization factor for the specific geometry), **Total Norm** (total normalization factor).



Isotope	Activity (uCi/Kg)	Weight (g)	Uncertainty (%)	Total Uncert. (%)	Matrix Uncer
AG-110M	5.8928E+00	1.2163E-08	.87	1.2148E+01	.00
SB-125	3.5374E+01	3.3591E-07	.47	1.2169E+01	.00
CO-60	1.0319E+01	8.9523E-08	.31	1.2122E+01	.00
CS-137	2.0284E+00	2.2939E-07	.72	1.2177E+01	.00

Container: cm 0.20

Matrix density: g/cc 0.10

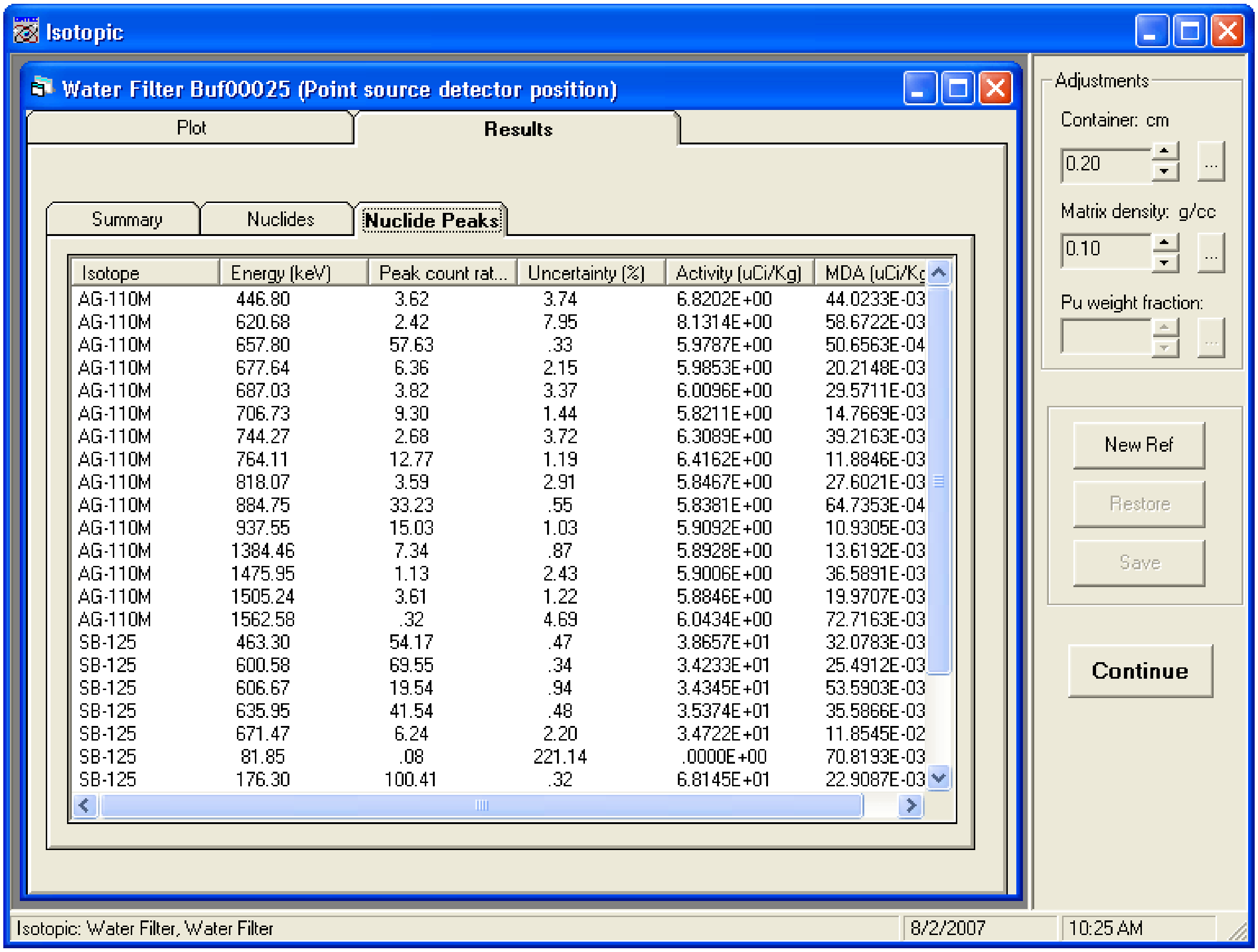
Pu weight fraction:

Isotopic: Water Filter, Water Filter 8/2/2007 10:25 AM

Figure 30. The Nuclides Tab.

4.1.2.3. Nuclide Peaks Tab

The **Nuclide Peaks** tab is shown in Fig. 31.



Container: cm 0.20

Matrix density: g/cc 0.10

Pu weight fraction:

Isotope	Energy (keV)	Peak count rat...	Uncertainty (%)	Activity (uCi/Kg)	MDA (uCi/Kg
AG-110M	446.80	3.62	3.74	6.8202E+00	44.0233E-03
AG-110M	620.68	2.42	7.95	8.1314E+00	58.6722E-03
AG-110M	657.80	57.63	.33	5.9787E+00	50.6563E-04
AG-110M	677.64	6.36	2.15	5.9853E+00	20.2148E-03
AG-110M	687.03	3.82	3.37	6.0096E+00	29.5711E-03
AG-110M	706.73	9.30	1.44	5.8211E+00	14.7669E-03
AG-110M	744.27	2.68	3.72	6.3089E+00	39.2163E-03
AG-110M	764.11	12.77	1.19	6.4162E+00	11.8846E-03
AG-110M	818.07	3.59	2.91	5.8467E+00	27.6021E-03
AG-110M	884.75	33.23	.55	5.8381E+00	64.7353E-04
AG-110M	937.55	15.03	1.03	5.9092E+00	10.9305E-03
AG-110M	1384.46	7.34	.87	5.8928E+00	13.6192E-03
AG-110M	1475.95	1.13	2.43	5.9006E+00	36.5891E-03
AG-110M	1505.24	3.61	1.22	5.8846E+00	19.9707E-03
AG-110M	1562.58	.32	4.69	6.0434E+00	72.7163E-03
SB-125	463.30	54.17	.47	3.8657E+01	32.0783E-03
SB-125	600.58	69.55	.34	3.4233E+01	25.4912E-03
SB-125	606.67	19.54	.94	3.4345E+01	53.5903E-03
SB-125	635.95	41.54	.48	3.5374E+01	35.5866E-03
SB-125	671.47	6.24	2.20	3.4722E+01	11.8545E-02
SB-125	81.85	.08	221.14	.0000E+00	70.8193E-03
SB-125	176.30	100.41	.32	6.8145E+01	22.9087E-03

Isotopic: Water Filter, Water Filter 8/2/2007 10:25 AM

Figure 31. The Nuclide Peaks Tab.

This lists all the peaks in the library with their energy, net peak count rate in this spectrum, the uncertainty in the net peak area, the activity of the isotope based on this peak only, and the MDA based on this peak only. The list can be ordered in several different ways by clicking the column headers. For example, to list all the peaks for one isotope in sequence (as shown), click the **Isotope** header. To arrange all the peaks by energy, click the **Energy** header.

4.2. Container/Surface Mode Report

The Container/Surface Mode report has been redesigned for ISOTOPIC v4. The new report is in HTML file format (the format used for web pages) and can be viewed in any web browser or other program that supports HTML. This report is in color so it is easier to read. It provides more information, automatically reformats onscreen as you resize the browser window, and displays bitmap images of the corresponding spectrum and fine-tuning plot. Be sure to see the note in Section 1.6 concerning archival of all ISOTOPIC database and associated files.

For multi-detector configurations, ISOTOPIC Operator generates one report for each detector and an averaged report of all the individual results. The filenaming conventions for these files are in Section 1.6. The reports are saved in the **Spectrum** directory specified on the Directories tab under **File/Settings...** in Supervisor. The individual detector report is shown in Figs. 32 through 38. The average report is discussed in Section 4.3.

The report for individual detectors is arranged in five general sections as follows.

4.2.1. Section 1 — Acquisition and Analysis Settings

The first page of the report, shown in Fig. 32, lists the acquisition and analysis parameters. The sample name (report title) reflects the **Container ID** for this acquisition, plus any additional text entered in the Sample Description dialog at the end of the acquisition.

Spectrum Filename

Self-explanatory.

Data Acquisition Parameters

These include the date and time data acquisition started, the live time and real time values, and MCB ID as stored in the spectrum file.

Calibration Information

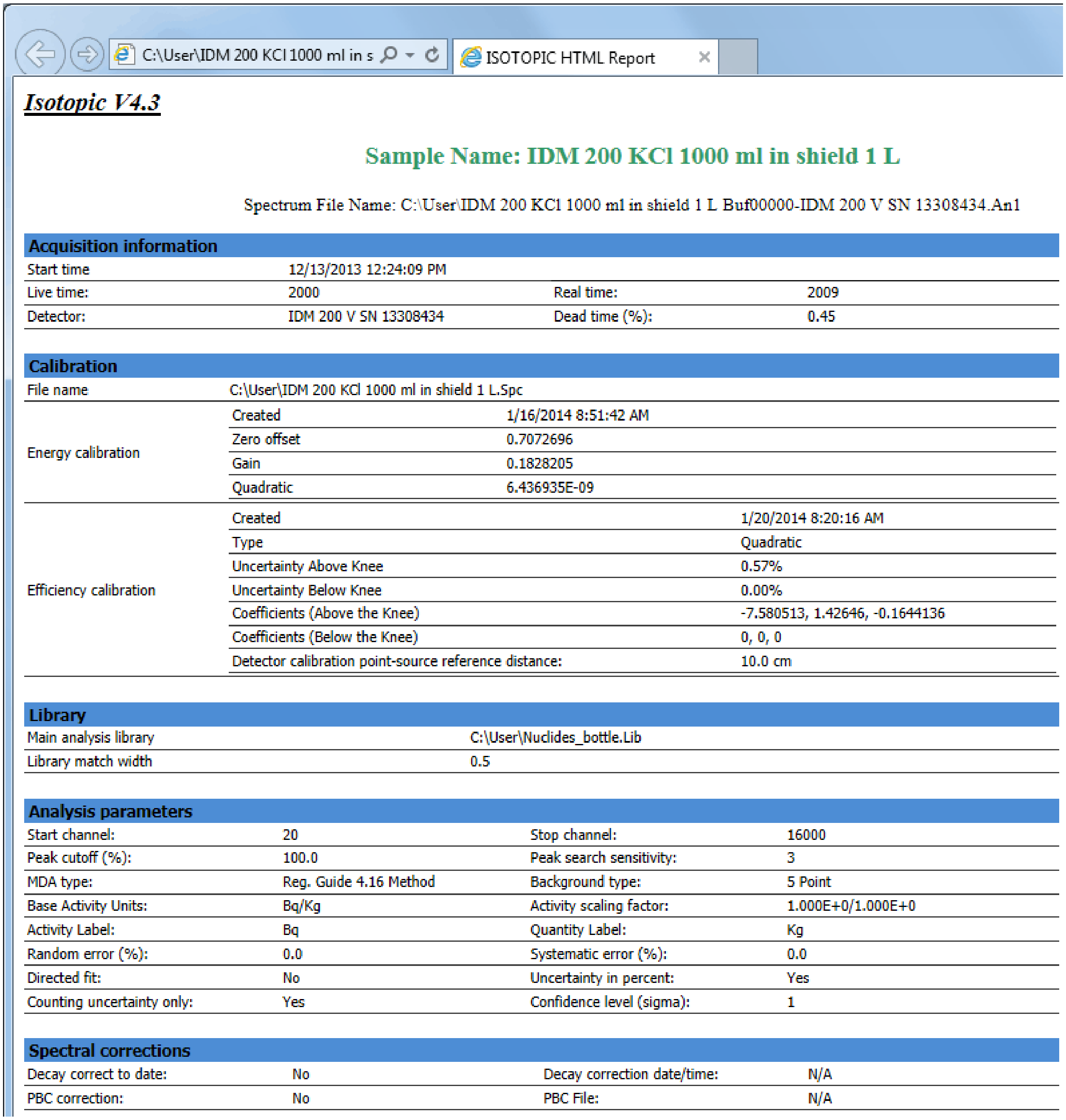
Includes the calibration filename, and information about each of the calibrations (energy, efficiency) performed. The filename and description are from the spectrum file if it is an `.SPC` file. Each set of calibration data shows the date the calibration calculation was performed (not the collection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

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,



Isotopic V4.3

Sample Name: IDM 200 KCl 1000 ml in shield 1 L

Spectrum File Name: C:\User\IDM 200 KCl 1000 ml in shield 1 L Buf00000-IDM 200 V SN 13308434.An1

Acquisition information

Start time	12/13/2013 12:24:09 PM		
Live time:	2000	Real time:	2009
Detector:	IDM 200 V SN 13308434	Dead time (%):	0.45

Calibration

File name	C:\User\IDM 200 KCl 1000 ml in shield 1 L.Spc	
Energy calibration	Created	1/16/2014 8:51:42 AM
	Zero offset	0.7072696
	Gain	0.1828205
	Quadratic	6.436935E-09
Efficiency calibration	Created	1/20/2014 8:20:16 AM
	Type	Quadratic
	Uncertainty Above Knee	0.57%
	Uncertainty Below Knee	0.00%
	Coefficients (Above the Knee)	-7.580513, 1.42646, -0.1644136
	Coefficients (Below the Knee)	0, 0, 0
	Detector calibration point-source reference distance:	10.0 cm

Library

Main analysis library	C:\User\Nuclides_bottle.Lib
Library match width	0.5

Analysis parameters

Start channel:	20	Stop channel:	16000
Peak cutoff (%):	100.0	Peak search sensitivity:	3
MDA type:	Reg. Guide 4.16 Method	Background type:	5 Point
Base Activity Units:	Bq/Kg	Activity scaling factor:	1.000E+0/1.000E+0
Activity Label:	Bq	Quantity Label:	Kg
Random error (%):	0.0	Systematic error (%):	0.0
Directed fit:	No	Uncertainty in percent:	Yes
Counting uncertainty only:	Yes	Confidence level (sigma):	1

Spectral corrections

Decay correct to date:	No	Decay correction date/time:	N/A
PBC correction:	No	PBC File:	N/A

Figure 32. Container Report — Part 1.

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.

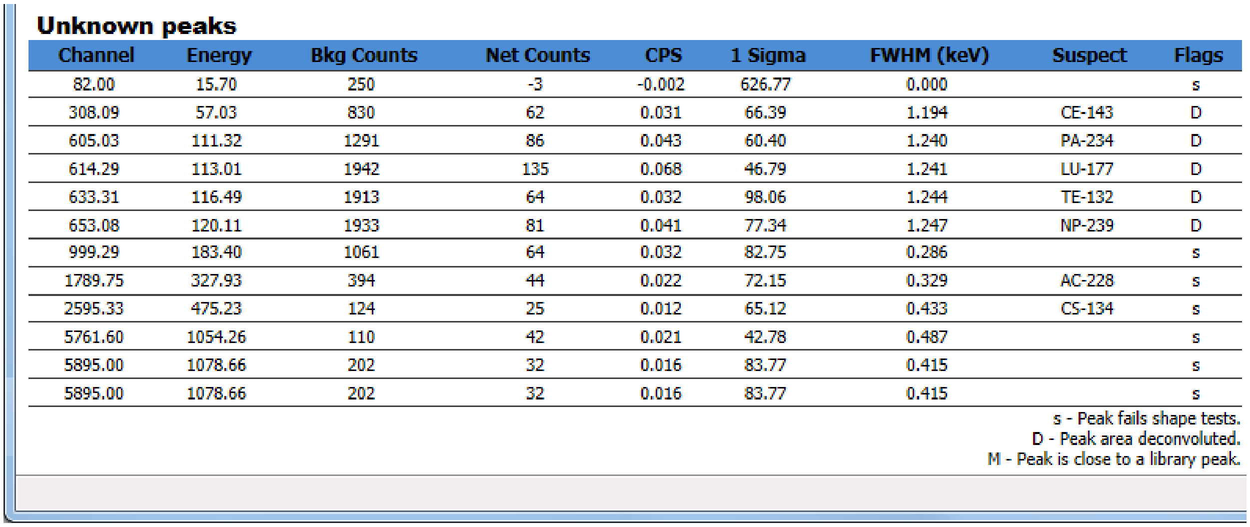
The normalization factor is the factor for changing the output activities to the requested units from the internal units of becquerels. It is the quotient of the input multiplier and input divisor. A value of 1.0 leaves the activities in becquerels.

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 may be small due to the ratio of the half-life to the real time, so the effect may not be seen in the output activity.

4.2.2. Section 2 — Unknown Peaks Table

Figure 33 shows Unknown Peaks table, showing the peak/energy matrix of unidentified peaks. This section can be suppressed.



Unknown peaks

Channel	Energy	Bkg Counts	Net Counts	CPS	1 Sigma	FWHM (keV)	Suspect	Flags
82.00	15.70	250	-3	-0.002	626.77	0.000		s
308.09	57.03	830	62	0.031	66.39	1.194	CE-143	D
605.03	111.32	1291	86	0.043	60.40	1.240	PA-234	D
614.29	113.01	1942	135	0.068	46.79	1.241	LU-177	D
633.31	116.49	1913	64	0.032	98.06	1.244	TE-132	D
653.08	120.11	1933	81	0.041	77.34	1.247	NP-239	D
999.29	183.40	1061	64	0.032	82.75	0.286		s
1789.75	327.93	394	44	0.022	72.15	0.329	AC-228	s
2595.33	475.23	124	25	0.012	65.12	0.433	CS-134	s
5761.60	1054.26	110	42	0.021	42.78	0.487		s
5895.00	1078.66	202	32	0.016	83.77	0.415		s
5895.00	1078.66	202	32	0.016	83.77	0.415		s

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

Figure 33. Container Report — Part 2.

The first column is the peak channel as determined by the peak-search routine. 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. 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 may 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.

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 the Unidentified Peak and Library Table Format flag in the `B30winds.ini`; this is discussed in the *Supervisor Manual*.

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.

The last column shows a symbol if the peak is too wide or too narrow as compared to the shape calibration; for good peaks the column is blank. This 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.

4.2.3. Section 3 — Library Peaks Table and Library Peak Matrix

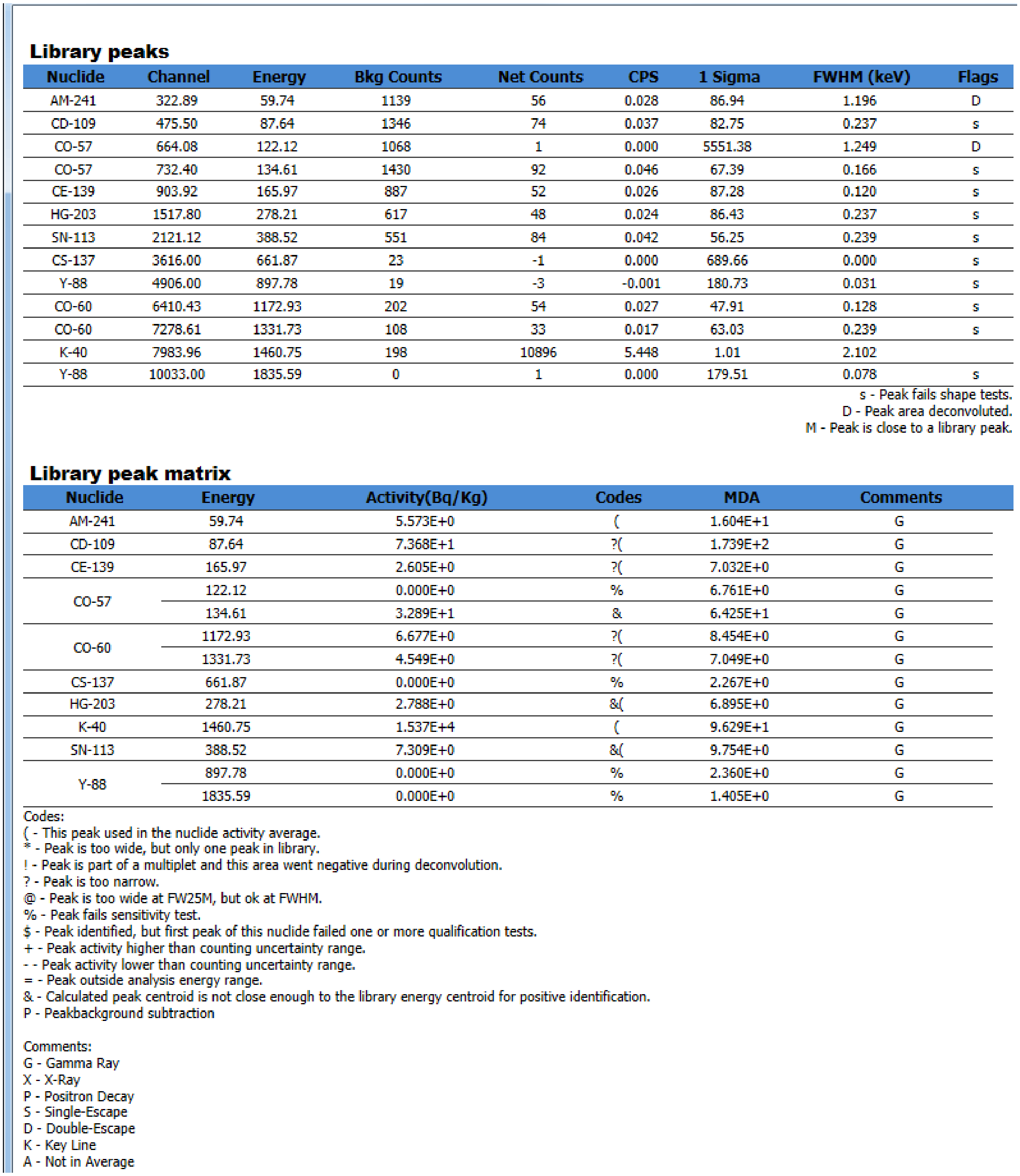
Figure 34 shows the Library Peaks table (the peak/energy matrix for the library peaks) and the Library Peak Matrix.

4.2.3.1. Library Peaks Table

The library name is printed at the beginning of the list. They are arranged in ascending energy order.

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

The second column is the peak channel as determined by the peak-search algorithm described in the analysis methods chapter in the *Supervisor Manual*. 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.



Library peaks

Nuclide	Channel	Energy	Bkg Counts	Net Counts	CPS	1 Sigma	FWHM (keV)	Flags
AM-241	322.89	59.74	1139	56	0.028	86.94	1.196	D
CD-109	475.50	87.64	1346	74	0.037	82.75	0.237	s
CO-57	664.08	122.12	1068	1	0.000	5551.38	1.249	D
CO-57	732.40	134.61	1430	92	0.046	67.39	0.166	s
CE-139	903.92	165.97	887	52	0.026	87.28	0.120	s
HG-203	1517.80	278.21	617	48	0.024	86.43	0.237	s
SN-113	2121.12	388.52	551	84	0.042	56.25	0.239	s
CS-137	3616.00	661.87	23	-1	0.000	689.66	0.000	s
Y-88	4906.00	897.78	19	-3	-0.001	180.73	0.031	s
CO-60	6410.43	1172.93	202	54	0.027	47.91	0.128	s
CO-60	7278.61	1331.73	108	33	0.017	63.03	0.239	s
K-40	7983.96	1460.75	198	10896	5.448	1.01	2.102	
Y-88	10033.00	1835.59	0	1	0.000	179.51	0.078	s

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

Library peak matrix

Nuclide	Energy	Activity(Bq/Kg)	Codes	MDA	Comments
AM-241	59.74	5.573E+0	(	1.604E+1	G
CD-109	87.64	7.368E+1	?(	1.739E+2	G
CE-139	165.97	2.605E+0	?(	7.032E+0	G
CO-57	122.12	0.000E+0	%	6.761E+0	G
	134.61	3.289E+1	&	6.425E+1	G
CO-60	1172.93	6.677E+0	?(	8.454E+0	G
	1331.73	4.549E+0	?(	7.049E+0	G
CS-137	661.87	0.000E+0	%	2.267E+0	G
HG-203	278.21	2.788E+0	&(	6.895E+0	G
K-40	1460.75	1.537E+4	(	9.629E+1	G
SN-113	388.52	7.309E+0	&(	9.754E+0	G
Y-88	897.78	0.000E+0	%	2.360E+0	G
	1835.59	0.000E+0	%	1.405E+0	G

Codes:
(- This peak used in the nuclide activity average.
* - Peak is too wide, but only one peak in library.
! - Peak is part of a multiplet and this area went negative during deconvolution.
? - Peak is too narrow.
@ - Peak is too wide at FW25M, but ok at FWHM.
% - Peak fails sensitivity test.
$ - Peak identified, but first peak of this nuclide failed one or more qualification tests.
\+ - Peak activity higher than counting uncertainty range.
\- - Peak activity lower than counting uncertainty range.
= - Peak outside analysis energy range.
& - Calculated peak centroid is not close enough to the library energy centroid for positive identification.
P - Peakbackground subtraction

Comments:
G - Gamma Ray
X - X-Ray
P - Positron Decay
S - Single-Escape
D - Double-Escape
K - Key Line
A - Not in Average

Figure 34. Container Report — Part 3.

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 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 may 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.

4.2.3.2. Library Peak Matrix

This is the isotope/peak summary of library peak usage.

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. This value is not decay-corrected.

The next column may 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.

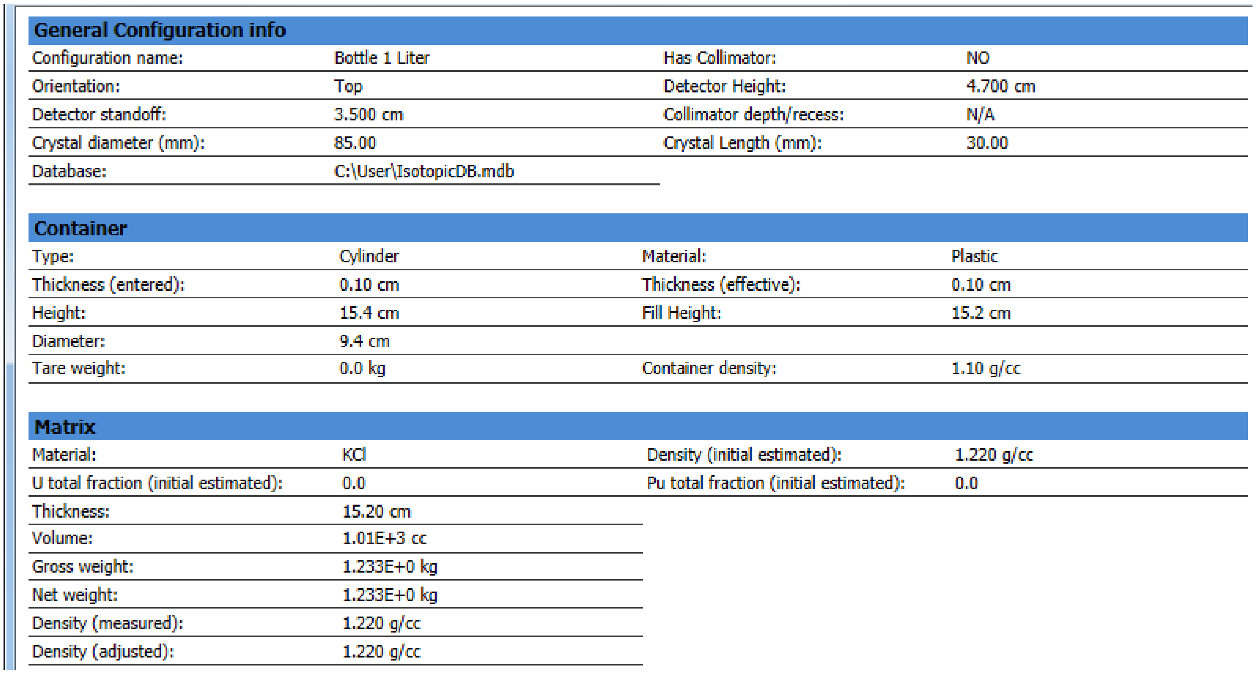
The symbols have the following meanings:

*****	The peak FW10M and FW25M were wider than the calibrated shape by more than 20% which would indicate that this may 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 may 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 may contain a symbol, **(** , that indicates which peaks were used in the average activity calculation for this nuclide. There may 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.

4.2.4. Section 4 — Configuration Settings

This section of the report (Fig. 35) shows the acquisition/analysis settings used for this measurement, including the configuration name, detector orientation and position, detector crystal size, container and matrix characteristics, and information about the collimator, if present.



General Configuration info

Configuration name:	Bottle 1 Liter	Has Collimator:	NO
Orientation:	Top	Detector Height:	4.700 cm
Detector standoff:	3.500 cm	Collimator depth/recess:	N/A
Crystal diameter (mm):	85.00	Crystal Length (mm):	30.00
Database:	C:\User\IsotopicDB.mdb		

Container

Type:	Cylinder	Material:	Plastic
Thickness (entered):	0.10 cm	Thickness (effective):	0.10 cm
Height:	15.4 cm	Fill Height:	15.2 cm
Diameter:	9.4 cm		
Tare weight:	0.0 kg	Container density:	1.10 g/cc

Matrix

Material:	KCl	Density (initial estimated):	1.220 g/cc
U total fraction (initial estimated):	0.0	Pu total fraction (initial estimated):	0.0
Thickness:	15.20 cm		
Volume:	1.01E+3 cc		
Gross weight:	1.233E+0 kg		
Net weight:	1.233E+0 kg		
Density (measured):	1.220 g/cc		
Density (adjusted):	1.220 g/cc		

Figure 35. Container Report — Part 4.

4.2.5. Section 5 — Analysis Results Tables

Figures 36 and 37 show the analysis results tables.

4.2.5.1. Isotopic Results

This table lists the grams of uranium or other material, the specific activity, and the uncertainty. If decay correction is enabled, the activity is decay-corrected.

4.2.5.2. MDA for Measured Geometry

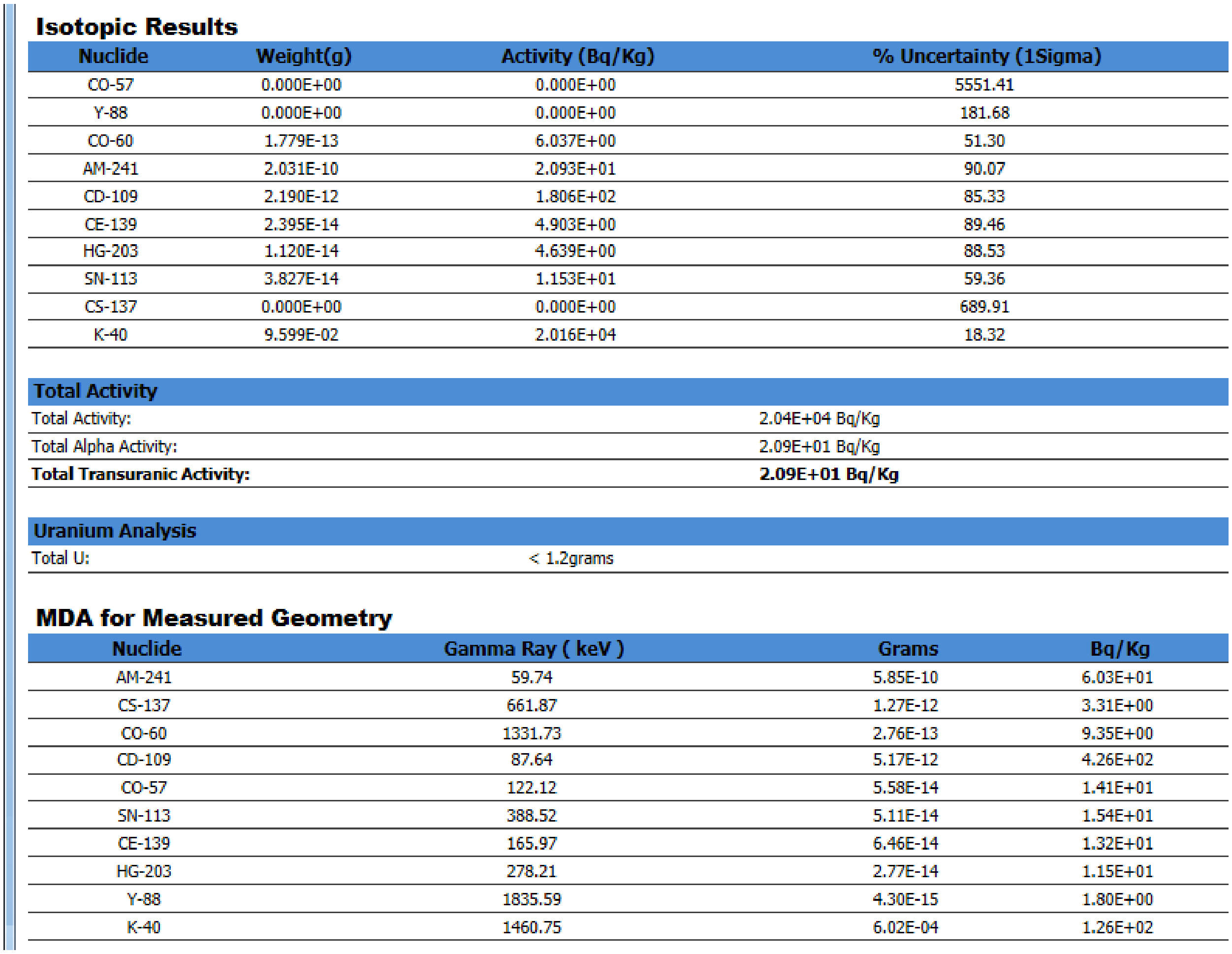
These values represent the MDA for each nuclide using the reference gamma ray and the selected MDA method.

4.2.5.3. Peak Correction Factors

These are the modeling correction factors used to convert peak activity to reportable item activity. The item correction factors include corrections for geometry and matrix attenuation; inner and outer container corrections; and collimator correction.

4.2.5.4. Peak Info. Sorted by Nuclide

This shows the gamma-ray peaks sorted by isotope. The first column shows the nuclide name. The second column shows the energy of the peak. The third column shows the difference between the spectrum peak energy and the gamma-ray energy in the library. The next column, **Activity**, shows the corrected peak area (in counts) of this peak. The last column indicates whether this peak had an interfering peak in the spectrum. In this example, there are no interfering peaks. The reference gamma ray is marked with a # in the list of peaks.



Isotopic Results

Nuclide	Weight(g)	Activity (Bq/Kg)	% Uncertainty (1Sigma)
CO-57	0.000E+00	0.000E+00	5551.41
Y-88	0.000E+00	0.000E+00	181.68
CO-60	1.779E-13	6.037E+00	51.30
AM-241	2.031E-10	2.093E+01	90.07
CD-109	2.190E-12	1.806E+02	85.33
CE-139	2.395E-14	4.903E+00	89.46
HG-203	1.120E-14	4.639E+00	88.53
SN-113	3.827E-14	1.153E+01	59.36
CS-137	0.000E+00	0.000E+00	689.91
K-40	9.599E-02	2.016E+04	18.32

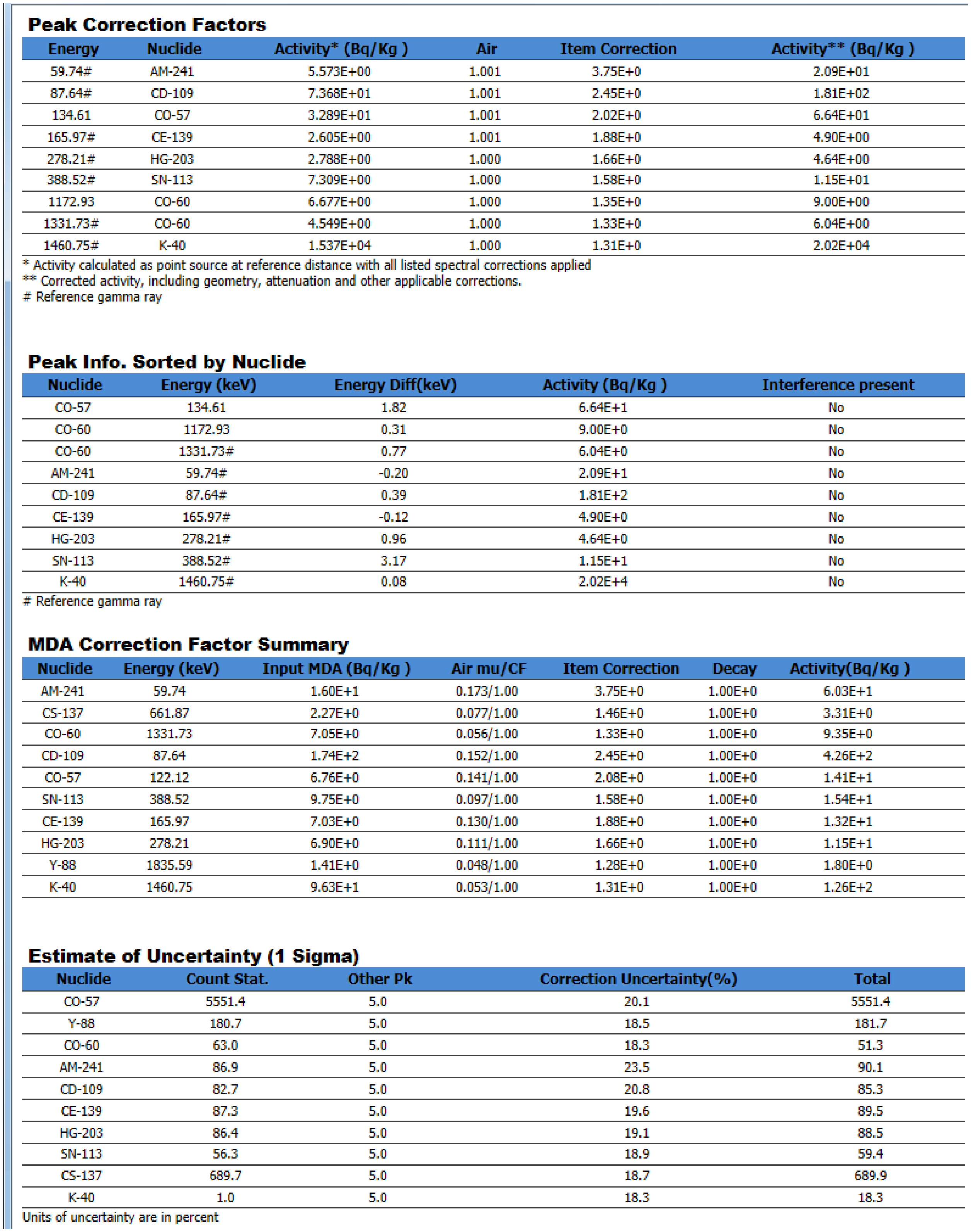
Total Activity	
Total Activity:	2.04E+04 Bq/Kg
Total Alpha Activity:	2.09E+01 Bq/Kg
Total Transuranic Activity:	**2.09E+01 Bq/Kg**

Uranium Analysis	
Total U:	< 1.2grams

MDA for Measured Geometry

Nuclide	Gamma Ray (keV)	Grams	Bq/Kg
AM-241	59.74	5.85E-10	6.03E+01
CS-137	661.87	1.27E-12	3.31E+00
CO-60	1331.73	2.76E-13	9.35E+00
CD-109	87.64	5.17E-12	4.26E+02
CO-57	122.12	5.58E-14	1.41E+01
SN-113	388.52	5.11E-14	1.54E+01
CE-139	165.97	6.46E-14	1.32E+01
HG-203	278.21	2.77E-14	1.15E+01
Y-88	1835.59	4.30E-15	1.80E+00
K-40	1460.75	6.02E-04	1.26E+02

Figure 36. Container Report — Part 5, ISOTOPIC Results and MDA Tables.



Peak Correction Factors

Energy	Nuclide	Activity* (Bq/Kg)	Air	Item Correction	Activity** (Bq/Kg)
59.74#	AM-241	5.573E+00	1.001	3.75E+0	2.09E+01
87.64#	CD-109	7.368E+01	1.001	2.45E+0	1.81E+02
134.61	CO-57	3.289E+01	1.001	2.02E+0	6.64E+01
165.97#	CE-139	2.605E+00	1.001	1.88E+0	4.90E+00
278.21#	HG-203	2.788E+00	1.000	1.66E+0	4.64E+00
388.52#	SN-113	7.309E+00	1.000	1.58E+0	1.15E+01
1172.93	CO-60	6.677E+00	1.000	1.35E+0	9.00E+00
1331.73#	CO-60	4.549E+00	1.000	1.33E+0	6.04E+00
1460.75#	K-40	1.537E+04	1.000	1.31E+0	2.02E+04

* Activity calculated as point source at reference distance with all listed spectral corrections applied
** Corrected activity, including geometry, attenuation and other applicable corrections.
# Reference gamma ray

Peak Info. Sorted by Nuclide

Nuclide	Energy (keV)	Energy Diff(keV)	Activity (Bq/Kg)	Interference present
CO-57	134.61	1.82	6.64E+1	No
CO-60	1172.93	0.31	9.00E+0	No
CO-60	1331.73#	0.77	6.04E+0	No
AM-241	59.74#	-0.20	2.09E+1	No
CD-109	87.64#	0.39	1.81E+2	No
CE-139	165.97#	-0.12	4.90E+0	No
HG-203	278.21#	0.96	4.64E+0	No
SN-113	388.52#	3.17	1.15E+1	No
K-40	1460.75#	0.08	2.02E+4	No

Reference gamma ray

MDA Correction Factor Summary

Nuclide	Energy (keV)	Input MDA (Bq/Kg)	Air mu/CF	Item Correction	Decay	Activity(Bq/Kg)
AM-241	59.74	1.60E+1	0.173/1.00	3.75E+0	1.00E+0	6.03E+1
CS-137	661.87	2.27E+0	0.077/1.00	1.46E+0	1.00E+0	3.31E+0
CO-60	1331.73	7.05E+0	0.056/1.00	1.33E+0	1.00E+0	9.35E+0
CD-109	87.64	1.74E+2	0.152/1.00	2.45E+0	1.00E+0	4.26E+2
CO-57	122.12	6.76E+0	0.141/1.00	2.08E+0	1.00E+0	1.41E+1
SN-113	388.52	9.75E+0	0.097/1.00	1.58E+0	1.00E+0	1.54E+1
CE-139	165.97	7.03E+0	0.130/1.00	1.88E+0	1.00E+0	1.32E+1
HG-203	278.21	6.90E+0	0.111/1.00	1.66E+0	1.00E+0	1.15E+1
Y-88	1835.59	1.41E+0	0.048/1.00	1.28E+0	1.00E+0	1.80E+0
K-40	1460.75	9.63E+1	0.053/1.00	1.31E+0	1.00E+0	1.26E+2

Estimate of Uncertainty (1 Sigma)

Nuclide	Count Stat.	Other Pk	Correction Uncertainty(%)	Total
CO-57	5551.4	5.0	20.1	5551.4
Y-88	180.7	5.0	18.5	181.7
CO-60	63.0	5.0	18.3	51.3
AM-241	86.9	5.0	23.5	90.1
CD-109	82.7	5.0	20.8	85.3
CE-139	87.3	5.0	19.6	89.5
HG-203	86.4	5.0	19.1	88.5
SN-113	56.3	5.0	18.9	59.4
CS-137	689.7	5.0	18.7	689.9
K-40	1.0	5.0	18.3	18.3

Units of uncertainty are in percent

Figure 37. Container Report — Part 5, Peak Correction Factors, Peak Info, MDA Correction Factor, and Estimated Uncertainty Tables.

4.2.5.5. MDA Correction Factor Summary

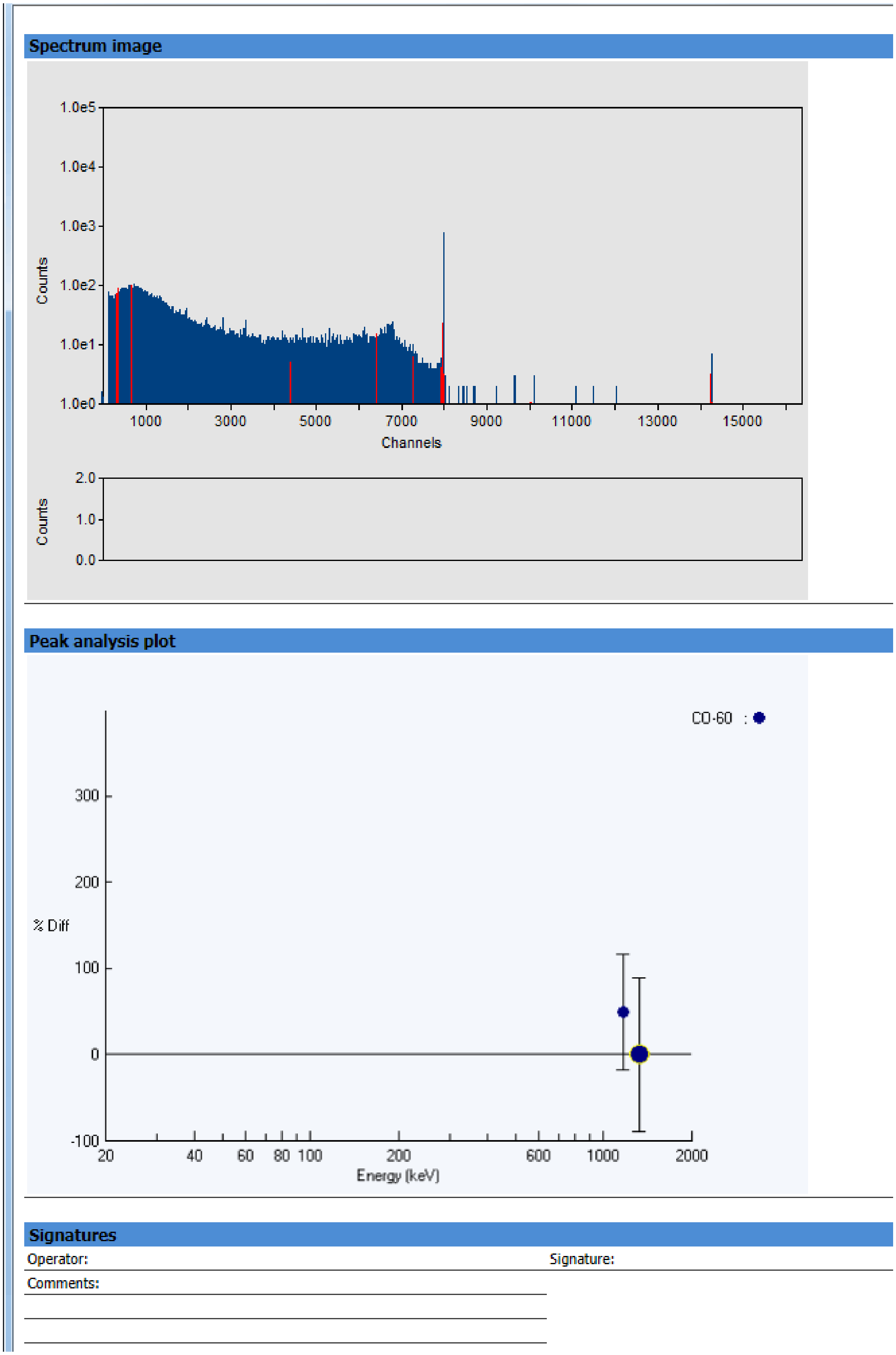
The energies in the library are listed in ascending energy in column 2. The nuclide name for each energy is given in column 1. The uncorrected MDA (**Input MDA**), as calculated from the spectrum is given in the next column. The next columns show the absorption coefficient (mu) and the correction factor (CF) for the different materials. The corrected MDA is shown in the next column and the last column lists the specific activity.

4.2.5.6. Estimate of Uncertainty (1 Sigma)

This shows the uncertainty estimate for each of the isotopes in the library and in the Isotopic Results table. The counting uncertainty (**Count Stat.**) is shown in column 2. The other uncertainties are given in the remaining columns. The total uncertainty is the square root of the sum of the squares of the individual uncertainties and is given in the last column.

4.2.6. Section 6 — Spectrum and Isotopic Analysis Plot

The last section of the report (Fig. 38) shows the spectrum image(s) and isotopic analysis plot(s), and the signature block.



Spectrum image

Peak analysis plot

Signatures

Operator:

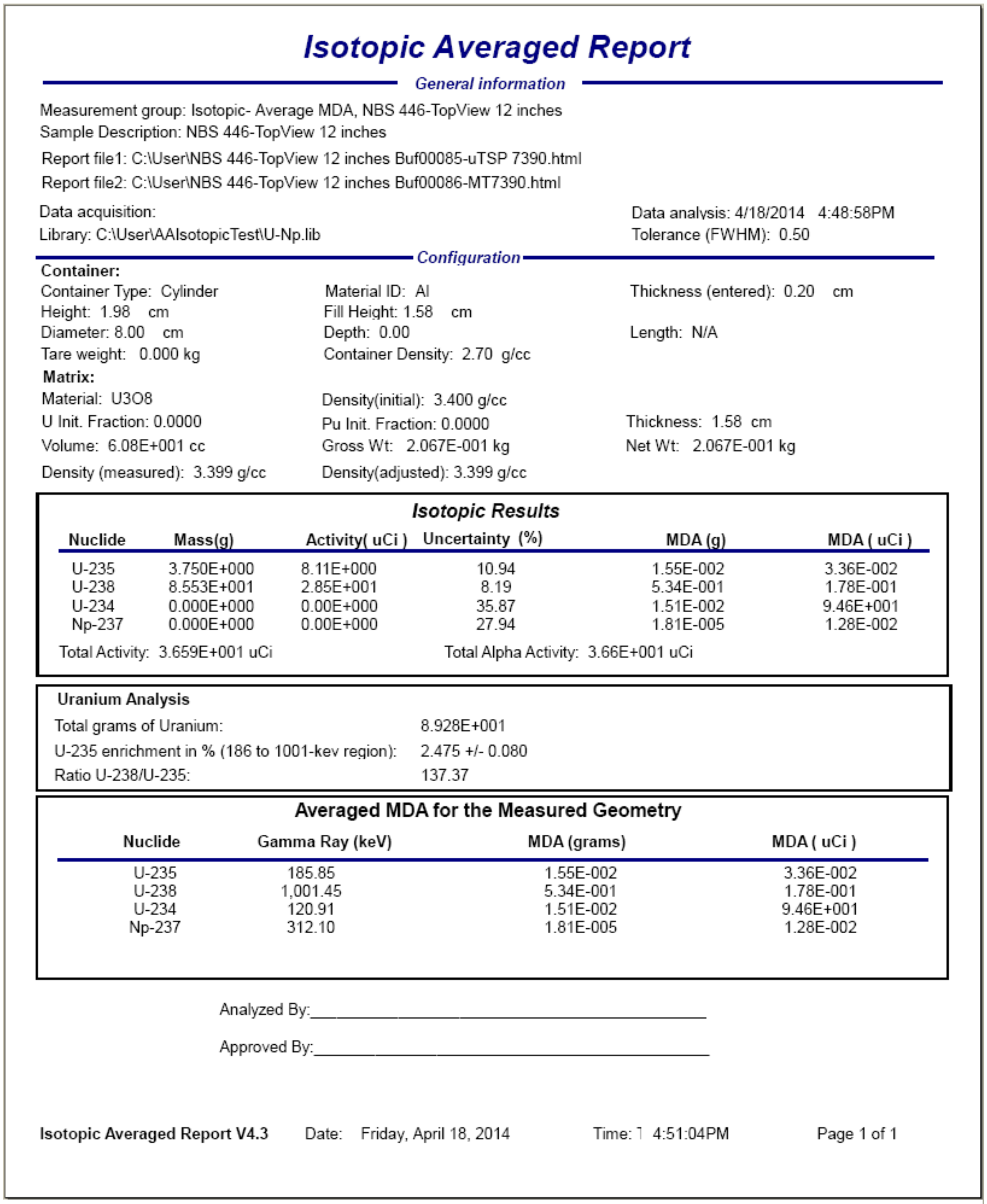
Signature:

Comments:

Figure 38. Container Report — Part 6.

4.3. The Averaged Container/Surface Mode Report

Figure 39 shows the averaged report for a configuration in which two detectors are each used in two orientations. The results are weighted according to the weighting factors entered in the Configuration Wizard. If the individual reports are decay-corrected, the average report is decay-corrected as well.



Isotopic Averaged Report

General information

Measurement group: Isotopic- Average MDA, NBS 446-TopView 12 inches
Sample Description: NBS 446-TopView 12 inches
Report file1: C:\User\NBS 446-TopView 12 inches Buf00085-uTSP 7390.html
Report file2: C:\User\NBS 446-TopView 12 inches Buf00086-MT7390.html

Data acquisition:
Library: C:\User\AAIsotopicTest\U-Np.lib
Data analysis: 4/18/2014 4:48:58PM
Tolerance (FWHM): 0.50

Configuration

Container:
Container Type: Cylinder
Height: 1.98 cm
Diameter: 8.00 cm
Tare weight: 0.000 kg
Material ID: Al
Fill Height: 1.58 cm
Depth: 0.00
Container Density: 2.70 g/cc
Thickness (entered): 0.20 cm
Length: N/A

Matrix:
Material: U3O8
U Init. Fraction: 0.0000
Volume: 6.08E+001 cc
Density (measured): 3.399 g/cc
Density(initial): 3.400 g/cc
Pu Init. Fraction: 0.0000
Gross Wt: 2.067E-001 kg
Density(adjusted): 3.399 g/cc
Thickness: 1.58 cm
Net Wt: 2.067E-001 kg

Isotopic Results

Nuclide	Mass(g)	Activity(uCi)	Uncertainty (%)	MDA (g)	MDA (uCi)
U-235	3.750E+000	8.11E+000	10.94	1.55E-002	3.36E-002
U-238	8.553E+001	2.85E+001	8.19	5.34E-001	1.78E-001
U-234	0.000E+000	0.00E+000	35.87	1.51E-002	9.46E+001
Np-237	0.000E+000	0.00E+000	27.94	1.81E-005	1.28E-002

Total Activity: 3.659E+001 uCi
Total Alpha Activity: 3.66E+001 uCi

Uranium Analysis

Total grams of Uranium:	8.928E+001
U-235 enrichment in % (186 to 1001-kev region):	2.475 +/- 0.080
Ratio U-238/U-235:	137.37

Averaged MDA for the Measured Geometry

Nuclide	Gamma Ray (keV)	MDA (grams)	MDA (uCi)
U-235	185.85	1.55E-002	3.36E-002
U-238	1,001.45	5.34E-001	1.78E-001
U-234	120.91	1.51E-002	9.46E+001
Np-237	312.10	1.81E-005	1.28E-002

Analyzed By:____

Approved By:____

Isotopic Averaged Report V4.3 Date: Friday, April 18, 2014 Time: 4:51:04PM Page 1 of 1

Figure 39. The Averaged Container/Surface Mode Report.

The General Information section of the report includes the individual detector reports from which the averaged report was generated, the date and time the averaged report was produced, and the analysis library.

The Configuration section lists the container and matrix parameters.

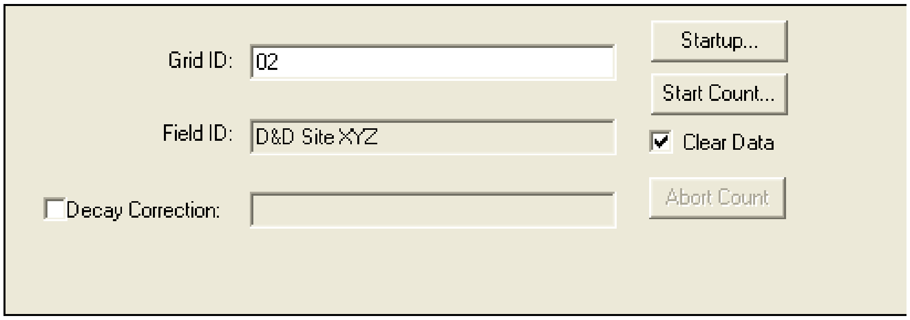
The remainder of the report provides the analysis tables (discussed in Section 4.2.5) and signature block.

5. USING SOIL MODE

This chapter describes how to use the Soil Mode (Fig. 40), and presumes you have completed all of the startup activities[2] in Chapter 3.

The **Field ID** is automatically retrieved based on the currently selected Soil Mode configuration.

To easily distinguish among sample results, be sure to assign a unique **Grid ID** to each sample (e.g., *Grid 001*, *Grid 002*), and to each reanalysis of an existing sample spectrum (e.g., *Grid 1*, *Grid 1 Reanalysis 1*). The **Grid ID** is stored in the database and printed on the report. If you discover an error after the analysis, correct the values, then use **Analyze/Configuration in Memory...** to repeat the analysis. All results for the original analysis and any reanalyses are stored in the ISOTOPIC database. In addition, a suite of spectrum, analysis, and report files are created as described in Section 1.6.



Grid ID: 02

Field ID: D&D Site XYZ

☐ Decay Correction:

☑ Clear Data

Figure 40. Scan Control Area — Soil Mode.

Mark the **Decay Correction** checkbox to correct the analysis results to a specific date. This date is stored in the database.

If the **Clear Data** box is marked, the data memory in the MCB automatically clears when you click **Start Count**.

When the detector is arranged properly above the soil, click **Start Count** to begin the data collection. The live spectrum for the detector will be displayed in the spectrum window, and the Status Sidebar will show the count values for the detector.

The spectrum acquisition continues until the preset conditions are met. To stop the count at any time, click **Stop Count**. The dialog in Fig. 41 will open.

Click **Resume** to continue the count with the data and settings unmodified. Click **Restart** to erase the spectrum and start the counting over. This is used when an error is discovered in the

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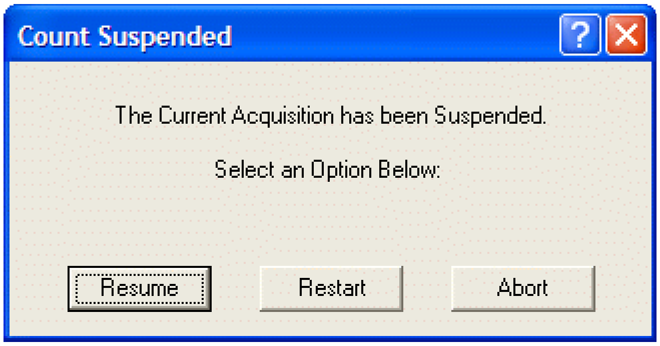
[2] Except **Update Background File**, which applies only to Container/Surface Mode.

count. The error should be corrected before **Restart** is clicked. **Abort** will stop the count and return to the idle state.



The Current Acquisition has been Suspended.

Select an Option Below:

Figure 41. Abort or Resume Count.

The report will be generated according to the Supervisor program settings on the Report tab in **Settings/Configurations...**, or the Operator program settings on the Report tab in **Analyze/ Configuration Settings...** (Section 8.3.2.4). If the **Allow Modification of Analysis Parameters** permission is enabled under **Services/Operator Permissions...** in the Supervisor program, you change the report settings with the **Analyze/Configuration Settings...** function as needed.

5.1. Soil Mode Report

A typical Soil Mode report is shown in Figs. 42 through 48. The exact details of the report depend on the options selected, the spectrum, the calibration, and the libraries.

5.1.1. First Page

Figure 42 shows the acquisition, configuration, and analysis information on the first page of the report. This is printed for all analyses and contains the bookkeeping data that are stored with the spectrum files along with other messages about the analysis. Some sections can be omitted from the report; see the discussion of the Report tab under **Analyze/Configuration Settings...** in Section 8.3.2.4, page 128.

Analysis Engine Version

This is useful when discussing program operation with the factory.

Generated

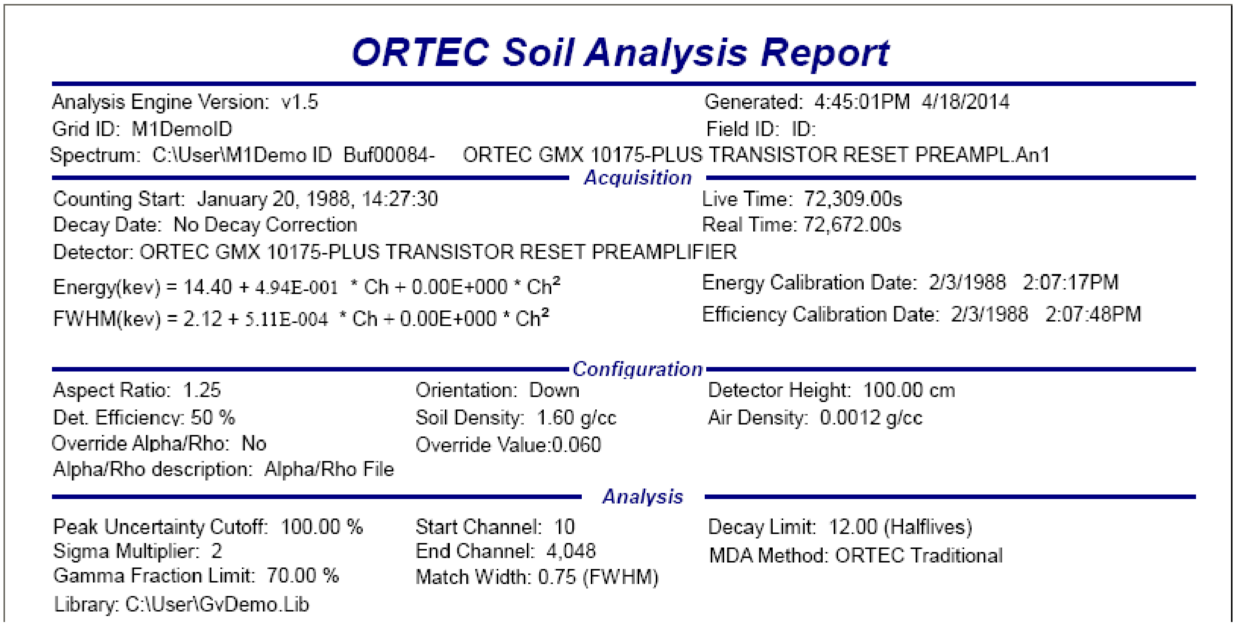
The date and time the analysis and report were generated.

Spectrum

The spectrum filename, including full path.

Grid ID and Field ID

The **Grid ID** (sample ID) entered by the operator when the data were collected (see the discussion concerning Fig. 40 on page 49); and the **Field ID** (primary project identifier) entered in the soil analysis configuration (see Section 8.3.2).



ORTEC Soil Analysis Report

Analysis Engine Version: v1.5
Generated: 4:45:01PM 4/18/2014
Grid ID: M1DemoID
Field ID: ID:
Spectrum: C:\User\M1Demo ID Buf00084- ORTEC GMX 10175-PLUS TRANSISTOR RESET PREAMPL.An1

Acquisition

Counting Start: January 20, 1988, 14:27:30
Live Time: 72,309.00s
Decay Date: No Decay Correction
Real Time: 72,672.00s
Detector: ORTEC GMX 10175-PLUS TRANSISTOR RESET PREAMPLIFIER
Energy(kev) = 14.40 + 4.94E-001 * Ch + 0.00E+000 * Ch²
Energy Calibration Date: 2/3/1988 2:07:17PM
FWHM(kev) = 2.12 + 5.11E-004 * Ch + 0.00E+000 * Ch²
Efficiency Calibration Date: 2/3/1988 2:07:48PM

Configuration

Aspect Ratio: 1.25
Orientation: Down
Detector Height: 100.00 cm
Det. Efficiency: 50 %
Soil Density: 1.60 g/cc
Air Density: 0.0012 g/cc
Override Alpha/Rho: No
Override Value:0.060
Alpha/Rho description: Alpha/Rho File

Analysis

Peak Uncertainty Cutoff: 100.00 %
Start Channel: 10
Decay Limit: 12.00 (Halflives)
Sigma Multiplier: 2
End Channel: 4,048
MDA Method: ORTEC Traditional
Gamma Fraction Limit: 70.00 %
Match Width: 0.75 (FWHM)
Library: C:\User\GvDemo.Lib

Figure 42. Software, Analysis, Acquisition, and Configuration Information.

Counting Start Date/Time, Decay Date

The collection date and time of the spectrum, and the decay correction date.

Collection Live and Real Times

The real and live time of the spectrum as recorded in the spectrum by the hardware.

Detector Description

The detector description of the MCB that collected the spectrum data. This description is entered in the MCB Configuration program. For portable units (such as the digiDART), it is stored in the unit and read out when the spectrum is stored. This is important for verifying the data. The example here of the HPGe detector type gives an added check that the correct values were used in the analysis.

Calibration Values

The energy and shape calibrations used in the analysis. These are stored when the system is calibrated in the Supervisor program. For portable units (such as the digiDART), the calibration is stored in the unit and read out when the spectrum is stored. This is important for verifying the data.

Calibration Date

The time and date of the calibration shown above. These are important for verifying that the correct calibration has been used.

Configuration

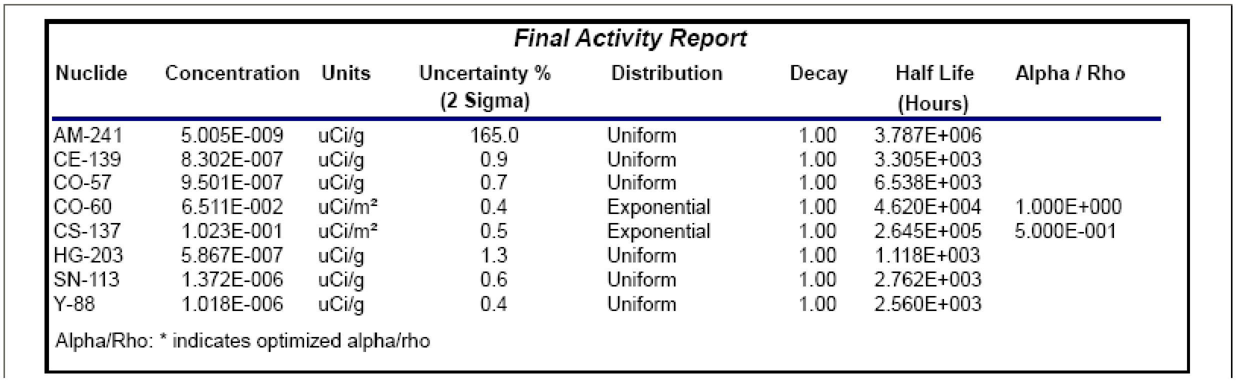
The detector aspect ratio and efficiency; geometry; and data collection parameters. These are entered in Setup, and are important for verifying that the correct information has been used.

Analysis Parameters

The analysis parameters entered in Soil Setup or the Supervisor program. These are important for verifying that the correct parameters have been used.

5.1.2. Final Activity Report

The Final Activity Report is shown in Fig. 43.



Final Activity Report

Nuclide	Concentration	Units	Uncertainty % (2 Sigma)	Distribution	Decay	Half Life (Hours)	Alpha / Rho
AM-241	5.005E-009	uCi/g	165.0	Uniform	1.00	3.787E+006	
CE-139	8.302E-007	uCi/g	0.9	Uniform	1.00	3.305E+003	
CO-57	9.501E-007	uCi/g	0.7	Uniform	1.00	6.538E+003	
CO-60	6.511E-002	uCi/m²	0.4	Exponential	1.00	4.620E+004	1.000E+000
CS-137	1.023E-001	uCi/m²	0.5	Exponential	1.00	2.645E+005	5.000E-001
HG-203	5.867E-007	uCi/g	1.3	Uniform	1.00	1.118E+003	
SN-113	1.372E-006	uCi/g	0.6	Uniform	1.00	2.762E+003	
Y-88	1.018E-006	uCi/g	0.4	Uniform	1.00	2.560E+003	

Alpha/Rho: * indicates optimized alpha/rho

Figure 43. Final Activity Report.

Nuclide

The nuclide name from the library.

Concentration and Units

The activity or concentration; and the units for the concentration in either activity units/g or activity units/m^2, depending on the alpha/rho selected. The activity units are selected in Soil Mode setup.

Uncertainty %

The activity or concentration uncertainty. The sigma value is 1, 2, or 3, as entered in Soil Mode setup, and is listed in the column header.

Distribution

Uniform or exponential, as entered in Soil Mode setup.

Decay

Calculated using the spectrum collection time, the decay-correction date, and the nuclide half-life. If the decay correction is turned off, the factor is 1.0 for no correction.

Half Life

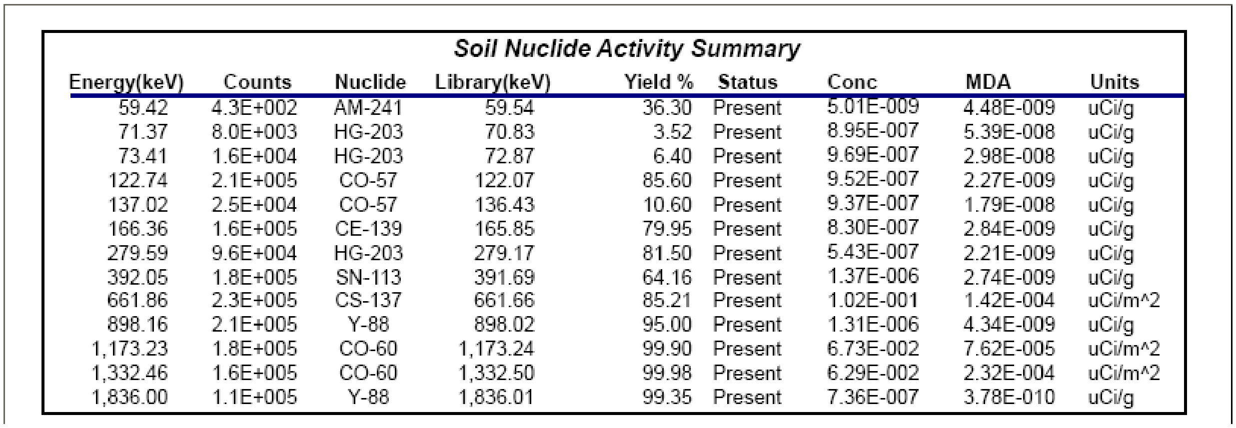
The unit of decay time is listed in the column header.

Alpha/rho

Self-explanatory.

5.1.3. Soil Nuclide Activity Summary

This section (Fig. 44) shows the list of putative isotope identifications.



Soil Nuclide Activity Summary

Energy(keV)	Counts	Nuclide	Library(keV)	Yield %	Status	Conc	MDA	Units
59.42	4.3E+002	AM-241	59.54	36.30	Present	5.01E-009	4.48E-009	uCi/g
71.37	8.0E+003	HG-203	70.83	3.52	Present	8.95E-007	5.39E-008	uCi/g
73.41	1.6E+004	HG-203	72.87	6.40	Present	9.69E-007	2.98E-008	uCi/g
122.74	2.1E+005	CO-57	122.07	85.60	Present	9.52E-007	2.27E-009	uCi/g
137.02	2.5E+004	CO-57	136.43	10.60	Present	9.37E-007	1.79E-008	uCi/g
166.36	1.6E+005	CE-139	165.85	79.95	Present	8.30E-007	2.84E-009	uCi/g
279.59	9.6E+004	HG-203	279.17	81.50	Present	5.43E-007	2.21E-009	uCi/g
392.05	1.8E+005	SN-113	391.69	64.16	Present	1.37E-006	2.74E-009	uCi/g
661.86	2.3E+005	CS-137	661.66	85.21	Present	1.02E-001	1.42E-004	uCi/m^2
898.16	2.1E+005	Y-88	898.02	95.00	Present	1.31E-006	4.34E-009	uCi/g
1,173.23	1.8E+005	CO-60	1,173.24	99.90	Present	6.73E-002	7.62E-005	uCi/m^2
1,332.46	1.6E+005	CO-60	1,332.50	99.98	Present	6.29E-002	2.32E-004	uCi/m^2
1,836.00	1.1E+005	Y-88	1,836.01	99.35	Present	7.36E-007	3.78E-010	uCi/g

Figure 44. Soil Nuclide Activity Summary.

Energy

The energy of the peak from the spectrum.

Counts

The net peak area.

Nuclide and Library (keV)

The nuclide identified from the library for this peak energy, and the library peak energy.

Yield

The yield (branching ratio) or gammas per disintegration, in percent.

Status

Lists the gamma ray as present, absent, or could not be calculated.

Conc

The activity for this nuclide, in the selected units, based on this energy only. This is marked "Invalid" for peak energies above 2.5 MeV, which is the upper limit of the angular correction range.

MDA

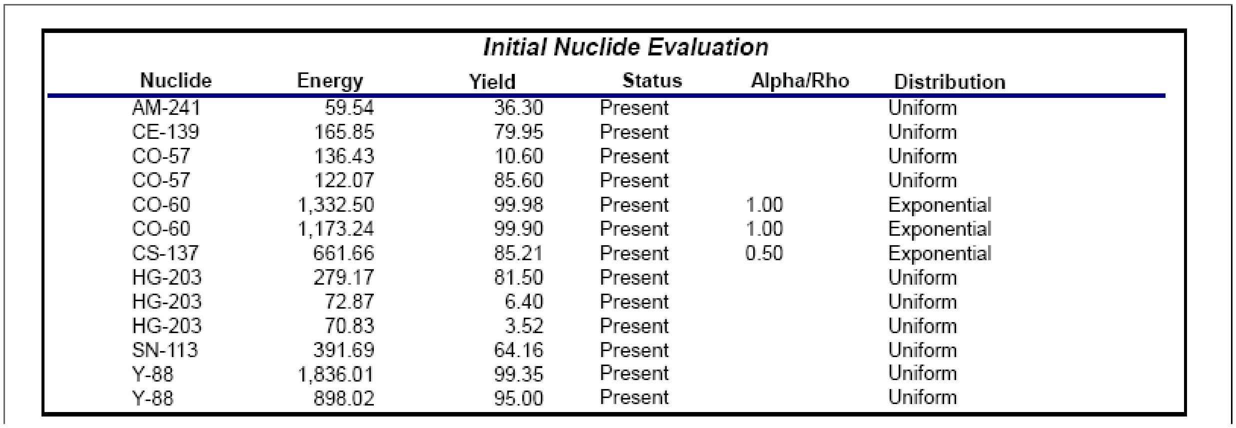
The MDA, in the selected units, based on this energy only. This is marked "Invalid" for peak energies above 2.5 MeV, which is the upper limit of the angular correction range.

Units

The units of measure used in the **Conc** and **MDA** calculations.

5.1.4. Initial Nuclide Evaluation

The Initial Nuclide Evaluation section is shown in Fig. 45. This section shows how each nuclide in the spectrum was determined to be present or absent.



Initial Nuclide Evaluation

Nuclide	Energy	Yield	Status	Alpha/Rho	Distribution
AM-241	59.54	36.30	Present		Uniform
CE-139	165.85	79.95	Present		Uniform
CO-57	136.43	10.60	Present		Uniform
CO-57	122.07	85.60	Present		Uniform
CO-60	1,332.50	99.98	Present	1.00	Exponential
CO-60	1,173.24	99.90	Present	1.00	Exponential
CS-137	661.66	85.21	Present	0.50	Exponential
HG-203	279.17	81.50	Present		Uniform
HG-203	72.87	6.40	Present		Uniform
HG-203	70.83	3.52	Present		Uniform
SN-113	391.69	64.16	Present		Uniform
Y-88	1,836.01	99.35	Present		Uniform
Y-88	898.02	95.00	Present		Uniform

Figure 45. Initial Nuclide Evaluation.

Nuclide

The nuclide name from the library.

Energy

This column has the library energy for each line in the library for this nuclide or "Total" for the summation line.

Yield

This column lists the library yield for this energy line.

Status

Lists the gamma ray as present, absent, or could not be calculated.

Alpha/rho

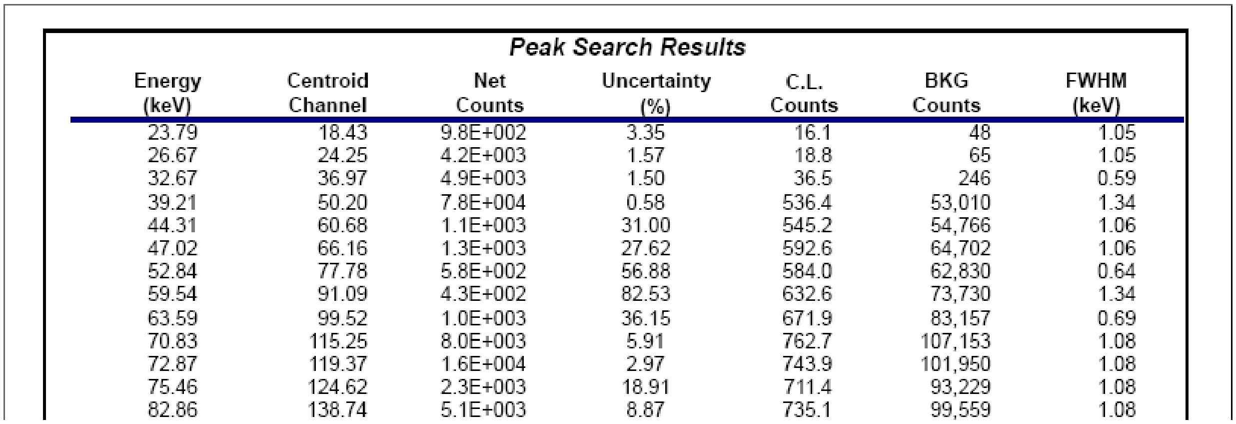
Self-explanatory.

Distribution

Uniform vs exponential.

5.1.5. Peak Search Results

Figure 46 shows the Peak Search results from the analysis of the spectrum.



Peak Search Results

Energy (keV)	Centroid Channel	Net Counts	Uncertainty (%)	C.L. Counts	BKG Counts	FWHM (keV)
23.79	18.43	9.8E+002	3.35	16.1	48	1.05
26.67	24.25	4.2E+003	1.57	18.8	65	1.05
32.67	36.97	4.9E+003	1.50	36.5	246	0.59
39.21	50.20	7.8E+004	0.58	536.4	53,010	1.34
44.31	60.68	1.1E+003	31.00	545.2	54,766	1.06
47.02	66.16	1.3E+003	27.62	592.6	64,702	1.06
52.84	77.78	5.8E+002	56.88	584.0	62,830	0.64
59.54	91.09	4.3E+002	82.53	632.6	73,730	1.34
63.59	99.52	1.0E+003	36.15	671.9	83,157	0.69
70.83	115.25	8.0E+003	5.91	762.7	107,153	1.08
72.87	119.37	1.6E+004	2.97	743.9	101,950	1.08
75.46	124.62	2.3E+003	18.91	711.4	93,229	1.08
82.86	138.74	5.1E+003	8.87	735.1	99,559	1.08

Figure 46. Peak Search Results.

Energy (keV)

The energy of the peak centroid calculated from the Centroid Channel in column 2 and the energy calibration shown on page 1 of the report.

Centroid Channel

The peak centroid value, in channels, as calculated by the analysis program for the peaks in the spectrum.

Net Counts

The net peak counts of this peak in the spectrum. Net peak is the gross counts minus the background.

Uncertainty (%)

The percent uncertainty of the net peak count as 1-sigma value.

C.L. Counts

The critical level for this peak.

BKG Counts

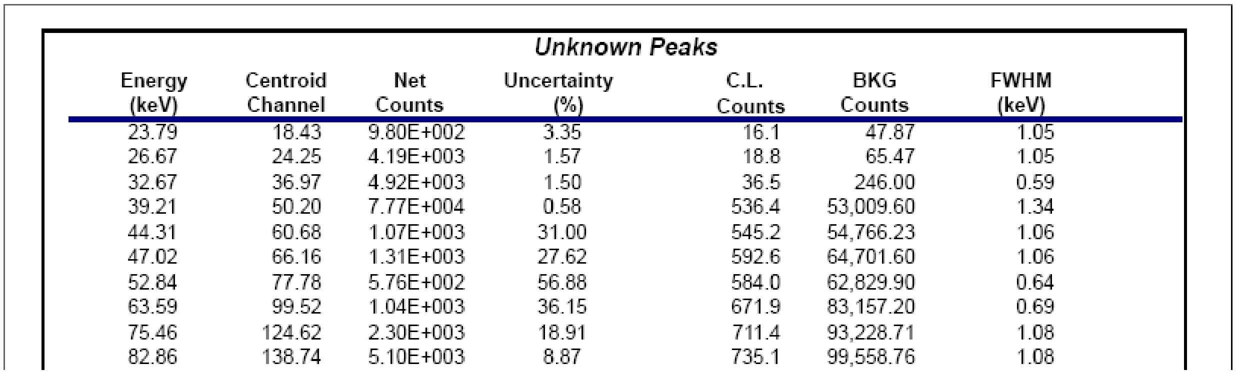
The Compton background under this peak.

FWHM (keV)

The actual peak full width half maximum, in keV.

5.1.6. Unknown Peaks

The Unknown Peaks section of the report (Fig. 47) shows the unidentified peaks (those peaks not in the library). This section is useful for verifying that all the significant peaks in the spectrum have been accounted for in the spectrum analysis.



Unknown Peaks

Energy (keV)	Centroid Channel	Net Counts	Uncertainty (%)	C.L. Counts	BKG Counts	FWHM (keV)
23.79	18.43	9.80E+002	3.35	16.1	47.87	1.05
26.67	24.25	4.19E+003	1.57	18.8	65.47	1.05
32.67	36.97	4.92E+003	1.50	36.5	246.00	0.59
39.21	50.20	7.77E+004	0.58	536.4	53,009.60	1.34
44.31	60.68	1.07E+003	31.00	545.2	54,766.23	1.06
47.02	66.16	1.31E+003	27.62	592.6	64,701.60	1.06
52.84	77.78	5.76E+002	56.88	584.0	62,829.90	0.64
63.59	99.52	1.04E+003	36.15	671.9	83,157.20	0.69
75.46	124.62	2.30E+003	18.91	711.4	93,228.71	1.08
82.86	138.74	5.10E+003	8.87	735.1	99,558.76	1.08

Figure 47. Unknown Peaks.

Energy

This column shows the energy of the peak centroid calculated from the Centroid Channel in column 2 and the energy calibration shown on page 1 of the report.

Centroid Channel

This is the peak centroid value as calculated by the analysis engine for the peaks in the spectrum.

Net Counts

This is the net peak counts of this peak in the spectrum. Net peak is the gross counts minus the background.

Uncertainty Percent

This is the uncertainty of the net peak count as 1-sigma value.

C.L. Counts

This is the critical level for this peak.

BKG Counts

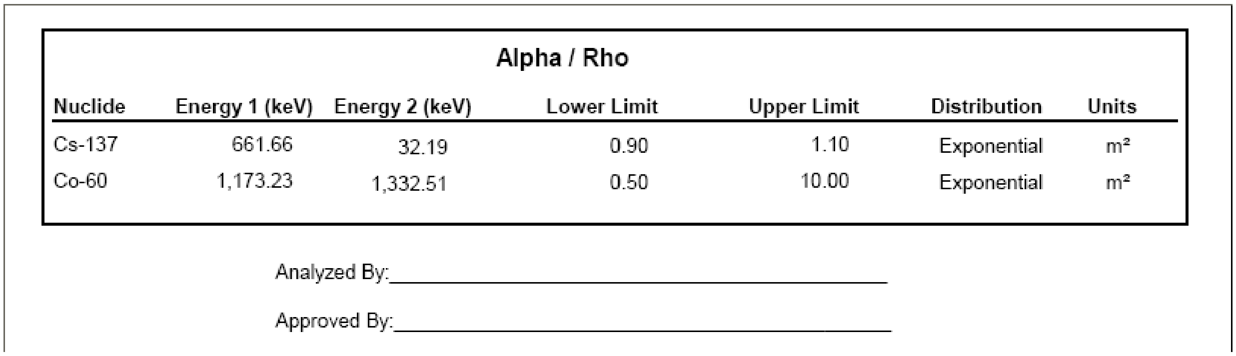
This is the background under this peak.

FWHM

This is the actual peak full width half maximum, in keV.

5.1.7. Alpha/Rho

The final section of the report (Fig. 48) gives the results of the alpha/rho validity check followed by the signature line. The validity check compares the expected intensity ratio of the two listed peaks with the actual ratio. See the “Concentration Ratio Limits” discussion on page 131 for more details.



Alpha / Rho

Nuclide	Energy 1 (keV)	Energy 2 (keV)	Lower Limit	Upper Limit	Distribution	Units
Cs-137	661.66	32.19	0.90	1.10	Exponential	m^2
Co-60	1,173.23	1,332.51	0.50	10.00	Exponential	m^2

Analyzed By:____

Approved By:____

Figure 48. Alpha/Rho Section.

Nuclide

This column lists the nuclides as shown.

Energy1

The energy, in keV, of the first peak of the nuclide.

Energy2

The energy, in keV, of the second peak of the nuclide.

Lower Limit

This is the lowest concentration ratio limit to be accepted as good. It is entered in the Soil Setup dialog.

Upper Limit

This is the highest concentration ratio limit to be accepted as good. It is entered in the Soil Setup dialog.

Distribution

Uniform or exponential.

Units

The concentration units in either activity units/g or activity units/m^2, depending on the alpha/rho selected. The activity units are selected in Soil Mode setup.

6. THE CRYSTAL REPORTS WINDOW

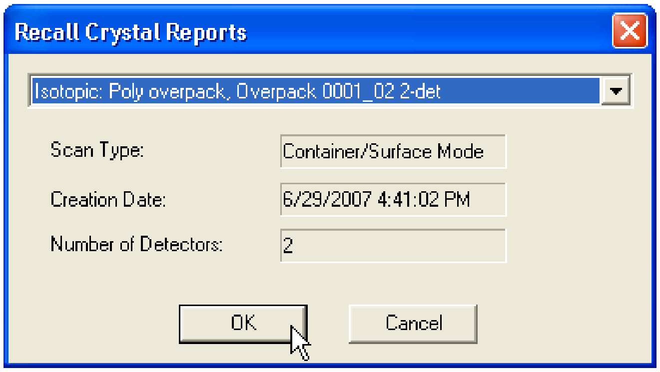
The Crystal Reports window opens when you issue the **File/Recall Reports...** command. If a Crystal Reports template has been specified in the Supervisor program with the **Settings/Crystal Reports...** command, this report window allows you to view, print, and export your report data from within the Operator program.

These reports are dynamic. That is, previously generated reports are not stored on disk. Each time you issue the **Recall Reports...** command, they are generated directly from the pertinent analysis record(s). The data retrieved and the output format are determined by (1) the customized Crystal Reports template your organization has developed with your own copy of SAP BusinessObjects Crystal Reports v11.5; or (2) one of three ISOTOPIC report templates (Section 6.1.1.1).

6.1.1. Viewing Reports

Figure 49 shows the Recall Crystal Reports dialog. Scan records are listed oldest first, and only the records for the currently selected **Scan Type** (Container/Surface or Soil) are available. Choose the desired scan from the droplist and click **OK**.

If a valid report template was not selected in the Supervisor program, the error message shown in Fig. 50 will be displayed. Return to Supervisor and select a valid template file.


Recall Crystal Reports

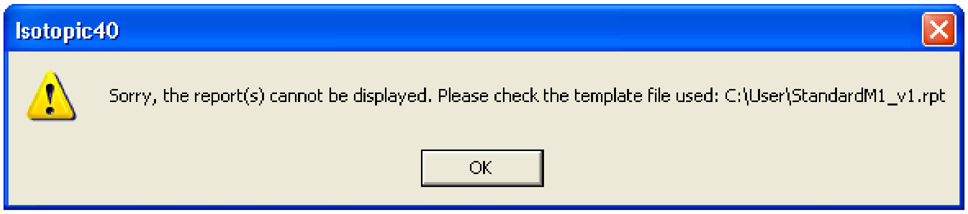
Isotopic: Poly overpack, Overpack 0001_02 2-det

Scan Type: Container/Surface Mode

Creation Date: 6/29/2007 4:41:02 PM

Number of Detectors: 2

Figure 49. Choose a Record to View in the Crystal Reports Window.

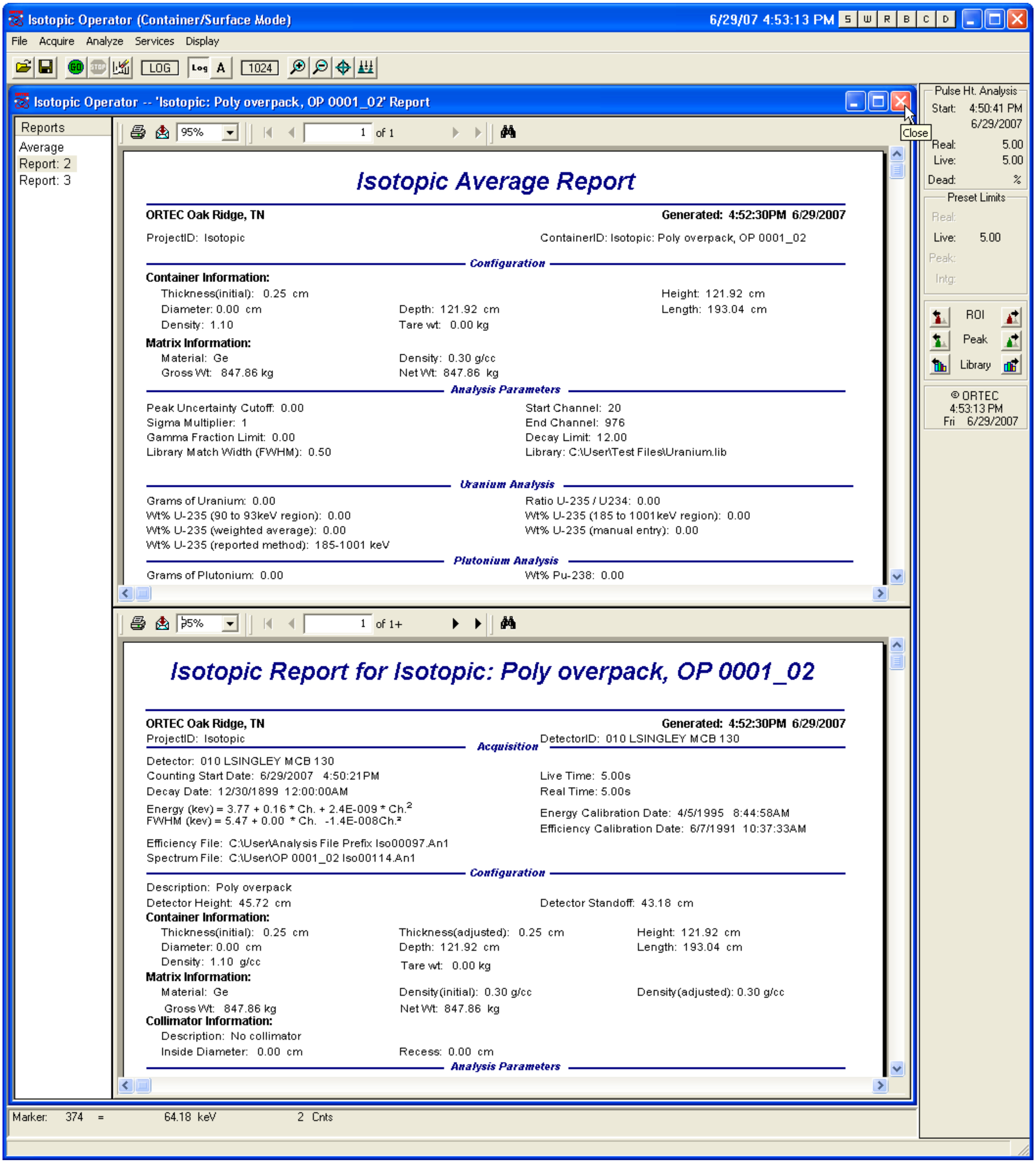

Isotopic40

Sorry, the report(s) cannot be displayed. Please check the template file used: C:\User\StandardM1_v1.rpt

Figure 50. Return to Supervisor and Select a Valid Crystal Reports Template.

If a valid report template was selected in Supervisor, the report window will open over the Operator window, as shown in Fig. 51.

To view the Crystal Report(s) for another scan data set, you must first close the report window.



Isotopic Average Report

ORTEC Oak Ridge, TN **Generated: 4:52:30PM 6/29/2007**

ProjectID: Isotopic ContainerID: Isotopic: Poly overpack, OP 0001_02

Configuration

Container Information:
Thickness(initial): 0.25 cm Height: 121.92 cm
Diameter: 0.00 cm Depth: 121.92 cm Length: 193.04 cm
Density: 1.10 Tare wt: 0.00 kg

Matrix Information:
Material: Ge Density: 0.30 g/cc
Gross Wt: 847.86 kg Net Wt: 847.86 kg

Analysis Parameters

Peak Uncertainty Cutoff: 0.00 Start Channel: 20
Sigma Multiplier: 1 End Channel: 976
Gamma Fraction Limit: 0.00 Decay Limit: 12.00
Library Match Width (FWHM): 0.50 Library: C:\User\Test Files\Uranium.lib

Uranium Analysis

Grams of Uranium: 0.00 Ratio U-235 / U234: 0.00
Wt% U-235 (90 to 93keV region): 0.00 Wt% U-235 (185 to 1001keV region): 0.00
Wt% U-235 (weighted average): 0.00 Wt% U-235 (manual entry): 0.00
Wt% U-235 (reported method): 185-1001 keV

Plutonium Analysis

Grams of Plutonium: 0.00 Wt% Pu-238: 0.00

Isotopic Report for Isotopic: Poly overpack, OP 0001_02

ORTEC Oak Ridge, TN **Generated: 4:52:30PM 6/29/2007**
ProjectID: Isotopic DetectorID: 010 LSINGLEY MCB 130

Acquisition

Detector: 010 LSINGLEY MCB 130
Counting Start Date: 6/29/2007 4:50:21PM Live Time: 5.00s
Decay Date: 12/30/1899 12:00:00AM Real Time: 5.00s
Energy (kev) = 3.77 + 0.16 * Ch. + 2.4E-009 * Ch.^{2} Energy Calibration Date: 4/5/1995 8:44:58AM
FWHM (kev) = 5.47 + 0.00 * Ch. -1.4E-008Ch.^{2} Efficiency Calibration Date: 6/7/1991 10:37:33AM
Efficiency File: C:\User\Analysis File Prefix Iso00097.An1
Spectrum File: C:\User\OP 0001_02 Iso00114.An1

Configuration

Description: Poly overpack
Detector Height: 45.72 cm Detector Standoff: 43.18 cm

Container Information:
Thickness(initial): 0.25 cm Thickness(adjusted): 0.25 cm Height: 121.92 cm
Diameter: 0.00 cm Depth: 121.92 cm Length: 193.04 cm
Density: 1.10 g/cc Tare wt: 0.00 kg

Matrix Information:
Material: Ge Density(initial): 0.30 g/cc Density(adjusted): 0.30 g/cc
Gross Wt: 847.86 kg Net Wt: 847.86 kg

Collimator Information:
Description: No collimator
Inside Diameter: 0.00 cm Recess: 0.00 cm

Analysis Parameters

Figure 51. Crystal Reports Window Showing Average Report and One of Two Individual Detector Reports for Container/Surface Mode.

6.1.1.1. The Default Example Templates

ISOTOPIC supplies you with three example Crystal Reports templates, which are installed in c:\User:

- StandardIso_v1.rpt — for individual detector reports in Container/Surface Mode.
- StandardIsoAve_v1.rpt — for the averaged Container/Surface Mode report in multi-detector systems.
- Soil.rpt — for Soil Mode reports.

StandardIso_v1.rpt and StandardIsoAve_v1.rpt, as well as your custom templates, can reside in any location.

6.1.2. Basic Report Window Functions

6.1.2.1. Reports Sidebar

The **Reports** sidebar, in the upper left corner of the window, shows the reports available for the selected scan.

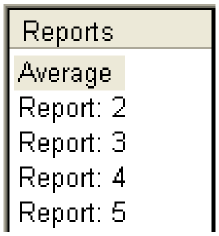


Figure 52. Choose from the List of Reports for this Scan.

- **Container/Surface Mode** — For a single-detector system, ISOTOPIC generates a report based on the original analysis parameters. This is always labeled **Report 1** on the Reports sidebar. Each time you adjust the isotopic parameters and click **Save** (Section 4.1.1), the program saves an additional analysis record in the database. The resulting reports will be labeled as **Report 2**, **Report 3**, and so on, on the Reports sidebar.

  If the scan was made with multiple detectors or with one detector in multiple positions, the Reports bar will list the averaged report and the individual reports for each detector; see the example in Fig. 52. Clicking **Average** will display the averaged report only. Clicking on any of the **Report** entries displays the averaged report and the selected individual detector report. Each time you adjust the isotopic parameters and click **Save**, the program saves an additional analysis record in the database. This adds more reports to the Reports sidebar.

- **Soil Mode** — Soil Mode measurements are made with only one detector, therefore, only the one individual detector report is available.

6.1.2.2. Report Window Tools

- Selecting the report window's zoom factor from the zoom droplist 100%
- Manually entering a zoom value other than those on the list 85
- Searching for a particular string of alphanumeric characters within the report
- Printing the report
- Exporting the analysis data, including selecting the data format and delimiters

The page number bar beside the zoom field (Fig. 53) shows the number of pages in the report and the page currently displayed. The accompanying arrow buttons allow you to advance to the first, previous, next, or last page of the report.

Figure 53.

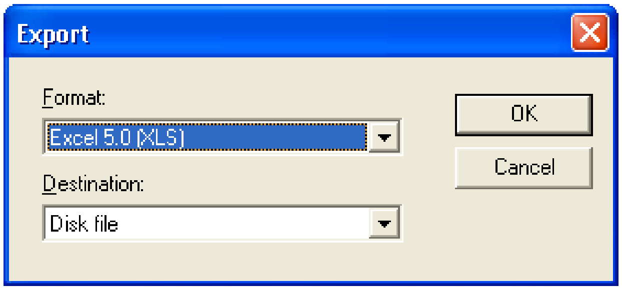
6.1.3. Exporting Report Data

ISOTOPIC allows you to export report data to disk in the following **Format**s (Fig. 54).

Adobe Acrobat	.PDF
Crystal Reports	.RPT
HTML 3.2	.HTML
HTML 4.0	.HTML
Microsoft Excel 97-2000	.XLS
Microsoft Excel 97-2000 — Data only	.XLS
Microsoft Word	.RTF
Microsoft Word — Editable	.RTF
Record Style — Columns with spaces	.REC
Record Style — Columns without spaces	.REC
Report Definition	.TXT
Rich Text Format	.RTF
Separated Values	.CSV
Tab Separated Values	.TTX
XML	
ODBC	

When you select a format and click **OK**, a standard file-save dialog opens so you can assign a location and filename.

NOTE *Be sure the correct Crystal Reports template has been selected with the* **Settings/Crystal Reports...** command in the Supervisor program or this export function might not function properly.



Format: Excel 5.0 (XLS)

Destination: Disk file

Figure 54. Select an Export Format.

[Intentionally blank]

7. IN SITU MEASUREMENTS WITH THE ISO-CART-85

This chapter covers the use of ISOTOPIC and the ISO-CART-85 to perform accurate nondestructive measurements of radioactive items in various containers and configurations. The discussion addresses mode selection, collimator settings, detector positioning, background measurements, counting times, and other best measurement practices in accord with ISO 17025.[3]

Definitions

Term	Description
Backshield	Shielding positioned behind the detector to minimize the activity entering the detector from the rear.
Blank	A prepared sample with no significant radioactivity whose density and average atomic number are similar to the items being measured.
Collimator Standoff	Distance from the face of the collimator to the surface of the item being measured.
Crosstalk	Unwanted activity from a nearby item that is detected by the counting system.
Detector/Collimator Assembly	A detector surrounded by a shield that defines a directional response on the collimated detector.
Detector Standoff	Distance from the face of the detector to the surface of the item being measured.
Effective Matrix Density	Density of the matrix that gamma rays penetrate between the activity and detector.
FOV	Detector field of view, i.e., the conical detection range in front of a collimated gamma-ray detector.
Holdup	Residual special nuclear material in processing or support equipment areas.
Item	Generic term used here to mean drum, pipe, object or surface to be measured.
Staging Areas	Locations for storing items prior to measurements.

ISO-CART-85 is the latest ORTEC mobile system for radioactive waste assay by high-resolution gamma spectroscopy. Through the use of a single, very large-area high purity germanium

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[3] General Requirements for the Competence of Testing and Calibration Laboratories.

(HPGe) detector, and a modular collimation system, ISO-CART-85 achieves, in many cases, free release levels in reasonable count times, for in-field measurements.

The HPGe detector is provided in the form of the ORTEC IDM-200-V, a revolutionary all-in-one integrated Gamma Spectrometer, which requires no liquid nitrogen to cool to operational temperature. Instead, a miniature Stirling cycle cryocooler is employed. An internal battery powers the cooler and the highly stable digital signal processing electronics for up to 3 hours or longer with battery life extending options or battery hot swap.

The new ISO-CART II, which is the measurement system transport, represents the latest generation of ISO-CART from ORTEC. It may be configured with conventional LN_2-cooled HPGe detectors or other gamma spectrometers, as required. In the remainder of this document, references to the ISO-CART-85 can generally be taken to apply to these alternative configurations.

The ISOTOPIC software is designed to control the spectroscopy system, calibrate the system, and develop models for the item being measured and use these models for accurate nondestructive analyses. Once the measurement system is set up, it functions as a turnkey system.

The ISOTOPIC software consists of two separate software components, a Supervisor program, and an Operator program. The Supervisor program is used to calibrate the HPGe detector, set up the analysis instructions, and establish models of the items being analyzed.

The Operator program is used to: (1) record weight and other minor equipment adjustments, (2) measure the activity, and (3) analyze the items in near-assembly line fashion. Archived data can be analyzed using the Operator program with previously established templates.

ISOTOPIC has two completely independent measurement modes, Container Mode and Soil Mode. Choice of measurement mode depends on the dimensions of the item of interest. If measuring an item with discrete parameters (height, length, diameter, or width), use the Container Mode. Use the Soil Mode for the measurement of fallout and naturally occurring radioactivity evenly distributed in the soil over a wide area.

7.1. Ways to Use ISOTOPIC and the ISO-CART-85 for In Situ Measurements

There are several ways to use ISOTOPIC software at a nuclear facility. It can be used for measurement stations at which the detector is relatively stationary, for holdup measurements where the detector is moved to the activity within a building, or for soil measurements.

- Measurement stations are used when the items to be measured have similar container and material characteristics. Usually the items are samples with ID numbers. Only a few templates are needed to model the waste stream. The detector can be raised or lowered to make minor positioning adjustments. Container Mode is used for these measurements.

- In process holdup measurements, each item being measured may have geometry, matrix, and container shapes that vary dramatically among the items. In this situation, a data sheet must be prepared for each item being measured (see Fig.). The data sheet contains critical parameter information necessary to establish a model which will be used to analyze the item. A typical data sheet is shown on the back of this brochure. Container Mode is used for these measurements.

- To measure radioactivity in soil, the collimator is removed and the detector is positioned facing downward. It is assumed that the activity is relatively homogeneous. The area of concern is mapped out in a grid, and each grid location is measured independently. Soil Mode is used in this situation.

7.2. Measurement Hints

7.2.1. Collimator Considerations

The collimator is used to shield the detector in order to reduce the radiation from surrounding areas and to define the field of view of the detector in container mode. Definition of the field of view is an important consideration because the container mode software corrects from what the system “sees” in its field of view to what it “does not see” that is the total container, as described by the parameters in the configuration for height, width, depth, density, etc.

Background radiation is everywhere, so always use a collimator except when measuring fallout or natural activity in the soil. Several collimator options are available for the ISO-CART. The ISO-CART-85 has a modular collimator, allowing the choice of an appropriate field of view collimator, followed by additional shielding segments to prevent background radiation from reaching the detector crystal. Overall, the modular collimator is intended to reduce system weight where possible.

The selection of the collimator depends on the measurement situation.

For soil mode, no collimator should be used for two reasons: (1) the general-purpose DOE Environmental Measurements Laboratory calibration was performed with uncollimated detectors, and (2) an uncollimated detector is much more efficient for infinite plane measurements because a large fraction of the gamma rays penetrate the detector from the side. The detector efficiency will increase by a factor of 2 to 4 (high energy to low energy) when the collimator is removed.

To reduce the detection of unwanted activity near the item being measured, recess the detector within the collimator. The length of recess will depend on where the unwanted activity is located in the measurement area. Staging areas have activity that could contribute to the item being measured if the staging area is within the FOV. A collimator recess can help reduce this effect.

For general purpose recess settings, use a 2.5 cm (1 in.) recess. If very large containers are being measured (more than about 2 m [6 ft] in length), reduce the collimator recess to zero if the background is low enough. For background areas with significant activity, approximately in the line of sight of the item being measured, increase the collimator thickness to 5.0 cm (2 in.).

Backshields are seldom necessary as the internal copper cup holding the germanium crystal, the cryostat and the liquid nitrogen in the Dewar are equivalent to 2 in. of lead shielding for most gamma rays.

7.2.2. Establishing the Collimator Standoff

Once the detector recess within the collimator is established, then the FOV of the detector/ collimator combination must be determined. Understanding the FOV is the key to knowing how to position the detector. See Fig. 55. Note that the FOV is a circle because the collimator is round.

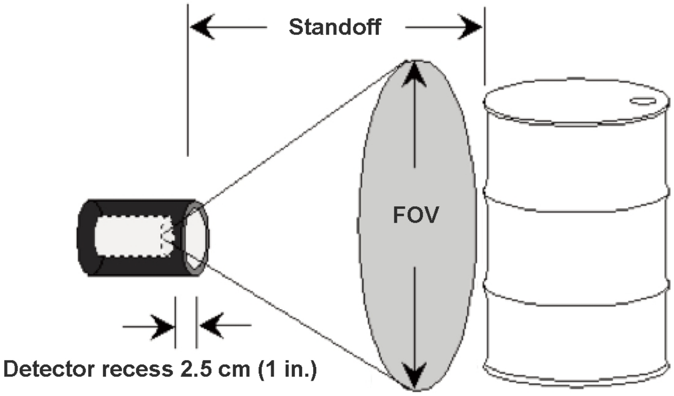


Figure 55. Collimator Standoff.

A helpful rule of thumb is: the ratio between the detector recess within a collimator and the inside collimator radius should be the same as the ratio of the detector standoff distance and the diameter of the FOV. That is, if the detector recess is 2.5 cm (1 in.) and the inside radius of the collimator is 5.0 cm (2 in.) then the minimum detector standoff distance to container height ratio is 1:2. Thus, for a drum that is 86 cm (34 in.) high, the detector standoff should be at least 43 cm (17 in.).

Use the FOV estimate in Table 1 to determine the minimum standoff for the detector. First, determine the largest container parameter (usually the height or length) that will be measured.

This is the FOV necessary for measurement. For 200 L (55 gal.) drums this will be 86 cm (34 in.), due to the height. For a B-25 box, the FOV is determined from the length of 183 cm (72 in.). For a detector recess of 5.0 cm (2 in.), the detector standoff-to-FOV ratio should be 1:1.

Table 1. Selection of Collimator Standoff for Typical Configurations.

Detector Recess (cm)	**FOV* (cm)**	**Minimum Detector Standoff (cm)**
2.54 (1 in.)	91.4 (36 in.)	45.7 (18 in.)
	183 (72 in.)	91.4 (36 in.)
5.08 (2 in.)	91.4 (36 in.)	91.4 (36 in.)
	183 (72 in.)	183 (72 in.)
7.62 (3 in.)	91.4 (36 in.)	137 (54 in.)
	183 (72 in.)	274 (108 in.)

*The FOV is intended to be approximate. Actual FOV dimensions vary with HPGe crystal diameter.

For more accurate FOV determinations where a sharp cutoff from nearby activity is needed, some additional experimentation may be necessary to establish an exact cutoff at a fixed distance. Measure sources along an axis perpendicular to the detector. Consider the definition of cut-off to be a drop-in count rate of 80% compared to an uncollimated measured count rate of a point source. This can be obtained from a deep detector recess in the collimator.

Other factors to consider when positioning the sample item:

1) Initial configurations as modeled in the software assume that the item being measured is homogeneous. Nearly all nuclear waste items are nonhomogeneous to some degree. If the radioactivity within the item is positioned closer or further away from the detector than assumed by the configuration, then the geometry and matrix correction will be incorrect. Both of these errors can be minimized by positioning the detector farther from the sample than the minimum distance the table recommends and/or rotating drums about a vertical axis, if possible, during a counting period to simulate a homogenous container.

2) Collimation, angular correlation, and geometry errors can be reduced if the gamma rays enter the detector at normal incidence. In other words, if the sample-to-detector distance is large, gamma rays entering the detector are closer to normal to the detector, which reduces errors associated with approximations in the model. Try not to position the detector closer than the FOV table recommends.

3) Sensitivity increases significantly if the detector is positioned closer to the item being measured. For example, sensitivity improves by a factor of 1.45 if the detector is positioned 30 cm (12 in.) from a 208 L drum rather than 46 cm (18 in.).

Thus, detector positioning becomes a compromise. The greater the distance from the face of the detector to the item being measured, the less the measurement uncertainty, but at the price of lower sensitivity. If there is enough activity to accommodate a reasonable counting time, then increase the detector standoff.

NOTE In ISOTOPIC, the **Collimator Standoff** is used to define the configuration, *not the detector standoff*. Thus, if the detector recess (depth) is 2.5 cm (1 in.), a detector standoff of 45.72 cm (18 in.) should be entered as a **Collimator Standoff** of 43.28 cm (17 in.). See Fig. 56.

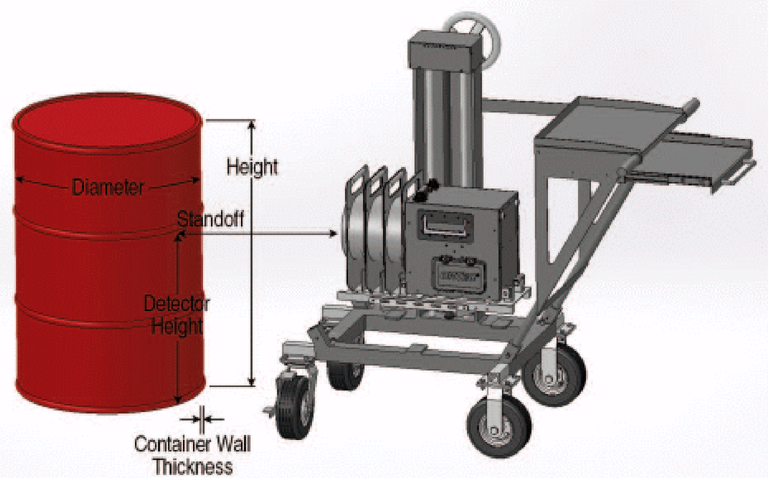


Figure 56. Detector Standoff Setting.

7.2.3. Background Measurements

The area used to measure items may contain gamma-ray activity that will appear in the spectrum. Therefore, it is important to subtract this activity, especially if the background activity contains some of the same nuclides being analyzed for in the item of interest. The collimator will shield much of this activity but not all. *Thus, it is good practice to obtain a background spectrum so this activity can be subtracted.*

If the radioactive items in the staging area are contributing significantly to the background, try to position the staging area as far as possible from the measurement station area. If background activity is a significant contribution to the activity of the item being measured, then the counting time for a background measurement should be at least twice the typical counting time of an item. Remember the background activity table may be used to subtract activity from many spectra. *Thus, it is important to obtain a background with good peak area counting statistics.* The

ISOTOPIC software provides a mechanism to develop a table for peaked background subtraction (see the *Supervisor Manual*).

HINTS Taking a background measurement is not as simple as it seems. One of the common mistakes is to measure the area with nothing in front of the detector. This will give an artificially high background because as an item is being measured it will shield some of the background activity. The best method is to position, measure, and analyze a blank as if it were a sample. The matrix of the blank should be as free as possible of radioactivity but should otherwise be as similar as possible to the sample item with respect to gamma-ray absorbing material and density.

If counting stations are positioned close together, crosstalk could occur between the detectors at different stations. Thicker collimators or additional separate shields minimize that effect.

7.2.4. Preliminary Survey with a Scanning NaI Detector

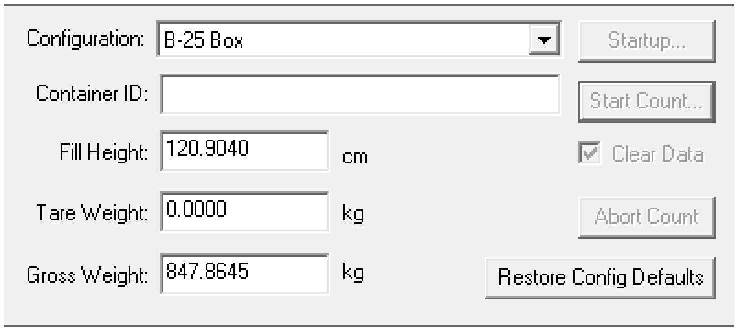
An extremely helpful tool for preliminary item measurements is a scanning NaI detector. This is an NaI detector interfaced to a rate meter, and is used to indicate the location of gamma-ray activity within the item being measured or to determine matrix fill heights within a container. The NaI detector should be lightly collimated to provide directional activity yet portable enough for personnel to use for long time periods. The size of the NaI detector will vary depending on the intensity of the activity in the container. For a 200 L drum, usually a 1 in. to 2 in. diameter NaI detector will suffice. For large containers such as a B-25 box, a 3 in. diameter NaI detector may be necessary. Dose rate meters will work if the activity in the container is high enough.

7.2.5. Sample Fill Height

It is good facility practice to completely fill the waste containers. If you cannot assume a container is full and if facility regulations prohibit removal of its lid, measure the fill height before the measurement. Error in effective (average) matrix density is one of the largest sources of measurement bias. *Thus, it is important to accurately determine the matrix density.* This is done by measuring the weight of the item, subtracting the weight of the empty container (the *tare*), and dividing by the volume. The ISOTOPIC software does this automatically. Measured results from containers improperly assumed to be full will be biased low because the average density has been computed based on the volume of a full drum. To determine the height of the contents without opening the drum, perform simple transmission measurements using a low-energy transmission source. Position the source on one side of the container and use a collimated NaI detector on the other side. Move both down the container concurrently, so that the collimated detector will always “see” the transmission source. A drop in count rate will reflect the top level of the matrix. Note that the activity of the sample being measured will contribute to the transmission source measurement, thus the activity of the transmission source should be more intense than the sample.

If the container is found to be less than full, the measured container **Fill Height** should be entered in the Operator program's Scan Control Area before the scan is started (Fig. 57).

If the **Ask for Detector Positions on Start** checkbox is marked in the configuration (Fig. 58),[4] the operator will be given the opportunity to adjust the detector position and enter the detector height and stand-off before starting the scan (Fig. 59).


Configuration: B-25 Box

Container ID:

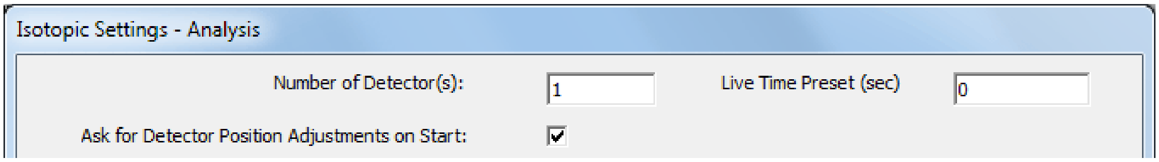
Fill Height: 120.9040 cm

Tare Weight: 0.0000 kg

Gross Weight: 847.8645 kg

☑ Clear Data

Figure 57. Adjust the Detector Position in the Operator Program as Needed.



Number of Detector(s): 1

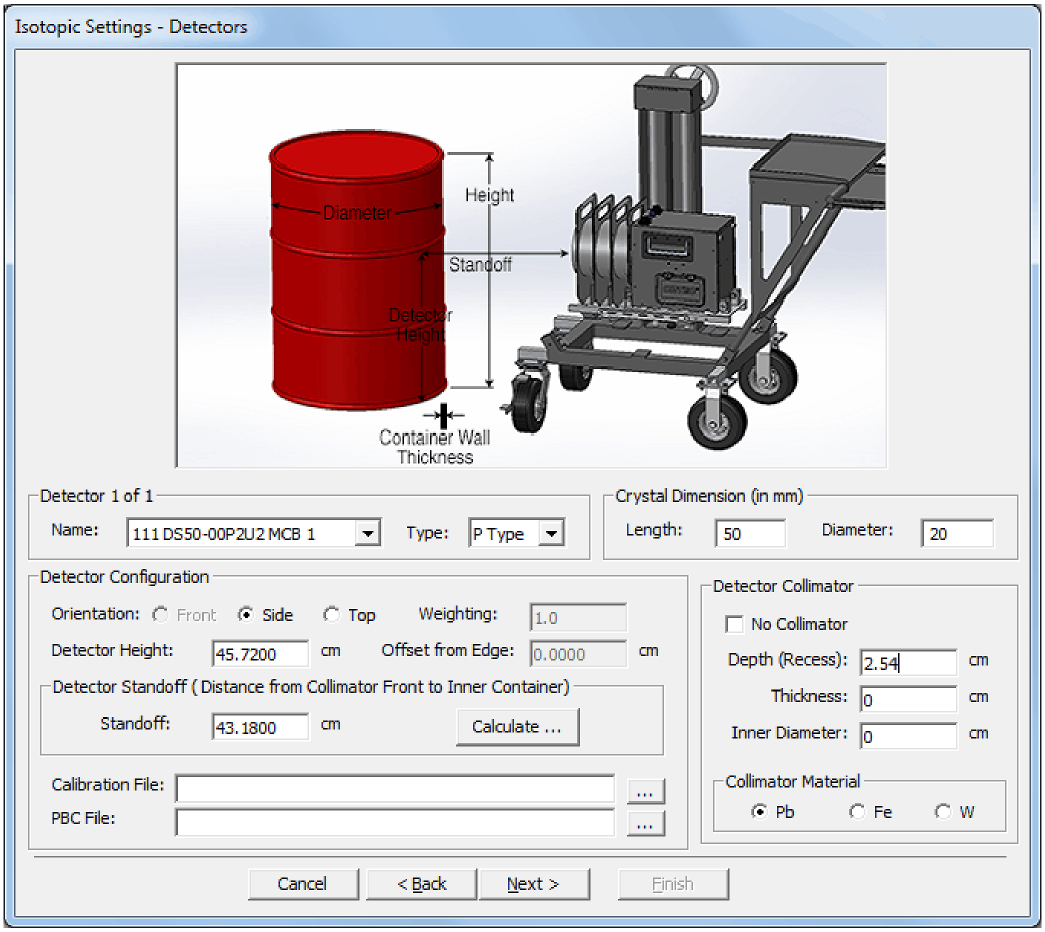
Live Time Preset (sec) 0

Ask for Detector Position Adjustments on Start: ☑

Figure 58. Adjust the Detector Position in the Operator Program as Needed.

---

[4] The configuration is typically set up in the Supervisor program, but if an operator has the **Allow Modification of Configuration Parameters** permission, set in Supervisor under **Services/Operator Permissions...**, configurations can be modified in the Operator program.



Isotopic Settings - Detectors

Detector 1 of 1

Name: 111 DS50-00P2U2 MCB 1

Type: P Type

Crystal Dimension (in mm)

Length: 50

Diameter: 20

Detector Configuration

Orientation: ○ Front ● Side ○ Top

Weighting: 1.0

Detector Height: 45.7200 cm

Offset from Edge: 0.0000 cm

Detector Standoff (Distance from Collimator Front to Inner Container)

Standoff: 43.1800 cm

Calculate ...

Calibration File:

PBC File:

Detector Collimator

☐ No Collimator

Depth (Recess): 2.54 cm

Thickness: 0 cm

Inner Diameter: 0 cm

Collimator Material

● Pb ○ Fe ○ W

Figure 59. Adjust the Detector Position Parameters Before Scanning the Sample.

7.2.6. Preliminary Gamma-Ray Scans for Model Adjustments

Model the activity to be measured as if the activity is homogeneously distributed in a container. As a precaution, scan the item with an NaI detector interfaced to a rate meter (Fig. 1). If the rate meter activity of a "hot spot" is approximately 10 times greater than the rate meter activity of the remaining item, then model the item being measured as a point source.

Figure 60. Scanning for a "Hot Spot."

7.2.7. Quantifying a "Hot Spot" in a Box, Drum or On the Floor

The important information necessary for the model adjustment is distance through the matrix (*Absorber 2*), container thickness (*Absorber 1*), and distance from the "hot spot" to the detector. The matrix density is obtained assuming average matrix density of the entire container. Use the point source model instead of models where volume is used for the geometry correction. See Fig. 1.

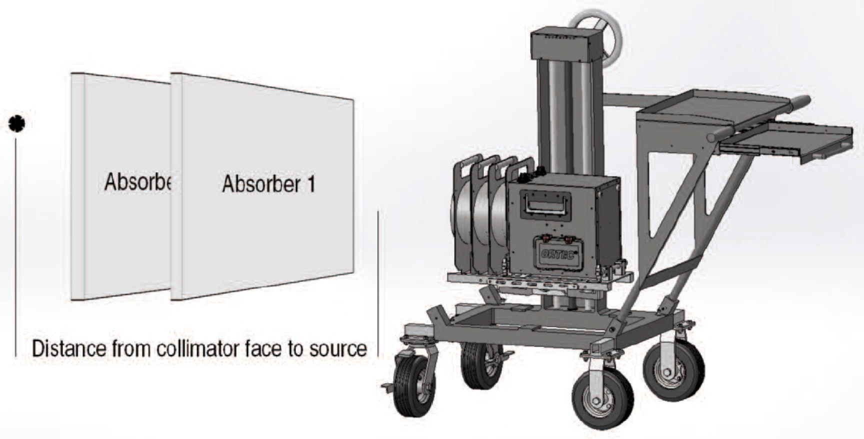


Figure 61. Template Used to Define a Hot Spot.

Results will be reported as activity (Bq) instead of a concentration (Bq/g). The information needed for the analysis is: (1) distance from the detector to the "hot spot"; (2) thickness, density, and material of matrix that the activity penetrates before reaching the detector; and (3) wall thickness of the container. The scanning NaI detector is useful to locate the item in the container to established the thickness of matrix. A separate weight measurement will be necessary to establish the average matrix density which is represented as the density of absorber 2.

It is important to model the activity within the container, not just the container itself. Consider a 200 L drum with the vast majority of the activity in the bottom fourth of the drum. This is frequently the case. Best results are obtained when the container is modeled to match what the gamma rays "see" as they exit the item and are collected in the detector. If all of the activity were located in the bottom half of the container then the software model should be set up as if the container is only one half the ***physical*** height in order to get the correct "per container" result. Use this information to develop a model and position the detector. Note however, that if the activity were only in the bottom fourth of the container, the gamma rays would still "see" the average density computed by the weight and volume of the matrix measured as if the drum were full.

In practice, it is not practical to set this measurement template before hand. Usually, the spectrum is archived and the data specific to the measurement is collected outside the ISOTOPIC program. Then a special template is prepared for that item in the Supervisor program and activity results obtained accordingly in the Operator program.

Frequently, activity is located in the bottom fourth of the container. In these cases, an adjustment to the model must be made. If more than one hot spot is located in the drum, best results will be obtained if the measurement model is kept simple and the item is modeled as if the activity is homogenous.

For nonuniform contamination on floors and walls, scan and identify areas of increased activity and treat as hot spots or small spill areas. Mark the contaminated area so that the contamination in the area can be modeled and later analyzed.

7.2.8. Measuring Activity in a Pipe

Use a preliminary scan with a NaI detector to indicate if the piping is evenly contaminated, contains localized activity, or has significant activity at all.

If the piping is evenly contaminated, then only a few sections need to be counted, analyzed, and averaged to obtain activity/length of piping. In this situation the FOV table (Table 1) will establish an approximate standoff. However, in this case, determine a more accurate FOV. Report the activity in units of activity/meter of piping. The difficult part is to determine where the FOV has a sharp cutoff. Note that the FOV calculations determine where collimator corrections begin. However, there may be considerable activity beyond the FOV that is partially collimated. Several HPGe measurements should be taken along the pipe to assure that the activity within the pipe is uniform.

If the pipe has an uneven continuous distribution of activity, then the pipe should be measured in overlapping segments and an average activity/meter given to the entire pipe. If there are only a few localized “hot spots” with no continuous activity, then best results will be obtained by measuring the activity of each “hot spot” separately.

7.2.9. Contaminated Wall and Floor Measurements

Contaminated walls and floors are similar to piping. A preliminary scan of the surface will help find localized activity. If the floor or wall is homogeneously contaminated, the FOV will establish the area of the circle of activity. Divide the item being measured into a matrix. The diameter of the circle is established by the field of view. See Figure 7. Average the results of the measured circles to obtain a measure of the item. Activity beyond the FOV may enter the detector to complicate the real area “seen.” Recess the detector to obtain a sharp cutoff and then experimentally determine when 80% of the activity is attenuated. This cutoff establishes the radius of the measured circle. Then determine the area measured. If there are hot spots, measure these separately.

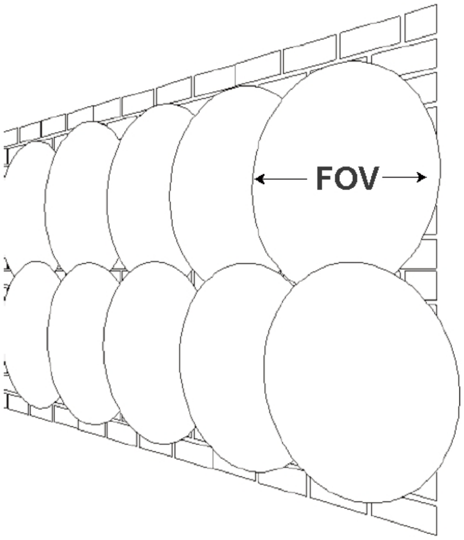


Figure 62. Map the Wall in Overlapping Circles.

7.2.10. ISOTOPIC Mode Selection — Container or Soil

Spills of radioactivity should be measured using a collimated system as the collimator masks out the surrounding activity. The critical parameter is a diameter of approximately 10 m (39 ft). That is, if the diameter of the spill activity is greater than 10 m and relatively homogenous, remove the collimator and use Soil Mode for that activity measurement. Otherwise, use Container Mode. Position the detector 1 m from the surface of the soil, facing downward, when take Soil Mode measurements. If the diameter of the soil spill is greater than 2 m, then do not recess the detector in the collimator. The soil mode algorithm also allows you to take account of the exponential "wash in" of fallout into the soil by rainfall over time.

7.3. Common Measurement Mistakes

7.3.1. Measuring the Opposite Side of the Container

In general, nuclear waste is very nonhomogeneous and matrix attenuation corrections dominate the correction factors for large containers. If drums can be rotated, the matrix "appears" to be more homogeneous and the uncertainty in matrix attenuation will be lower. This does not solve the geometry error of different activity levels within a drum, but the geometry error is usually smaller than the matrix error.

For large boxes with a depth greater than 46 cm (18 in.) it is very important to measure from both sides. ISOTOPIC has the option to use multiple detectors for item counting. If multiple detectors are available, then concurrently measure both sides of the box. If multiple detectors are not available, then measure both sides successively. In both cases ISOTOPIC will average the results.

7.3.2. Minimizing Uncertainty

There are several measurement techniques that can be used to minimize the measurement uncertainty. These can be characterized by minimizing the correction factors. The following tips will help make detector position decisions.

1) Increasing the item-to-detector distance will reduce the error due to geometry correction. Counting statistics are seldom a major contributing factor to the overall uncertainty, so you don’t have to worry about the reduced count rate. You may have to count longer if the activity is too low to meet sensitivity requirements.

2) Matrix attenuation corrections usually dominate the correction factors. Count boxes through the thinnest [front to back) dimension [maximum area normal to the detector) to minimize this correction and thus the uncertainty in the correction. See Fig. 1.

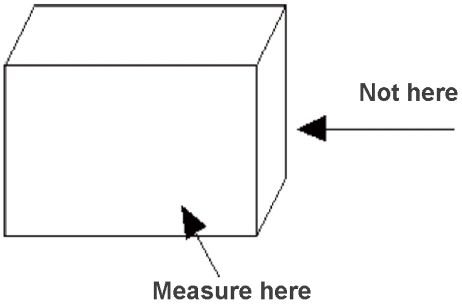


Figure 63. Measure Correctly to Minimize Uncertainty.

3) Position the item at the distances shown in Table 1 or greater to avoid collimator corrections. The corrections should not vary significantly from 1.00 (no correction).

7.4. Software Hints

7.4.1. Working with the Fine-Tuning Adjustments

When an item being measured is initially modeled, it is assumed that the activity within a matrix is homogeneous. In practice, however this is seldom the case. Nonhomogeneity will affect the results in several ways.

1) The matrix within a container usually has several air pockets. Alternately, the activity being measured might be situated near an item with high attenuation properties. This is common for samples such as large containers of contaminated steel.

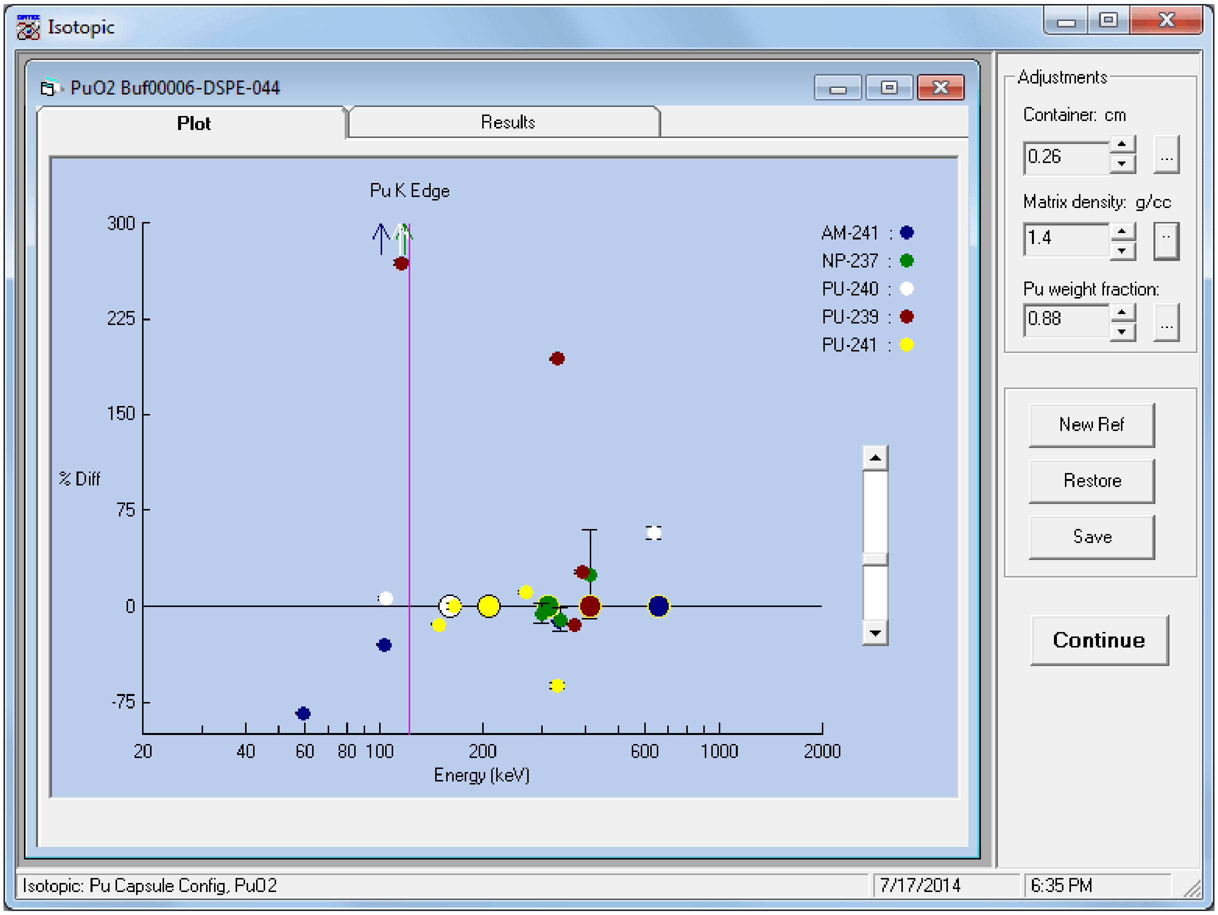
2) Note also that gamma rays will likely penetrate the container at an angle that is not normal to the detector. Thus, the container attenuation will be greater than is generally considered from the wall thickness only. The container correction accounts for this but it assumes that the activity is homogeneously distributed within the container.

3) Heavy elements such as uranium and plutonium often exhibit self-attenuation of their emitted gamma-rays. The matrix mass attenuation coefficients need to include contributions from uranium or plutonium when these elements are present. As the weight percentage of uranium or plutonium is increased, the mass attenuation correction in ISOTOPIC will adjust the mass attenuation coefficients according to the entered weight percent of uranium or plutonium. This simulates what the gamma ray "sees" as it penetrates the matrix. This provides a good "lump" correction for uranium and plutonium.

ISOTOPIC has a fine-tuning adjustment that allows you to vary the modeled values of matrix density, container thickness, and heavy-element contributions. You must decide how much of these adjustments are necessary from each of the contributions. If the product of all the gamma-ray corrections at each energy is correct, the corrected gamma-ray peak areas from the same nuclide will show the same activity. If the item has been incorrectly modeled, the low-energy gamma-ray corrected peak areas will be higher or lower than high-energy gamma ray peak areas. This is graphically presented in a graph of % deviation (**% Diff**) from the reference gamma-ray activity vs energy as shown in Fig. 64

It is important to know your spectrum when working with the adjustment plot. Use the nuclide with the most intense activity and the widest range of gamma-ray energies. Disregard the nuclides with low activity because their gamma-ray peak areas may add scatter to the plot. In Fig. 64, five nuclides are plotted, but ^{239}Pu is the nuclide with the widest gamma-ray energy range and gamma-ray intensity. Thus, ^{239}Pu should be the isotope used to adjust the parameters. In this example the 413-keV gamma ray is chosen as the reference gamma ray. As shown in this plot there is some scatter. This scatter is primarily because the peaks cannot be fit well in complicated multiplets. That is, when analyzing a plutonium item, there are many gamma- and x-ray peaks positioned in difficult-to-fit multiplets. These peaks should generally be disregarded for the fine-tune adjustments. A few well separated and intense peaks are better to use for the adjustment than many poorly-fitted peaks. Using this reasoning, on the Report tab of the container wizard's Analysis tab, set the number of peak count rates/nuclide shown on the plot to a number between 5 and 10 as shown in Fig. 65. Make certain that the reference gamma rays are not eliminated from display in the process of selecting the highest quality peaks for adjusting.

CAUTION Be careful with your adjustments. Do not increase or decrease the density of the sample to more than twice the average density of the sample. Keep in mind that the effective container thickness will always be greater than the measured thickness as most gamma rays go through the container wall at an angle. However do not increase the thickness by more that 50% of the actual thickness. Usually, the matrix adjustment is the first adjustment to be made and container thickness is the last fine-tune adjustment.



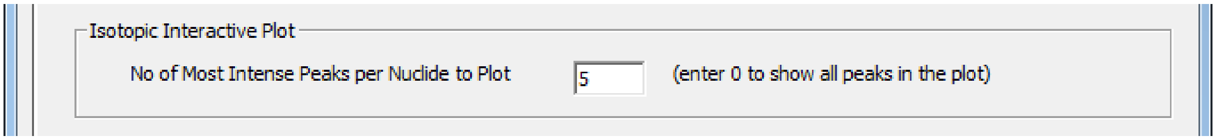
Container: cm 0.26

Matrix density: g/cc 1.4

Pu weight fraction: 0.88

Isotopic: Pu Capsule Config, PuO2 7/17/2014 6:35 PM

Figure 64. Fine-Tune Adjustment for a Plutonium Spectrum.



No of Most Intense Peaks per Nuclide to Plot 5 (enter 0 to show all peaks in the plot)

Figure 65. Fine-Tune Adjustment for a Plutonium Spectrum.

7.4.2. Hints for Setting Up the Analysis Library

Developing a library is a continuous process. Typically, the more analyses you perform on a particular type of sample or at a particular site, the more you will modify the library. There are a number of considerations to understand before you start.

1) Determine from the facility which daughter nuclides to report.

2) Gamma rays from the daughters that are not reported should be included as parent gamma rays in the library if they appear to exhibit the half-life of the parent. That is, the activities of the daughters are in secular equilibrium.

3) The reported activity for a nuclide is based on the activity from the first gamma ray listed in the library. This reference gamma ray peak should be well resolved from neighboring gamma ray peaks.

4) Select an intense, high-energy gamma ray for reference. It may not have to be the most intense high energy gamma ray, if that specific one is in an interference for example, but remember that high-energy gamma rays characterize nonhomogeneous matrices better than low-energy gamma rays because of the greater penetration.

5) Minimize the primary library to nuclides known to be present in the facility, but be alert to unexpected nuclide gamma-ray activity.

6) Investigate unidentified peaks for unexpected nuclides. To minimize the unidentified peak list record every gamma ray ever seen by each nuclide, but do not include gamma rays in the library that have never been seen before in the spectrum as this will introduce clutter. Thus, the library development will be somewhat continuous.

7) It is important to be sure that the energy calibration is accurate. If the computed energy of the peak is outside the library tolerance, a nuclide could inadvertently be classified as unidentified. As a general rule of thumb, check the energy of a high-energy gamma ray such as ^{40}K. If the energy of the peak is approximately 1.0 keV high or low, then energy recalibration may be necessary. The **Auto-Energy Calibration** feature works well if the library is simple and there are not many low-energy x-rays and gamma rays in it. If the normal sample library gives spurious results when the **Auto Calibrate** feature is used, then prepare an additional simple library containing only 5 or 10 gamma rays spaced throughout the energy range; these should be gamma rays that are likely to be in any spectrum. Select that library before using the Auto Calibrate feature if the sample library will not work. Alternately, calibrate using manual calibration with a few well established peaks.

Channel: 6510.05

E= 1764.5000 keV

15 Energies

● Energy

○ FWHM

☑ No FWHM Cal

Figure 66. No FWHM Calibration.

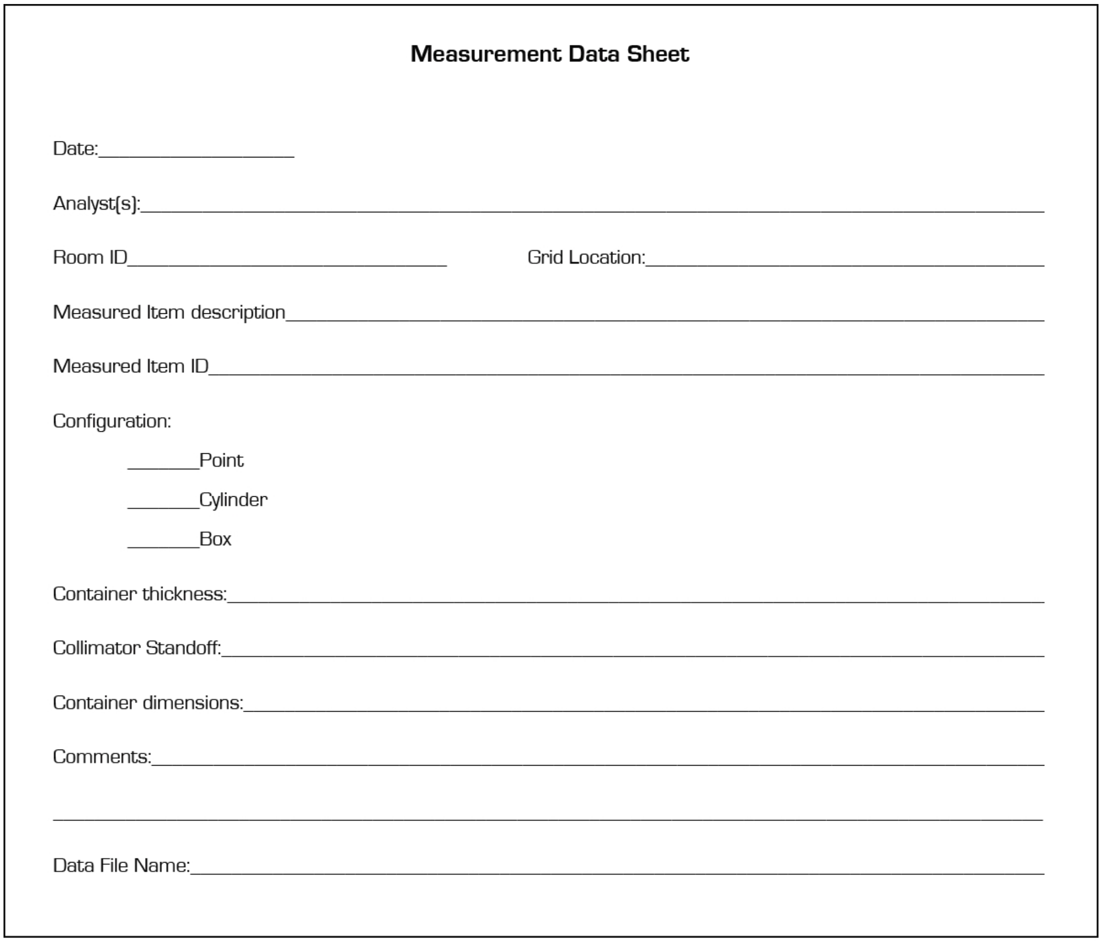
CAUTION When adjusting the energy calibration using the auto-energy calibration feature, do not change the FWHM calibration that has already been carefully established. Be sure to mark the **No FWHM Cal** checkbox as shown in Fig. 66.

7.4.3. Hints for Uranium Analysis

Frequently the weight percent (wt%) of ^{235}U for a waste item is known with high accuracy. This information can be used to obtain more accurate uranium results by normalizing the activity to either the ^{238}U or ^{235}U results. For example, if it is known that the wt% of ^{235}U is 5.0% and the analysis results report 5.0 grams of ^{235}U, the ^{238}U analysis can be forced to 95.0 grams. In situations where item densities are high and samples exhibit a high degree of nonhomogeneity, such as a barrel or box of metal parts, the user should select the ^{238}U analyses on which to normalize, because it is likely that the ^{238}U analysis obtained from referencing on higher-energy gamma rays will be better than the ^{235}U analysis because the gamma rays from the ^{235}U isotope are more highly attenuated.

Normally, the ^{235}U isotope is more accurately determined. However, if the matrix has high density it may be better to use the ^{238}U isotope to adjust the ^{235}U activity.

Figure 67 shows an example Measurement Data Sheet.



Measurement Data Sheet

Date:____________________

Analyst(s):____

Room ID____________________ Grid Location:____________________

Measured Item description____________________________________

Measured Item ID____

Configuration:

_______Point

_______Cylinder

_______Box

Container thickness:____

Collimator Standoff:____

Container dimensions:____

Comments:____

____

Data File Name:____

Figure 67. Example Measurement Data Sheet.

[Intentionally blank]

8. MENU COMMANDS

This chapter describes all of the ISOTOPIC Operator 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. The menus are:

File
- Recall configuration and file(s) / Recall File
- Recall Scan Data Set...
- Recall Reports...
- Save As...
- Compare...
- Exit
- About ISOTOPIC...

Acquire
- High Voltage...
- MCB Properties...
- Start   Alt + 1
- Stop   Alt + 2
- Clear   Alt + 3
- Download Spectra
- QA...   ▸
  - Measure Background
  - Measure Sample
  - Status
  - Control Charts

Analyze
- Configuration Settings...
- Create Background File...
- Configuration in Memory...

Services
- Set Presets/Recalibrate Energy
- Peak Info
- Clear All ROIs
- Recall ROI File...
- Calculate Field of View...

Display

Logarithmic	Keypad /
Automatic	Keypad *
Baseline Zoom	
Zoom In	Keypad +
Zoom Out	Keypad −
Center	Keypad 5
Full View	Alt + F7

Right-Mouse-Button Menu

Start
Stop
Clear
Zoom In
Zoom Out
Undo Zoom In
Peak Info
Input Count Rate
Sum
MCB Properties...

8.1. File

The **File** menu contains the commands for saving spectrum files; recalling configurations, reports, and spectra; and comparing spectra, as shown in Fig. 68.

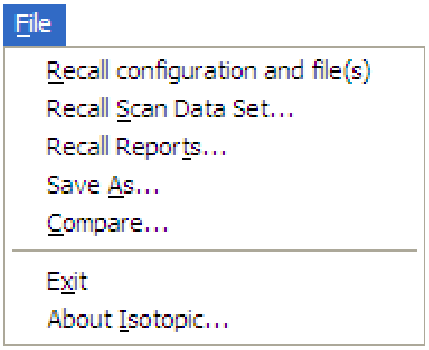


Figure 68. File Menu.

8.1.1. Recall configuration and file(s) / Recall File

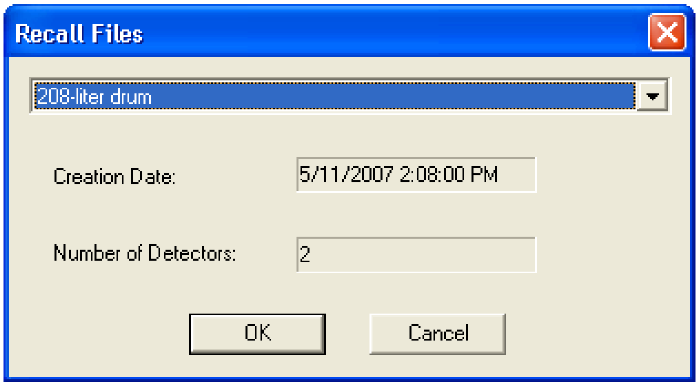
This function allows you to recall a previously acquired spectrum file (as distinguished from a scan data set in the database) for subsequent analysis or reanalysis with the **Analyze/Configuration in Memory** command (Section 8.3.4). It is especially useful when data have been acquired in a digiDART or other MCB in "Field Mode," without an attached computer. The command is labeled as **Recall configuration and file(s)** in Container/Surface Mode, and **Recall File** in Soil Mode.

To load the database record (as distinguished from a standalone spectrum file) for a previous measurement, use the **Recall Scan Data Set...** command.

- **Recall configuration and file(s)** lets you associate previously acquired spectra with an analysis configuration. Together these two elements constitute a set of scan data which can then be analyzed with the **Configuration in memory...** command.

- **Recall File** lets you recall a single spectrum file, at which point it is ready for analysis.

Fig. 69 shows the Recall Files dialog for Container/Surface Mode, with which you choose an existing configuration to act as a template of analysis parameters, then click **OK**. The number of spectra to be recalled for the analysis is based on the **Number of Detectors** in the configuration. A standard file-open dialog opens as many times as needed for you to select the spectrum files to be analyzed.



208-liter drum

Creation Date: 5/11/2007 2:08:00 PM

Number of Detectors: 2

Figure 69. Recall Template and Spectra

The only step in Soil Mode is to select a single spectrum with the file-open dialog.

When the file(s) has been recalled, select **Configuration in Memory**. The analysis creates a new scan record in the database for the results, as well as the standard set of spectrum, analysis, and report files.

CAUTION If the recalled spectrum file was acquired on a detector different from the one in the recalled configuration, the configuration is altered to include the detector used to acquire the spectrum file. *If the configuration is to be reused for actual data acquisitions, it must be re-edited to the correct detector.* ***The crystal diameter and length parameters have a major influence on the final results.***

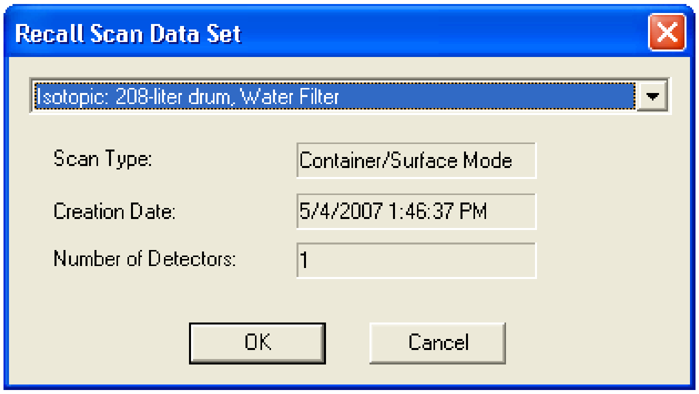
As an alternative, you might want to create a configuration specifically for this procedure. The analysis parameters associated with the imported spectrum are also loaded.

8.1.2. Recall Scan Data Set...

This function recalls the spectra — one for each MCB defined in the configuration — for a previously collected measurement (scan data set). The spectrum windows open for each MCB, and all the collection and analysis parameters are loaded. Use the droplist shown in Fig. 70 to select a scan from the database. The scan type, date, and number of detectors are shown in the dialog. These cannot be changed. After recalling, the data can be reanalyzed with new settings and re-saved in the database using the **Configuration in Memory** command (Section 8.3.4).

8.1.3. Recall Reports...

This function (Fig. 71) allows you to select a scan data set and generate a corresponding Crystal Report, if a custom Crystal Reports template was specified in the Supervisor program with the **Settings/Crystal Reports...** command. For detailed information on this feature and the resulting reports, see Chapter 6.



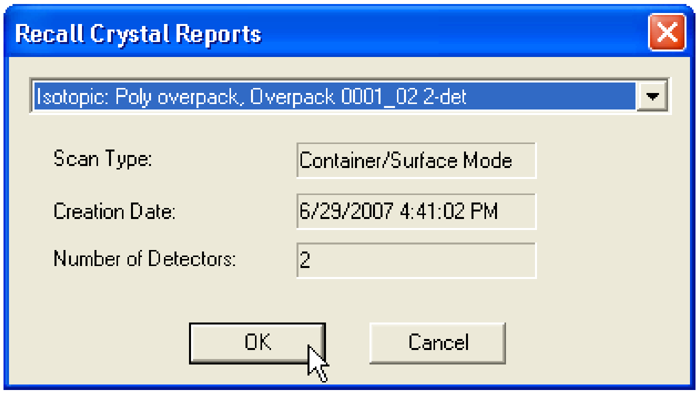
Isotopic: 208-liter drum, Water Filter

Scan Type: Container/Surface Mode

Creation Date: 5/4/2007 1:46:37 PM

Number of Detectors: 1

Figure 70. Recall Scan Data Set.



Isotopic: Poly overpack, Overpack 0001_02 2-det

Scan Type: Container/Surface Mode

Creation Date: 6/29/2007 4:41:02 PM

Number of Detectors: 2

Figure 71. Open a Crystal Reports Window.

8.1.4. Save As...

This command opens a standard file-save dialog that allows you to save the current spectrum to disk. Enter any valid filename in the **File name** field and click on **Save**. If that file already exists, a message box will ask if you wish to overwrite the existing file or cancel the operation. After the disk file has been saved, its filename will be displayed on the spectrum window title bar.

This command saves only the active spectrum. If the configuration has more than one detector, each detector must be saved individually (click in each window, then save). The scan data set (which includes all the spectra for a scan) is automatically saved with each scan. For hardware that support multiple spectra (such as ZDT mode in the DSPEC Pro), all spectra are automatically saved in the file.

8.1.5. Compare...

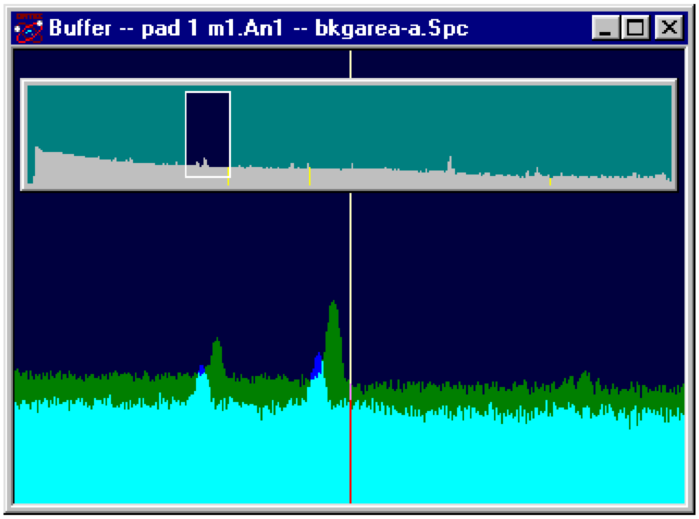


Figure 72. Comparing Two Spectra.

This function displays a spectrum from disk along with the active spectrum so the two can be visually compared. When **Compare...** is selected, a standard file-recall dialog box opens. Once the desired spectrum file is selected, the active spectrum window shows both spectra, as illustrated in Fig. 72. The comparison spectrum's ROIs (if any were saved with the file) are not marked.

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 the *Supervisor Manual* for details).

For units that support zero-dead-time (ZDT) mode, 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 <↓>.

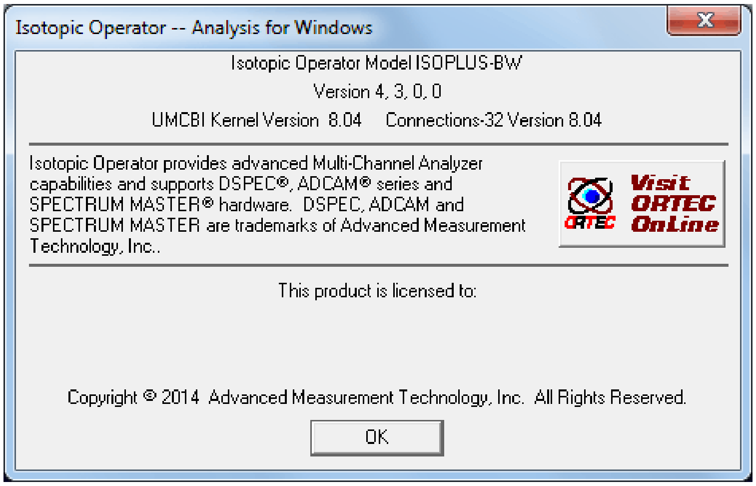
Press <**Esc**> to leave Compare mode.

8.1.6. Exit

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

8.1.7. About ISOTOPIC...

Figure 73 shows the **About** dialog for ISOTOPIC. It provides software version information that will be useful should you need customer support. Click the **Visit ORTEC Online** button to browse the ORTEC website, which includes application notes, technical papers, information on training courses, product information, and access to our Global Service Center.


Isotopic Operator -- Analysis for Windows

Isotopic Operator Model ISOPLUS-BW
Version 4, 3, 0, 0
UMCBI Kernel Version 8.04 Connections-32 Version 8.04

Isotopic Operator provides advanced Multi-Channel Analyzer capabilities and supports DSPEC®, ADCAM® series and SPECTRUM MASTER® hardware. DSPEC, ADCAM and SPECTRUM MASTER are trademarks of Advanced Measurement Technology, Inc..

This product is licensed to:

Copyright © 2014 Advanced Measurement Technology, Inc. All Rights Reserved.

Figure 73. About ISOTOPIC.

8.2. Acquire

The **Acquire** menu is shown in Fig. 74. Access to the various functions depends on whether the active spectrum window is for an MCB or a buffer.

NOTE In some cases, a command may be disabled because it is not valid for the current MCB (while it may be valid for another MCB in the system, or for this unit under different conditions).

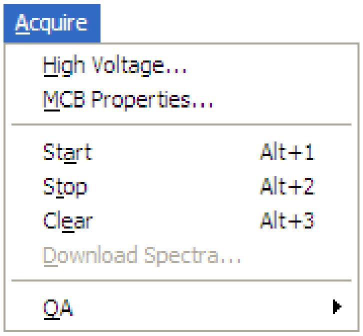
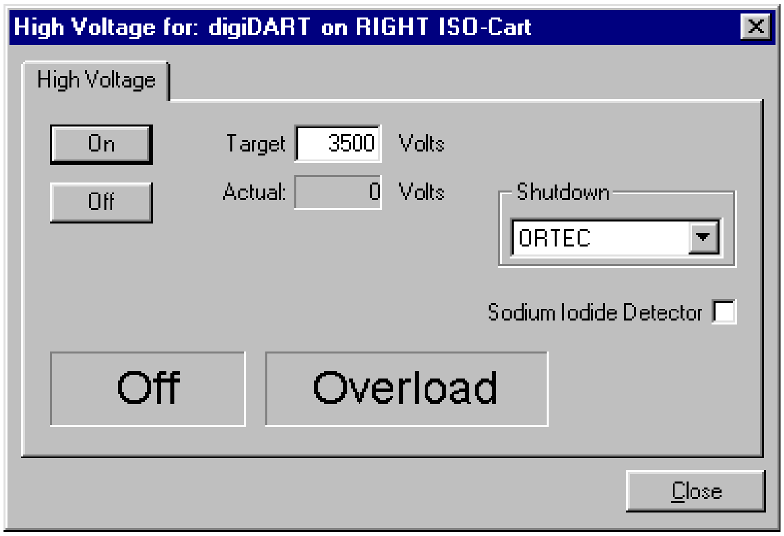


Figure 74. Acquire Menu.

8.2.1. High Voltage...

This function displays the high voltage properties page for the active Detector, as shown in Fig. 75. You can view this dialog even if the MCB Properties have not been enabled in the Supervisor program. The details of the dialog depend on the MCB type. For an example, see the discussion for the digiDART High Voltage tab on page 94.


High Voltage for: digiDART on RIGHT ISO-Cart

Target 3500 Volts
Actual: 0 Volts
Shutdown: ORTEC
Sodium Iodide Detector ☐

Figure 75. The High Voltage Properties.

8.2.2. MCB Properties...

CONNECTIONS applications use a uniform dialog for data acquisition setup, accessed with the **Acquire/MCB Properties...** command. The property pages for the digiDART are described here. To see the Properties dialog for other CONNECTIONS MCBs, refer their respective hardware manuals.[5]

Depending on the currently selected MCB, the Properties dialog displays several tabs of hardware controls that may include ADC setup parameters, acquisition presets, high-voltage controls, amplifier gain adjustments, gain and zero stabilizers, pole-zero and other shaping controls, the InSight™ Virtual Oscilloscope,[6] digital noise-suppression filters, and radionuclide detection reports. In addition, some MCBs monitor conditions such as detector temperature, external input status, alpha chamber pressure, charge remaining on batteries, and the number of spectra collected in remote mode, which are reported on a Status tab. Simply move from tab to tab and set your hardware parameters, then click **Close**. Note that as you enter characters in the data entry fields, the characters will be underlined until you move to another field or until 5 seconds have lapsed since a character was last entered. During the time the entry is underlined, no other program or computer on the network can modify this value.

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

8.2.2.1. digiDART

Amplifier

Figure 76 shows the Amplifier tab. This tab contains the controls for **Gain**, **Baseline Restore**, **Preamp-lifier Type**, **Input Polarity**, and optimization. The **Start Auto** (optimize) button should be clicked only *after* all of the controls on the tabs have been set.

NOTE The changes you make on this tab ***take place immediately***. *There is no cancel or undo for this dialog.*

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

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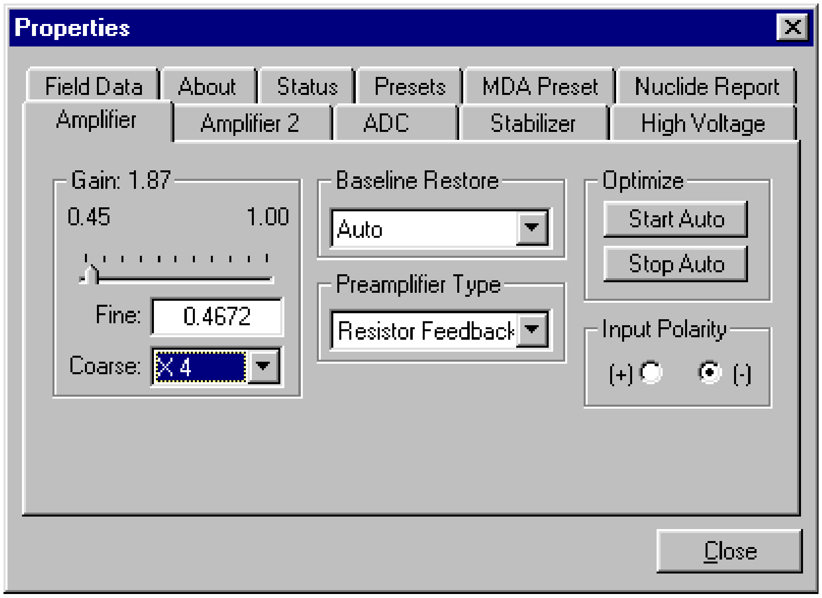
[5] For setup of pre-2005 MCBs, ORTEC can supply an electronic copy of the *ORTEC MCB Connections-32 Hardware Property Dialogs Manual* (P/N 931001).

[6] Gain and zero stabilization, setting the rise time in ORTEC digital MCBs, and the InSight virtual oscilloscope are discussed in the *Supervisor Manual*.

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 100.



Gain: 1.87
0.45 1.00
Fine: 0.4672
Coarse: X 4
Baseline Restore: Auto
Preamplifier Type: Resistor Feedback
Input Polarity: (+) ○ ● (-)

Figure 76. The digiDART Amplifier Tab.

Input Polarity — These 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 — This 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**,[7] **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 digiDART even when the power is off. The time constant can be manually set on the InSight display (see the *Supervisor Manual*).

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

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

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[7] U.S. Patent 5,912,825.

Optimize

The digiDART is equipped with both automatic pole-zero logic[8] and automatic flattop logic.[9] The **Start Auto** (optimize) button uses these features to automatically choose the best pole zero and flattop tilt settings. Pole zero is not performed for **Transistor Reset** preamplifiers.

As with any system, the digiDART should be optimized any time the detector is replaced or if the flattop width is changed. For optimization to take place, the digiDART must be processing pulses. The detector should be connected in its final configuration before optimizing is started. Position a radioactive source near the detector so the count rate causes a dead time of ~5% (typically, this will be at a count rate of 1000–5000 cps). Dead time is displayed on the digiDART front panel and the ISOTOPIC Status Sidebar during data acquisition.

Select either the **Resistive Feedback** or **Transistor Reset** option and click **Start Auto**. The optimize command is sent to the digiDART at this time and, if the digiDART 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 digiDART 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 digiDART, the optimize function does not need to be repeated for each possible rise time. If the source count rate is sufficient, optimization should take 3–5 minutes.

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 might not change enough to be seen. The most visible effect of incorrect settings is high- or low-side peak tailing or poor resolution. For small changes in the settings, the change in the shape of the spectrum peaks might be too small to see.

Amplifier 2

Figure 77 shows the Amplifier 2 tab, which accesses the advanced digiDART shaping controls including the InSight Virtual Oscilloscope mode, which is discussed in the *Supervisor Manual*.

The many choices of **Rise Time** allow a precise control in the tradeoff between resolution and throughput. The value of the rise time parameter in the digiDART is roughly equivalent to twice

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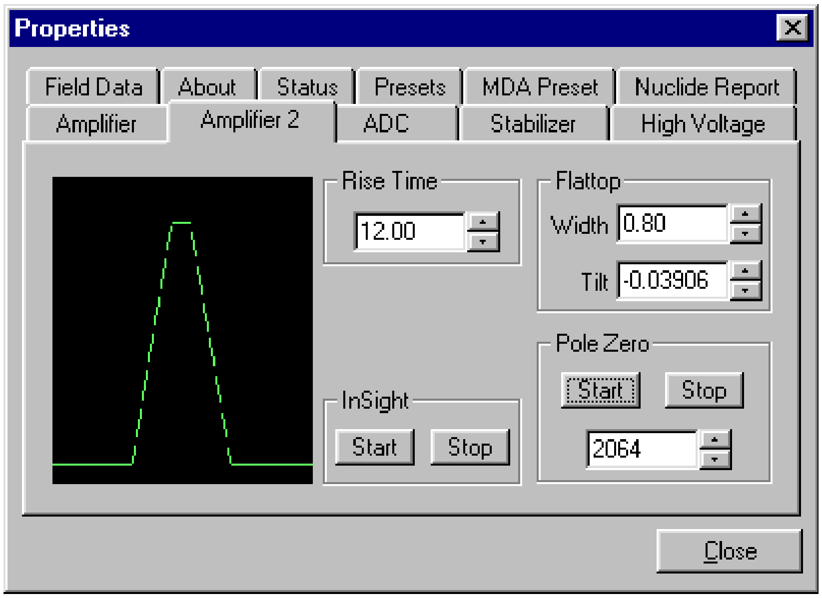
[8] Patent number 5,872,363.

[9] Patent number 5,821,533.

the integration time set on a conventional analog spectroscopy amplifier. Thus, a digiDART value of 12 µs corresponds to 6 µs in a conventional amplifier. Starting with the nominal value of 12 µs, increase 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. Increasing the rise time to a large value can increase (worsen) the resolution due to the increase in the signal noise included in the peak signal.



Rise Time: 12.00

Flattop

Width: 0.80

Tilt: -0.03906

Pole Zero: 2064

Figure 77. The digiDART Amplifier 2 Tab.

Use the up/down arrows to adjust the **Rise Time** within the range of 0.2 to 23.0. After all the controls have been adjusted, return to the Amplifier tab and click **Start Auto**. The most recent settings are saved in the digiDART firmware even when the power is turned off.

For the more advanced user, the InSight mode gives a direct view of all the parameters and the controls to adjust them interactively while collecting live data. To access the InSight mode, go to the **InSight** section on the Amplifier 2 tab and click **Start**.

The **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 $(3 \times \textit{Rise Time}) + (2 \times \textit{Flattop Width})$.

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.

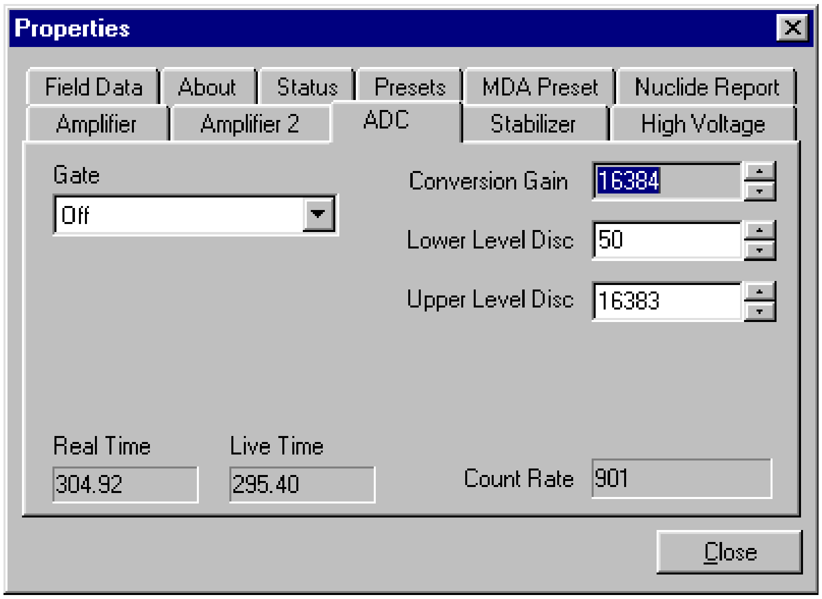
When the settings are correct, **Close** the Properties dialog and prepare to acquire data.

Once data acquisition is underway, the advanced user might wish to return to **MCB Properties...** and click the **Insight** section **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.

ADC

This tab (Fig. 78) contains the **Gate**, **ZDT Mode**, **Conversion Gain**, **Lower Level Disc**riminator, and **Upper Level Disc**riminator controls. In addition, the current real time, live time, and count rate are monitored at the bottom of the dialog.

Gate — This control allows you to select a 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 nanoseconds beyond peak detect (peak maximum).



Gate: Off

Conversion Gain: 16384

Lower Level Disc: 50

Upper Level Disc: 16383

Real Time: 304.92

Live Time: 295.40

Count Rate: 901

Figure 78. The digiDART ADC Tab.

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 (e.g., 8192, 4096, 2048, ...). The up/down arrow buttons step through the valid settings.

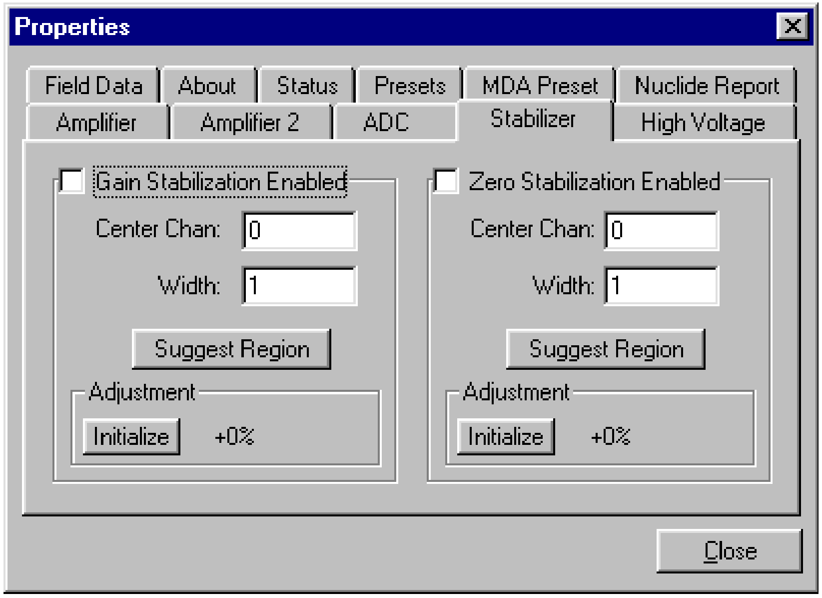
Upper- and Lower-Level Discriminators

In the digiDART the lower- and upper-level discriminators are under computer control. The **Lower Level Disc**riminator 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. Setting that level above random noise increases useful throughput because the MCB is not unproductively occupied processing noise pulses.

The **Upper Level Disc**riminator sets the level of the highest amplitude pulse that will be stored. This level establishes an upper-level cutoff by channel number for ADC conversions.

Stabilizer

The digiDART has both a gain stabilizer and a zero stabilizer. Gain and zero stabilization are discussed in detail in Section 3.2.8.2. The Stabilizer tab (Fig. 79) 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 Chan**nel and **Width** fields show the peak currently used for stabilization.



☐ Gain Stabilization Enabled
Center Chan: 0
Width: 1
Adjustment +0%

☐ Zero Stabilization Enabled
Center Chan: 0
Width: 1
Adjustment +0%

Figure 79. The digiDART Stabilizer Tab.

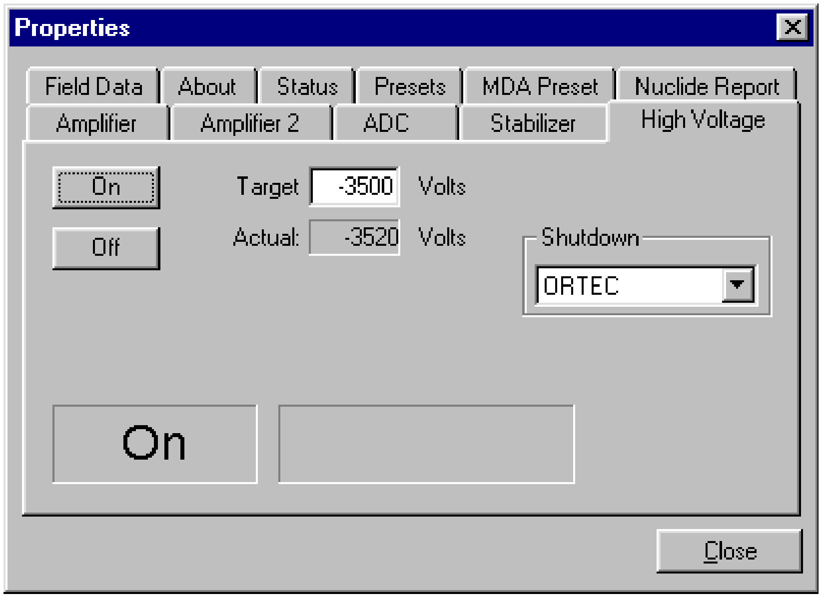
To enable the stabilizer, enter the **Center Chan**nel and **Width** values manually or click the **Suggest Region** button. **Suggest Region** reads the position of the marker and inserts values into the fields. If the marker is in an ROI, the limits of the ROI are used. If the marker is not in an ROI,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

High Voltage

Figure 80 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.

Enter the detector high voltage in the **Target** field, click **On**, and monitor the voltage in the **Actual** field. To turn the high voltage off, click the **Off** button.

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. The Overload indicator means there is a bad connection in your system. The Shutdown indicator means that either the detector is warm or you have chosen the wrong **Shutdown** mode.



Target -3500 Volts

Actual: -3520 Volts

Shutdown ORTEC

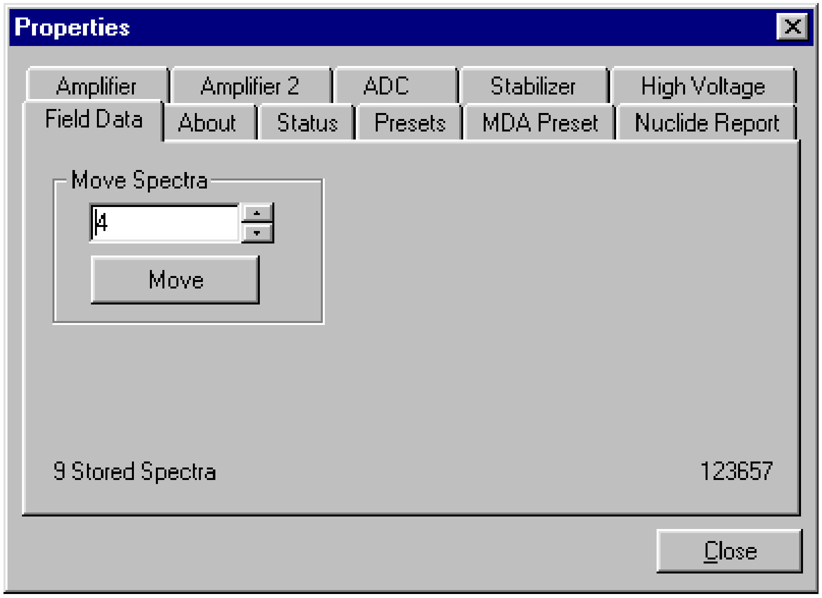
Figure 80. The digiDART High Voltage Tab.

The shutdown can be **ORTEC**, **TTL**, or **SMART**. The **ORTEC** mode is used for all ORTEC detectors except SMART-1® detectors, which use the **SMART** setting. For other detectors, check with the manufacturer. The **TTL** mode is used for most non-ORTEC detectors.

The high voltage in the digiDART 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.

Field Data

This tab (see Fig. 81) is used to view the spectra in the digiDART collected in field mode, that is without a computer attached. The digiDART is always in field mode when the computer is disconnected. The spectrum can then be viewed as the “active” spectrum in the digiDART. The active spectrum is the spectrum where the new data are collected. The current active spectrum is lost.



Move Spectra 4

9 Stored Spectra 123657

Figure 81. The digiDART Field Data Tab.

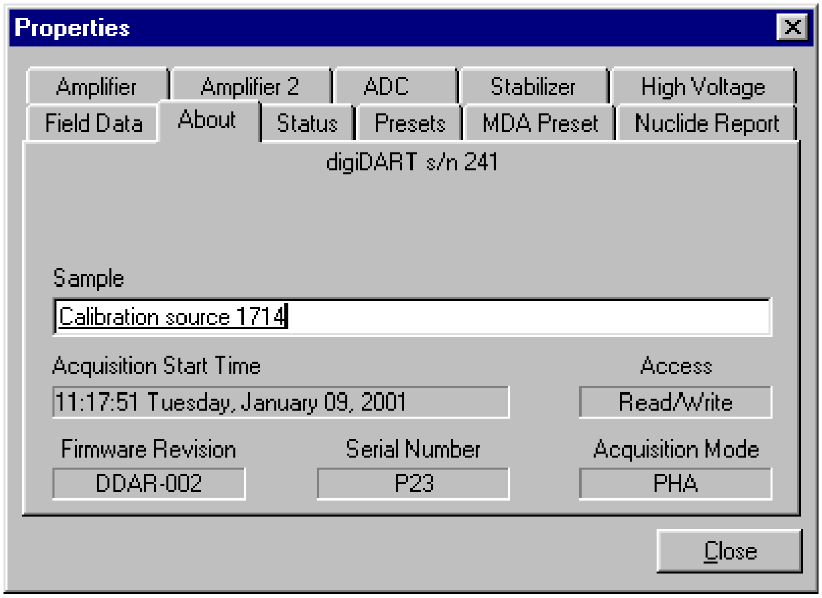
The lower left of the tab shows the total number of spectra (not counting the active spectrum) stored in the digiDART memory. The spectrum ID of the active spectrum is shown in the lower right. The stored spectra cannot be viewed or stored in the computer until they are moved to the active spectrum position.

To move a spectrum from the stored memory to the active memory, enter the spectrum number and click **Move**. Use the up and down arrow buttons to scroll through the list of spectra. The label on the lower right does not update until a spectrum is moved. The numbers are the same as the numbers on the digiDART display. This only moves the spectrum to active memory. To save the spectrum on the computer disk, use the **File/Save** commands.

The **Acquire/Download Spectra** can also be used to download all the stored spectra and save on disk automatically. They can then be viewed in the Buffer.

About

This tab (Fig. 82) displays hardware and firmware information about the currently selected digiDART as well as the data **Acquisition Start Time** and **Sample** description. *Note that creating an entry in the **Sample** field is the only way to add a sample description to a spectrum file created in Supervisor.* The **Access** field shows whether the MCB is currently locked with a password (see the *Supervisor Manual*). **Read/ Write** indicates that the MCB is unlocked; **Read Only** means it is locked.



digiDART s/n 241

Sample: Calibration source 1714

Acquisition Start Time: 11:17:51 Tuesday, January 09, 2001

Access: Read/Write

Firmware Revision: DDAR-002

Serial Number: P23

Acquisition Mode: PHA

Figure 82. The digiDART About Tab.

Status

Figure 83 shows the Status tab. Twenty-one values are monitored at all times. Use the droplists to select any six parameters to be displayed simultaneously on the Status tab (normally these would be the six that are most important to you). The values you select can be changed at any time, so you can view each of them as needed. Two types of values are presented: **OK** or **ERR**, and numeric value. The state-of-health (SOH) 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 digiDART. **Security**, **Detector temperature**, and **Live detector temperature** are available only for SMART-1 detectors. For non-SMART-1 detectors, they display **N/A**.

The available parameters are:

Detector State of Health

Reads OK if all the SOH are within operating limits and ERR if any one is outside the limits.

DIM +24V State of Health

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

DIM +12V State of Health

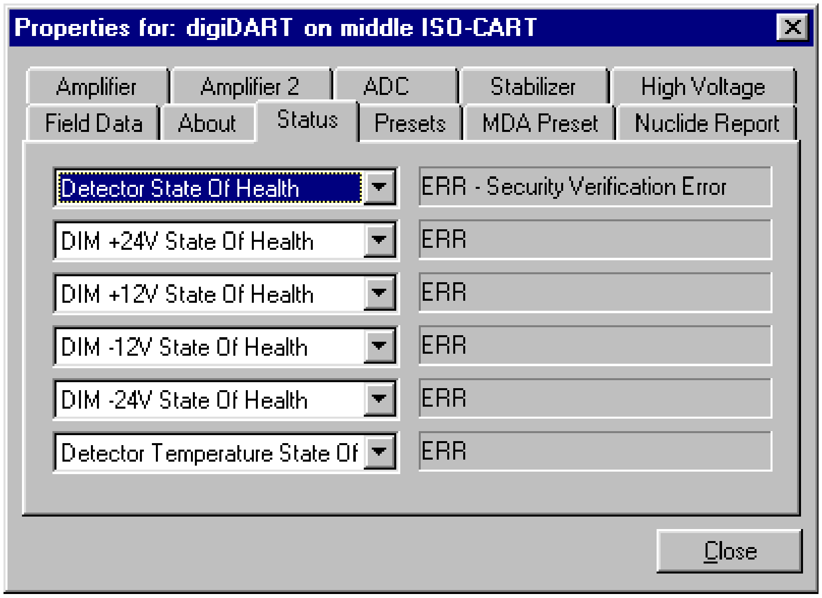
Reads OK if the +12 volt supply in the DIM has stayed within 200 mV of +12 V since the last time the SOH was cleared.

DIM -12V State of Health

Reads OK if the −12 volt supply in the DIM has stayed within 200 mV of −12 V since the last time the SOH was cleared.

DIM -24V State of Health

Reads OK if the −24 volt supply in the DIM has stayed within 200 mV of −24 V since the last time the SOH was cleared.



Detector State Of Health	ERR - Security Verification Error
DIM +24V State Of Health	ERR
DIM +12V State Of Health	ERR
DIM -12V State Of Health	ERR
DIM -24V State Of Health	ERR
Detector Temperature State Of	ERR

Figure 83. The digiDART Status Tab.

Temperature State of Health

Reads 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

Reads 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

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

Preamplifier overload State of Health

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

Security State of Health

Reads 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

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

+24 volts

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

+12 volts

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

−12 volts

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

−24 volts

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

High Voltage

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

Detector temperature

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

Live detector temperature

The detector temperature at the current time. This is available only for SMART-1 detectors. This information is helpful to determine if the detector is cold enough to operate The normal operation temperature should be 88–100 K. Do not ship the detector when the temperature is below 296 K.

Battery voltage

The current voltage of the internal battery.

Battery % full

The estimated amount of power remaining in the battery.

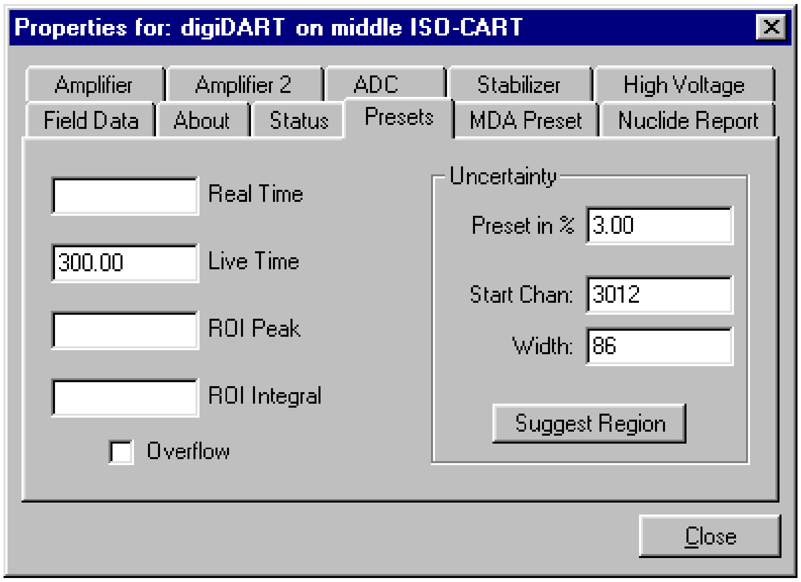
Battery time remaining

The estimated time remaining when operating the digiDART on the internal battery.

Presets

Figure 84 shows the Presets tab. MDA presets are shown on a separate tab.

The presets can only be set on an MCB that is not acquiring data (during acquisition the preset field backgrounds are gray indicating that they are inactive). Any or all of the presets can be used at one time. To disable a preset, enter a value of zero. If all of the presets are disabled, data acquisition will continue until manually stopped.


Properties for: digiDART on middle ISO-CART

Real Time:
Live Time: 300.00
ROI Peak:
ROI Integral:
☐ Overflow

Uncertainty
Preset in %: 3.00
Start Chan: 3012
Width: 86

Figure 84. The digiDART Presets Tab.

When more than one preset is enabled (set to a non-zero value), the first condition met during the acquisition causes the MCB to stop. This can be useful when samples of widely varying activity are analyzed and the general activity is not known 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 both the **ROI Peak** preset and the **Live Time** preset are set, the low-level samples will be counted to the desired fixed live time while the very active samples will be counted for the ROI peak count. In this circumstance, the **ROI Peak** preset can be viewed as a “safety valve.”

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

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

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

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

The **Uncertainty** preset stops acquisition when the statistical or counting uncertainty of a user-selected net peak reaches the value 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. The peak is the region selected here. The region must be at least 7 channels wide with 3 channels of background on each side of the peak. Note that ISOTOPIC calculates this preset once per 40 seconds. Therefore, the software will continue data acquisition up to 40 seconds after the preset has been reached, and the uncertainty achieved for a high count-rate sample may be lower than the preset value.

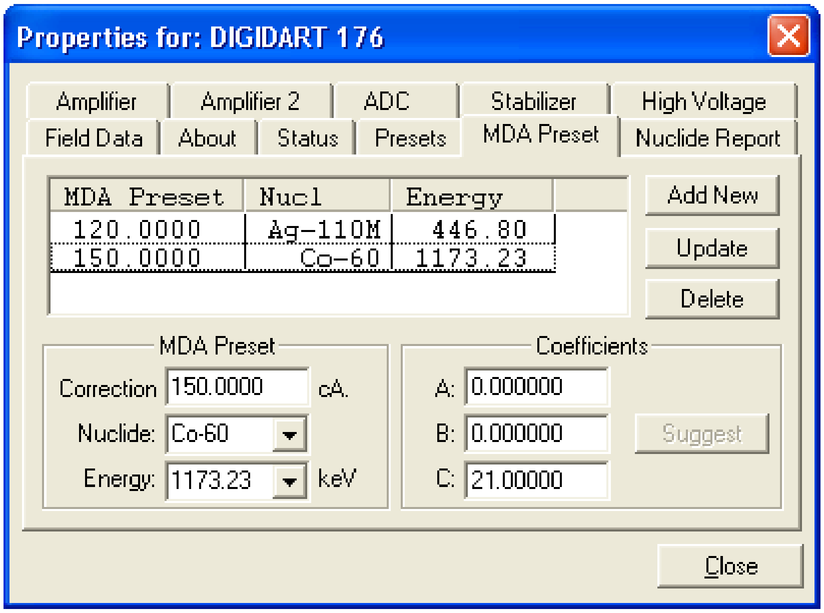
Use the **Start Chan**nel and **Width** fields to enter the channel limits directly, or click **Suggest Region**. If the marker is positioned in an ROI around the peak of interest, **Suggest Region** reads the limits of the ROI with the marker and display those limits in the **Start Chan** and **Width** 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 **Calculate/ Peak Info** (see Section 8.4.2, 8.6.6).

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

MDA Preset

The MDA preset (Fig. 85) can monitor up to 20 nuclides at one time, and stops data collection when the values of the minimum detectable activity (MDA) for *all* of the user-specified MDA nuclides reach the needed value. Presets are expressed in Bq, and are evaluated every 40 seconds. The detector must be calibrated for energy in all spectroscopy applications, and for efficiency in all applications but MAESTRO.



MDA Preset	Nucl	Energy
120.0000	Ag-110M	446.80
150.0000	Co-60	1173.23

Correction 150.0000 cA.
Nuclide: Co-60
Energy: 1173.23 keV
A: 0.000000
B: 0.000000
C: 21.00000

Figure 85. The digiDART MDA Preset Tab.

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

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

where:

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

Counts is the gross counts in an ROI that is 2.5×FWHM around the target peak energy.

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

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

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

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

To remove a preset, click to high-light it in the table, then click **Delete**.

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

Nuclide Report

The Nuclide Report (Fig. 86) displays the activity of up to nine user-selected peaks. Once the report is set up, the Nuclide Report can be viewed at any time on the digiDART display when it is not connected to a computer. The peak area calculations in the hardware are the same as the calculations done here, so the Nuclide Report display is the same as the Peak Info display on the selected peak in the spectra stored in the computer. The calculated value is computed by multiplying the net peak count rate by a user-defined constant. If the constant includes the efficiency and yield, the displayed value will be activity. The nuclide label and the activity units are entered by the user.

The report has this format:

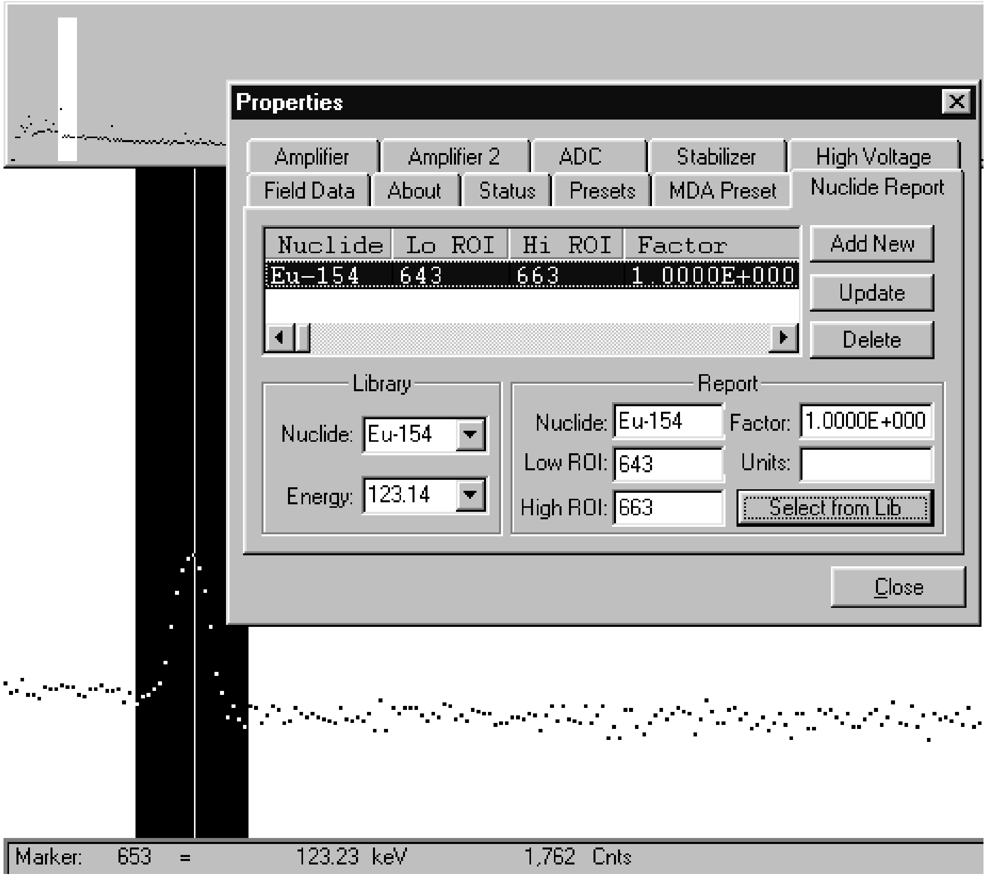
Nuclide	keV	µCi/m2	±%
CO-60	1332.5	12.1	10.2
CO-60	1173.2	10.9	12.3
CO-57	122.1	1.8	86.2

See the *Supervisor Manual* for the calculations.

Add New

You can add Nuclide Peaks to the report manually or by selecting the peaks from the current working library. The spectrum must be energy calibrated to use the library method.

- **Defining Peaks Manually** — To manually define peaks, enter the **Nuclide** name, ROI **Low** (start) and **High** (end) channels, multiplicative **Factor** and **Units** in the Report section; then click **Add New**. All nuclides in the table use the same units, so that value need only be entered once.



Nuclide	Lo ROI	Hi ROI	Factor
Eu-154	643	663	1.0000E+000

Library
Nuclide: Eu-154
Energy: 123.14

Report
Nuclide: Eu-154
Factor: 1.0000E+000
Low ROI: 643
Units:
High ROI: 663

Marker: 653 = 123.23 keV 1,762 Cnts

Figure 86. Nuclide Report Setup Tab.

- **Selecting Peaks from the Working Library** — To define report peaks using the library, select the **Nuclide** and gamma-ray **Energy** in the Library section. This defines which gamma ray to use. Now, in the Report section, click the **Select from Lib** button. Enter the **Factor** and **Units**, then click **Add New** to add this nuclide to the list. The ROI for this peak will be marked in the MCB’s spectrum window, centered on the peak energy and 3 times the width of the calibrated FWHM.

Edit

To change any of the current nuclides, select the nuclide in the list (use the scroll bars if needed). This will show the current settings for this nuclide. Make any changes needed. Any or all of the entries can be changed. When finished with the changes, click **Update**.

Delete

- To remove an entry, select the entry and click **Delete**.
- When the properties dialog is closed, all the values are written to the digiDART and will be used when the Nuclide Report is displayed on the digiDART display.

8.2.3. Start

This initiates data collection in the active MCB. 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 MCB 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 MCB is already started or if a buffer is the active spectrum, this entry is gray.

8.2.4. Stop

Stop terminates data collection in the active MCB. If the MCB is not collecting data or the active spectrum is a buffer, the entry is gray (inactive). The MCB 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.

8.2.5. 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 may **not** operate on some types of MCBs 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.

8.2.6. QA

This is explained in Chapter 9, "Quality Assurance."

8.3. Analyze

Figure 87 shows the **Analyze** menu, which contains the commands for analysis setup, the peak background correction (PBC), and data reanalysis.

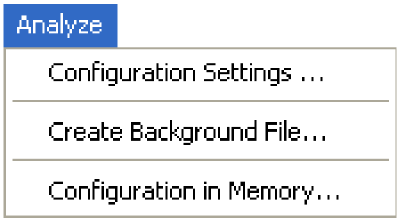


Figure 87. Analyze Menu.

The mode of operation for the Operator program — Container/ Surface (Isotopic) or Soil (EML 1-meter method) — determines which **Configuration Settings...** dialog is displayed. The details of the setup depend on the mode, which can only be selected in the Supervisor program. The Container/Surface Mode, with the **Point Source** configuration and **Surface/Disk** container shape, is used for spills or other small floor areas where the Soil Mode is not appropriate.

8.3.1. Container/Surface Mode: Configuration Settings...

This opens the Configuration Wizard ***for Container/Surface Mode.*** (To create a Soil Mode configuration, see Section 8.3.2.)

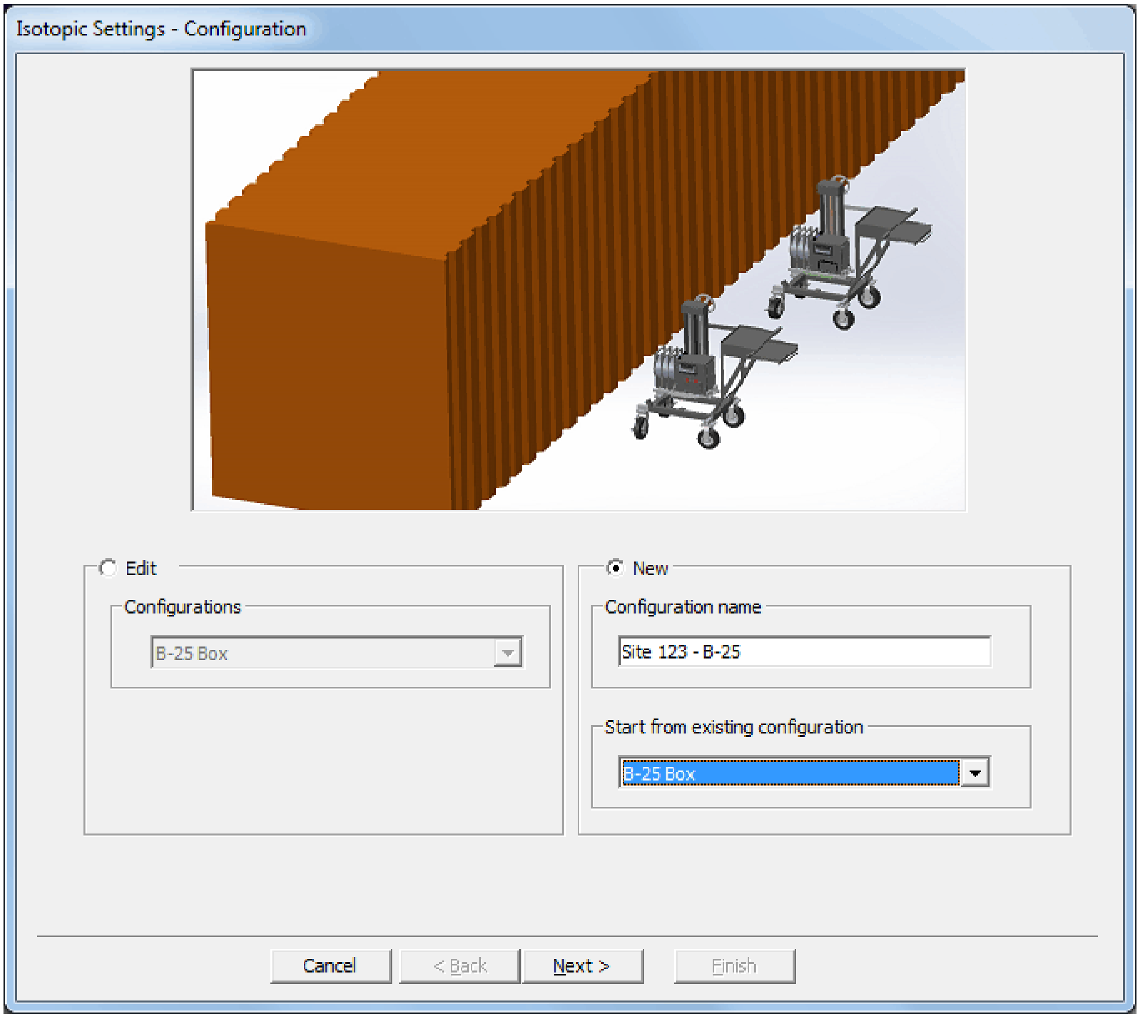
NOTE The Configuration Wizard is a feature of ISOTOPIC v4.x that combines the former Analysis Options, Operator Container Parameters, and Collimator dialogs. The result is a data acquisition and analysis *configuration* which is stored in the ISOTOPIC database. Sample description (`.SDF`) files are now used only in QA (see Section 9 in the *Supervisor Manual*).

A configuration is similar to an `.SDF` file in that it directs data acquisition, analysis, and reporting for container measurements. However, it also contains information about container type, detector geometry, and uranium/plutonium enrichment.

The configurations settings are automatically saved in the database when you click **Finish** on the last page of the wizard. If you cancel out of the wizard, the changes are not stored.

8.3.1.1. Configuration Page

Figure 88 shows the first page of the Configuration Wizard.



Isotopic Settings - Configuration

○ Edit

Configurations: B-25 Box

● New

Configuration name: Site 123 - B-25

Start from existing configuration: B-25 Box

Figure 88. Configuration Page.

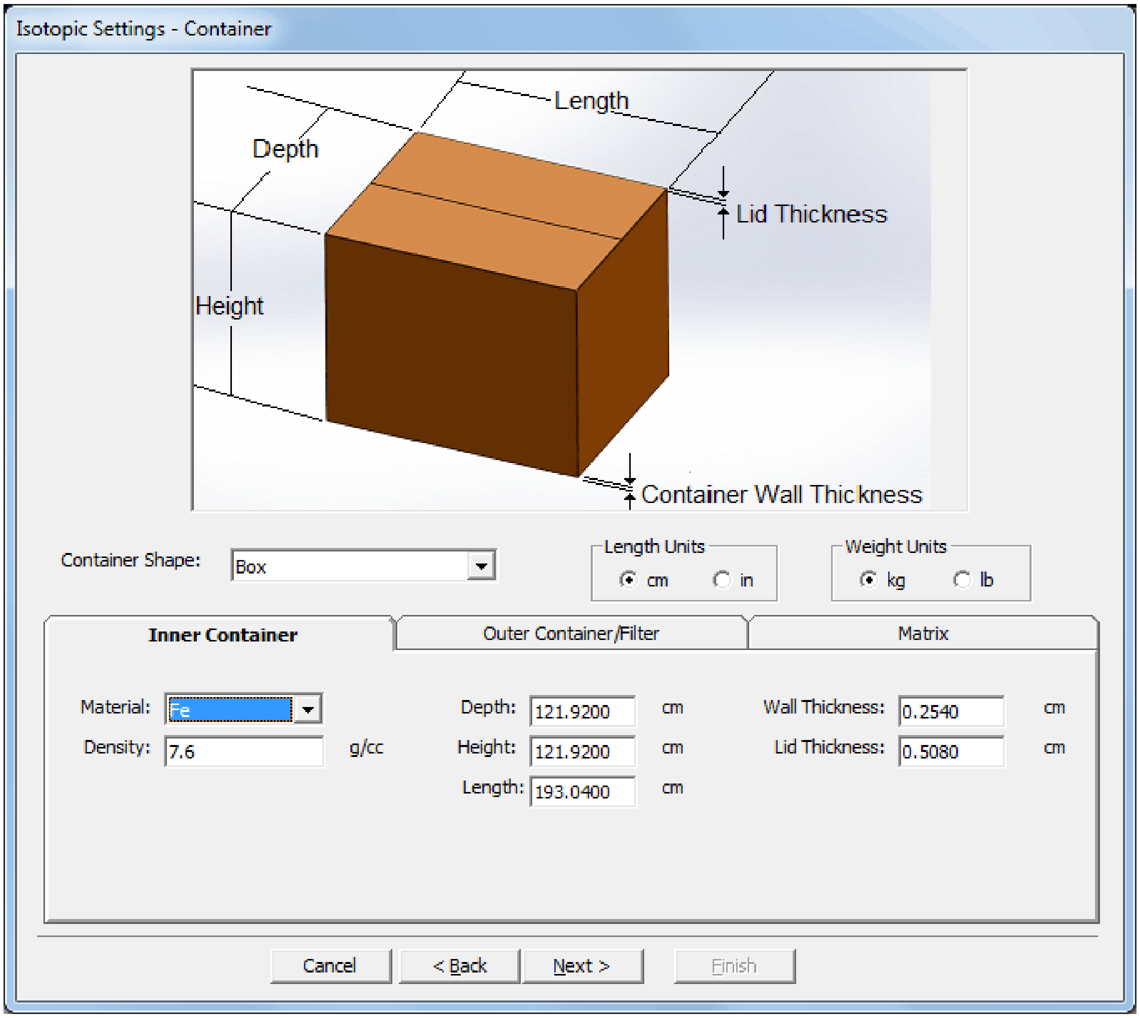
You can use the existing configurations as is or **Edit** them at any time to suit your measurement configuration. You can also create as many **New** configurations as desired. The **Start from existing configuration** feature allows you to use an existing active configuration as a template for your new configuration.

Select an existing configuration or mark the **New** radio button and enter a new **Configuration name**. If you wish, choose an **existing configuration** as a template. All of the settings from the existing configuration will be copied to the new configuration. Modify them as needed.

Click **Next**.

8.3.1.2. Container Page

Use the Container page (Fig. 89) to characterize the item to be counted.



Isotopic Settings - Container

Container Shape: Box

Length Units: ● cm ○ in

Weight Units: ● kg ○ lb

Material: Fe

Density: 7.6 g/cc

Depth: 121.9200 cm

Height: 121.9200 cm

Length: 193.0400 cm

Wall Thickness: 0.2540 cm

Lid Thickness: 0.5080 cm

Figure 89. Inner Container Tab, Container Page.

CONTAINER SETUP SUGGESTIONS

- Model the *activity* rather than the *container*. Note that usually, but not always, the activity takes the shape of the inner container. The following shapes are available from the **Container shape** droplist:
  - — **Cylinder** — For drums or filled pipes, thick disks.
  - — **Box** — For HEPA filters or other rectangular-shaped or square-shaped objects.
  - — **Lined cylinders** — For contaminated piping.
  - — **Point-source in a container** — For points sources in a cylinder or heavily shielded hot sources where the activity has a small volume and there are three containers (e.g., lead, steel, and concrete) used to reduce the shielding.
  - — **Disk or spill** — For thin, circular-shaped activity, point sources, floor spills of a relatively small diameter. Large areas of contaminated ground (diameter >10 m) are best analyzed in the Soil Mode (see Section 8.3.2).
  - — **Bottle** — For 1-liter bottles or other small cylinders placed on endcap.

- Determine the container thickness. For nested containers, if several have the same material and density, you can sum the thicknesses and enter the result as the thickness of a single container.

- Estimate the density of the matrix for the waste stream. The matrix density is a major contributor to the item attenuation correction. If possible, each item of the waste stream should be weighed to improve the matrix density determination. The weight can only be entered in the Operator program.

- Select the units of measure for **Length** and **Weight** to be used in the Container report in Operator. ISOTOPIC can use both SI (metric) units and U.S. customary (inches/pounds) units. It allows you to mix and match units according to the preference of your facility. Regardless of the units selected, all densities are in g/cc.

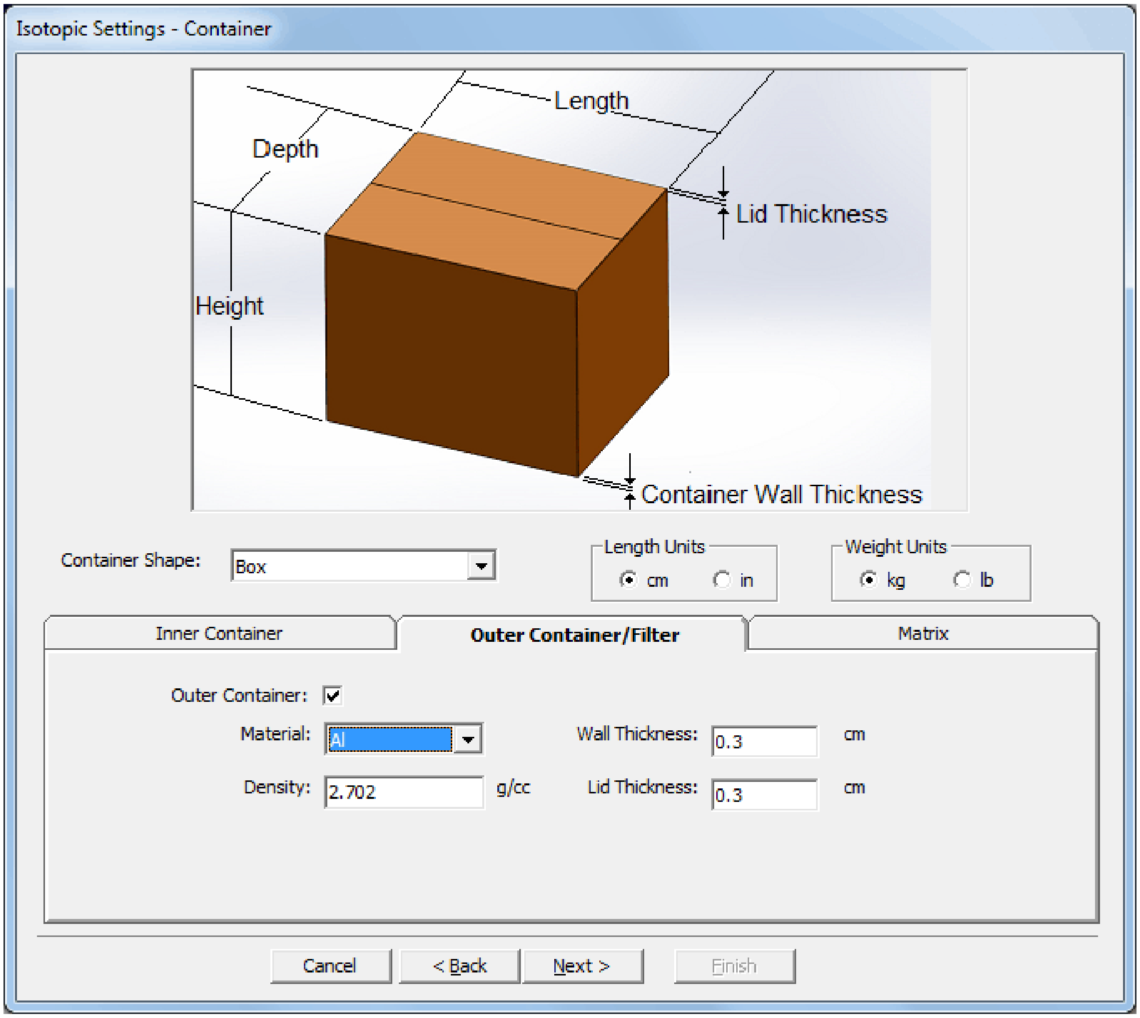
  NOTE The units of measure selected here also affect the units available in the Operator program, e.g., the Scan Control Area on the main Operator screen. These units can be changed in the Operator program if the **Allow Modification of Configuration Parameters** checkbox is marked in Operator Permissions in the Supervisor program.

Inner Container

On the Inner Container tab (Fig. 89), choose a **Material** from the droplist. The entries on this list are taken from the attenuation database, which contains most common materials. New materials can be added in the Supervisor program.

If the object to be counted is not in a container (e.g., a milling machine), select **None** for the inner container **Material**.

If the object to be counted is not in a container (e.g., a milling machine), select **None** for the inner container **Material**.



Container Shape: Box

Length Units: ● cm ○ in

Weight Units: ● kg ○ lb

Outer Container: ☑

Material: Al

Density: 2.702 g/cc

Wall Thickness: 0.3 cm

Lid Thickness: 0.3 cm

Figure 90. Outer Container Tab, Container Page.

The **Density** is read from the database. If you know that the actual density differs from the value in the database, enter the known value here. It will be saved ***for this Container Type only***. Enter the container dimensions according to the definitions in the figure at the top of the dialog. Some shapes do not use all of the available dimensions on the dialog; the unused dimensions are gray.

Outer Container/Filter Page

Click the Outer Container/Filter tab (Fig. 90). This allows you to characterize the outer container or a filter or absorber inserted between the detector and the container. The **Material** list here contains the same entries as the list on the Inner Container tab. The dimensions are calculated from the inner container dimensions. For containers, enter the wall and lid thickness; for filters, enter the filter thickness for both the wall and lid thicknesses.

Matrix Page

Figure 91 shows the Matrix tab. The matrix is the material in the container enclosing the radioactive substances. The matrix density and attenuation corrections are usually the dominant source of corrections for gamma-ray attenuation.

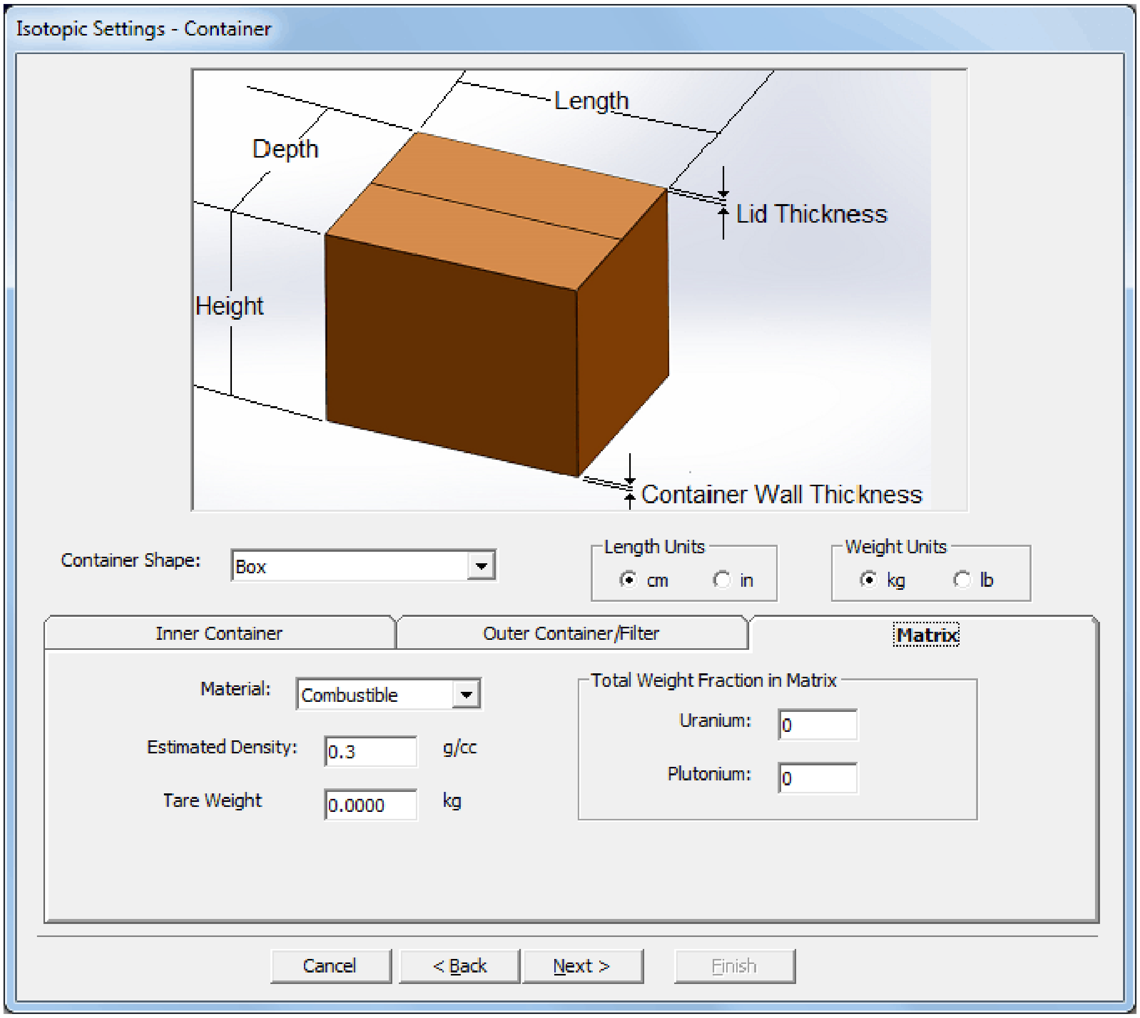
The **Material** list is drawn from the attenuation database. New materials can be added in the Supervisor program.

A default **Estimated Density** for the material is used unless you enter a new density here. The default value is typically the crystalline density of the material. In practice, however, the fill density of a pure material is much less than its crystalline density. If you know the actual density, enter it here.

The **Tare wt** is the weight of the empty container.

If uranium or plutonium is present, the possibility of self-attenuation exists. Self-attenuation effects are corrected in the software. These corrections are almost impossible to estimate initially. The program will calculate an initial selection. When uranium is detected in the sample, if the sample is nonhomogeneous, ISOTOPIC assigns an initial value of 0.001 weight fraction uranium. The presence of uranium fluorescence X rays at 98.44 keV indicates that a significant amount of uranium self-attenuation is present. If you know the matrix contains a greater fraction of uranium or plutonium, you should enter that greater fraction in the appropriate **Total Weight Fraction** field. If you enter a value here, it is used as the default value on the **Adjustments** sidebar in the Results Plot window.

Click **Next** to go to the Analysis page.



Container Shape: Box

Length Units: ● cm ○ in

Weight Units: ● kg ○ lb

Material: Combustible

Estimated Density: 0.3 g/cc

Tare Weight 0.0000 kg

Total Weight Fraction in Matrix

Uranium: 0

Plutonium: 0

Figure 91. Matrix Tab, Container Page.

8.3.1.3. Analysis Page

This page allows you to specify the analysis parameters as well as the contents of the Container/ Surface report.

Analysis Tab

Figure 92 shows the Analysis tab.

ANALYSIS SETUP SUGGESTIONS FOR CONTAINER MODE

- When analyzing containers, high attenuation is usually an issue. In such cases, averaging the activity of a high-energy gamma ray with that of a lower-energy gamma ray could bias the results unless your container modeling is "perfect." To minimize this problem, no activity averaging is done in Container Mode, and the **Not In Average (A)** flag is ignored. Instead, only one gamma ray for each library nuclide is used as a reference gamma ray for activity reporting. Because of this, *you must optimize your library as follows*. Use the **Cut**, **Insert**, and **Paste** buttons to rearrange the library as required (see the *Supervisor Manual*).

  - For each nuclide in the library, choose one high-energy gamma ray as the reference peak to be used for determining activity.
  - Move all the reference gamma rays so they are listed in the library *ahead of any other gamma rays*. In other words, if the library contains 10 nuclides, the library should start with the 10 reference gamma rays.
  - The remaining gamma rays for all of the library nuclides can then follow in any order.

- In all cases make certain that the most intense, clean (no interferences likely) gamma ray for a particular nuclide is referenced first in your library. The next three most intense gamma rays should be listed next in the library.

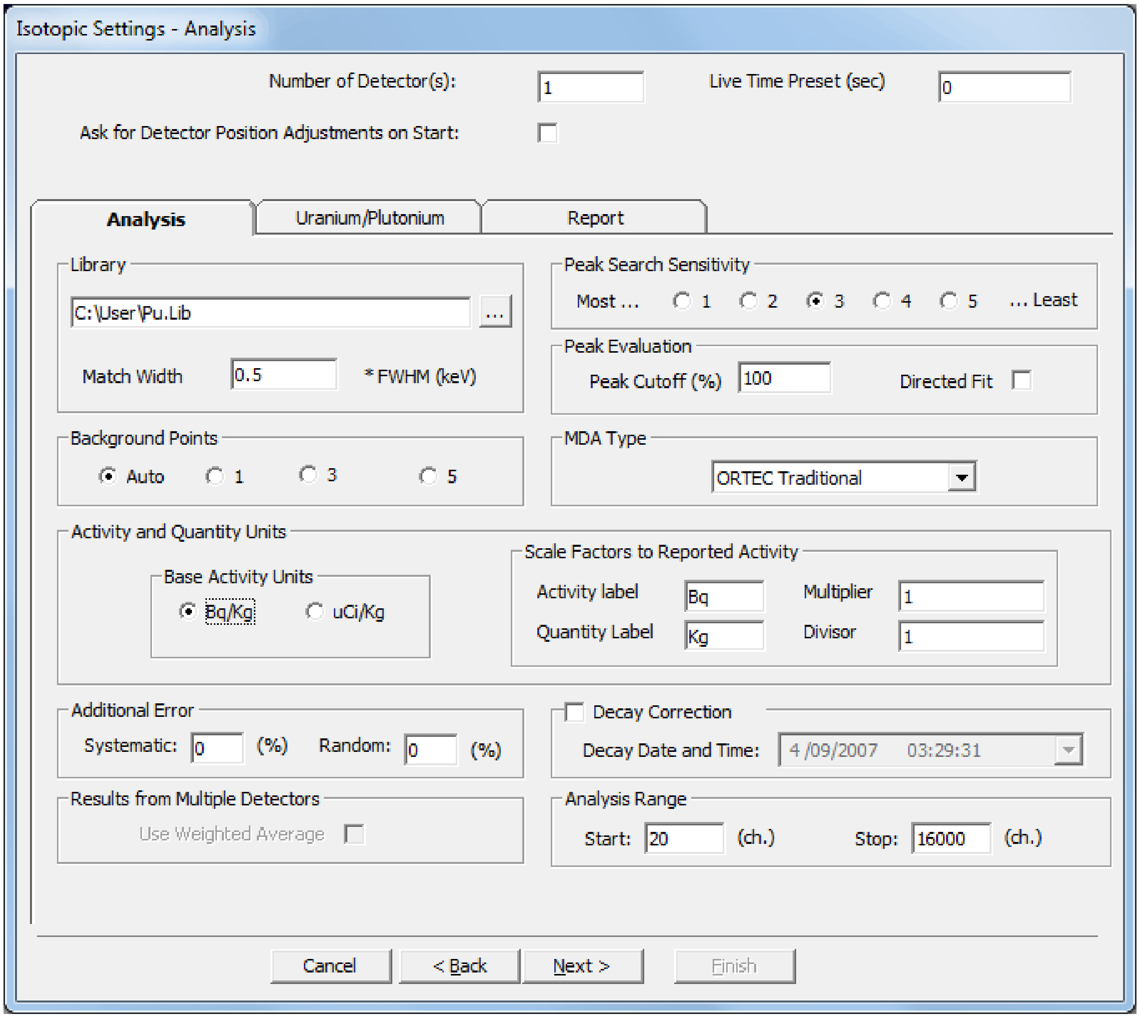
- The following parameters can affect the detection of weak peaks:
  - Peak search sensitivity
  - Match width (set to **0.5**)
  - Peak cutoff (set to **40%** and increase if necessary)
  - Background type (default set to **Auto**, but adjust to **5** if necessary for very weak peaks)

- Do not "clutter" your library with too many nuclides and gamma rays. The search engines will not be very effective in this situation. Use only the nuclides and gamma rays that are likely to be present.

- When creating libraries, if you work from the supplied `Lib0` or `Lib1` master library, it might be helpful to delete all X rays from the list of gamma rays for each nuclide. The energy **Auto-calibrate** feature works better if the library includes no X rays.

First, enter the **Number of Detectors** and the **Live Time Preset** (in seconds). If the operator will be adjusting detector positions before each measurement, mark the **Ask for Detector Position Adjustments on Start** checkbox. For measurements from a single, fixed detector position, leave this box unmarked.

Enter the **Library** file and **Match Width** to be used for the analysis. The **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.



Number of Detector(s): 1
Live Time Preset (sec) 0
Ask for Detector Position Adjustments on Start: ☐

Library
C:\User\Pu.Lib ...
Match Width 0.5 * FWHM (keV)

Peak Search Sensitivity
Most ... ○ 1 ○ 2 ● 3 ○ 4 ○ 5 ... Least

Peak Evaluation
Peak Cutoff (%) 100 Directed Fit ☐

Background Points
● Auto ○ 1 ○ 3 ○ 5

MDA Type
ORTEC Traditional

Activity and Quantity Units
Base Activity Units
● Bq/Kg ○ uCi/Kg

Scale Factors to Reported Activity
Activity label Bq Multiplier 1
Quantity Label Kg Divisor 1

Additional Error
Systematic: 0 (%) Random: 0 (%)

☐ Decay Correction
Decay Date and Time: 4 /09/2007 03:29:31

Results from Multiple Detectors
Use Weighted Average ☐

Analysis Range
Start: 20 (ch.) Stop: 16000 (ch.)

Figure 92. Analysis Tab, Analysis Page.

HINTS If your final report includes false positives, add more key line flags. This is especially helpful for the ISOWAN32 analysis engine.

If multiplets are not present, the **Match Width** can be set to values as great as 1.0. This is helpful when there is a slight gain shift and the identification of critical peaks is missed.

The **Background Points** can be set to **Auto**, **1-pt.**, **3-pt.**, **or 5-pt.** These are explained in more detail in the analysis methods chapter in the *Supervisor Manual*.

The **Peak Search Sensitivity** sets the sensitivity for the full-spectrum analysis. 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 may 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. The parabolic background method is disabled for energies above 200 keV if the sensitivity is set to 1.

In the **Peak Evaluation** section, the **Peak Cutoff** limits the unknown peak list to peaks with 1-sigma uncertainty below this value. Mark the **Directed Fit** box if you wish to allow for negative peak areas in low-level spectra. Directed fit is described in the *Supervisor Manual*.

MDA Type allows you to choose the MDA calculation to be used for calculating the MDA for the report. The MDA is a measure of how little activity could be present without being detected. The MDA is reported in units of activity, such as becquerels. The calibration geometry, backgrounds (system and source-induced), detector resolution, and particular nuclide all seriously affect the MDA reported. The *Supervisor Manual* provides explanations of the different MDA formulas used by ISOTOPIC. The default is Method 12, Regulatory Guide 4.16. To use another MDA method, change the **MDA type** parameter in the `B30winds.ini` file.

The parameters in the **Additional Error** section are used in the calculation of the total uncertainty. Total uncertainty is composed of error estimates that follow a normal distribution and error estimates that follow a uniform distribution over a range. Most errors in gamma spectroscopy, whether systematic or random, follow a normal distribution. Error estimates are included for counting, random summing, absorption, nuclide uncertainty, efficiency, and geometry. Enter additional errors (%) related to the measurement that follow a normal distribution at the 1-sigma level. Enter uniform distribution errors (%) at the complete range of the uniform error limit. That is, if the likelihood of an uncertainty is uniform over 3% of the reported results, enter 3.0 in this field. The error estimates from all corrections are explained in the “Analysis Methods” chapter of the *Supervisor Manual*.

If you wish to decay correct the concentrations of the nuclides to a specific date, mark the **Decay Date** checkbox and enter the date in the format displayed below the date field. This date format is determined by the current Windows date format setting.

Enter the **Analysis Range**, in channels. 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 the *Supervisor Manual*) 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.

The **Activity and Quantity Units** section determines how activity is reported.

All Container Shapes Except Surface/Disk and Point Source

Choose the appropriate **Base Activity Units** — either becquerels per kilogram (**Bq/Kg**) or microcuries per kilogram (**µCi/Kg**).

Next, use the **Activity** and **Quantity** fields as follows to determine whether ISOTOPIC reports the ***total activity*** for a measured item or the item's ***activity per unit measure***:

- To report total activity, enter *only* the **Activity** field and leave the **Quantity** field *blank* (do not enter zero).

- To report activity per unit measure, enter *both* fields.

CAUTION ***A mistake here can affect your results by multiple orders of magnitude.*** For instance, if you wish to report total item activity but do not remove the default **Kg** entry from the **Quantity** field, your results will be high by a factor of 1000. Likewise, if you replace the **Quantity** entry with one or more blank spaces, ISOTOPIC will read those spaces as characters and will assume you wish to apply a factor of 1000.

Next, enter a **Multiplier** and **Divisor** to scale the numbers up or down. 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 label** field. The combined label (activity/quantity) is limited to 14 characters.

Surface/Disk and Point Source Shapes

When you select either the **Surface/ Disk** or **Point Source** shape on the Container page, if either the **Diameter** or **Depth** is zero,[10] ISOTOPIC allows you to report only in activity units (i.e., total activity of the item measured), not concentration units (i.e., activity per unit measure); see Fig. 93.

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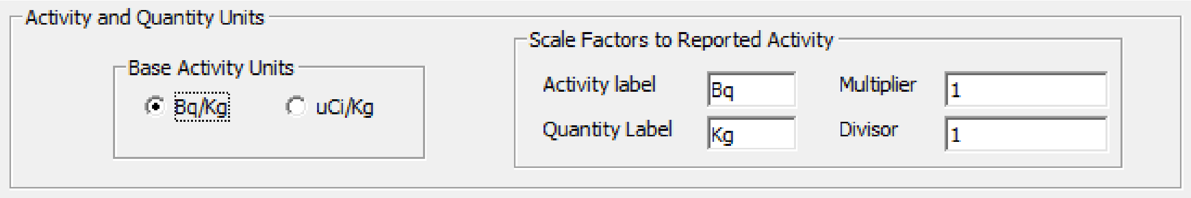
[10] An example would be a smear, which has a diameter but no depth.



Activity and Quantity Units

Base Activity Units

● Bq/Kg ○ uCi/Kg

Scale Factors to Reported Activity

Activity label: Bq

Quantity Label: Kg

Multiplier: 1

Divisor: 1

Figure 93. Activity and Quantity Units for Surface/Disk and Point Source Container Shapes.

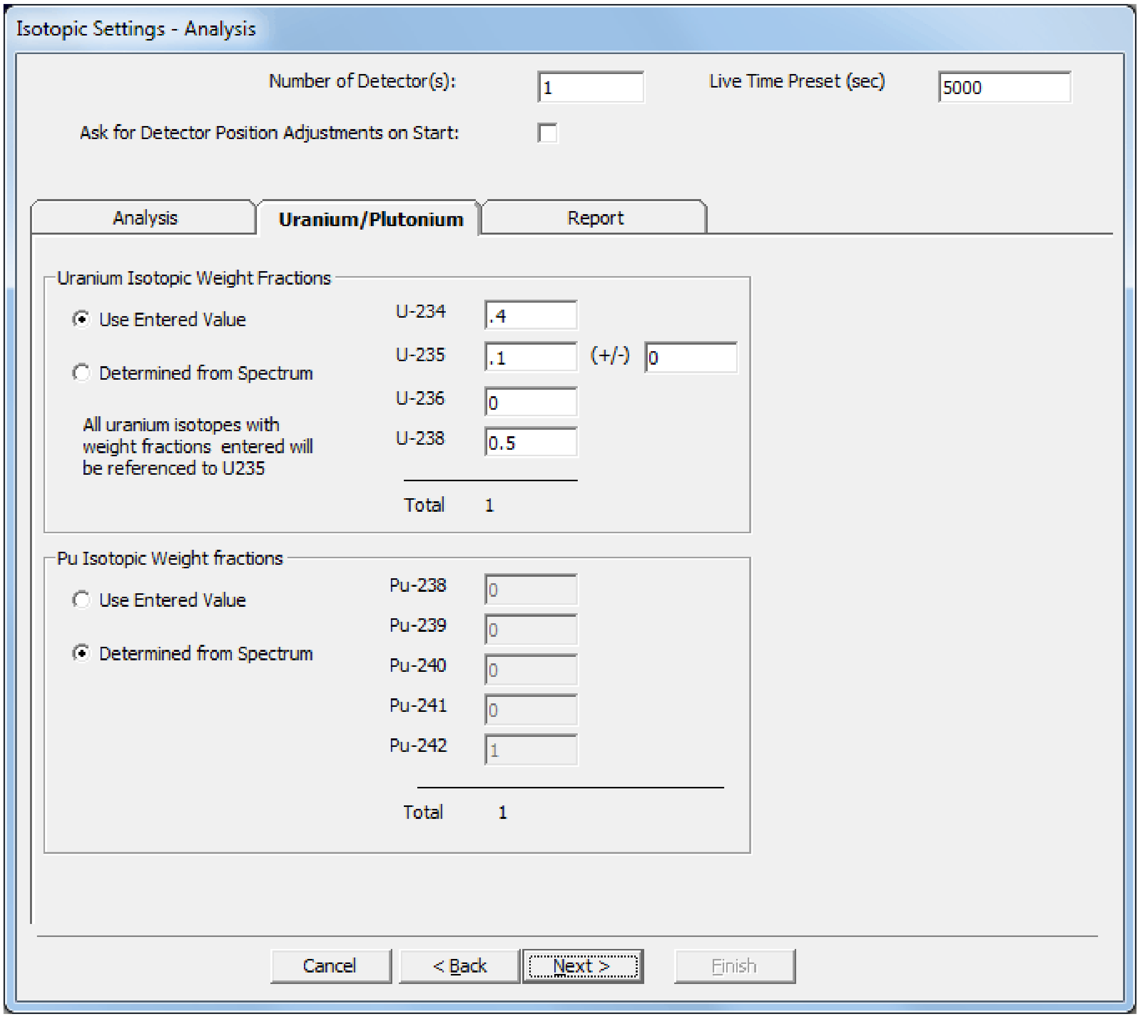
Uranium/Plutonium Tab

Use this tab (Fig. 94) to set the parameters for calculating the uranium and plutonium enrichment.

The **Uranium** and **Plutonium Isotopic Weight Fractions** can be entered or determined from the spectrum. If you choose **Use Entered Value**, you must enter all the weight fractions and an uncertainty value, **(+/-)** before moving to the next wizard page. The values should sum to 1.

In most uranium samples, ^{235}U is the most easily analyzed isotope. The other uranium isotopes can be computed from the ^{235}U determination if the weight fractions are known. In this case, mark **Use Entered Value** and enter the weight fractions. Values for all isotopes will be computed based on their corresponding weight fractions. If you do not know the weight fractions, select **Determined from Spectrum**. The final results will then reflect activity determined from the gamma rays for each isotope. If no gamma rays are detected for a particular uranium isotope, it will not be reported in this mode.

Similarly, in most plutonium samples, ^{239}Pu is the most easily measured isotope, and you can compute the other plutonium isotopes from the ^{239}Pu determination if you know the weight fractions.



Isotopic Settings - Analysis

Number of Detector(s): 1

Live Time Preset (sec) 5000

Ask for Detector Position Adjustments on Start: ☐

Uranium Isotopic Weight Fractions

● Use Entered Value

○ Determined from Spectrum

All uranium isotopes with weight fractions entered will be referenced to U235

U-234 .4

U-235 .1 (+/-) 0

U-236 0

U-238 0.5

Total 1

Pu Isotopic Weight fractions

○ Use Entered Value

● Determined from Spectrum

Pu-238 0

Pu-239 0

Pu-240 0

Pu-241 0

Pu-242 1

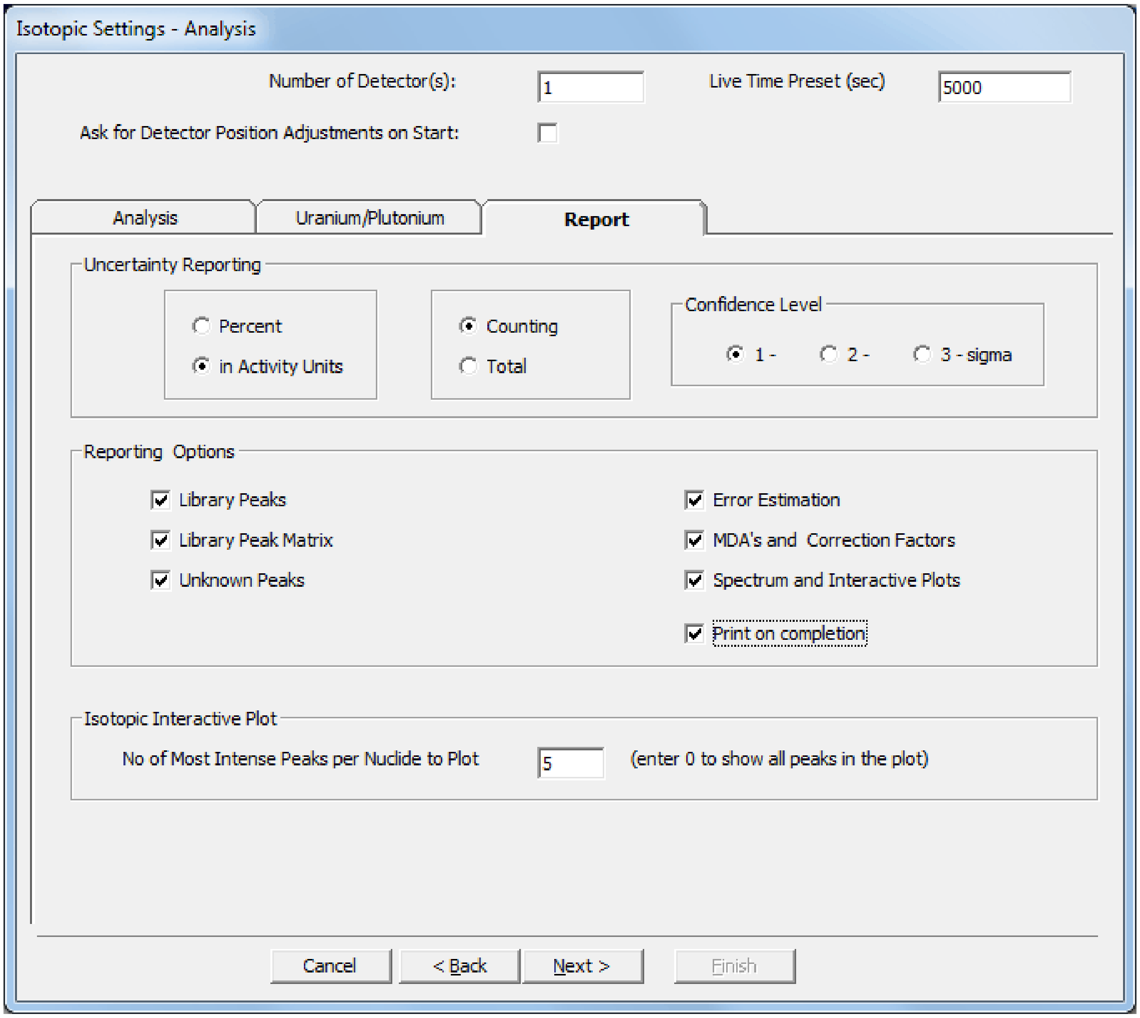
Total 1

Figure 94. Uranium/Plutonium Tab, Analysis Page.

Report Tab

The settings on this tab (Fig. 95) govern the content and generation of the Container/Surface Mode report.

Choose the **Uncertainty Reporting** options. The **Confidence level** multiplier shown here is used *on the report only*. All internal checks on peak uncertainty are performed at the 1-sigma level. The uncertainty can be in **Activity** (e.g., 200 Bq ± 10 Bq) or **Percent** (e.g., 200 Bq ± 5%). If **Counting** is selected, counting uncertainty will be printed. If **Total** is selected, both the counting and total uncertainty will be printed.



Number of Detector(s): 1

Live Time Preset (sec) 5000

Ask for Detector Position Adjustments on Start: ☐

Uncertainty Reporting

○ Percent
● in Activity Units

● Counting
○ Total

Confidence Level
● 1 - ○ 2 - ○ 3 - sigma

Reporting Options

☑ Library Peaks
☑ Library Peak Matrix
☑ Unknown Peaks
☑ Error Estimation
☑ MDA's and Correction Factors
☑ Spectrum and Interactive Plots
☑ Print on completion

Isotopic Interactive Plot

No of Most Intense Peaks per Nuclide to Plot 5 (enter 0 to show all peaks in the plot)

Figure 95. Report Tab, Analysis Page.

The **Reporting Options** show the tables that can be included in the HTML port in the Operator program. Note that these settings apply only to the standard Container/Surface HTML report. If you are using a custom Crystal Reports template to output your results, that template will define the contents of your custom report.

The points on the **Isotopic Interactive Plot** are the activities relative to the key line. Typically, only the most intense gamma rays have meaningful data. The plot can contain as many gamma rays as are defined in the library, up to the number specified here. Not many nuclides have more than 10 useful gamma rays. The activity is based on the gamma ray count rate, the detector efficiency, the gamma-ray yield (branching ratio), and attenuation. Thus, the gamma ray peak with the highest count rate may not be the peak with the highest activity. Enter zero to plot all of the gamma rays for each nuclide.

HINT Be sure that the reference gamma ray is included in the **No of Most Intense Peaks per Nuclide to Plot**. If, for instance, you use a setting of **5** but the reference gamma ray is the sixth most intense peak, your reference gamma ray will not be used.

Click **Next** to go to the Detectors page.

8.3.1.4. Detectors Page

Use the Detectors page (Fig. 96) to define the position of each detector relative to the container.

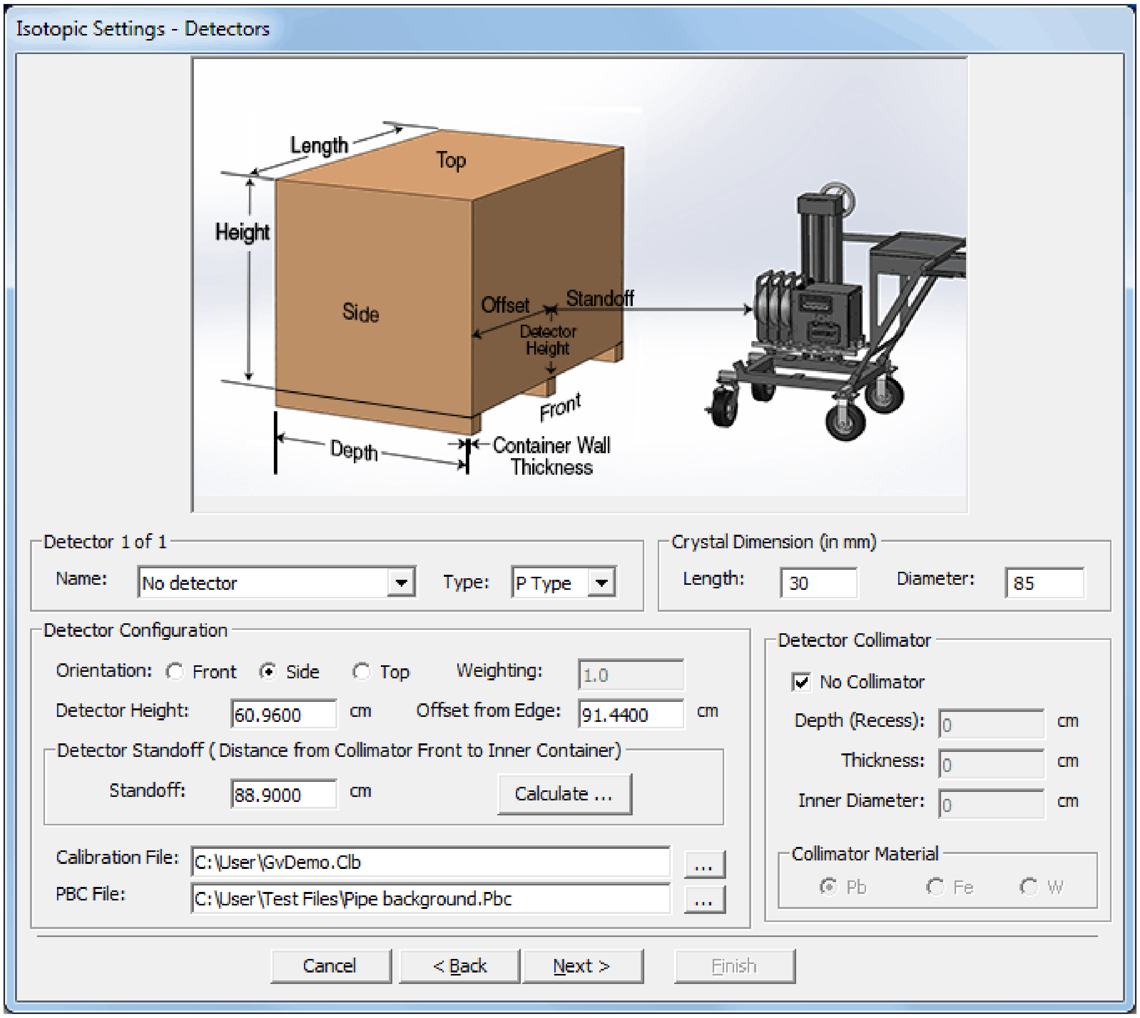
DETECTOR SETUP SUGGESTIONS FOR CONTAINER MODE

- Select the orientation of the detector with respect to the item. For a box, the most common orientation position is the **Front**, which ISOTOPIC defines as the wide side. Try to measure activity through the least thickness of matrix to minimize the item correction factor. Normally, you will not use the **Side** position (narrow width) for routine measurements unless you are making multiple measurements. For cylinders, the most common position is the **Side**. If measuring a thick disk looking down on the disk (i.e., along its cylindrical axis), use the **Top** position for the cylinder orientation.

- Typically, you will consider the largest dimension of the item to be measured, then position the detector at a distance half the size of the largest dimension. For example, if a drum is 100 cm high, the detector is usually positioned approximately 50 cm from the face of the collimator to the inner container. It is important to measure the **Standoff distance** from the front of the collimator, not the detector end cap, unless a collimator is not used. If you are not sure of the appropriate detector-to-item distance, use the **Calculate** button to help determine the field of view (FOV). For most common measurements, position the detector so the item being measured is within the field of view.

- Generally, you will position the detector at the horizontal center of the item. For box-shaped items, the detector can be positioned off center. It is important to enter the proper **Distance for the edge** parameter.

Note the **Detector 1 of [*x*]** indicator on the left, immediately below the diagram in Fig. 96. This number reflects the number of detectors in this configuration. For multi-detector configurations or configurations in which the same detector is used in different orientations, when you click the **Next** button, this same page will be presented for each of the remaining detectors in the configuration.



Detector 1 of 1

Name: No detector Type: P Type

Crystal Dimension (in mm)

Length: 30 Diameter: 85

Detector Configuration

Orientation: ○ Front ● Side ○ Top Weighting: 1.0

Detector Height: 60.9600 cm Offset from Edge: 91.4400 cm

Detector Standoff (Distance from Collimator Front to Inner Container)

Standoff: 88.9000 cm Calculate ...

Calibration File: C:\User\GvDemo.Clb ...

PBC File: C:\User\Test Files\Pipe background.Pbc ...

Detector Collimator

☑ No Collimator

Depth (Recess): 0 cm

Thickness: 0 cm

Inner Diameter: 0 cm

Collimator Material

● Pb ○ Fe ○ W

Figure 96. Detectors Page.

Choose the **Name** of the Detector to be configured and its **Type**; then enter the detector crystal **Length** and **Diameter**, in millimeters, from the detector data sheet.

NOTES Each time you add an MCB or move it to a different computer or port, be sure to rerun the MCB Configuration or the Name list will not be up to date. If you subsequently do not see the new (or moved) detector on the **Name** list, close Operator, return to the Supervisor program, select **Services/Edit Detector List...**, make sure this detector is on the ISO Pick List, and click **OK**. Restart Operator.

If you permanently remove an MCB from the system, any configurations that use it will have to be edited. This is discussed in detail in the *Supervisor Manual*.

Next, refer to the diagram at the top of the page and select the detector's **Orientation**. The position of the physical detector in this counting situation is defined by the **Detector Height**, **Offset from Edge**, and **Standoff** (to auto-calculate the standoff, see below). The definitions of these dimensions are illustrated in the figure on the wizard screen. ***It is important that these values be accurate as they are used in the model to calculate the detection efficiency and the matrix attenuation.*** Note that if the detector is on the **Top** of the container, the container lid thickness is used for the container absorption calculation (both containers), otherwise the container wall thickness is used.

In the case where the analysis uses two spectra collected by a single detector in two positions, assign each position the same detector **Name** but either (1) a different **Orientation**; or (2) a different height, offset, and/or standoff.

Enter the **Weighting** factor for this detector. This factor is used in the averaging of results from multiple spectra. The factors do not need to total 1.

If you are using a **Detector Collimator**, enter the **Depth (Recess)**, **Thickness**, and **Inner Diameter** in cm; then specify the **Collimator Material**. The depth dimension is the distance from the front of the collimator to the front of the detector. If the front of the detector is flush with the face of the collimator, the distance is 0 (zero). If no collimator is used, mark the **No Collimator** checkbox.

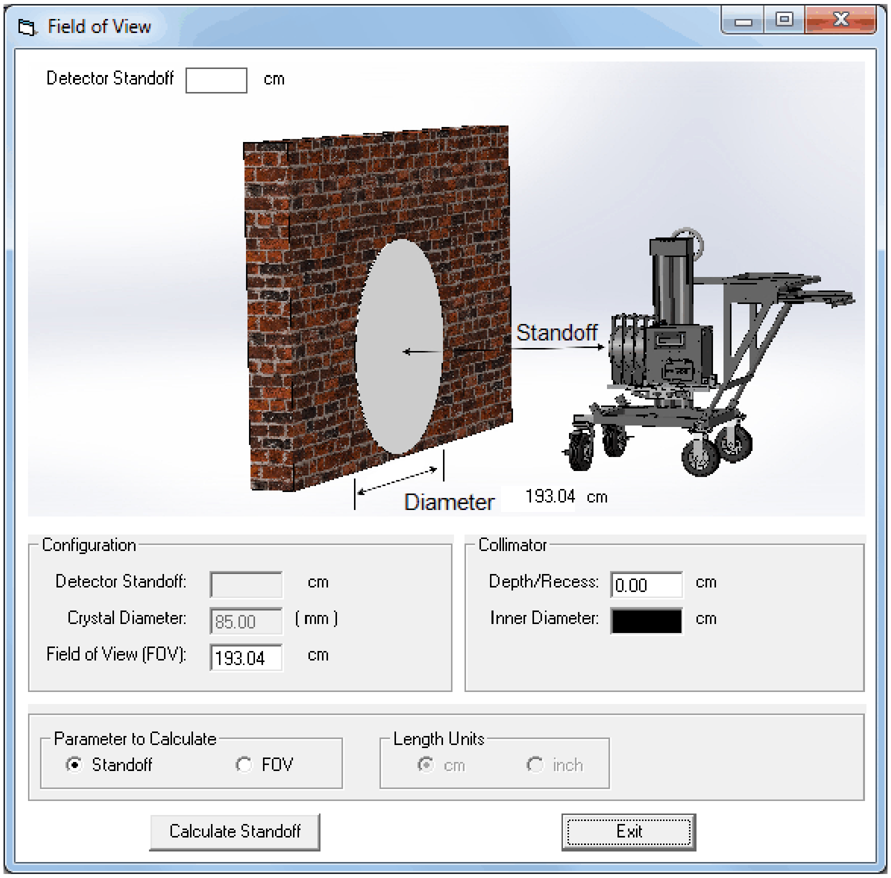
To use the energy calibration from an existing ORTEC **Calibration** (`.CLB`) **File**, click the browse (**...**) button and select the desired file. To use an existing PBC table, browse and select the desired `.PBC` file.

Field of View/Detector Standoff

ISOTOPIC includes a utility for calculating the **Standoff** for the current detector/collimator combination and the detector **Field of View (FOV)**. FOV is the space subtended in front of and coaxial with a collimated detector. The FOV must be computed to establish the area necessary for a source's activity to be detected without a collimator correction.

To use this tool, click the **Calculate** button to open the Field of View dialog (Fig. 97). The calculation is based on the **Crystal Diameter**, **Collimator** depth and inner diameter, and **Length Units** for the current configuration.

First choose the **Parameter to Calculate**. When you select **Standoff**, the **FOV** field becomes active and the lower left button label reads **Calculate FOV**. Enter the detector's FOV and click the **Calculate** button. The result is the effective detector diameter facing the sample. Use it to find the optimum detector standoff, the use of which will reduce measurement uncertainty. The new FOV is displayed both in the **FOV** field and just below the "stone wall" on the diagram.



Detector Standoff: cm

Configuration
Detector Standoff: cm
Crystal Diameter: 85.00 (mm)
Field of View (FOV): 193.04 cm

Collimator
Depth/Recess: 0.00 cm
Inner Diameter: cm

Parameter to Calculate
● Standoff ○ FOV

Length Units
● cm ○ inch

Figure 97. Calculate the FOV or Standoff.

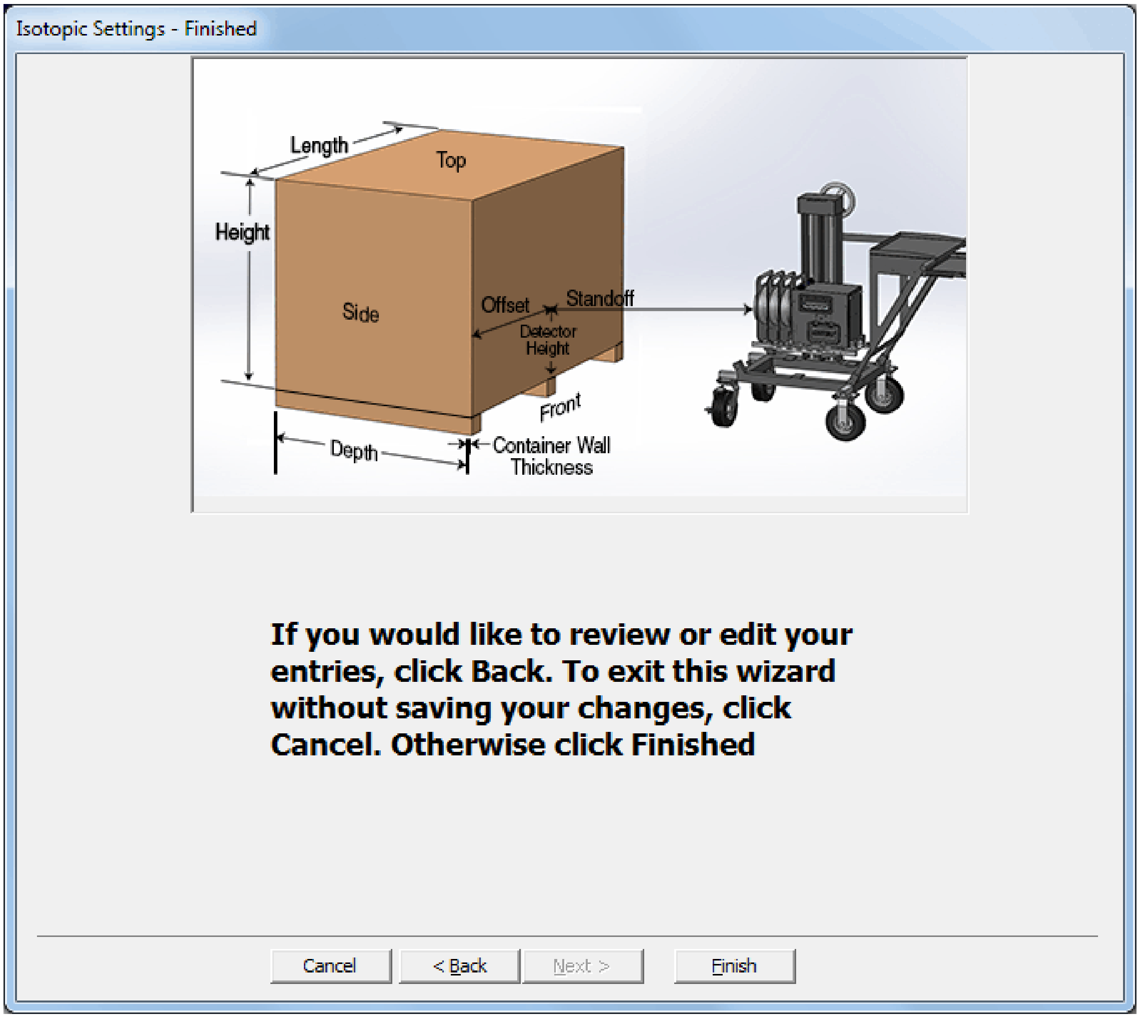
When you select **FOV**, the **Detector Standoff** field becomes active and the lower left button reads **Calculate Standoff**. Enter the standoff distance and click the **Calculate** button. The result is the detector-to-item distance at which there is no attenuation caused by the collimator. If you position the detector closer to the item being measured than the FOV would recommend, the uncertainly will increase. The new standoff is displayed in the **Standoff** field and above the detector in the diagram.

Click **Exit** to return to the Detectors page. If you calculated the standoff, the new value will be displayed in the **Detector Standoff (to Collimator Front)** field.

Click **Next** to go to the Finished page.

8.3.1.5. Final Page

This page (Fig. 98) gives you the opportunity to go **Back** and review the settings for this configuration before finishing the wizard and returning to the Supervisor program.



If you would like to review or edit your entries, click Back. To exit this wizard without saving your changes, click Cancel. Otherwise click Finished

Figure 98. Final Page.

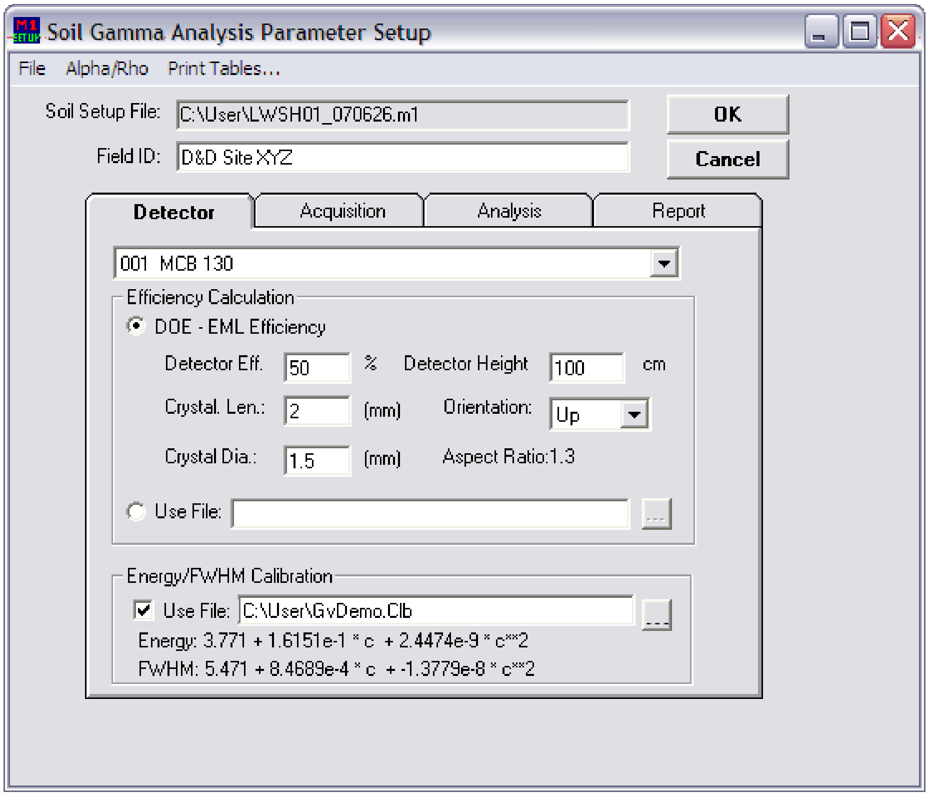
8.3.2. Soil Mode: Configuration Settings...

This opens the Soil Gamma Analysis Parameter Setup dialog ***for Soil Mode*** (Fig. 99). (To create a Container/Surface Mode configuration, see Section 8.3.1.)

Use this dialog to specify the detector, calibrations, data acquisition, analysis, and reporting settings for soil monitoring. Typically, you will save this suite of analysis parameters so it can be retrieved for reuse with the dialog's **File/Recall** command (Section 8.3.2.5). The parameter set is saved in a file with the extension `.M1` file. The current settings are retained for use in the analysis, but are not saved if there is no filename in the **Soil Setup File** field. However, the settings are stored in the analysis database as part of the scan data set for each sample measurement.

The Soil Mode user interface allows you to capture two levels of site and sample information. The top-level information is entered in this dialog, in the **Field ID** field. Typically, this refers to the top-level identifier for the project, for instance, the overall project or facility name. Additionally, the Operator interface has a **Grid ID** field in which the operator can enter a sampling grid number or other sample ID/description. The **Field ID** entered here is prepended to the filename for the `.SPC`, `.An1`, `.UFO`, and `.RPT` files generated during measurements.

8.3.2.1. Detector



Soil Setup File: C:\User\LWSH01_070626.m1

Field ID: D&D Site XYZ

001 MCB 130

● DOE - EML Efficiency

Detector Eff. 50 %   Detector Height 100 cm

Crystal. Len.: 2 (mm)   Orientation: Up

Crystal Dia.: 1.5 (mm)   Aspect Ratio:1.3

○ Use File:

☑ Use File: C:\User\GvDemo.Clb

Energy: 3.771 + 1.6151e-1 * c + 2.4474e-9 * c**2

FWHM: 5.471 + 8.4689e-4 * c + -1.3779e-8 * c**2

Figure 99. Soil Mode Operator Settings Dialog.

This tab (Fig. 99) describes the germanium detector and the energy and efficiency calibrations currently stored in the MCB. Click the droplist and choose the Detector to be used.

Next, select either the **DOE-EML Efficiency** (detector) calibration method or use the efficiency calibration from an existing calibration **File**.

The **DOE-EML Efficiency** method is very simple. The advantage of the **Use File** (alternate) method is that you get increased accuracy at energies below 200 keV. The gamma attenuation by the dead layer of germanium is especially important at these energies.

DOE-EML Efficiency

Complete the five associated fields. The **Detector Efficiency** is the actual stated efficiency of the detector from the manufacturer’s data sheet.

The **Orientation** is either up or down and is selected from the droplist. **Down** means the detector endcap is facing down or toward the ground and **Up** is the opposite. For a detector to face downward, it must be supported on a tripod or table. The preferred orientation is down.

The **Length** and **Diameter** of the germanium crystal are entered from the manufacturer's data sheet for the detector. The **Aspect Ratio** is calculated from these two numbers.

NOTE The efficiency, orientation, and crystal dimensions are used in the calculation of the absolute efficiency factors in the DOE-EML method. Care should be taken to enter the proper numbers. These are not used if **Use File** is specified.

Use File

For this method, click the browse button to find the efficiency file to be used in the analysis. This is the same format as the GammaVision `.CLB` file and can be created with the commands on the **Calibrate** menu, but the efficiency must be for the infinite plane geometry for the report to be meaningful.

NOTES Before selecting the **Use File** option, take a point-source calibration at a distance 5× the diameter of the detector, and save it with the **Save Calibration** command under the **Calibrate** menu. Detector crystal diameters will range from 25 mm to 85 mm, depending on the efficiency of the detector. If the detector crystal diameter is 50 mm, then calibrate with a point source at 250 mm (25 cm). The diameter of the detector crystal is given on the data sheet shipped with your detector. ***Be sure to use the crystal diameter, not the diameter of the endcap***.

In Container/Surface Mode, when deciding on the detector-to-source distance for efficiency calibration with the calibration wizard, we suggest 30 cm as a typical distance. However, if you position the calibration source at 5× the diameter of the detector crystal, you can use the same calibration in Soil Mode and Container/Surface Mode.

The normal height of the detector is 1 meter or 100 cm. It can be placed at different heights and the software will adjust the efficiency in the DOE-EML (Beck) method for the actual height entered here.

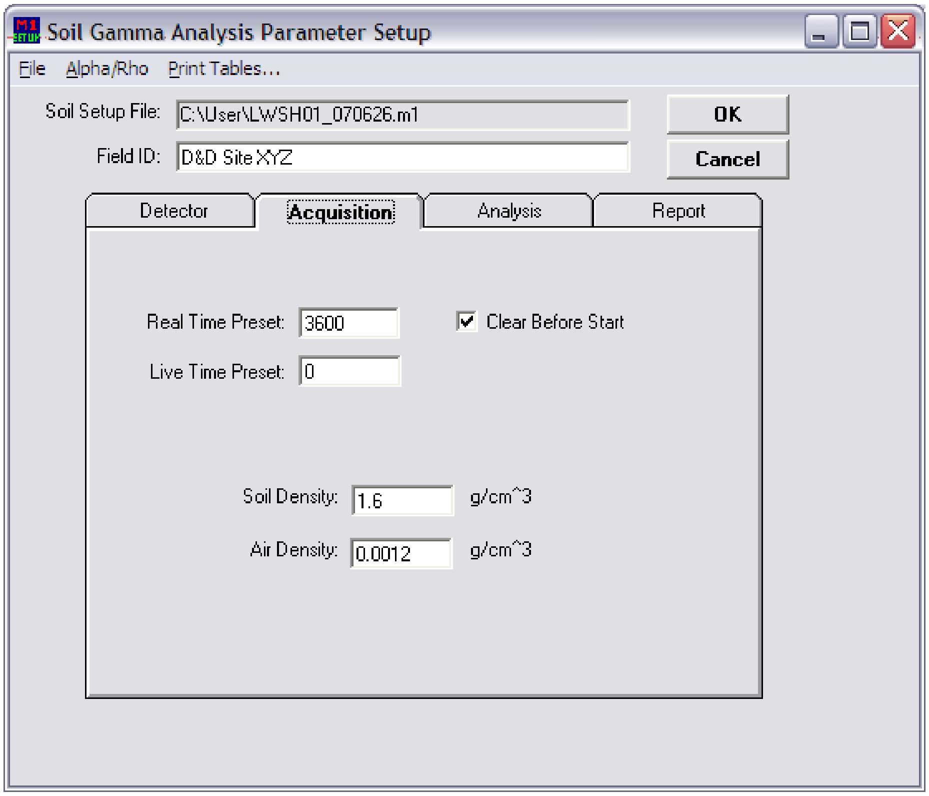
The **Energy/FWHM Calibration** section at the bottom of the dialog shows the current energy calibration stored in the MCB. A specific calibration from a `.CLB` file can be used to override the calibration currently stored in the MCB. To select a file, mark the **Use File** box and enter or browse for the filename.

8.3.2.2. Acquisition

The Acquisition tab is shown in Fig. 100. The **Live Time Preset** and **Real Time Preset** are entered here. If no presets are entered, spectrum acquisition will continue until manually stopped.

To clear the data before each start operation, mark the **Clear Before Start** box. This is the normal case. This clear flag is also on the Operator display, so it can be changed in the field.

The **Soil Density** and **Air Density** can be changed from the normal values in the fields here. These are used to calculate the attenuation of the gamma rays in air and in the soil. The soil density is used in the depth profile with the alpha/rho values.



Soil Setup File: C:\User\LWSH01_070626.m1

Field ID: D&D Site XYZ

Real Time Preset: 3600

☑ Clear Before Start

Live Time Preset: 0

Soil Density: 1.6 g/cm^3

Air Density: 0.0012 g/cm^3

Figure 100. Soil Mode Acquisition Parameters.

8.3.2.3. Analysis

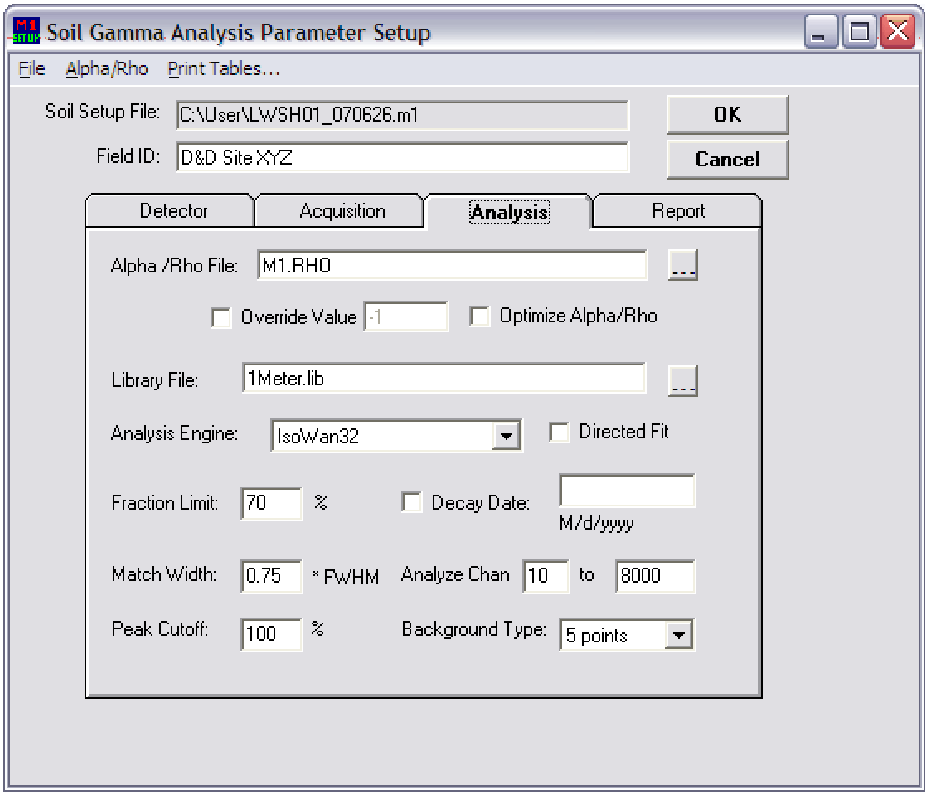
The Analysis tab is shown in Fig. 101. See Section 8.3.2.5, page 129, for information on the alpha/rho calculation and creating and editing alpha/rho files. See also Section 8.3.2.6, which contains instructions on determining an accurate α/ρ value.

Click the browse (**...**) button to locate the **Alpha/Rho File** to be used in the correction calculation.

In some circumstances, advanced users might wish to override the **Alpha/Rho File**. To do this, mark the **Override Value** checkbox and specify the alpha/rho value to be used for nonhomogeneous nuclides (i.e., where α/ρ >0).

The **Optimize Alpha/Rho** feature is also for advanced users and is only rarely used; Mark this checkbox to enable the automatic adjustment of the alpha/rho value based on the relative intensities of gamma rays from a single nuclide. These gamma rays are user-defined in the **Concentration Ratio Limits** section of the Alpha/Rho dialog (see page 129).

Enter the name of the **Library File** to be used in the analysis of the spectrum. This library can be in the NuclideNavigator™ or GammaVision format. Use the browse button to find the file on the system.



Soil Setup File: C:\User\LWSH01_070626.m1

Field ID: D&D Site XYZ

Alpha /Rho File: M1.RHO

☐ Override Value -1 ☐ Optimize Alpha/Rho

Library File: 1Meter.lib

Analysis Engine: IsoWan32 ☐ Directed Fit

Fraction Limit: 70 % ☐ Decay Date: M/d/yyyy

Match Width: 0.75 * FWHM Analyze Chan 10 to 8000

Peak Cutoff: 100 % Background Type: 5 points

Figure 101. The Soil Mode Analysis Parameters.

LIBRARY SETUP SUGGESTIONS FOR SOIL MODE

- In Soil Mode analyses, all gamma rays in the library are averaged, weighted by their yield (branching ratio). To exclude a particular gamma-ray from the averaged activity calculation, mark its **Not In Average (A)** peak flag (see the discussion on editing nuclide libraries in the *Supervisor Manual*).

- In all cases make certain that the most intense, clean (no interferences likely) gamma ray for a particular nuclide is referenced first in your library. The next three most intense gamma rays should be listed next in the library.

- ISOTOPIC libraries are limited to 500 peaks. Do not "clutter" your library with too many nuclides and gamma rays. The search engines will not be very effective in this situation. Use only the nuclides and gamma rays that are likely to be present.

- If using the supplied `Lib0` or `Lib1` master library, it might be helpful to delete all X rays from the list of gamma rays for each nuclide. The energy **Auto-calibrate** feature works better if the library includes no X rays.

The **Fraction Limit** is used to reject nuclides if enough different gamma rays are not detected. The gamma-ray detected fraction is the ratio of the sum of the yields of the peaks for a specific nuclide (in the library) located in the spectrum and the sum of the yields of all the peaks for that nuclide in the library. The **Fraction Limit** is the lowest ratio that will be accepted for the nuclide to be considered present.

For example, ^{60}Co has two peaks with about 99% branch for each peak. If both peaks are found, the ratio is (99+99)/(99+99) or 100%. In this case, ^{60}Co will be marked present because the ratio is above the 70% fraction limit shown in the figure. If one peak is not located, the ratio is (0+99)/(99+99) = 50%. Since this is below the 70% fraction limit in the figure, ^{60}Co will not be marked present in this spectrum.

If you wish to decay correct the concentrations of the nuclides to a specific date, mark the **Decay Date** checkbox and enter the date in the format displayed below the date field. This date format is determined by the current Windows date format setting.

The **Match Width** set the upper limit on how far the spectrum peak energy can be from the library energy and still assigned to the library nuclide. That is, the difference between the gamma-ray peak energy in the spectrum and the gamma-ray peak energy in the library must be less than this match width value or the spectrum peak will not be associated with that library peak. Note that the tolerance is in multiples of the full width at half maximum (FWHM). This allows the tolerance to be wider at higher energies (where the FWHM is larger) and smaller at the lower energies.

The **Analyze Chan** (analysis channels) are the channel limits for the analysis of the spectrum. The lower limit should be set above the lower-level discriminator (LLD) cutoff. The high limit should be at the high limit of useful data in the spectrum.

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. The default value is 100%.

The **Background Type** can be **Auto**, **1-point**, **3-point**, or **5-point**. These are explained in the *Supervisor Manual*. In most *in situ* spectra, the best choice will be **3-point** for 8K or fewer channels, and **5-point** for 16K channels.

Note that Soil Mode analysis uses MDA Method 12, Regulatory Guide 4.16, by default. To use another MDA method, change the **MDA type** parameter in the `B30winds.ini` file, as described in the *Supervisor Manual*.

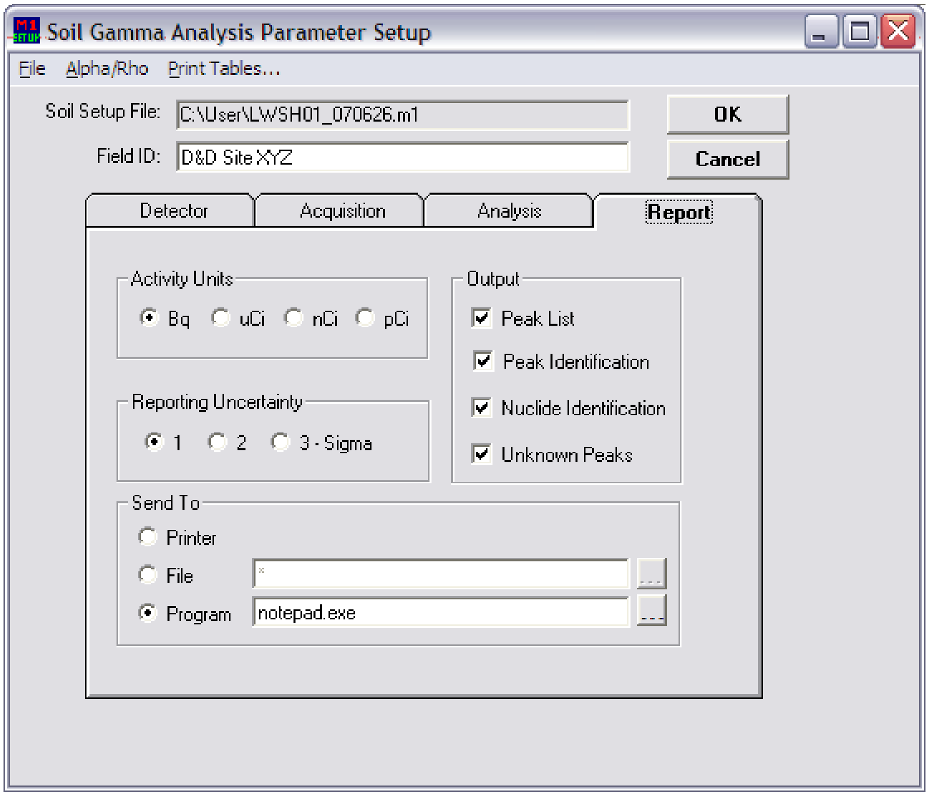
8.3.2.4. Report

The Report tab (Fig. 102) specifies the options for the final Soil Mode report, which is described in Chapter 5.1.

The **Activity Units** can be in becquerels (**Bq**), microcuries (**µCi**), nanocuries (**nCi**), or picocuries (**pCi**) for the activity. The selection of per unit area or per unit weight is done in the alpha/rho table.

The four **Output** sections of the report can be turned on or off by marking or unmarking the corresponding checkbox.

The **Unknown Peaks** list should be included to check that the spectrum does not contain significant amounts of any nuclides not included in the library.



Soil Setup File: C:\User\LWSH01_070626.m1

Field ID: D&D Site XYZ

Activity Units: ● Bq ○ uCi ○ nCi ○ pCi

Reporting Uncertainty: ● 1 ○ 2 ○ 3 - Sigma

Output:
- ☑ Peak List
- ☑ Peak Identification
- ☑ Nuclide Identification
- ☑ Unknown Peaks

Send To:
- ○ Printer
- ○ File *
- ● Program notepad.exe

Figure 102. Soil Mode Report Options.

Reporting Uncertainty can be 1, 2, or 3 sigma. The uncertainty is reported at the selected confidence limit on the reports; the value is printed on the report.

The output report can be sent directly to a **Printer**, **File**, or **Program**. When the output is sent to a program, that program will be started with the report filename as an argument. Windows Notepad can be used to view the report as soon as it is available. To browse for the program or filename, use the browse button beside the field. If an asterisk (*) is entered as the filename, the report will be assigned the spectrum filename with the extension `.RPT`. In all cases, the report file will be saved to disk.

8.3.2.5. Menu Commands for the Soil Setup Dialog

File

The **File** menu is shown in Fig.103. These commands will recall settings (`.M1`) files from or save them to disk. Using the settings files is an easy way to restore the system to a known state. Any number of settings files can be saved.

Figure 103. Soil Setup File Menu.

New — This opens the Create Soil Settings File dialog, a standard file-save dialog. Enter a filename for the new `.M1` file and click **Save**. The file-save dialog will close and the fields (all the inputs on the Detector, Acquisition, Analysis, and Report tabs) will be set to blanks or to their default values. Enter the new settings, then use **File/Save** to save them.

NOTE If the current settings have not already been saved, be sure to do so before selecting **New**; otherwise, they will be lost.

Open — Use this command to open an `.M1` file from a standard file-open dialog. The contents of the file replace the current settings, which are lost unless they have been saved.

Save — This saves the current settings to the `.M1` file most recently retrieved during this work session. Use it to save any changes to the parameters in a particular settings file. If no settings file has been retrieved during this configuration session, this command functions the same as **Save As...**.

Save As — This saves the current settings in an `.M1` file using a standard file-save dialog. Enter a filename and click **Save**.

Alpha/Rho

The **Alpha/Rho** menu is shown in Fig. 104. Use these functions to create, change, print, and display the alpha/rho tables.

Figure 104. Alpha/Rho Menu.

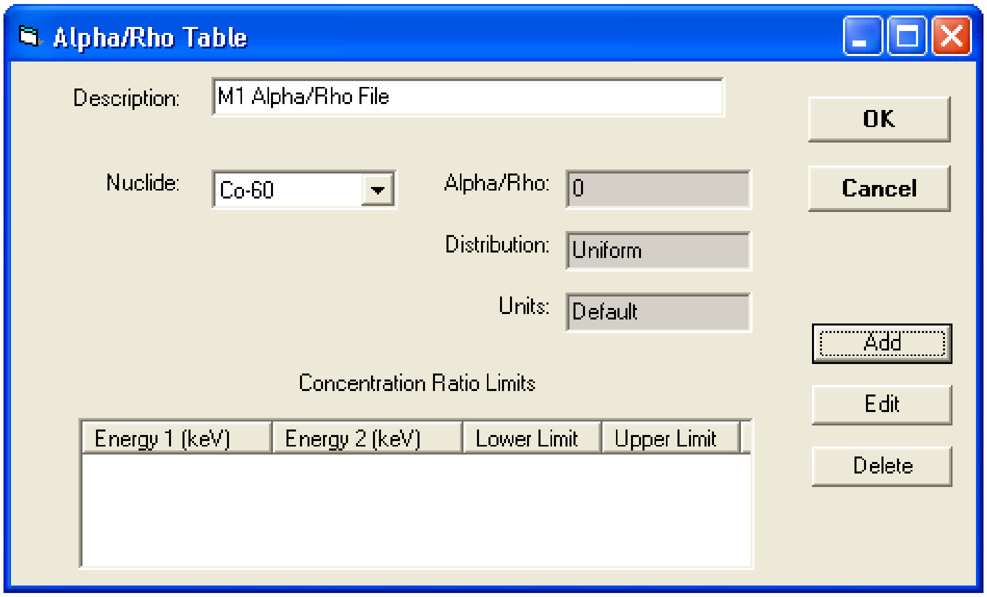
NOTE If a nuclide is in the analysis library but not in the alpha/rho table, it is assumed to be uniformly distributed in the soil, that is, the alpha/rho is 0.0. If the **Override** box on the Analysis tab is marked (see Section 3.1.3), the table values are ignored and all table nuclides use **the Override** value.

New

This command will create a new alpha/rho (`.RHO`) file. The first dialog is a standard file-open dialog. Enter a name for the new file and click **Save**. A second dialog (Fig. 105) will open, allowing you to build a list of nuclides and alpha/rho values.

Enter a **Description** that will easily distinguish this particular `.RHO` file from all others.

To begin adding nuclides to the table, click **Add**. This will open the Alpha/Rho Value dialog shown in Fig. 106. Enter a **Nuclide** name; it must be entered exactly as entered it is in the nuclide library, including metastable state (e.g., Ag-110m for ^{110m}Ag). The software will add correct capitalization and place a dash between the nuclide and its atomic weight. For example, if you enter **co60**, it will be reformatted as **Co-60**. The droplist shows the nuclides already in the table.



Description: M1 Alpha/Rho File

Nuclide: Co-60

Alpha/Rho: 0

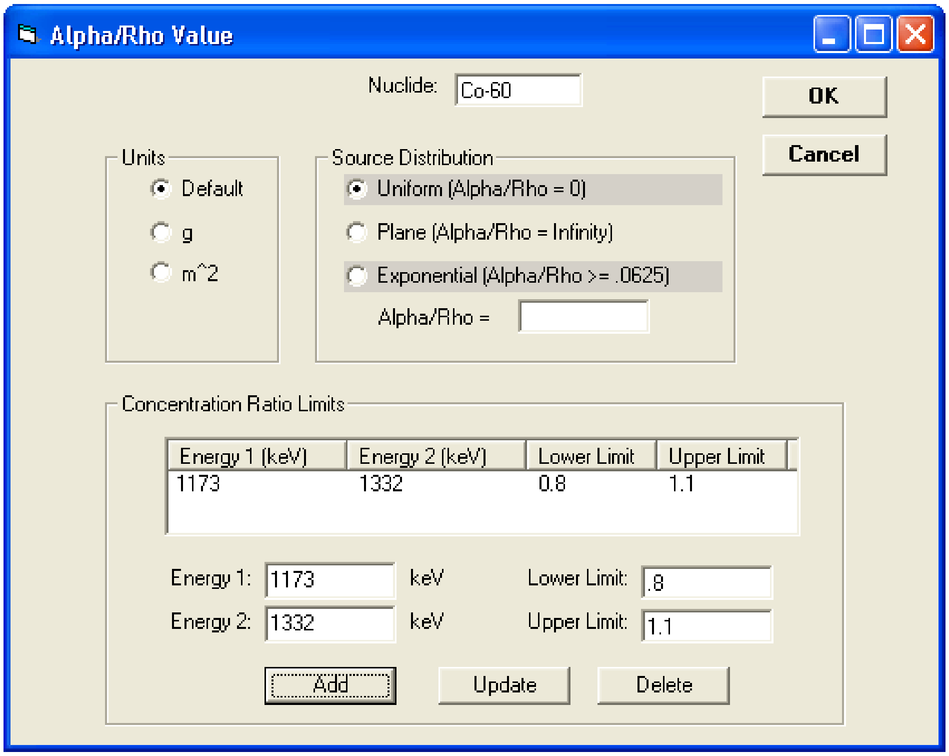
Distribution: Uniform

Units: Default

Figure 105. Alpha/Rho File Entry Dialog.

NOTE Do not duplicate entries; this will result in ambiguous results because the report will not show which value was used.

Select the **Source Distribution** for this nuclide by clicking one of the radio buttons. If the distribution is **Exponential**, enter the nuclide **Alpha/Rho** value, which can be any positive number. **Uniform** distribution in the soil means the type of distribution that might be expected for naturally-occurring nuclides. A planar distribution (**Plane**) means a uniform thin layer on the surface of the soil, such as recent fallout. By default, the activity of planar and exponentially distributed sources are listed in units of activity/m^2, while uniform nuclides are in units of activity/g. See the *Supervisor Manual* for more details on the alpha/rho parameter.



Nuclide: Co-60

Units
● Default
○ g
○ m^2

Source Distribution
● Uniform (Alpha/Rho = 0)
○ Plane (Alpha/Rho = Infinity)
○ Exponential (Alpha/Rho >= .0625)
Alpha/Rho =

Concentration Ratio Limits

Energy 1 (keV)	Energy 2 (keV)	Lower Limit	Upper Limit
1173	1332	0.8	1.1

Energy 1: 1173 keV
Energy 2: 1332 keV
Lower Limit: .8
Upper Limit: 1.1

Figure 106. Add Nuclide to Alpha/Rho Table.

Concentration Ratio Limits

Advanced spectroscopists can use the **Concentration Ratio Limits** (the activity of two peaks) to develop a more accurate alpha/rho value. If the alpha/rho value is correct, the activity ratio of **Energy 1** to **Energy 2** will approach 1.0. The **Lower Limit** and **Upper Limit** represent the acceptable **Energy 1/Energy 2** ratios. The alpha/rho value might need to be adjusted if the ratio is outside these limits. If **Energy 1/Energy 2** is outside these limits, the concentration ratio section of the report will show “Failed.”

To use the concentration ratio limits for one or more nuclides, set up your entries as described below, then mark the **Optimize Alpha/Rho** checkbox on the Analysis tab of the Soil Mode configuration dialog (see Section 8.3.2.3).

CAUTION This is a rarely used and advanced feature that should be approached with caution. If a nuclide has two intense gamma rays at least 500 keV apart (to reflect different attenuations), the α/ρ value can be determined from information obtained from these two gamma rays. However, long count times could be necessary to obtain the excellent counting statistics required to make this feature useful.

Enter the two energies and the upper and lower limits of the ratio for the nuclide activity for these two energies. Now click **Add** to add these values to the table shown above the entry fields.

To delete an entry, click the entry to highlight it and then click **Delete**. To change an entry, click the entry to highlight it, change the values, and click **Update**.

Repeat for all the nuclides to be added to the table.

Click **OK** to return to Fig. 105. Click **Cancel** to return to Fig. 105 without saving the changes made here.

To modify an existing nuclide values, select the nuclide from the droplist, then click **Edit** to open the dialog shown in Fig. 106. Make any changes and click **OK.**

To remove an entry from the table, click the **Nuclide** field to open the list, highlight the nuclide to be removed, and click **Delete**.

When the table is completed, click **OK** to save it. A pop-up box will ask if this file is to be used as the default alpha/rho file on the Analysis tab. Click **Yes** to use the new file or **No** to retain the currently assigned file.

Edit — Use this function to change the values in an alpha/rho table. A standard file-open dialog is displayed; select the `.RHO` file to be edited and click **Open**. The `.RHO` file will be displayed as in Fig. 105. Follow the **Add/Edit/Delete** instructions above. When the changes are complete, click **OK** to save them.

Print — This prints the current alpha/rho table, in table form, to the default printer.

View — This displays the table in a dialog in the same format as the printed table.

Print Tables

The **Print Tables** menu is shown in Fig. 107. This will print the **N_f/N_0 Curves** and **Flux** tables used in calculating the detector efficiency based on the detector Description entered on the Detector tab.

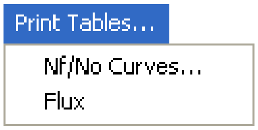


Figure 107. Print Soil Files.

8.3.2.6. Helpful Hints for Establishing α/ρ Values

It is not easy to determine an accurate α/ρ value for the soil activity you are measuring. The α/ρ values apply only to radioactive fallout that has penetrated the soil over a number of years. Usually the activity will seep into the soil in an exponential manner, with the highest concentration of activity located near the top of the soil. To determine the value accurately, core samples must be taken and the activity mapped per centimeter of depth. The α value is the reciprocal of the relaxation length for the activity. The relaxation value is determined by measuring the activity changes determined from core samples. The soil depth above which 63% of the activity lies remains is the relaxation length. Table 2 equates the relaxation value with a usable number for the α value.

If you have no idea how much activity seepage has occurred over time, a value of 0.6 is commonly used.

Table 2. Estimating α/ρ (density) at an Estimated Soil Density of 1.65 g/cc.

Relaxation length (mm)*	α (cm^{-1})	α/density
1	10.00	6.061
5	2.00	1.212
10	1.00	0.606
20	0.50	0.303
30	0.33	0.202
40	0.25	0.152
50	0.20	0.121
60	0.17	0.101
70	0.14	0.087
80	0.13	0.076
90	0.11	0.067
100	0.10	0.061
200	0.05	0.030

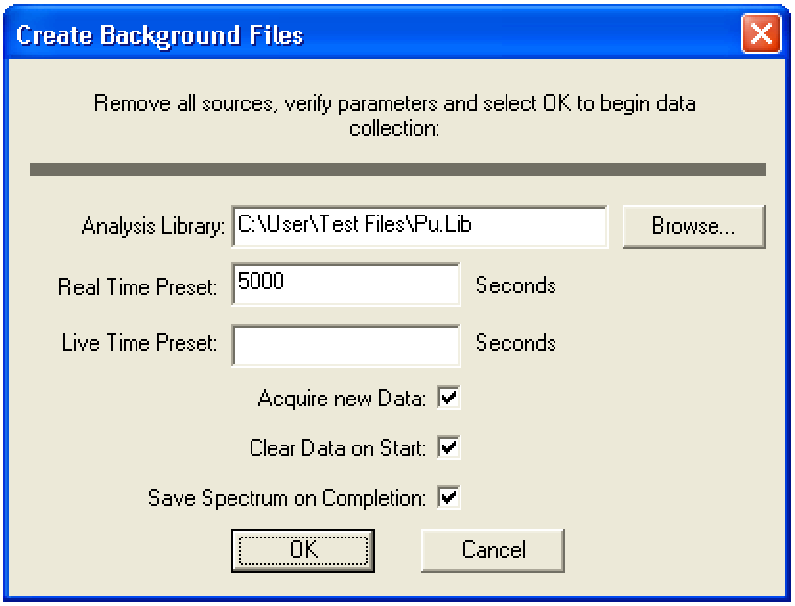
NOTES In moist areas the α/density number usually ranges from 0.03 to 0.2.
In dry areas the α/density number usually ranges from 0.2 to 1.
1 mm represents a fresh deposit with minimum activity seepage.

8.3.3. Create Background File...

This starts the PBC wizard, which creates `.PBC` files automatically from a live spectrum. the command is inactive for buffer windows and does not apply to Soil Mode. See also Section 3.3.5.

- Select a configuration that is associated with a detector.
- Select **Create Background File...** to open the dialog shown in Fig. 108.
- Browse for the **Analysis Library**. This will normally be a library of background nuclides.
- Enter the **Real** 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** options are used to control data acquisition in the MCB.
  - — To clear the MCB and collect a new spectrum for the preset time, mark both the **Acquire** and **Clear** checkboxes.
  - — If the MCB contains a good spectrum and no more data is needed, unmark both the **Acquire** and **Clear** check-boxes. This will ignore the counting presets and read the spectrum in the MCB.
  - — To add more count time to a spectrum in MCB memory, mark the **Acquire** box and unmark the **Clear** box. Adjust the preset(s) to the original count time plus the additional count time (i.e., the preset value will reflect the total time for the data collection, not just the additional time). It the preset is less than the actual time, no new data will be added to the existing spectrum.


Create Background Files

Remove all sources, verify parameters and select OK to begin data collection:

Analysis Library: C:\User\Test Files\Pu.Lib

Real Time Preset: 5000 Seconds

Live Time Preset: Seconds

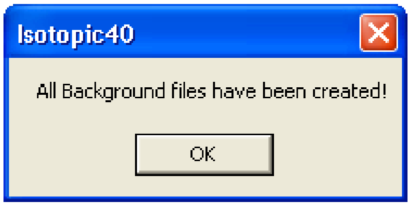
Acquire new Data: ☑

Clear Data on Start: ☑

Save Spectrum on Completion: ☑

Figure 108. Creating a .PBC File from Live Spectral Data.

- Mark the **Save Spectrum on Completion** checkbox to save the spectrum after the analysis.
- Prepare the detector, remove all sources, and click **OK** to start data collection. At the end of the count, enter a **Sample Description** if desired. ISOTOPIC will analyze the spectrum file, create the background file, and display the dialog shown in Fig. 109.


Isotopic40

All Background files have been created!

Figure 109.

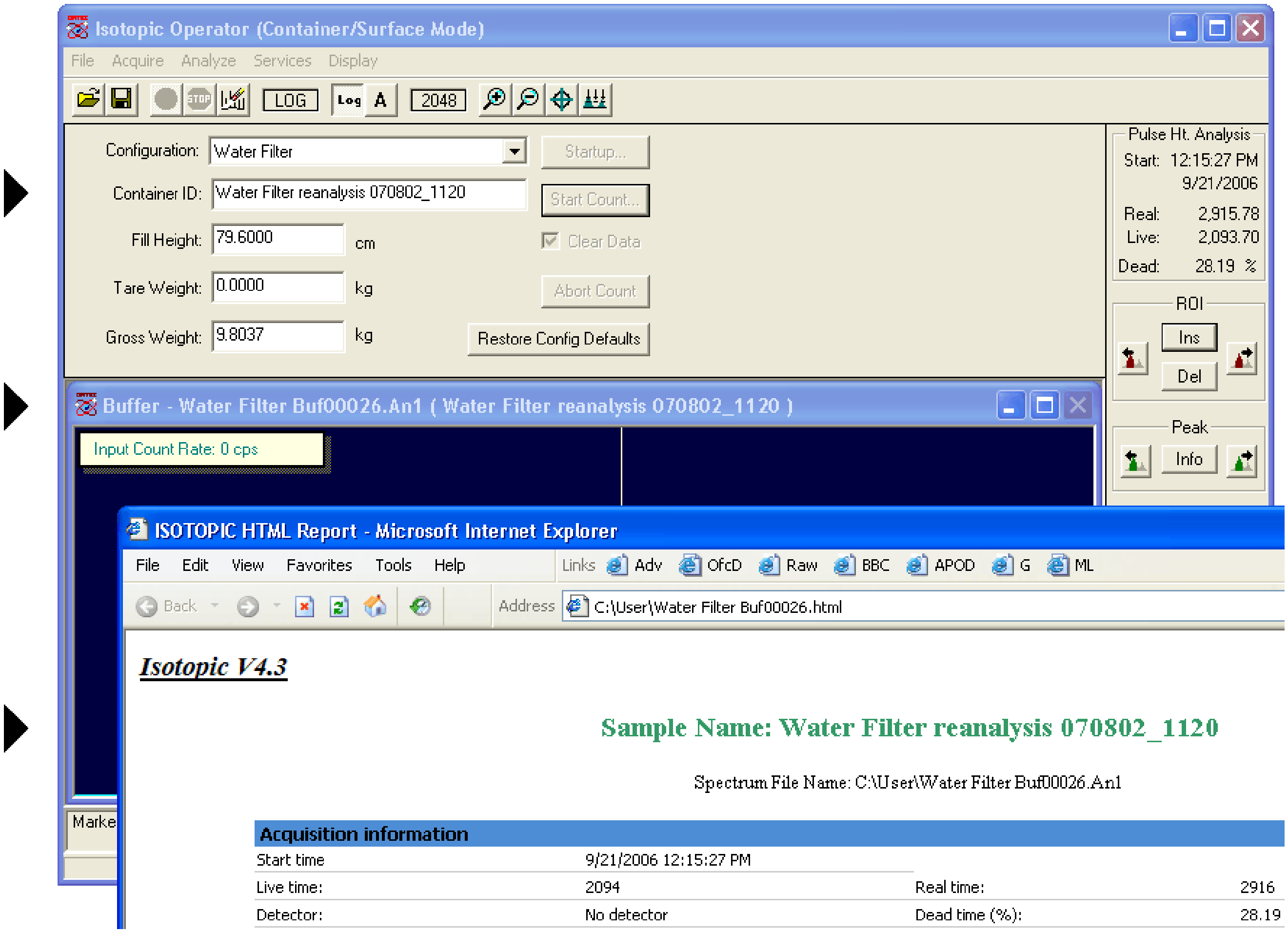
- The title bar of the spectrum window will display the MCB; the name of the .PBC file; and the sample description, if any. You might find it useful to change the filename to make it more descriptive.

8.3.4. Configuration in Memory...

This analyzes the scan data set currently loaded in memory. This can be either a newly collected data set, a data set recalled using **Recall Scan Data Set...** (Section 8.1.2), or a spectrum file recalled with **Recall configuration and file(s)** (Section 8.1.1). A new entry for the results is made in the database; and a new set of spectrum, analysis, and report files is created. When the analysis is complete, the results are displayed according to the settings in the applicable configuration.

NOTE Be sure all detectors in your system are efficiency calibrated; if not, all reanalyzed nuclide activities will be reported as zero.

When reanalyzing an existing scan data set or spectrum file, we recommend that you enter a descriptive name for the reanalysis in the **Container ID** field (for Container/Soil Mode) or **Grid ID** field (for Soil Mode). This name will be displayed on the spectrum window and at the top of the report, as shown in Fig. 110.



Isotopic Operator (Container/Surface Mode)

Configuration: Water Filter

Container ID: Water Filter reanalysis 070802_1120

Fill Height: 79.6000 cm

Tare Weight: 0.0000 kg

Gross Weight: 9.8037 kg

☑ Clear Data

Pulse Ht. Analysis
Start: 12:15:27 PM
9/21/2006
Real: 2,915.78
Live: 2,093.70
Dead: 28.19 %

Buffer - Water Filter Buf00026.An1 (Water Filter reanalysis 070802_1120)

Input Count Rate: 0 cps

ISOTOPIC HTML Report - Microsoft Internet Explorer

Address C:\User\Water Filter Buf00026.html

Isotopic V4.3

Sample Name: Water Filter reanalysis 070802_1120

Spectrum File Name: C:\User\Water Filter Buf00026.An1

Acquisition information			
Start time	9/21/2006 12:15:27 PM		
Live time:	2094	Real time:	2916
Detector:	No detector	Dead time (%):	28.19

Figure 110. Revised Container ID is Displayed on Spectrum Window, Title Bar, and HTML Report.

8.4. Services

The **Services** menu (Fig. 111) contains several functions and utilities.

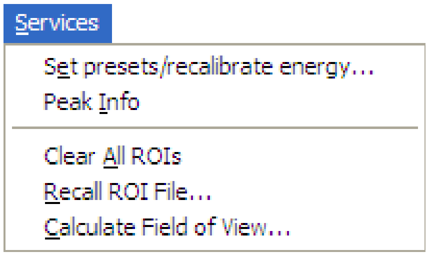


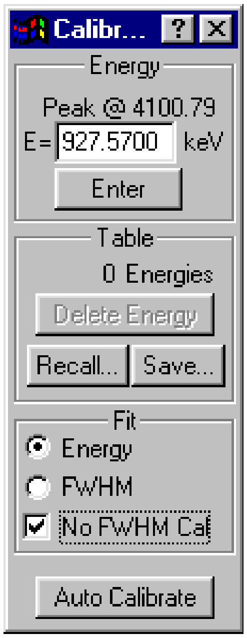
Figure 111. Services Menu.

8.4.1. Set Presets/Recalibrate Energy...

This function is used to correct the energy calibration in case it has changed. If a good spectrum is collected in this step, you can save it and use it for later energy recalibrations. Only the energy calibration is changed, so a high-quality spectrum (as needed for the FWHM calibration) is not necessary. You will need a multi-nuclide source and a corresponding library file. This recalibration is only performed on the spectrum in the active window. The result is stored in the MCB and subsequently written to any .SPC files generated during acquisition. No calibration file is created.

CAUTION You can obtain an excellent spectrum for energy recalibration in only a few minutes. However, a good FWHM calibration requires a much longer acquisition. Before using the **Auto Calibrate** function, be sure to disable the FWHM calibration by marking the **No FWHM Cal** checkbox on the Energy Calibration Sidebar (Fig. 112).

At times you might notice a slight gain shift in the spectrum. You can remedy this incorrect energy calibration by using the **Auto Calibrate** function at the bottom of the Energy Calibration Sidebar. Note, however, that the library used for the sample analysis might contain too many gamma rays for the auto-calibrate feature to work properly. It is good practice to have another, simpler library available that contains only the most intense gamma rays in the spectrum. This library should contain no more than 10 gamma rays covering the energy range of the spectrum. If the counting uncertainties for on the peaks are adequate for proper peak identification., you might not have to collect new data. Try to avoid using gamma rays with energies below 55 keV in the **Auto Calibrate** library.



Peak @ 4100.79
E= 927.5700 keV
0 Energies
● Energy
○ FWHM
☑ No FWHM Cal

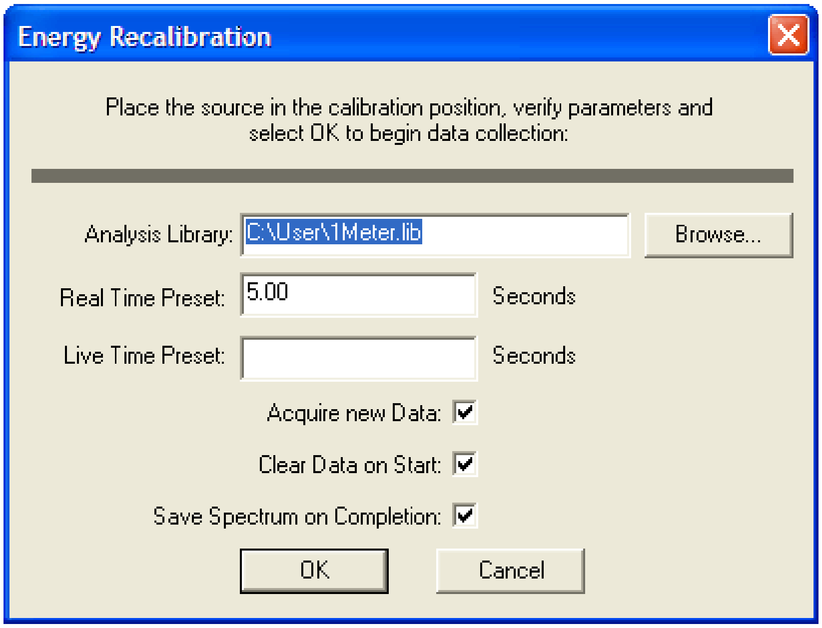
Figure 112. Disable the FWHM Calibration.

The starting dialog is shown in Fig. 113. When you click **OK**, the spectrum will be collected according to the selected checkboxes, the calibration performed, and the results stored without any other operator actions.

The **Analysis Library** selected must contain the nuclides in the calibration source.

Set the preset **Live Time** or **Real Time Preset** to count for a period long enough to accumulate about 10000 counts in the peak areas. The dead time should not be about 15% for best results, so either preset can be used.

If the MCB contains a valid spectrum of this source, it can be used as is or more counts can be added to it. To keep the existing data, unmark the **Clear Data on Start** box. To add data to it (that is, count for more time), click the **Acquire new Data** box. To save the spectrum to disk when the calibration is complete, click the **Save Spectrum on Completion** box.



Place the source in the calibration position, verify parameters and select OK to begin data collection:

Analysis Library: C:\User\1Meter.lib

Real Time Preset: 5.00 Seconds

Live Time Preset: Seconds

Acquire new Data: ☑

Clear Data on Start: ☑

Save Spectrum on Completion: ☑

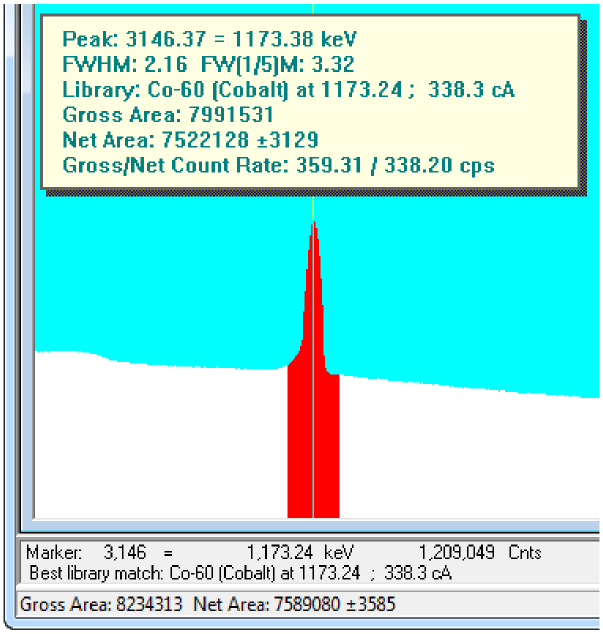
Figure 113. Start the Energy Recalibration.

When the entries are complete, click **OK**. This will start the process of collecting the data, performing the calibration, and saving the spectrum to disk. When complete, a message box will inform you.

8.4.2. Peak Info

This command operates when the marker is positioned in a peak or in an area marked as an ROI. It displays the following information in a popup box and on the Supplementary Information Line (Fig. 114):

- If the spectrum is not calibrated, the centroid channel, FWHM, FW1/xM (all in channels), gross area, net area, and net area uncertainty are displayed for the ROI.
- If the spectrum is calibrated, the centroid channel, FWHM, FW1/xM in channels and calibration units (e.g., energy), library “best match” energy and activity, gross area, net area, and net-area uncertainty are displayed for the ROI.



Peak: 3146.37 = 1173.38 keV
FWHM: 2.16 FW(1/5)M: 3.32
Library: Co-60 (Cobalt) at 1173.24 ; 338.3 cA
Gross Area: 7991531
Net Area: 7522128 ±3129
Gross/Net Count Rate: 359.31 / 338.20 cps

Marker: 3,146 = 1,173.24 keV 1,209,049 Cnts
Best library match: Co-60 (Cobalt) at 1173.24 ; 338.3 cA
Gross Area: 8234313 Net Area: 7589080 ±3585

Figure 114. Peak Info Beneath Marker and Above Peak.

If the MCB is acquiring data, the displayed values are continuously updated.

NOTE If the marker is in an ROI, peak information is displayed whether or not the area is a detectable peak. If no ROI is marked, the peak limits are the same as the limits for the **ROI Insert** button on the Status Sidebar. If a peak is detected, its information is displayed (otherwise a "could not fit peak properly" message is displayed).

The **Next Peak** and **Previous Peak** buttons on the Status Sidebar will move the Peak Info box up and down in the spectrum. To close it, click it or press **<Esc>**.

See the *Supervisor Manual* for peak calculation details.

8.4.3. Clear All ROIs

This resets all the ROI bits in the displayed spectrum (i.e., removes all ROI markings from the spectrum).

8.4.4. Recall ROI File...

Recall File... sets the ROIs in the buffer or active MCB to the table in the disk file created by **ROI/Save File...** (see the *Supervisor Manual*), 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 a standard Windows file-open dialog. When you select a file, the ROIs in the buffer or active MCB are set to conform to the table in the file. The previous ROIs are cleared. The data contents of the buffer or MCB are not altered by this operation, only the ROI bits in the buffer or MCB.

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.

8.4.5. Calculate Field of View

This is discussed on page 120.

8.5. Display

The spectrum display can be controlled by the **Display** menu (Fig. 115), which is only displayed on the full menu. These commands act on the active spectrum windows. These functions are duplicated by hot keys, some on the toolbar, and some are on the right-mouse-button menu (see Section 8.6).

8.5.1. Logarithmic

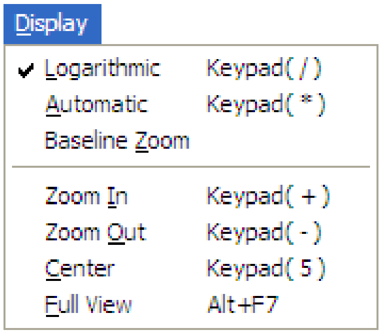


Figure 115. Display Menu.

Logarithmic toggles the vertical scale of the Expanded Spectrum View between the logarithmic and linear modes. This function is duplicated by **Keypad</>** and the **Log/ Linear Display** button on the toolbar.

8.5.2. Automatic

Automatic switches the Expanded Spectrum View 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.

8.5.3. Baseline Zoom

Baseline Zero switches to autoscale mode, then sets and keeps the baseline of the Expanded Spectrum View at zero counts. Autoscale is then switched off. This function is duplicated by the **Baseline Zoom** toolbar button.

8.5.4. Zoom In

Zoom In adjusts the horizontal and vertical scales in the Expanded Spectrum View 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. 116).

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

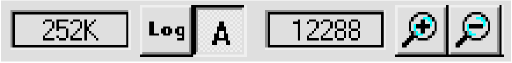


Figure 116. Vertical and Horizontal Full-Scale Setting on the Toolbar.

8.5.5. Zoom Out

Zoom Out adjusts the horizontal and vertical scales in the Expanded Spectrum View 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.

8.5.6. 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 Spectrum View. **Center** is duplicated by **Keypad<5>** and the **Center** button on the toolbar.

8.5.7. Full View

Full View adjusts the horizontal and vertical scaling to display the entire spectrum in the Expanded Spectrum View. This command is duplicated by **<Alt + F7>**.

8.6. Right-Mouse-Button Menu

Figure 117 shows the right-mouse-button menu. To open it, move the mouse pointer into the spectrum display, right-click to open the menu, then left-click to select the desired command.

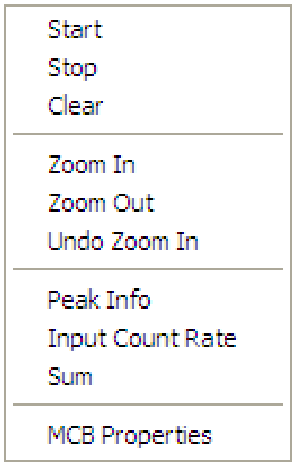


Figure 117. Right-Mouse-Button Menu.

8.6.1. Start

This starts data acquisition in the selected MCB; see Section 8.2.3.

8.6.2. Stop

Ends data collection in the selected MCB; see Section 8.2.4.

8.6.3. Clear

Clears the MCB memory; see Section 8.2.5.

8.6.4. Zoom In / Zoom Out

See Sections 8.5.4 and 8.5.5, respectively.

8.6.5. Undo Zoom In

This undoes or reverses 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**.

8.6.6. Peak Info

This command is explained in Section 8.4.2.

8.6.7. Input Count Rate

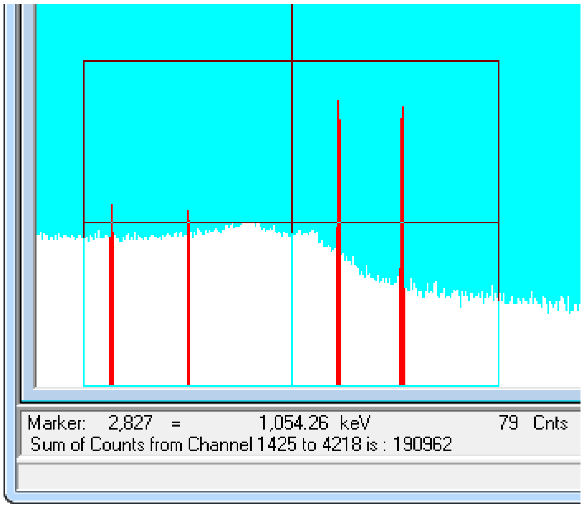
On supported ORTEC MCBs, the input count rate can be shown in the upper left corner of the spectrum window; see item 5 on page 8. This is the input count rate and not the number of processed pulses. The buffer shows the input count rate when the spectrum from an MCB that supports this feature is transferred to the buffer from the MCB or saved to disk. In MCB windows, if the MCB is not acquiring data, the value displayed is the current input count rate value, not the count rate when the MCB was stopped.

8.6.8. Sum

The **Sum** function performs its calculation as follows, and displays the sum on the Marker Information Line:

1) If the marker is not in an ROI, the counts in all data channels in the buffer (e.g., channel 1 to the maximum channel currently selected) are summed.

2) 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.



```
Marker:   2,827   =           1,054.26  keV              79  Cnts
Sum of Counts from Channel 1425 to 4218 is : 190962
```

Figure 118. Summing the Channels In a Rubber Rectangle.

3) You can also sum a region by marking it with a rubber rectangle, then selecting **Sum**. This is illustrated in Fig. 118.

8.6.9. MCB Properties...

This command accesses the MCB setup dialogs discussed in Section 8.2.2.

[Intentionally blank]

9. QUALITY ASSURANCE

The accuracy and reproducibility of results of a data acquisition system should be verified on a periodic basis. Quality Assurance (QA) in ISOTOPIC 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. The latter measurements use a check source. These results are stored in the ISOTOPIC database, `GvQa32.mdb` 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.
- **Average peak shift**, the average of the deviation of actual peak centroids from expected library energies within a specified range (the **Match Width** entered on the Analysis tab under **Settings/Configurations...**).
- 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 isotopic 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. This activity calculation uses the general analysis program to ensure that the total system is checked.

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 have not changed.

Figure 119 shows the **QA** submenu under the **Acquire** menu. These commands allow you to accomplish the three major QA functions in ISOTOPIC:

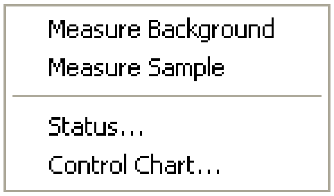


Figure 119. QA Submenu.

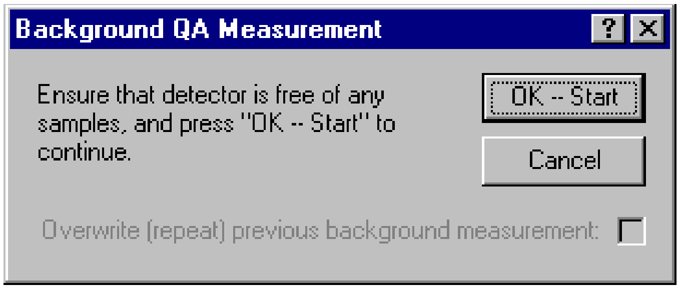
1) Establishing and entering the settings, or "ground rules," for QA. This is typically performed in the Supervisor program; see the "Quality Assurance" chapter in the *Supervisor Manual* for instructions.

2) Measuring background and sample. This is performed periodically, and is automatically logged into the QA database.

3) Analyzing the QA database and generating reports. This includes ISOTOPIC **Status** and **Control Chart** features, to view the current status of measurements for the MCB and/or view and print the data stored in the database as a control-chart display.

9.1. Measure Background

This command opens the dialog in Fig. 120, to verify that all sources have been removed from near the detector before proceeding. Confirm that all sources have been removed for a background measurement, click **OK–Start**. The remaining functions are performed automatically.



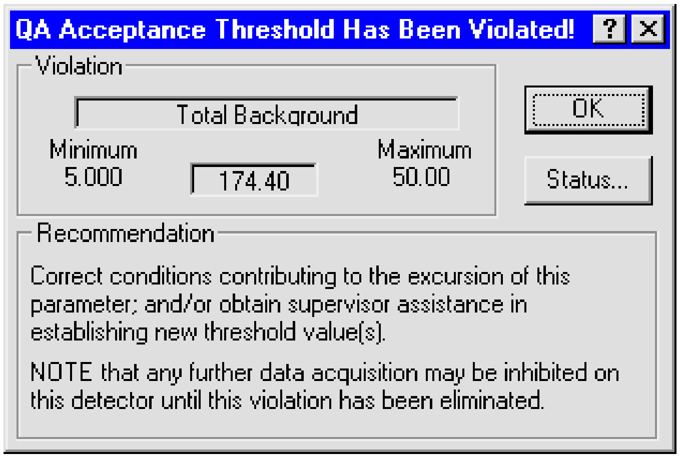
Ensure that detector is free of any samples, and press "OK -- Start" to continue.

Overwrite (repeat) previous background measurement: ☐

Figure 120. Begin Count for Background QA.

Mark the **Overwrite (repeat) previous background measurement** checkbox (by clicking it) if the previous measurement was in error. For example, if a problem was detected, fixed, and this run is to verify the repairs, mark the box so the "bad" value is not kept in the database. Click **OK**.

If the background is outside the set limits, a warning similar to Fig. 121 is displayed.



Total Background

Minimum 5.000

174.40

Maximum 50.00

Correct conditions contributing to the excursion of this parameter; and/or obtain supervisor assistance in establishing new threshold value(s).

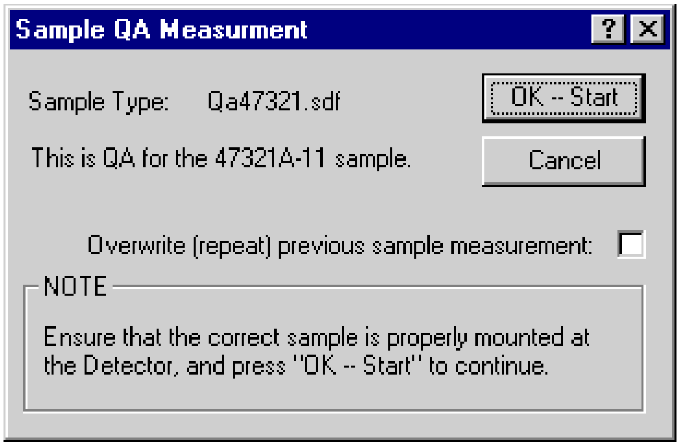
NOTE that any further data acquisition may be inhibited on this detector until this violation has been eliminated.

Figure 121. Background Warning Message.

9.2. Measure Sample

This command opens the Sample QA Measurement dialog (Fig. 122). It contains a reminder to place the QA source on the detector. Click **Overwrite** to replace the last measurement. Click **OK–Start** to begin the count.

The QA source spectra are collected for the preset time and analyzed automatically. The analysis results are compared with the limits. If the result is outside the limits, a warning is displayed. The results are also stored in the QA database.



Sample Type: Qa47321.sdf

This is QA for the 47321A-11 sample.

Overwrite (repeat) previous sample measurement: ☐

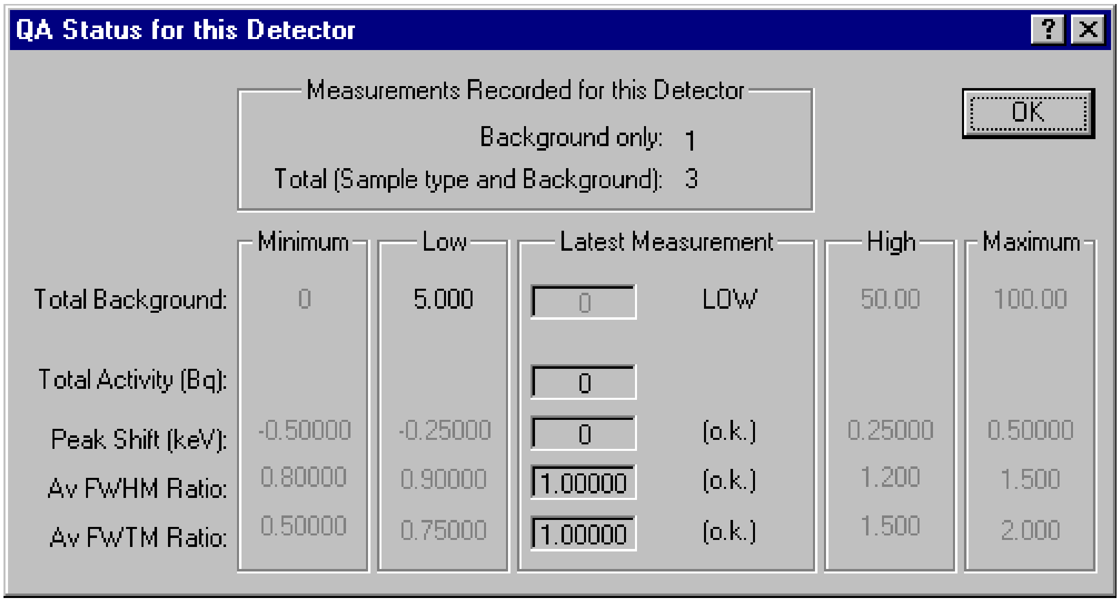
NOTE

Ensure that the correct sample is properly mounted at the Detector, and press "OK -- Start" to continue.

Figure 122. Starting Sample Type QA Measurement.

9.3. Status...

The QA status for the currently selected Detector is displayed as shown in Fig. 123. Click **OK** to close the dialog.



Measurements Recorded for this Detector

Background only: 1

Total (Sample type and Background): 3

	Minimum	Low	Latest Measurement		High	Maximum
Total Background:	0	5.000	0	LOW	50.00	100.00
Total Activity (Bq):			0			
Peak Shift (keV):	-0.50000	-0.25000	0	(o.k.)	0.25000	0.50000
Av FWHM Ratio:	0.80000	0.90000	1.00000	(o.k.)	1.200	1.500
Av FWTM Ratio:	0.50000	0.75000	1.00000	(o.k.)	1.500	2.000

Figure 123. Showing Status of QA Measurements for a Detector.

9.4. Control Charts...

The **Control Chart...** functions 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. 124. The short dashed lines represent the warning limits and the long dashed lines represent the acceptance threshold limits.

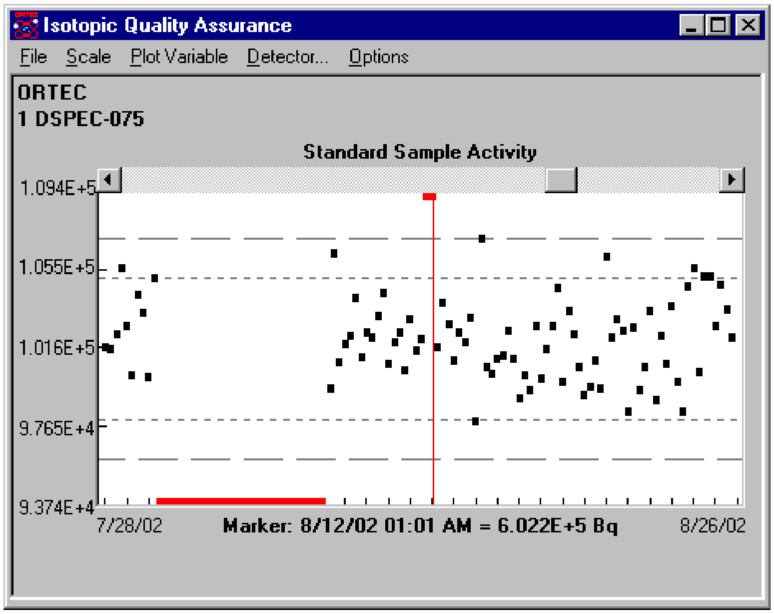


Figure 124. Control Chart Example.

Figure 125 shows the control chart **File** menu, which contains the **Print Graph** command for printing the current graph on the current printer; the **Exit** command for closing the QA Chart Program (this duplicates the dialog upper-right Close box); and an **About** box providing version information about the chart program.

Choose the chart time period (**Week**, **Month**, or **Quarter**) from the **Scale** menu (Fig. 126).

The **Plot Variable** menu (Fig. 127) contains functions for selecting **Activity**, **Peak Energy**, **Peak Width @ Half Max**, **Peak Width @ Tenth Max**, or **Background**.

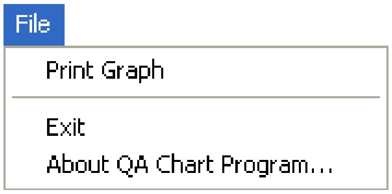


Figure 125. QA Chart File Menu.

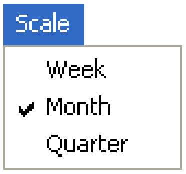


Figure 126. Scale Menu.

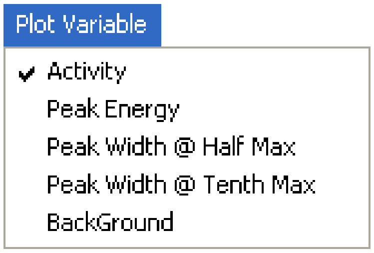


Figure 127. Plot Variable Menu.

The **Detector** menu item opens the list of MCBs for which background and sample measurements have been made (Fig. 128). Select an MCB for this control chart and click **OK**.

Offline processing of the QA database (including detailed trend analyses) can be done outside of ISOTOPIC. The database format used is well-documented and compatible with a number of popular software products including Microsoft Access.

IMPORTANT ***We strongly recommend that you back up any ISOTOPIC database files before performing manipulations on them outside of ISOTOPIC.***

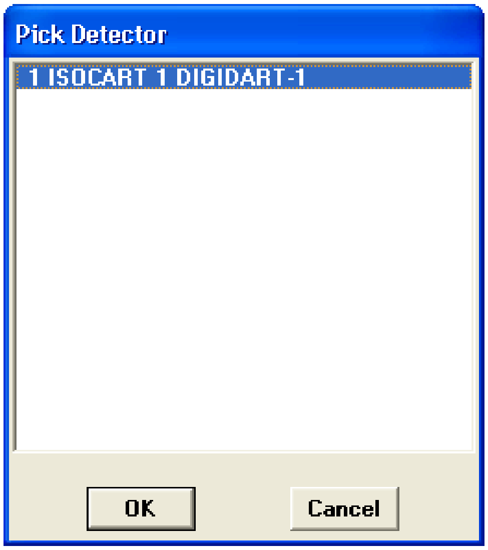


Figure 128. Detector Pick List.

The **Options** menu (Fig. 129) includes an **Always On Top** command, which keeps the QA window on top of all other windows, no matter which window (in ISOTOPIC or any other program) might be active.

The **Fixed Vertical Scale** command adds flexibility in displaying control charts both on-screen and on printouts, for comparison with other charts.

Figure 129.

- **Fixed Vertical Scale Off** (no checkmark) — 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 may be quite compressed vertically.

- **Fixed Vertical Scale On** (checkmark) — 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 the menu item to mark it with a checkmark or unmark it.

Figures 130 through 133 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. 130 and 131 to the location of the question marks in Figs. 132 and 133.

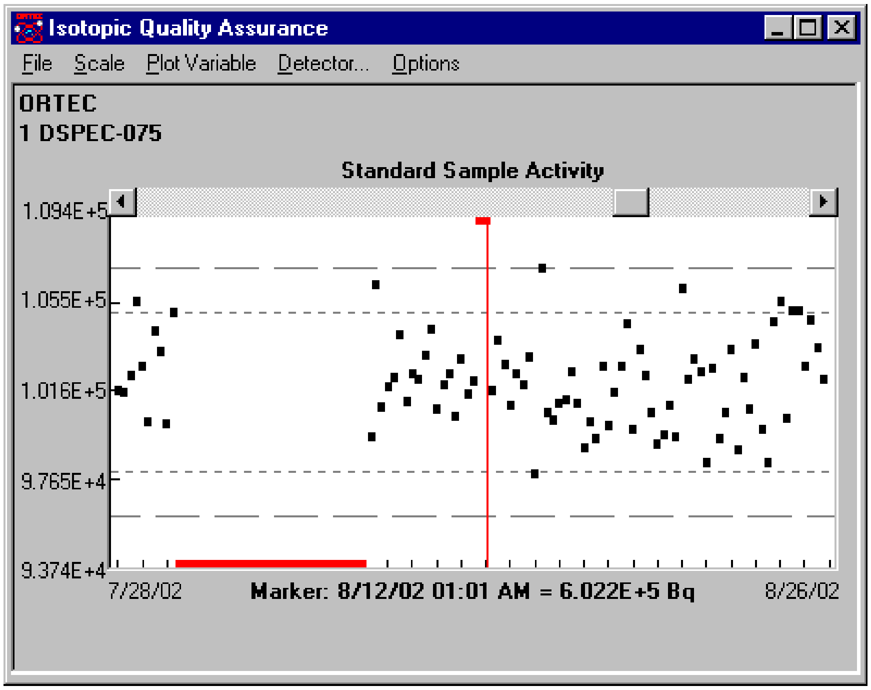


Figure 130. Control Chart On Screen with Fixed Vertical Scale On.

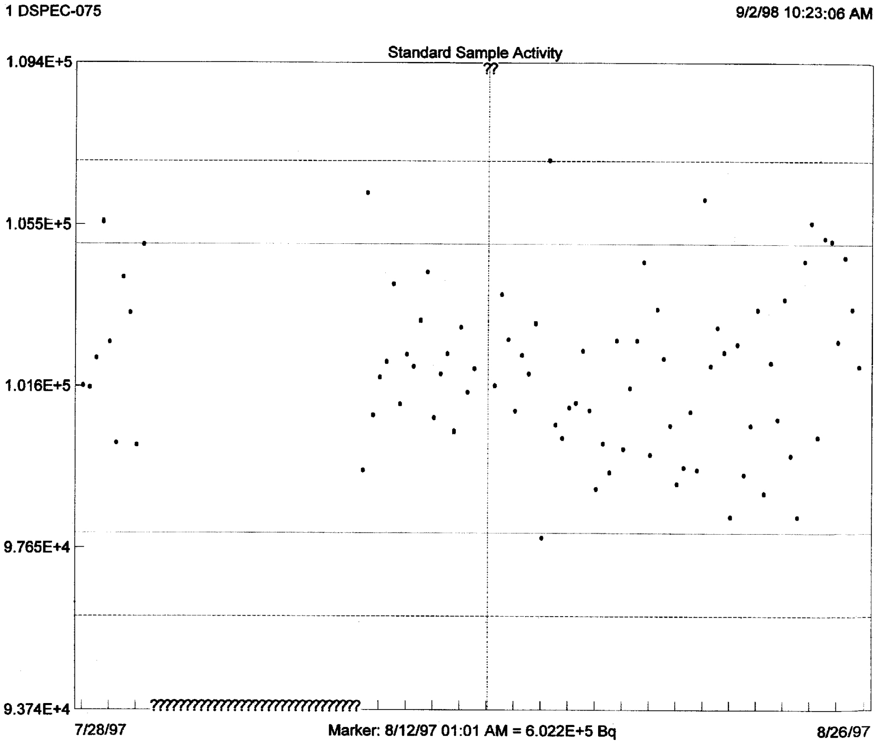
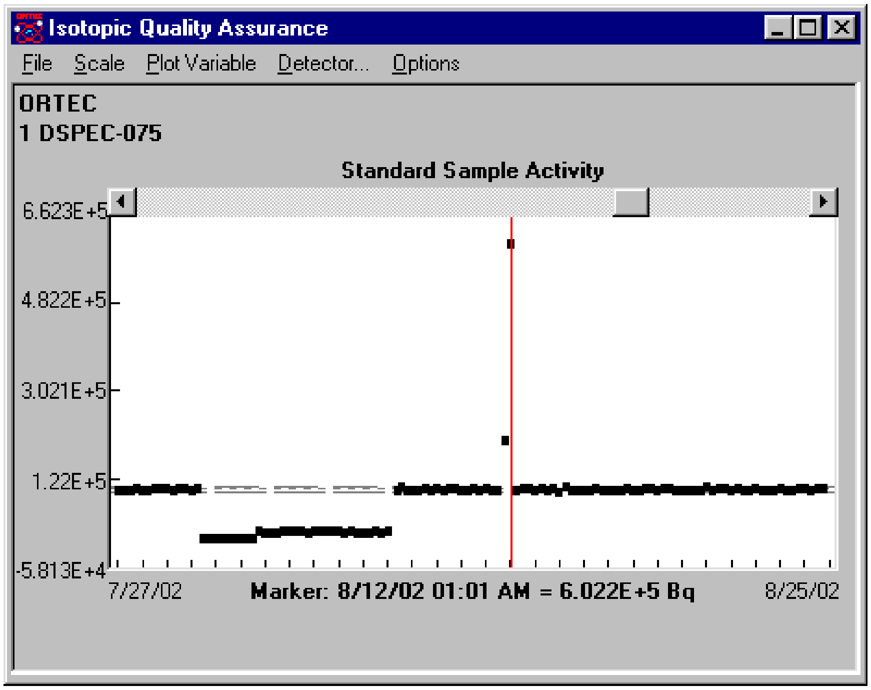
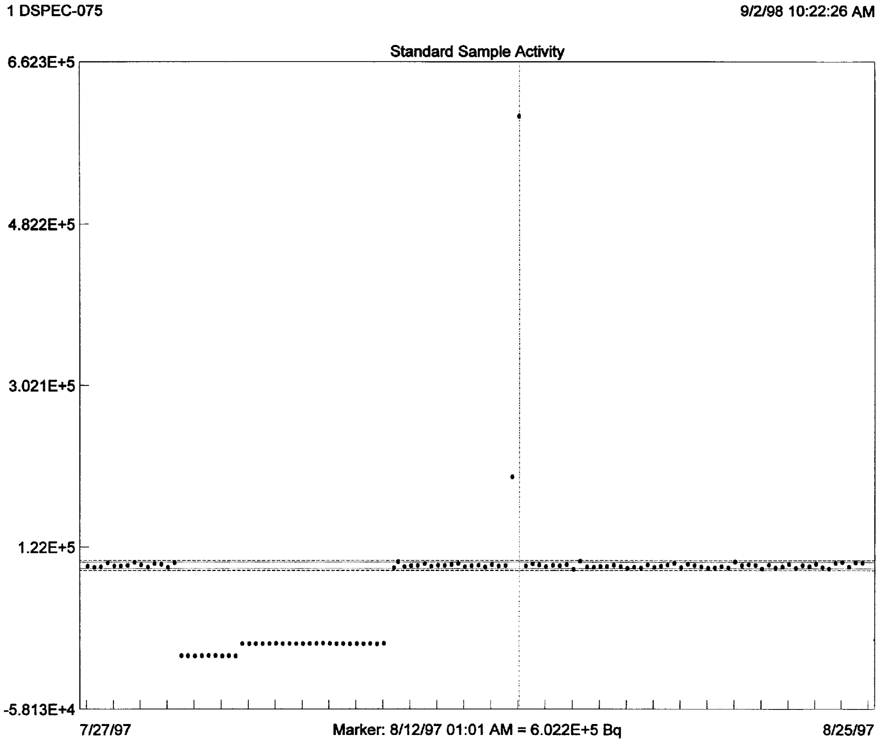


Figure 131. Printout of Control Chart with Fixed Vertical Scale On.



Marker: 8/12/02 01:01 AM = 6.022E+5 Bq

Figure 132. Control Chart On Screen with Fixed Vertical Scale Off.



Marker: 8/12/97 01:01 AM = 6.022E+5 Bq

Figure 133. Printout of Control Chart with Fixed Vertical Scale Off.

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10. KEYBOARD ACCELERATORS

This chapter describes the ISOTOPIC Operator accelerator keys.

10.1. Introduction

Table 3 and Fig. 134 provide a quick reference to all of the ISOTOPIC Operator keyboard and keypad functions, which are discussed in more detail in the remainder of the chapter.

The accelerators operate only in the active window, and the cursor must be in the active spectrum window.

The multi-key functions, such as **<Alt + 1>** or **<Shift + →>**, are executed by simultaneously pressing and releasing both keys (e.g., **<Alt>**, **<Shift>**, or **<Ctrl>**). Commands that use the keypad begin with the word **Keypad**, e.g., **Keypad<5>**.

The menus are accessed by clicking them with the mouse, or by using the **Alt** key plus the key that matches the <u>underlined</u> letter in the menu item name. For example, to open the **<u>F</u>ile** menu, press **<Alt + F>**.

The ISOTOPIC accelerator keys do not interfere with Windows menu operations or task switching.

10.2. Marker and Display Function Keys

10.2.1. 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 may 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 2.1).

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 the *Supervisor Manual*.)

Table 3. Quick Reference to ISOTOPIC Keyboard Commands.

Key	Function
<↓> or <F5>	Change vertical scale so spectrum peaks are smaller.
<↑> or <F6>	Change vertical scale so spectrum peaks are larger.
<→>	Move marker to higher channel.
<←>	Move marker to lower channel.
<−> or <F7>	Narrow the horizontal scale.
<+> or <F8>	Widen the horizontal scale.
<Ctrl + →>	Jump to next (higher-energy) peak.
<Ctrl + ←>	Jump to previous (lower-energy) peak.
<Shift + →>	Jump to next higher ROI.
<Shift + ←>	Jump to next lower ROI.
<Alt + →>	Move to next (higher-energy) library entry.
<Alt + ←>	Move to previous (lower-energy) library entry.
<PageUp>	Jump to higher channel number in 1/16th-screen-width increments.
<PageDown>	Jump to lower channel number in 1/16th-screen-width increments.
<Home>	Jump to first channel of the full spectrum.
<End>	Jump to last channel of the full spectrum.
<Ctrl + Fi>	Select Detector i (i = 1 to 12, in pick list order).
<F2>	Switch ROI bit control from OFF to SET to CLEAR.
<F3>	In supported ORTEC digital MCBs, switch between the two spectra stored in ZDT mode.
<Shift + F3>	In supported ORTEC digital MCBs, switch the disk spectrum to compare normal to disk ZDT spectrum or ZDT spectrum to disk normal spectrum.
<F5> or <↓>	Change vertical scale so that spectrum peaks are smaller.
<F6> or <↑>	Change vertical scale so that spectrum peaks are larger.
<F7> or <−>	Narrow the horizontal scale.
<F8> or <+>	Widen the horizontal scale.
<Alt + F7>	Reset both horizontal and vertical scaling to view complete spectrum.
Keypad<−>	Zoom out.
Keypad<+>	Zoom in.
Keypad<5>	Center expanded display on cursor.
Keypad</>	Switch to logarithmic vertical scale.
Keypad<*>	Switch to auto vertical scale.
<Shift + ↑>	Shift the compare spectrum upwards.
<Shift + ↓>	Shift the compare spectrum downwards.
<Alt + 1>	Start acquisition in selected Detector.
<Alt + 2>	Stop acquisition in selected Detector.
<Alt + 3>	Clear data in selected Detector.
<Alt + −>	Decrease amplifier fine gain by smallest increment (where supported).
<Shift + Alt + −>	Decrease amplifier fine gain by several increments.
<Alt + +>	Increase amplifier fine gain by smallest increment.
<Shift + Alt + +>	Increase amplifier fine gain by several increments.
<PrintScreen>	Capture screen to Windows Clipboard.

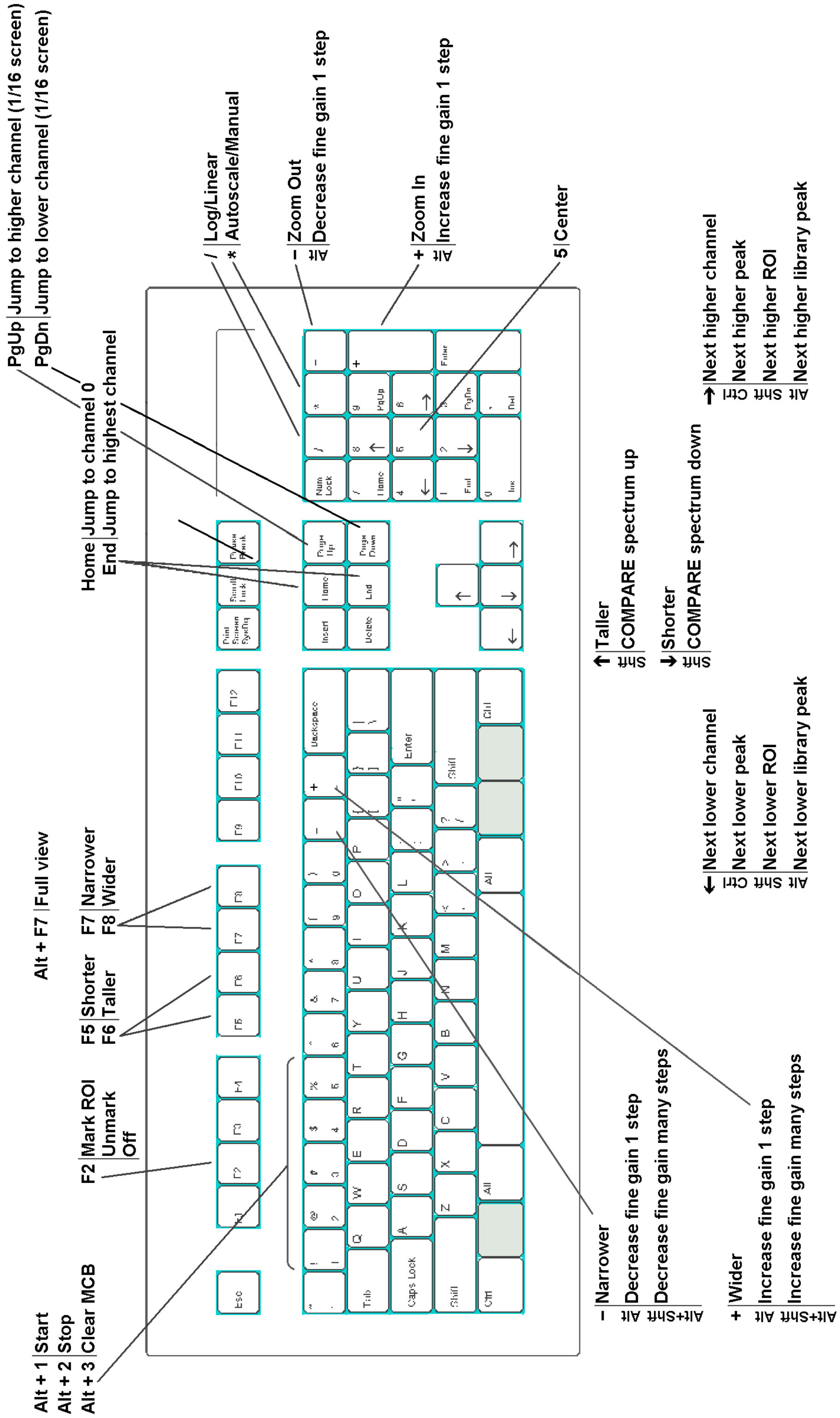

Figure 134. ISOTOPIC Operator Keyboard and Keypad Accelerators.

10.2.2. 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.

10.2.3. 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.

10.2.4. 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.

10.2.5. First/Last Channel <Home>/<End>

These keys move the marker to the first or last channel of the spectrum.

10.2.6. Jump (Sixteenth Screen Width) <PageDown>/<PageUp>

<PageDown> and **<PageUp>** jump the marker position to the left (to lower channel numbers) or right (to higher channel numbers), respectively, 1/16 of the window width, regardless of the horizontal scale. The status of the ROI bit is not altered when the marker is moved with these keys, that is, the **Mark/UnMark/Off** state is ignored. The marker channel contents and Marker Information Line are continuously updated as the marker jumps, so when the jump is complete, the marker information is up-to-date for the current channel.

10.2.7. 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. These keys duplicate the function of the <**F6**>/<**F5**> keys.

Note that if the number of counts exceeds the full-scale value, the data points will be displayed at the full-scale value.

10.2.8. Compare Vertical Separation <Shift+↑>/<Shift+↓>

In Compare mode, the <**Shift** + ↑> or <**Shift** + ↓> keys decrease or increase the vertical separation between the two spectra. Each successive key press will increase or decrease the separation by moving the spectrum read from disk. The spectrum from disk can be moved below the first spectrum if it has fewer counts.

10.2.9. Zoom In/Zoom Out Keypad<+>/<−>

Keypad<+> decreases the scale of both axes in the Expanded Spectrum View so the peaks appear larger, while **Keypad**<−> does the opposite, making the peaks look smaller. The scale value for both axes is always shown on the toolbar. These functions are duplicated by the **Zoom In**/**Zoom Out** buttons on the toolbar and **Zoom In** and **Zoom Out** under the **Display** menu. See Section 2.1 for a more detailed discussion.

10.3. Keyboard Number Combinations

NOTE Only the key*board* numbers will function in the following combinations. The key*pad* number keys will *not* perform these functions.

10.3.1. Start <Alt + 1>

<**Alt + 1**> starts the acquisition in the selected MCB. Any presets desired must be entered before starting acquisition. This accelerator duplicates the **Start** toolbar button.

10.3.2. Stop <Alt + 2>

<**Alt + 2**> stops acquisition in the selected MCB. This duplicates the **Stop** toolbar button.

10.3.3. Clear <Alt + 3>

<Alt + 3> clears the displayed MCB histogram data and its descriptors (e.g., real time, live time). This accelerator duplicates the **Clear Spectrum** toolbar button.

10.3.4. Narrower/Wider <+>/<−>

The <+> key decreases the horizontal scale of the Expanded Spectrum View so the peaks appear wider, while the <−> key increases 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**>.

10.4. Function Keys

10.4.1. Taller/Shorter <F5>/<F6>

These keys decrease or increase the vertical full scale of the displayed spectrum so the peaks appear taller or shorter, respectively. They duplicate the function of the <↑> and <↓> keys. The vertical scale value is always shown on the toolbar.

10.4.2. Narrower/Wider <F7>/<F8>

These keys increase or decrease the horizontal scale of the data display so the peaks appear narrower or wider, respectively. They duplicate the function of <−> and <+> keys. The horizontal scale value is always shown on the toolbar.

10.4.3. Show Full View <Alt + F7>

This key will force the Expanded Spectrum View for the active spectrum to be the full spectrum width. This is duplicated by the **Display/Show Full View**.

10.5. Keypad Keys

10.5.1. Log/Linear Keypad</>

Keypad</> toggles the active spectrum window between logarithmic and linear vertical display. This is duplicated by the **Log** toolbar button. The vertical scale can be controlled with the **Zoom In/Zoom Out** toolbar buttons, **Keypad**<+>/<−>, the <↑> and <↓> keys, and <**F5/F6**>.

10.5.2. Auto/Manual Keypad<*>

Keypad<*> switches the spectrum window between automatic and manual vertical full scale (see the discussion in Section 8.5.2). This is duplicated by the **Vertical Auto Scale** button on the toolbar.

10.5.3. Center Keypad<5>

Keypad<5> forces the marker to the center of the screen by shifting the spectrum without moving the marker from its current channel. This is duplicated by the **Center** button on the toolbar. For more information, see Section 8.5.6.

10.5.4. Zoom In/Zoom Out Keypad<+>/<–>

Keypad<+> decreases the scale of both axes in the Expanded Spectrum View so the peaks appear larger, while **Keypad<–>** does the opposite, making the peaks look smaller. The scale value for both axes is always shown on the toolbar. These functions are duplicated by the **Zoom In/Zoom Out** toolbar buttons.

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INDEX

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