Genie™ 2000 Tutorials

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The information in this document describes the product as accurately as possible, but is subject to change without notice.

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1. Introduction to the Tutorials

Though these tutorials are written for Genie™ 2000's Model S501 Gamma Analysis Software, the Model S509 Alpha Analysis Software is similar enough that using these tutorials shouldn't cause any confusion.

- The user interface, starting on page 2.
- Basic Genie 2000 operations, starting on page 11.
- Basic energy calibration techniques, starting on page 21.
- Basic efficiency calibration techniques, starting on page 25
- Basic analysis techniques in three parts, starting on page 29.
  - Executing a Module Interactively
  - Executing an Analysis Sequence
  - Editing an Analysis Sequence

The first tutorial, "The User Interface", describes the main features of the application's user interface.

The remaining tutorials are brief introductions; their functions are covered more thoroughly in one of two documents:

- The *Gamma Acquisition and Analysis* chapter of the *Genie 2000 Operations Manual*.
- The *Model S509 Genie 2000 Alpha Analysis User's Manual*, which is included at the back of the *Genie 2000 Operations Manual*.

Glossary

A comprehensive glossary of nuclear spectroscopy terms is included at the back of this document, starting on page 39.

A Prerequisite to Using the Tutorials

Before you can use these Tutorials with Genie 2000, you must have created at least one MCA Input Definition with either the MID Wizard or the MID Editor. Instructions for using both of these are provided in the *MCA Input Definition* chapter of the *Genie 2000 Operations Manual*.

2. The User Interface

The Acquisition and Analysis window (Figure 1) is Genie™ 2000's user interface for acquiring and analyzing nuclear spectra. Since the Gamma A&A window (GAA) is similar to other Genie 2000 application windows, it'll be used as a quick introduction to the parts of the window.

It consists of the Title Bar, the Menu Bar, the Toolbar and the Display Status Line at the top of the screen, the Control Panel, the Spectral Display, the Status Pages, and the Report Window in the main part of the window, and, at the bottom of the screen, the Analysis Status Line.

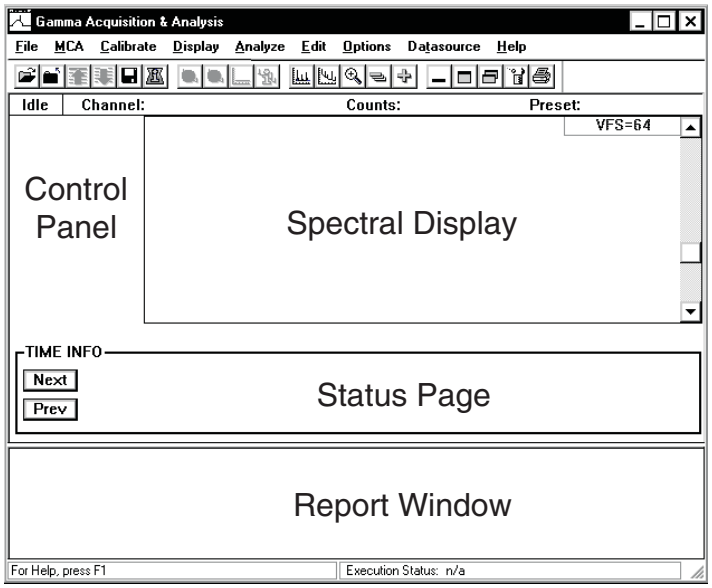

Figure 1 The Basic Acquisition and Analysis Window

The Top Four Lines

The four lines at the top of the screen are the Title Bar, the Menu Bar, the Toolbar and the Display Status Line.

The Title Bar

The Title Bar, at the top of the screen, always shows the application's name. If a datasource has been opened, the datasource's file name will also be displayed (Nbsstd.cnf in Figure 2). If more than one datasource is open, the name of the current one is displayed.

Figure 2 The Title Bar

The Menu Bar

The Menu Bar, just below the Title Bar, presents you with a choice of top-level menu functions (Figure 3). Each of the submenus' functions is covered in detail in your *Gamma Acquisition and Analysis* chapter or *Alpha Analysis Manual*.

Figure 3 The Menu Bar

The Toolbar

The Toolbar (Figure 4), directly under the Menu Bar, contains buttons corresponding to common menu commands. Throughout these tutorials, you'll find examples of using Toolbar buttons, each with an illustration of its icon. If you rest the mouse cursor (page 13) on an icon for a short time, you'll see a tooltip describing its action.

Figure 4 The Toolbar

If you don't see the tooltips, select the "Show Tooltips" checkbox in **Display | Preferences | Toolbar Setup | Toolbars**. Before closing the Toolbar Setup page, check or uncheck the "Cool Look" checkbox. You'll immediately see another way of displaying the Toolbar. Figure 4 shows the Toolbar with the "Cool Look" box unchecked.

Display Status Line

The Display Status Line (Figure 5) is between the Menu Bar and the spectrum. It displays the current status, such as Idle, Busy or Done, and the position of the spectrum cursor (page 13) in terms of both channel and energy, and the total counts at that location. The Preset at the right shows 2000/1826.00, the values for the preset setting and the elapsed preset.

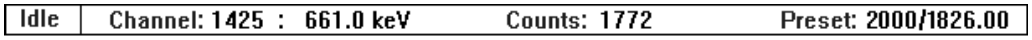

Figure 5 The Display Status Line

How to Use the Control Panel

The Control Panel (Figure 6), on the left-hand side of the screen, provides easy access to the functions used in daily operations: Acquire Start/Stop, Expand On/Off, Clear data and time, ROI Indexing, and moving forward/backward through the list of all open datasources.

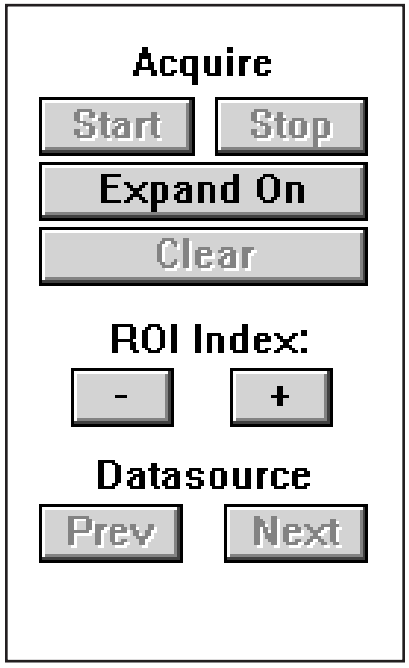

Figure 6 The Control Panel

You can make the spectral display area larger by hiding the Control Panel: select **Display | Preferences**, then remove the check from the **Control Panel Shown** check box.

Acquire Start/Stop

Clicking on these buttons starts or stops data acquisition. The buttons are disabled for files and for detector datasources that are opened as Read Only.

Expand On

Clicking on this button toggles the state of the Expanded Display. See "Expand" on page 16 for more information.

Clear

Clicking the **Clear** button, which is enabled only for detector datasources, clears all spectral data and time information from the currently displayed datasource.

ROI Index

To quickly move the markers through the spectrum, from one ROI (Region of Interest) to the next, you can:

- Click one of the Control Panel's **ROI Index** buttons. The (+) button moves one ROI to the right and the (–) button moves one ROI to the left.
- Use the keypad's (+) and (–) keys.
- Click one of the ROI Index buttons in the Toolbar. 

Datasource

If more than one datasource is open, you can click on **Next** or press the F6 key to change the display to the next datasource in the list of all open datasource. If you click on **Prev** or press SHIFT+F6, you'll display the previous datasource.

If less than two datasources are open, these buttons will be disabled (grayed out).

Up to 48 Detector and File Inputs in any combination may be opened and up to eight can be displayed simultaneously.

Similarly, other open Detector Inputs or File Inputs (as well as multiple memory groups) can be selected for display from the list of currently open Detector Inputs or File Inputs.

How to Use the Spectral Display

The Spectral Display (Figure 7) shows the current spectrum. The upper right corner of this area will show the display's current VFS (vertical full scale) setting.

Changing the VFS

The scroll bar on the right side of this area lets you manually adjust the VFS.

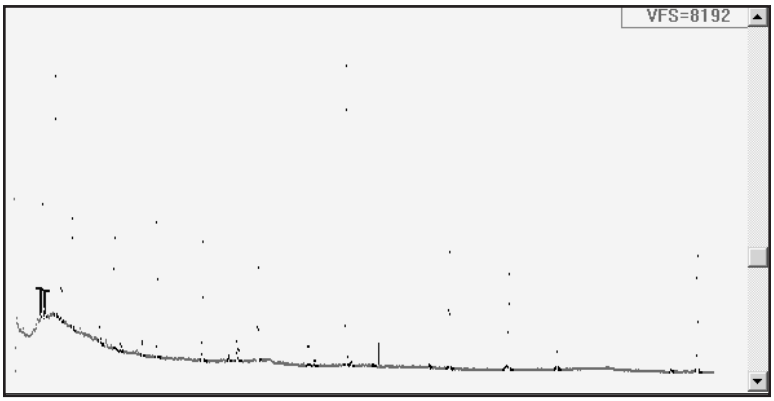

Figure 7 The Spectral Display

How to Use the Status Pages

Detailed information about the current datasource can be seen in the Status Pages displayed below the spectrum.

You can move through the pages by selecting the **Next** or **Prev** button in the Status Page area or by pressing keyboard's PG DN or PG UP key. You can make the spectral display area larger by hiding the Status Pages: select **Display | Preferences**, then remove the check from the **Status Page Shown** check box. In addition, you can chose which status pages to display by selecting **Display | Preferences**, then the **Status Pages** button.

Note that some of the data shown on the Status Pages is the result of a rough calculation for the region between the markers. This means that this displayed data may not agree with the data you see in a report generated by your analysis application.

Only the four default Status Pages are described here. For information on the other pages, refer to the "Display Menu | Screen | Status Pages" section of your *Gamma Acquisition and Analysis* chapter or *Alpha Analysis Manual*.

The Time Info Page

The **Time Info** status page (Figure 8) includes: acquire start time, percent dead time, computational preset region, and elapsed and preset values.

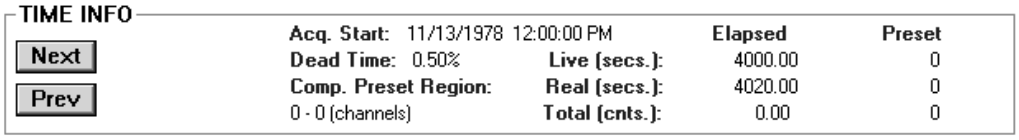

Figure 8 The Time Info Page

The Sample Info Page

The **Sample Info** status page (Figure 9) includes sample-related information: Title, ID, sample type, quantity and units, sample geometry, geometry id, and buildup type.

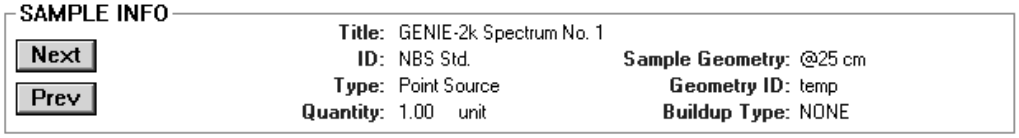

Figure 9 The Sample Info Page

The Nuclide Info Page

The **Nuclide Info** status page (Figure 10) includes estimated nuclide information for the location of the spectrum cursor (page 13): Nuclide, Energy, Half-life, and percent Yield. If the cursor is within an ROI then the FWHM, Area, and estimated Activity are also displayed.

Figure 10 The Nuclide Info Page

The Marker Info Page

The **Marker Info** status page includes data related to the current Region of Interest (ROI): left and right marker channel and energy, centroid channel and energy, area and percent error, FWHM and FWTM, Gaussian ratio, ROI type, and integral.

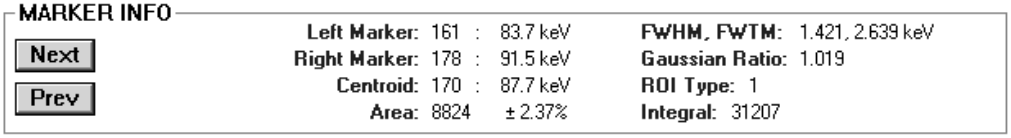

Figure 11 The Marker Info Page

How to Use the Report Window

The Report Window (Figure 12) displays reports that have been created either interactively or automatically by the system.

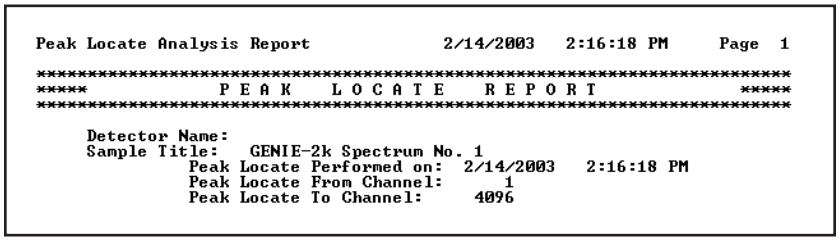

Figure 12 The Report Window

Select the Options menu item, then Report Window to see commands to copy the data to the clipboard, to clear the data from the window, and to change the size of the window for easier report viewing.

Copy (Highlighted) Data to Clipboard

To copy the entire report, select **Options | Report Window | Copy Contents to Clipboard**.

To copy just the highlighted portion, created by dragging your mouse cursor (page 13) over the data of interest, select **Options | Report Window | Copy Highlighted to Clipboard**.

Printing the Report Window

To print the data in the Report Window, select **File | Print Report Window**.

Clearing the Report Window

You'll have to clear the Report Window if you want to display the next report's data by itself. If you don't clear the Report Window, the next report will be appended to the current report.

There are two ways to clear the window:

- Select the menu's **Options | Report Window | Clear Contents** command.
- Click the Toolbar's "trashcan". 

Resizing the Report Window

There are two ways to make the Report Window larger or smaller or reset it to its default size:

- Select the menu's **Options | Report Window | Minimize** or **Maximize** or **Default Size** command.
- Click one of the Toolbar's report window icons. 

How to Use the Analysis Status Line

The Analysis Status Line at the bottom of the screen (Figure 13) displays the execution status during various phases of an analysis.

Figure 13 The Analysis Status Line

How to Use the the Menu Commands

The Gamma Acquisition and Analysis window's Menu Bar contains the title of each of eight main command groups: File, MCA, Calibrate, Display, Analyze, Edit, Options and Datasource, as well as Help.

The File Menu

The **File** menu lets you open, close or save a datasource, save it under another name (save as), access print options for the current spectrum and Report Window, access workspace files, and exit the program.

The MCA Menu

The MCA Menu's commands include starting and stopping data acquisition, setting up the acquisition parameters, clearing the spectral display, adjusting the hardware datasource's programmable controls, checking the status of all MCA devices, advancing to the next sample in a sample changer, and loading a data file into the current datasource.

The Calibrate Menu

The Calibrate Menu lets you set up calibration preferences, perform energy, efficiency and peak-to-total calibrations, show the results of a calibration graphically, and load a calibration file into the current datasource or store the datasource's calibration as a file.

The Display Menu

In the Display Menu, you'll find commands for expanding and scaling the display, comparing two datasources, entering or deleting ROIs (regions of interest), and setting display preferences.

The Analyze Menu

The Analyze Menu's commands let you execute a single analysis step or a sequence of analysis steps. Every Genie 2000 system includes the acquisition, peak locate, peak area, reporting, post-NID processing and datasource saving steps.

If your system includes the Model S501 Gamma Analysis option, the area correction, efficiency correction, nuclide identification and detection limits steps are added. Any other installed options will add their own steps.

The Edit Menu

The Edit Menu allows you to enter and edit Sample Information and define and edit Analysis Sequences.

The Options Menu

The Options Menu lets you change the operator's name, initiate interactive NID, launch the geometry composer, perform strip and smooth, and work with the report window.

The Datasource Menu

The Datasource Menu lets you display up to eight of the currently open datasources. If the datasource is a multi-memory group input, you'll be able to move from one group to another.

3. Basic Genie 2000 Operations

For the procedures covered in this chapter, the Model S500/502/504 Basic Spectroscopy Software must be running.

This tutorial is intended to be a brief overview of the basic Gamma Spectroscopy Analysis window and of some of its functions. The Alpha Spectroscopy Analysis window is very similar, so Alpha users can benefit from this tutorial as well.

The first step in learning how to use Gamma Spectroscopy Analysis is to get some data to work with. This process is called opening a datasource, where the source for the data can be a Detector or a data file. For this tutorial, we'll open a data file.

How to Open a Datasource

There are two ways to open a datasource:

- Select the menu's **File | Open Datasource** command.
- Click the Toolbar's open datasource icon. 

Either way, the dialog box in Figure 14 will be displayed.

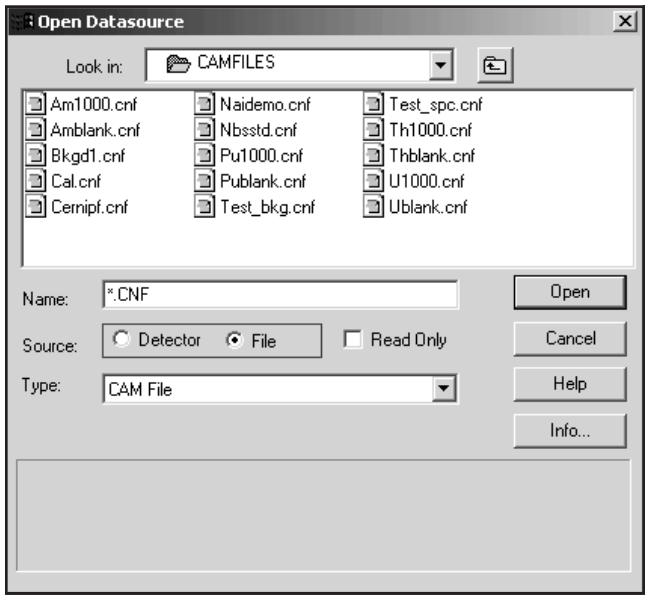

Figure 14 Opening a Datasource

1. **Source:** If it's not already highlighted, select the **File** button.

2. **Type:** Select CAM File. CAM stands for Configuration Access Method, a type of data file which contains a spectrum, its Regions of Interest (ROIs), its calibration information, etc.

3. **Read Only:** This checkbox should *not* be checked.

4. **Look in:** Navigate to C:\GENIE2K\CAMFILES and select Nbsstd.cnf, the NBS Standard spectrum file.

5. Click **Open**.

How to View the Data

The name of the datasource you just opened can be seen in the window's Title Bar, and the data itself in the window's Spectral Display area as seen in Figure 15.

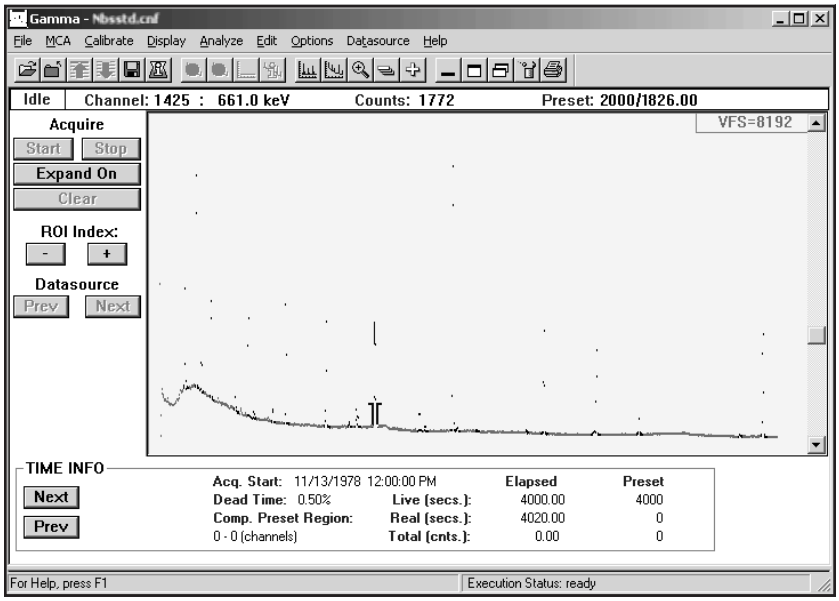

Figure 15 A Typical Gamma Display

A. The Display's Vertical Full Scale

The spectral display's Vertical Full Scale (VFS) defaults to Linear Autoranging. That is, the vertical scale is linear rather than logarithmic, and the smallest VFS which will contain the tallest peak in the data is automatically picked for you.

The VFS being used is always displayed in the upper right-hand corner of the spectral display as either VFS=nnnn for a Linear scale or LOG=nnnn for a Logarithmic scale, where nnnn is the vertical full scale value.

How to Change the Scale Manually

There are several ways to change the Vertical Full Scale by a factor of two (1024, 2048, 4096, etc.):

- Click on the upper or lower part scroll bar at right of the data display.
- Drag the scroll bar's slider up or down.
- Use the keyboard's up and down arrow keys. Each press of an arrow key is the same as clicking once on the corresponding end of the scroll bar.

To toggle between Auto and Manual, press the keyboard's F5 key.

Linear or Log Mode

There are two ways to change between Linear and Log data display:

- Select the menu's **Display | Scale | Linear** or **Log** command.
- Click one of the Toolbar's display mode icons. 

How to Use the Cursors

Genie 2000 uses two kinds of cursor:

- The mouse cursor. 
- The spectrum cursor. 

Move the mouse cursor to the middle of the spectrum, hold down the left mouse button and move the cursor to the left and right. You'll see a short vertical bar, the spectrum cursor, following your mouse's movement.

Moving the Spectrum Cursor

Any time you point and click within the data display, the spectrum cursor will immediately jump to the channel which corresponds to the horizontal location of the mouse cursor. In addition, you can also move the spectrum cursor by:

- Dragging it across the data by holding the left mouse button down while you move the mouse.

- Using the keyboard's left and right arrow keys to move the spectrum cursor through the data.

As you move the spectrum cursor, watch the Display Status Line (Figure 16). You'll see the information displayed there, the current channel number, its energy, and the number of counts in that channel, change with the cursor's movement. The word Idle at the far left lets you know that no data acquisition is under way.

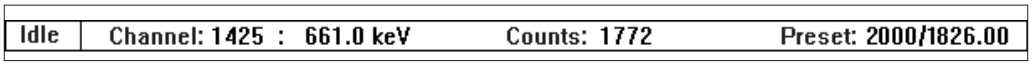

Figure 16 The Display Status Line

How to Use the Markers

In addition to the spectrum cursor, which is used to examine individual channels of data, the spectrum also includes a pair of region markers that are used to measure things like peak areas and centroids. These are initially located on either side of the first ROI (Region of Interest), if there is one. If there is no ROI, they are at either end of the full spectrum.

The region markers look like an "upside down L", with the horizontal part pointing to the left for the left marker, and right for the right marker. Figure 17 on page 15 illustrates the region markers.

Moving the Region Markers

The region markers can be moved independently by either of two methods:

1. With the mouse: Move the spectrum cursor to the outside edge of the marker you want to move. When the cursor turns into a vertical bar with an arrow attached to it (see Figure 17 on page 15), dragging with the mouse will move the region marker.

2. From the keyboard: First, use the keypad's arrow keys to move the spectrum cursor to the new location for a region marker. Press CTRL+L for the Left marker or CTRL+R for the Right marker and the selected marker will jump to the cursor location.

In addition, a keyboard command, CTRL+M, is available to the markers from where ever they happen to be in the Reference (lower) Spectrum to the edges of the Expanded Spectrum. The Expand Mode is covered in detail in "Expanding the Display" on page 16.

While the region markers can be moved individually, we've found the following to be the easiest way to quickly place the markers on either side of a peak of interest when the markers are close together:

1. Move the mouse cursor (not the spectrum cursor) to the region markers. When it reaches a marker, it will change into a vertical bar with an arrow attached to it. Dragging the mouse will move that marker.

   Figure 17 shows the mouse cursor on the left (with an arrow), the two region markers and the spectrum cursor, the vertical line at the top of the peak.

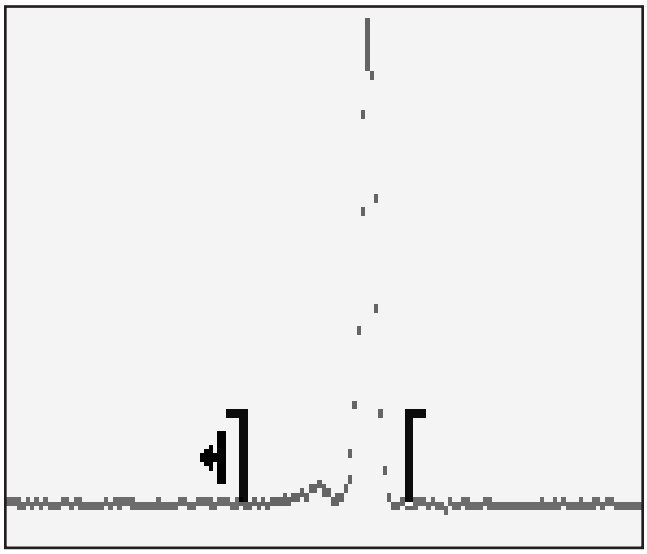

Figure 17 The Mouse Cursor, the Two Region Markers and the Spectrum Cursor

2. When the mouse cursor has a left-pointing arrow, it means that you have selected the left marker for movement. Similarly, a right-pointing arrow affects only the right marker.

3. Drag the left marker toward the right until it is just to the right of the peak you want to analyze. You'll notice that both markers will move together when you do this, because the left marker will "push" the right marker along in front of it.

4. Now drag the left marker back to the left until it is at the left edge of the region you want to analyze. When you do that the right marker will stay where it was; the markers are now bracketing the region.

How to Add, Use and Delete ROIs

Since Genie 2000 has the ability to create and use Regions of Interest (ROIs), let's take a look at them.

Creating an ROI

In the previous section, you moved the markers so that they would bracket a peak, which is the first step in creating an ROI. The second step is to press the keyboard's INS key to create an ROI between the two markers.

Using the ROIs

When there are ROIs in your spectrum, you can quickly move the markers to the region you want to examine by:

- Clicking one of the Control Panel's **ROI Index** buttons. The (**+**) button moves one ROI to the right and the (**–**) button moves one ROI to the left.
- Using the keypad's (**+**) and (**–**) keys.
- Clicking one of the ROI Index buttons in the Toolbar. 

Deleting an ROI

Deleting an ROI is just as easy as entering one. Just Index the markers to the ROI you want to remove, then press the keyboard's DEL key.

How to Expand the Display

To create ROIs accurately, you really need to take a closer look at the data, and for that, we use the expand mode.

Turning Expand On and Off

There are three ways to turn the expand mode on:

- Click on the Control Panel's **Expand On** button.
- Press the F8 key on the keyboard.
- Click the Toolbar's expand icon. 

The result will be a display like the one in Figure 18. The Reference Spectrum, the lower half of the display, contains the full spectrum and the Expanded Region, the upper half of the display, shows the expanded data.

Turning the expand mode on changes the button's name to **Expand Off**, so the next time you click on it (or press F8), the display will change back to normal.

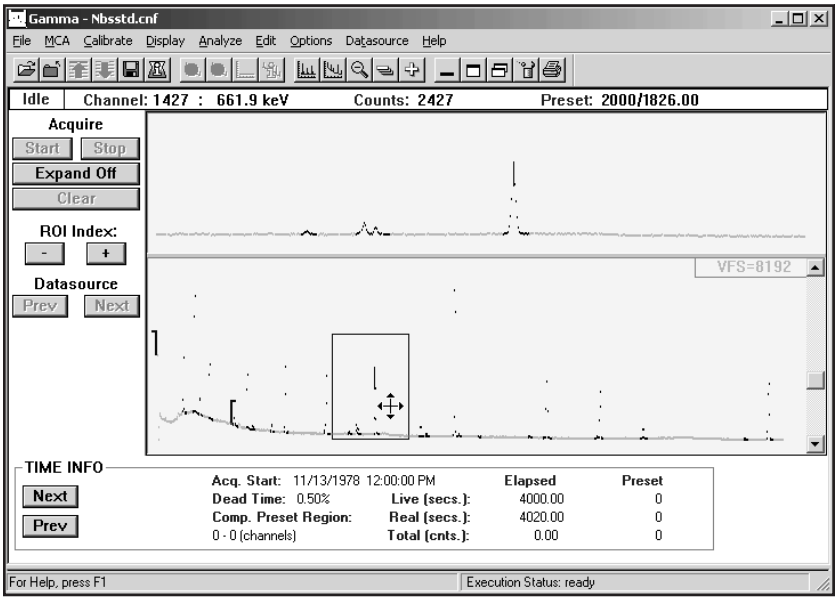

Figure 18 Expand Has Been Turned On

The Expand Rectangle

At the spectrum cursor's location in the Reference Spectrum, you'll see a large rectangle in the spectrum (Figure 18). What you see in the Expanded Region is the data within the rectangle.

Moving the Rectangle

To view a different portion of the Reference Spectrum in the Expanded Region, all you have to do is move the rectangle to a new section of the data. To do that:

1. Move the mouse cursor into the rectangle; it will change into the four-headed arrow  shown inside the Expand Rectangle in Figure 18.

2. Press the left mouse button and drag the rectangle to the new location. The Expanded Region will track the movement so you can view the data as the Expand Rectangle is moved.

Viewing the Data in ROIs

You can to move to and examine the ROIs in the Expanded Display by using any of the methods described in "Using the ROIs" on page 16.

Changing the Size of the Rectangle

To change the amount of data shown in the Expanded Region all you have to do is change the size and shape of the rectangle. This is done by stretching or shrinking the rectangle.

To change one side of the rectangle:

1. Move the mouse cursor to the side you want to change until it changes into a horizontal or vertical double-headed arrow (Figure 19).

2. Click and drag the side to the new position.

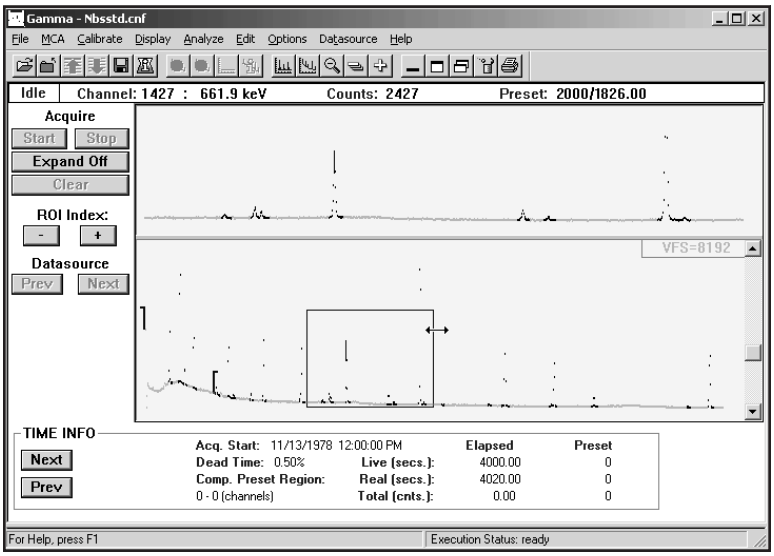

Figure 19 Stretching the Expand Rectangle

To change two adjacent sides at the same time:

1. Move the mouse cursor to any corner of the rectangle until it changes into a diagonal double-headed arrow.

2. Click and drag with the mouse, which moves the rectangle's corner, changing the size of the rectangle in two directions at once.

Using either of these two methods you can change the size and shape until the data you want to view is displayed in the Expanded Region.

Using the Expanded Region

The spectrum cursor, the markers, and adding and clearing ROIs all work in the usual way in the Expanded Region, allowing you to examine individual data channels and "fine tune" your ROI locations. When you've finished working with the expanded display, click **Expand Off** and you'll be ready to continue.

How to Describe the Data

When you've acquired a spectrum, the next step is to enter some descriptive information before saving it for later analysis.

Editing the Sample Information

There are two ways to open the Sample Information dialog box shown in Figure 20:

- Select the menu's **Edit | Sample info** command.
- Click the Toolbar's edit sample information icon. 

The Sample Information editor lets you add a description of the sample to the data file. Note this information does not have to be entered at this time; it can be added at analysis time.

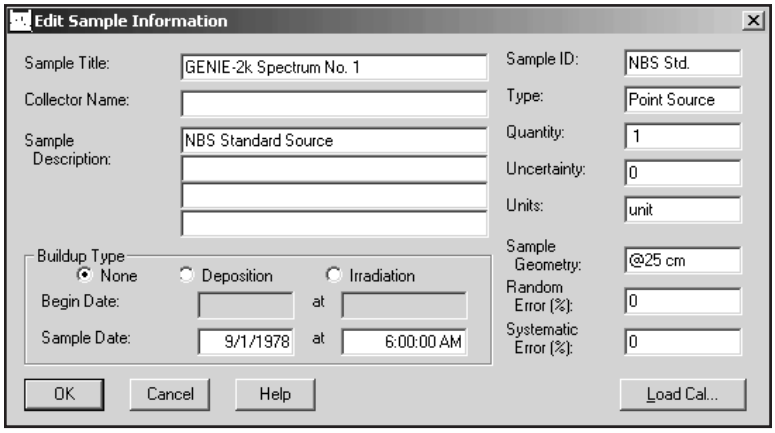

Figure 20 Editing Sample Information

Most of the fields in this dialog box are for descriptive purposes only. That is, the text you type in is stored with the data and will be included with the analysis reports to provide a better description of the sample.

You can also enter information in the sample Quantity, Uncertainty, Units, Sample Geometry, percent Random Error and percent Systematic Error fields, all of which are used during sample analysis. Their use is beyond the scope of this tutorial; for complete information, refer to "The Information Fields" in your *Gamma Acquisition and Analysis* chapter or *Alpha Analysis Manual*.

Viewing the Sample Information

To see the Sample Information for the current datasource, click on the **Next** button in the window's Status Page area until the SAMPLE INFO page appears. You'll find a summary of the information you've entered displayed there.

If the Sample Info page is not available, you can enable it through the **Display | Preferences** menu selection.

How to Save the Data

There are three ways to save the data and its description:

- Select either the menu's **File | Save** command or the Toolbar's save icon , which will save directly to an existing file.
- If there is no existing file, you'll see the "Save as" dialog box shown in Figure 21, which lets you save to a new file name
- Select the menu's **File | Save as** command. You'll see the "Save as" dialog box (Figure 21).

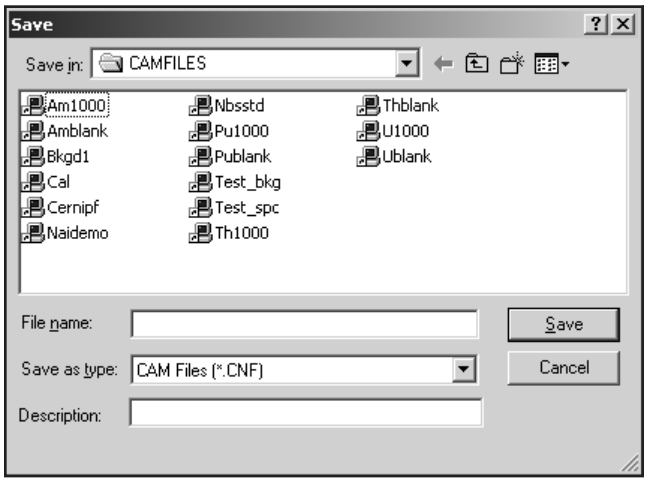

Figure 21 The Save As Dialog

Description

For CAM files, you can enter an optional description of up to 32 characters, making it easier to identify this data file at a later date.

Save as Type

Use the default file type: CAM Files (*.CNF).

File Name

All you need to do is type in the file's name. The dot and the extension (file type) will be automatically added by Genie 2000 when you click **Save**.

4. Basic Energy Calibration Techniques

Energy calibration establishes a linear relationship between the spectrum's channels and their energy levels. By calibrating two peaks, one at each end of the spectrum, the energy of any other peak can be estimated fairly accurately.

Though Genie 2000 Spectroscopy Analysis includes several methods for Energy Calibrating a spectrum, we'll use only one of these methods in the tutorial.

Calibration Setup

Before we create a new energy calibration, we'll take a look at a system-wide parameter used in energy calibration. Select **Calibrate | Setup** to see the screen in Figure 22.

You can see two Tolerance parameters in the upper right corner of the window. The first parameter, Energy Cal, is used in Energy Calibration, discussed below; the second parameter, Eff Match, is used in Efficiency Calibration (page 25).

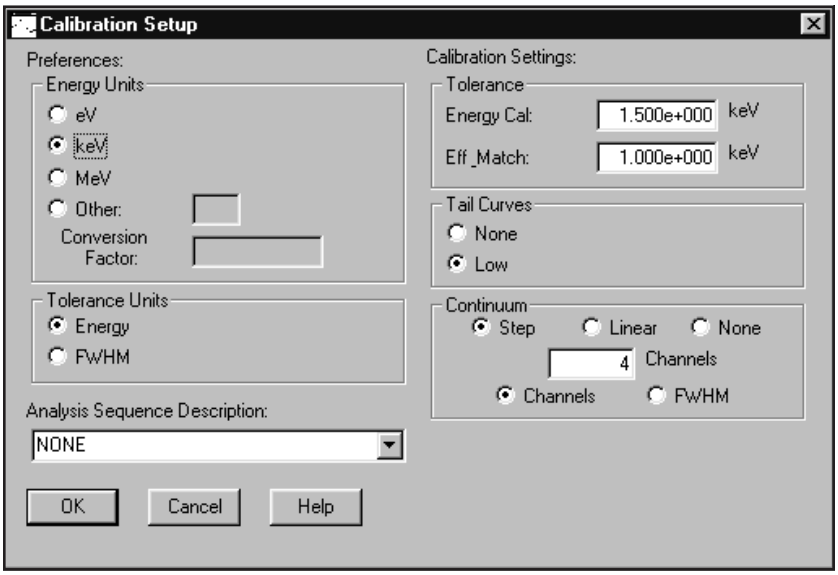

Figure 22 Calibration Setup

Energy Cal Tolerance

During energy calibration, the spectrum's peaks are matched with the energies specified in the selected certificate file, plus or minus this tolerance value. The default value of 1.50 keV means that if a spectrum's peak is within 1.50 keV of a matching energy in the certificate file, it will be accepted as valid.

If you use a higher value, more of the spectrum's peaks will be seen, which could lead to false peaks being accepted. On the other hand, using a lower value may cause valid peaks to be overlooked. Determining the best setting for a given spectrum is beyond the scope of this tutorial, so we'll leave the parameter set to its default value.

How to Create a New Energy Calibration

To create a new Energy Calibration, we'll look at calibration by Certificate File. A mixed radionuclide calibration source includes a certificate that defines the source's radionuclides, their peak energies, the calibrated activity for each, and so forth. A Certificate File is this information stored in a computer file.

- For details on the other Energy Calibration methods, refer to the "Energy Only Calibration", "Energy Full", and "Energy Calibration | Full" subsections of the "Calibrate Menu" section in your *Gamma Acquisition and Analysis* chapter of, or the *Alpha Analysis Manual* in, the *Genie 2000 Operations Manual*.

- For information on how Certificate Files are created and maintained, refer to the *Using the Certificate File Editor* chapter in your *Genie 2000 Operations Manual*.

A. Starting the Calibration

Since we've already opened a datasource (page 11), we'll calibrate its spectrum by entering peak locations and their corresponding energies.

1. Click on **Calibrate | Energy Full | By Certificate File**.

2. In the Open Certificate File box, double click on Nbsstd.ctf.

The energies of the peaks in the datasource will be loaded into the calibration list for you (Figure 23).

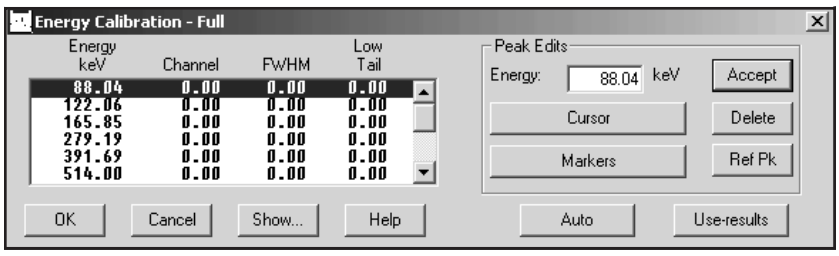

Figure 23 The Energy Calibration – Full Dialog

To establish an energy calibration, we have to locate at least two of the datasource's peaks, one at the low end of the spectrum and one at the high end, which correspond to the energy of the entries in the calibration file, ±1.50 keV, the Energy Calibration Tolerance value.

B. Entering the Peak Locations

The first energy line in Figure 23 is 88.04, which is the line for ^{109}Cd. To enter that peak, place the spectrum cursor on the 88 keV peak at the low end of the spectrum, then click the **Cursor** button to add the cursor's channel position to the Channel column. The FWHM and Low Tail values will be calculated and added to the list.

Now scroll down the list in Figure 23 to the 1836 line (^{88}Y), place the spectrum cursor on the ^{88}Y peak at the high end of the spectrum, then click the **Cursor** button to add the cursor's channel position.

C. Viewing the Energy Calibration

To view the new calibration, click the **Show** button to see the display in Figure 24.

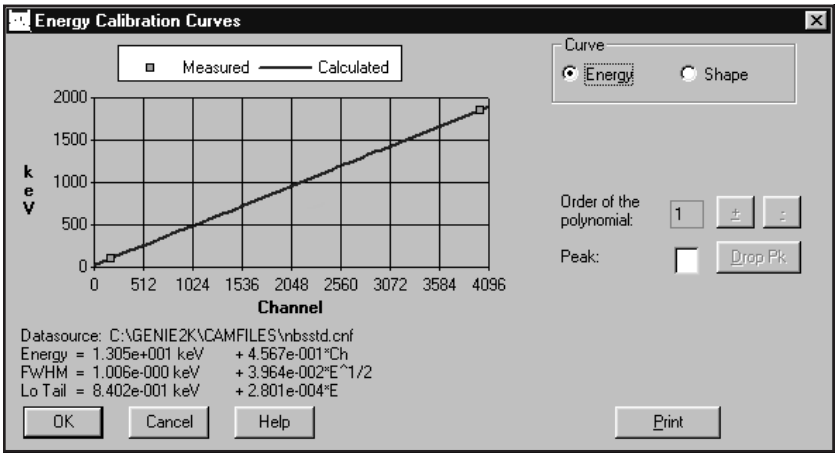

Figure 24 A Two-Point Energy Calibration Graph

Below the graph, you'll see the Datasource's file name and the equation's values for Energy, FWHM and Low Tail.

D. Labeling the Peaks

When the spectrum is calibrated, select **Display | Preferences**. On the left side of the Display Preferences dialog (Figure 25), check the Display Nuclide ID on Spectrum and Display Peak Information checkboxes.

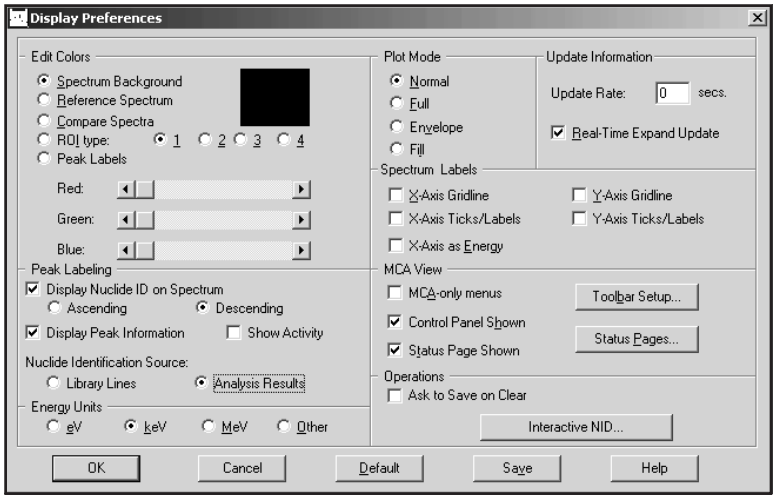

Figure 25 The Display Preferences Dialog

This will add two kinds of peak information to the spectral display: Peak Labels, identifying the nuclide for each peak, and a Peak Information Bubble for the current peak, listing the peak's: Nuclide ID, Energy, Net Area with percent error and the nuclide's Activity (optional).

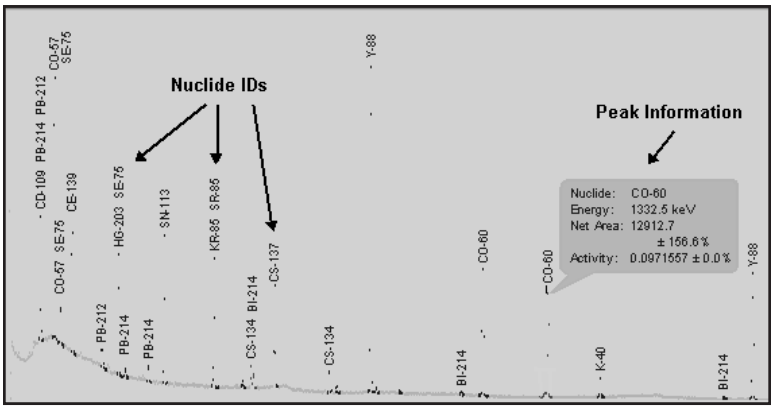

Figure 26 Nuclide IDs and ^{60}Co Peak Information

5. Basic Efficiency Calibration Techniques

Put very simply, a detector's efficiency changes at different levels of gamma-ray energy. The efficiency calibration allows us to compensate for these changes.

Assuming you've gone through the procedures on Energy Calibration and the use of Certificate Files, you'll find Efficiency Calibration to be a similar process.

To create an efficiency calibration, your spectrum must be energy calibrated. If you haven't done that yet, go back to page 22 and follow the procedure in "How to Create a New Energy Calibration".

Eff Match Tolerance

The Efficiency Match Tolerance parameter (Eff Match in Figure 27) is used during efficiency calibration to match calculated peaks with the peaks in the specified certificate file, plus or minus the specified tolerance value.

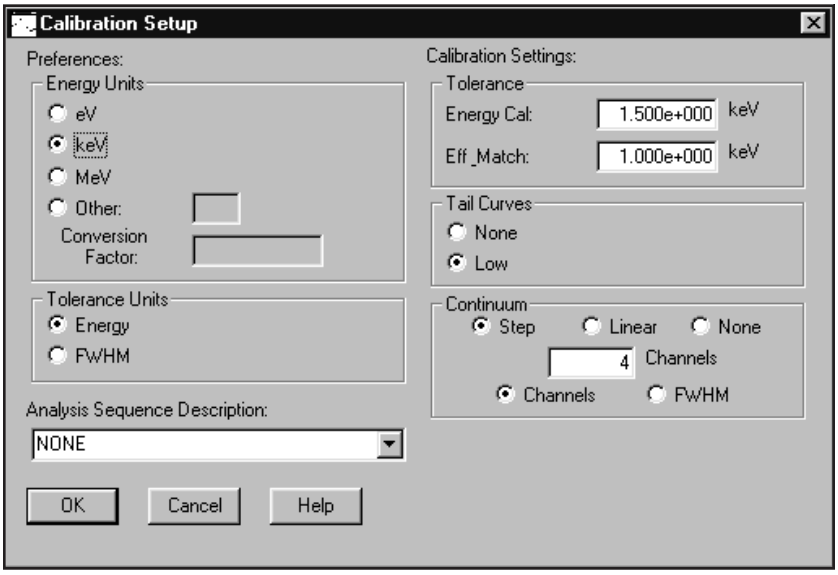

Figure 27 Calibration Setup

The default value of 1.00 keV means that if a spectrum's peak is within 1.00 keV of a matching energy in the certificate file, it will be accepted as valid.

If you use a higher value, more of the spectrum's peaks will be seen, which could lead to false peaks being accepted. On the other hand, using a lower value may cause valid

peaks to be overlooked. Determining the best setting for a given spectrum is beyond the scope of this tutorial, so we'll leave the parameter set to its default value

How to Create a New Efficiency Calibration

To create a new Efficiency Calibration, we'll use calibration by Certificate File, which is similar to the Energy Calibration by Certificate File process.

- For details on the other Efficiency Calibration methods, refer to the "Calibrate Menu | Efficiency" section in your *Gamma Acquisition and Analysis* chapter or *Alpha Analysis Manual*.

- For information on how Certificate Files are created and maintained, refer to the *Using the Certificate File Editor* chapter in your *Genie 2000 Operations Manual*.

A. Starting the Calibration

To calibrate the spectrum, we have to enter peak locations and their corresponding energies.

1. Click on **Calibrate | Efficiency | By Certificate File**.

2. In the Open Certificate File box, double click on Nbsstd.ctf (the same Certificate File we used in Energy Calibration).

The energy lines in this file will populate the list box, as shown in Figure 28.

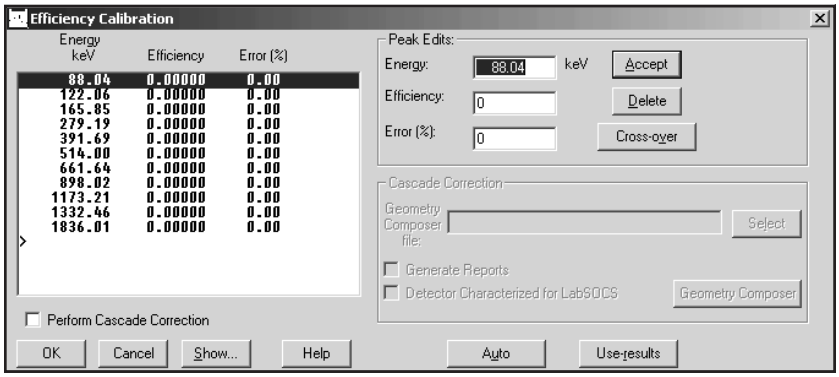

Figure 28 Efficiency Calibration

B. Adding the Efficiency Data

The next step is to add efficiency and percent error values to each energy in the list. There are two ways to do this:

- If you know that the current datasource contains peak area analysis results, you can click the **Use-results** button to populate the list box with that data. If you're not sure whether the current datasource contains peak area data, you'll have to use the second method.

- Click the **Auto** button to have the system automatically perform a Peak Locate and Peak Area analysis, then calculate and display the efficiency and percent error values for each energy in the list box.

With either method, for each peak found that matches one in the list box, ±1.00 keV, the Efficiency Match Tolerance value, an efficiency is calculated based on the peak net area and the calibration data contained in the Certificate File.

Dual Polynomial Curve

For the dual polynomial curve, the overall Efficiency Curve can be a combination of two curves, one for the lower energies and a second for the higher energies (above 150–200 keV or so).

To use two curves, highlight an energy, then click the **Cross-over** button to specify the point where you want the low energy curve to end and the high energy curve to start. If no crossover point is specified, a single equation is used across the entire energy range.

1, Click on the 165.85 keV line in the list to select it.

2. Click the **Cross-over** button to put an X to the right of the peak in the list. This will mark it as the energy used as the crossover point.

Peak Edits

The Peak Edits section lets you enter or change the **Energy**, **Efficiency**, and **Error (%)** data by hand. You can use up to 45 calibration triplets; any more than that will be ignored. The **Accept** button verifies the entered values and displays them in the list box; the **Delete** button deletes the highlighted entry from the list box.

Cascade Correction

The Cascade Correction function, which is enabled only under certain conditions, produces an efficiency calibration that is free from cascade summing effects. Its use is beyond the scope of this tutorial. You'll find a full description of this function in the *Correcting for Cascade Summing* appendix of the *Genie 2000 Operations Manual*.

C. Viewing the Efficiency Calibration

To check the results of the Efficiency Calibration, click on the **Show** button, which will display the dual efficiency curves and the fit to the data points.

The Dual Energy Curves

The low energy curve, a second order equation, is shown in red (white in Figure 29); the high energy curve, a fifth order equation, is shown in blue (black in the figure). The two share the data point at 165.85 keV to ensure continuity from one curve to the other.

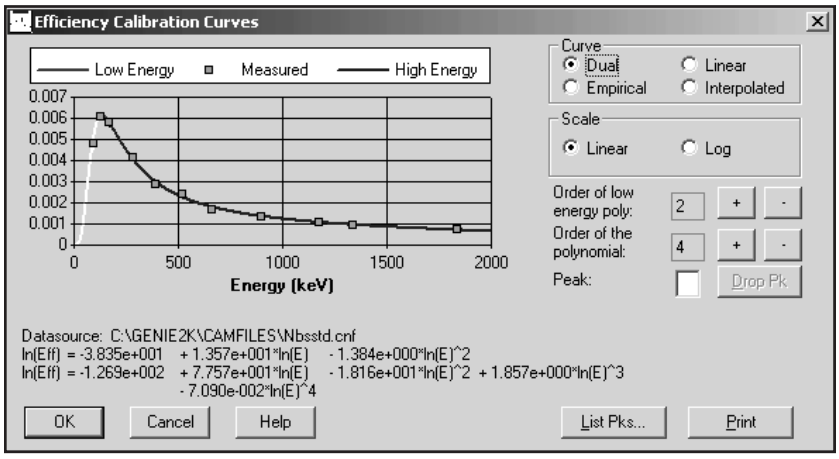

Figure 29 Show Efficiency Calibration

In addition to the default Dual Curve, you can display the calibration as an Empirical Curve, a Linear Curve or an Interpolated Curve by selecting the appropriate button in the Curve section of the data window.

To return to the Efficiency Calibration screen, click **OK** or **Cancel**.

D. Accepting the Efficiency Calibration

When you are satisfied with the calibration, click **OK** to have this calibration become your current calibration.

6. Basic Spectroscopy Analysis Techniques

Now that we have a calibrated system let's look at Genie 2000's analysis and reporting routines. We'll also find that the reports generated by the basic routines can include the calibration used during the analysis.

What Are Analysis Modules?

Before we discuss the analysis modules, such as peak locate and area measurements, we'll examine the philosophy behind them.

All of the Genie 2000 analyses use modules: programs that take one data set – such as spectral data – perform a process on it, then output the results – such as peak centroid locations. Depending on the options installed on your system, you'll find modules for functions like Peak Location, Peak Area Measurement and Nuclide Identification.

All of these modules share the following general features:

- All look to the datasource for their input data.
- All (with one exception) place their results back into the datasource so other modules can use that data. For example, the output from the Peak Location Module – Peak Centroids – is used as input data by the Peak Net Area and Nuclide ID Modules. Their outputs, in turn, are used as inputs to other modules.
- None, with the one exception, are capable of generating a printed report; all they can do is get data from a datasource, process it, and send results back to that datasource.
- The one exception is the Report Module. It doesn't analyze data; it uses the data generated by the other modules to create a report.

These modules can be run interactively, as demonstrated in the next section, or stored as an Analysis Sequence File (ASF) that lets you automatically implement a sequence of analysis modules as discussed in "Executing an Analysis Sequence" on page 32.

How Are the Modules Used?

The modules are the building blocks from which you create analysis procedures. For example, consider the following spectroscopy questions.

- Is Nuclide 'X' present in my spectrum?
  For this you would use the Peak Locate Module, the Peak Area Module, the Efficiency Correction Module, the Nuclide ID Module, and the Report Module.

- Several days (weeks, months) later you're asked "Since Nuclide X did not appear to be present, what was its Minimum Detectable Activity (MDA)?".
  The results from step 1 were stored in the datasource with the data, so all you have to do is apply the MDA Module to the datasource and run the Report Module again.

- Are you sure that's right? What calibration did you use?
  Since the calibration equations are also stored in the datasource, all you need to do is use the Report Module to generate a Calibration Report. The report which will include the calibration.

In short, by running the modules you need in the order you need them, you can easily tailor your analyses to answer your questions. And, as you'll see in "Editing an Analysis Sequence" on page 34, a module's parameters can easily be modified to refine the results.

As we just learned, performing an analysis consists of running a series of analysis modules one after the other, then generating a report. This sequence of events can be stored as an Analysis Sequence File (ASF). Executing the ASF file automatically performs the stored sequence of events.

Depending on which modules you use and how you modify them, you might have several automatic analysis sequences for various types of analyses.

How to Execute a Module Interactively

Before you start defining your own custom analysis sequences, you might ask, "How do I know just which steps to use and which parameters must be modified to get a particular job done?"

For this, we'll look at an individual module, which you can interactively modify and execute so you can see just what their impact will be. We'll see how this works by modifying the Peak Locate module.

Locating the Peaks

You can run the Peak Locate module interactively by selecting **Analyze | Peak Locate | Unidentified 2nd Diff.** You'll see the dialog box in Figure 30.

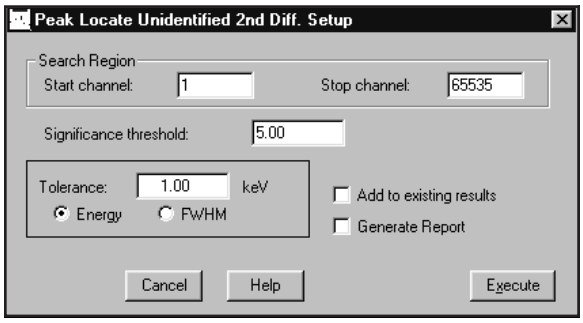

Figure 30 The Peak Locate Module

The Significance Threshold

The Significance Threshold determines how large a peak must be (relative to the background) to be recognized as a peak. For instance, if the Threshold is set to 5.00, as in the figure, running the Peak Locate module will result in 26 peaks being found in the Nbsstd.cnf spectrum.

To see the effects of a higher setting (less sensitivity), change the Significance Threshold value to 12.00, check the Generate Report checkbox, then click on **Execute**. When you look at the results in the Report Window (Figure 31), you'll see that a higher threshold (12.00) results in a lower sensitivity: only 17 peaks have been found, nine less than with a Threshold setting of 5.00.

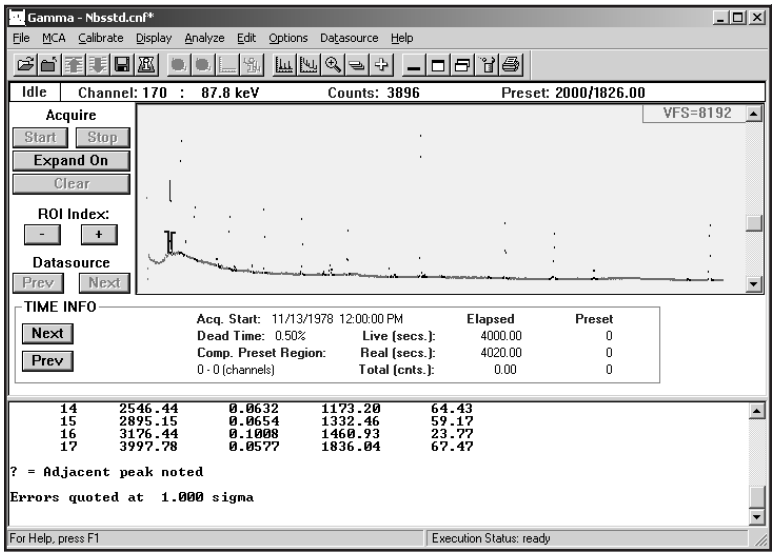

Figure 31 Threshold Set to 12

The Report Window Option

This is a good time to take a look at the Report Window options. There are commands to copy the data to the clipboard, to clear the data from the window, and to change the size of the window for easier report viewing.

Clearing the Report Window

You'll have to clear the Report Window if you want to display the next report's data by itself. If you don't clear the Report Window, the next report will be appended to the current report.

There are two ways to clear the window:

- Select the menu's **Options | Report Window | Clear Contents** command.
- Click the Toolbar's clear report icon. 

Creating a Printed Report

There are two ways to create a printed record of this report:

- Select the menu's **File | Print Report Window** command.
- Click the Toolbar's print report icon. 

How to Execute an Analysis Sequence

As we'll see in "How to Edit an Analysis Sequence" on page 34, Genie 2000 includes an editor both for changing a module's parameters and for custom-assembling the analysis modules into any type of sequence you may need.

In addition, your custom sequences can be added to the Analyze Menu, allowing you to tailor your system's automatic analysis to your specific application needs.

To gain an understanding of what an analysis sequence can do, we'll examine a sequence that's included with Genie 2000. It automatically executes three analysis modules in a specified order.

When you select **Analyze | Execute Sequence**, you'll see a list of the sequences installed on your system (Figure 32).

Remember that this tutorial assumes that the Model S501 Gamma Analysis option is installed on your system, so the list in Figure 32 includes the option's sequences, as well as those for the Basic Spectroscopy software.

To use any sequence, there must be a spectrum in the Gamma window. If a spectrum is not displayed, open C:\GENIE2K\CAMFILES\Nbsstd.cnf.

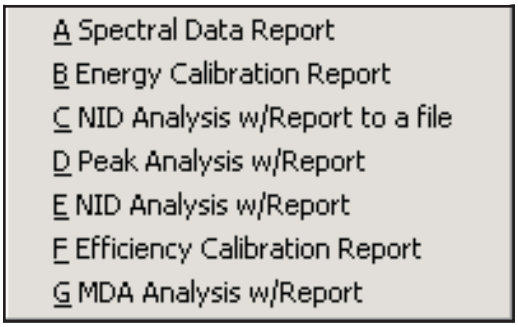

Figure 32 Execute Sequence Menu

Running the Peak Analysis w/Report Sequence

The fourth sequence in the list, Peak Analysis w/Report, runs four modules, or steps, sequentially. To run the sequence, click on **Analyze | Execute Sequence | Peak Analysis w/Report**.

The Report Window will display a report of the Peak Analysis of the spectrum (at the bottom of Figure 33).

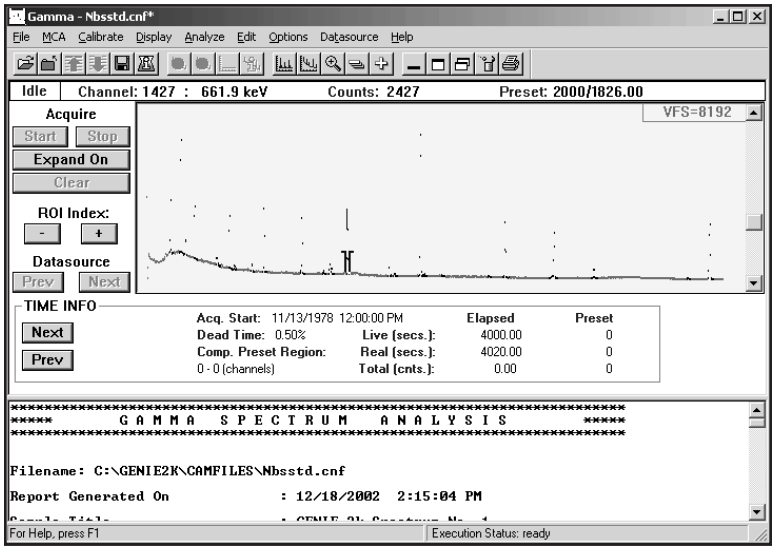

Figure 33 A Peak Analysis Report

Creating a Printed Report

There are two ways to create a printed record of this report:

- Select the menu's **File | Print Report Window** command.
- Click the Toolbar's print report icon. 

How to Edit an Analysis Sequence

If the standard Peak Analysis sequence isn't quite what you want, you can edit it. You can even define entirely new sequences. To open the Analysis Sequence Editor, select **Edit | Analysis Sequence**. You'll see the dialog box in Figure 34.

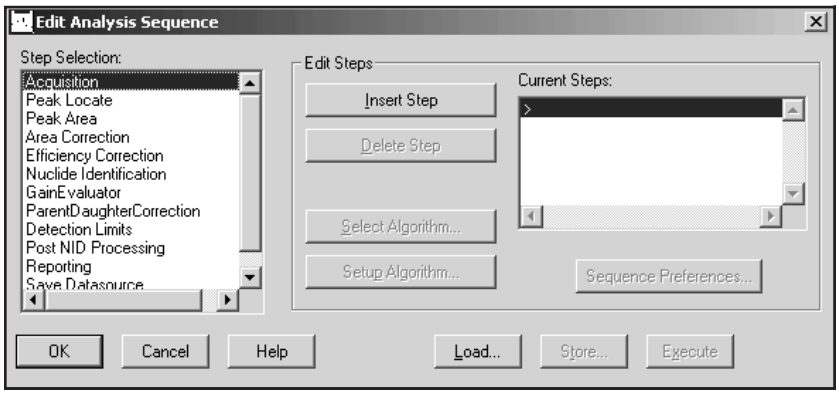

Figure 34 The Edit Analysis Sequence Dialog

As an example of how to use this editor, we'll modify the standard Peak Analysis w/Report sequence to make it less sensitive, just as we did interactively.

A. Load the Sequence

To select the sequence to be edited, click on the **Load** button. You'll see the dialog box in Figure 35, which lets you pick the sequence to be loaded into the editor.

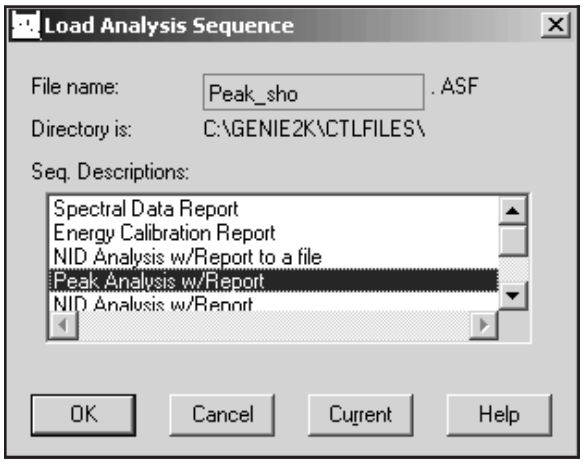

Figure 35 Loading a Sequence

The Seq. Descriptions list in Figure 35 shows all of the Sequences in the Analyze Menu. The one we want to change is **Peak Analysis w/Report**. Double click on its name to load its steps into the Edit Analysis Sequence window's Current Steps list, as shown in Figure 36.

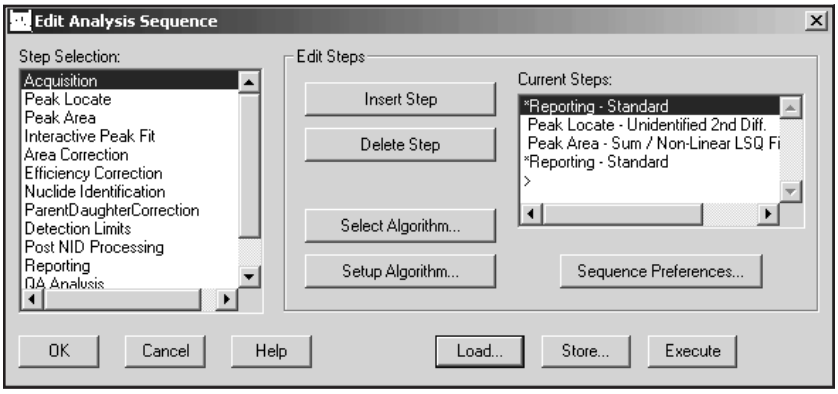

Figure 36 Editing the Peak Report Sequence

In the Current Steps window, you'll see the four steps in this sequence:

- Reporting – Standard
- Peak Locate – Unidentified 2nd Difference

- Peak Area – Sum/Non-linear LSQ Fit
- Reporting – Standard.

The report module is run twice because each instance uses a different section of the Analysis template to create its part of the report. When the first instance runs, the report Header is created. When the second instance runs, the Peak Analysis report is sent to the Report Window.

The second step in the sequence is the Peak Locate module we ran interactively. Since we already know how to use this module interactively, we'll use it again as to see how it can be modified and run in a sequence.

B. Modify the Peak Locate Step

To modify the step's parameters, double click on **Peak Locate – Unidentified 2nd Diff** in the Current Steps list to open the Peak Locate Setup dialog in Figure 37.

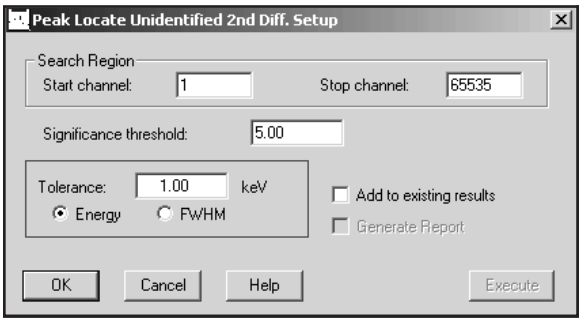

Figure 37 Modifying Peak Locate

Since we want to change the sensitivity, we'll edit the **Significance Threshold** parameter to show 12.00 as the new value, as we did for the interactive version. When you're finished, click on **OK** to return to the Edit Analysis Sequence dialog box.

C. Store the Modified Sequence

You have two options here: Save the changes to the original ASF file or save the changes to a new ASF file.

Saving to the Original File

To save the changed Significance Threshold value to the original file:

1. Click the Edit Analysis Sequence screen's **Store** button. You'll see the Store Analysis Sequence dialog box in Figure 38.

2. Click **OK** to save the changed definition.

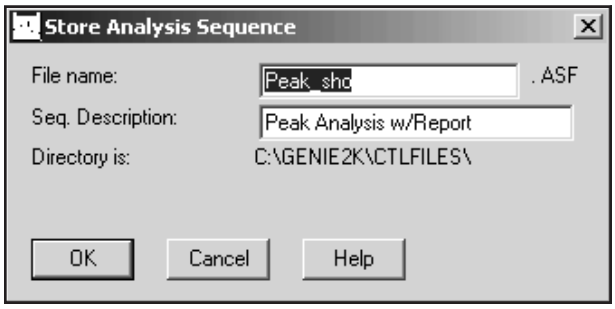

Figure 38 Storing the Modified Sequence

Saving to a New File

To save the changed Significance Threshold value to a new file:

1. Click the Edit Analysis Sequence screen's **Store** button.

2. Type a new file name, such as Peak_NEW, in the **File name** box (Figure 39).

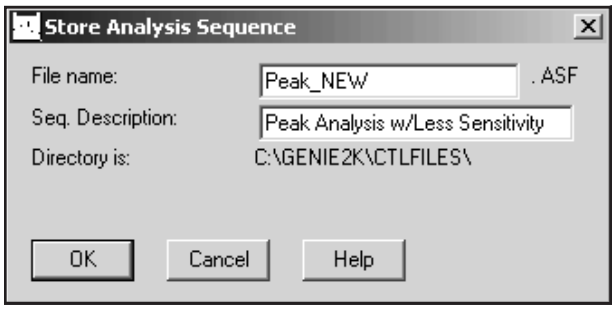

Figure 39 Renaming the Modified Sequence

3. Type a new description in the **Seq. Description** box. Since this description will be the sequence's name in your Execute Sequence Menu, it should be both meaningful and fairly short. For this example, the revised sequence has been named Peak Analysis w/Less Sensitivity.

4. After you've completed your entries, click on **OK** to save the definition.

Using the procedures we've just covered, you can create any number of custom sequences or edit existing sequences. For further information on defining a sequence, refer to the "Edit Menu | Analysis Sequence" section of your *Gamma Acquisition and Analysis* chapter or *Alpha Analysis Manual*.

D. Use the Modified Sequence

To use the new definition file, click on **OK** in the Edit Analysis Sequence dialog box to close it, then click on **Analyze | Execute Sequence** in the Menu Bar. Your new sequence will be at the end of the list (Figure 40).

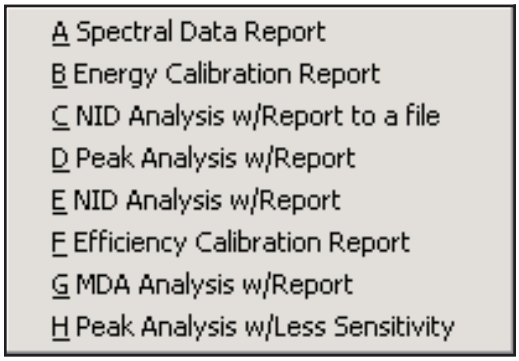

Figure 40 New Execute Sequence

Creating Your Own Sequence

Creating a sequence isn't any more complicated than modifying the parameters of the Peak Locate – Unidentified 2nd Difference step. The only difference is that you'll be modifying the parameters of several modules instead of just one.

Of course, it'll take a little study to determine which modules will be best for your sequence. You'll find that referring to either of the following documents will be very useful for that study.

All of the modules are fully described in the "Analyze Menu" section of your *Gamma Acquisition and Analysis* chapter or *Alpha Analysis Manual*.

Glossary

Underlined terms are defined elsewhere in this glossary. These terms and their cross references can also be researched online at http://www.canberra.com.

A

ABSORBED DOSE Absorbed dose is the amount of energy deposited in any material by ionizing radiation. It is a measure of energy absorbed per gram of material. The SI unit of absorbed dose is the gray. The special unit of absorbed dose is the rad.

ACCURACY The degree of agreement between an individual measurement or average of measurements and the accepted reference value of the quantity being measured. See also precision.

ACTIVATION ANALYSIS A method of chemical analysis (for small traces of material) based on the detection of characteristic radionuclides in a sample after it has been subjected to nuclear bombardment.

ADC Analog to Digital Converter. A device which changes an analog signal to a digital signal.

AIM Acquisition Interface Module: a type of multichannel analyzer.

ALGORITHM A set of well-defined rules for solving a problem.

ALARA Since exposure to radiation always carries some risk, the exposure should be kept "As Low As Reasonably Achievable", as defined by 10 CFR 20.

ALPHA PARTICLE [Symbol: α] A particle made up of two neutrons and two protons; it is identical to a helium nucleus and is the least penetrating of the three common types of radiation (the other two are beta particles and gamma rays), being stopped by a sheet of paper or a few centimeters of air. An alpha-emitting substance is generally not dangerous to a biological system, such as the human body, unless the substance has entered the system. See decay.

AMPLIFICATION The process by which weak signals, such as those from a detector are magnified to a degree suitable for measurement.

ANALOG MULTIPLEXER An electronic instrument that accepts several inputs and stores each one in a separate section of MCA memory. Also called a mixer/router.

ANNIHILATION RADIATION Radiation produced by the annihilation of a positron and an electron. For particles at rest, two photons with an energy of 511 keV each are produced.

ANTICOINCIDENCE CIRCUIT A circuit with two inputs. The circuit delivers an output pulse if one input receives a pulse within a predetermined time interval, usually on the order of milliseconds, but not if both inputs receive a pulse. A principle used in pulse height analysis. See also coincidence circuit.

AREA The number of counts in a given region of a spectrum that are above the continuum level.

ASCII An acronym for American Standard Code for Information Interchange, a method for encoding alphabetical, numeric, and punctuation characters and some computer control characters.

ATTENUATION CORRECTION Correction to the observed signal for the attenuation of radiation in a material between the sample and the detector or within the sample itself.

B

BACKGROUND RADIATION Radiation due to sources other than the sample, such as cosmic rays, radioactive materials in the vicinity of a detector or radioactive components of the detection system other than the sample.

BACKGROUND SUBTRACTION The statistical process of subtracting the background level of radiation from a sample count.

BACKSCATTERING The process of scattering or deflecting into the sensitive volume of a measuring instrument radiation that originally had no motion in that direction. The process is dependent on the nature of the mounting material, the shield surrounding the sample and the detector, the nature of the sample, the type of energy of the radiation, and the geometry. See also scattering.

BASELINE In biology, a known base state from which changes are measured. In electronics, a voltage state (usually zero volts) from which a pulse excursion varies.

BECQUEREL [Symbol: Bq] The SI unit of activity, defined as one disintegration per second (dps).

BETA PARTICLE [Symbol: β] An elementary particle emitted from a nucleus during radioactive decay with a single electrical charge and a mass equal to 1/1837 that of a proton. A negatively charged beta particle is identical to an electron. A positively-charged beta particle is called a positron.

BIOLOGICAL HALF-LIFE [Symbol: T_b] The time required for a biological system to eliminate half of the amount of a substance (such as radioactive material) by natural processes. Compare effective half-life and half-life.

BREMSSTRAHLUNG Radiation produced by the sudden deceleration of an electrically charged particle when passing through an intense electrical field.

C

CASCADE SUMMING Also referred to as true coincidence summing, it occurs when two or more pulses from the same decay are summed because they deposit energy in the detector at the same time. It is a function of the measurement efficiencies and occurs only with susceptible cascading nuclides (^{60}Co, ^{88}Y, ^{152}Eu, ^{133}Ba, etc.)

CENTROID The center of a peak; usually not an exact channel number.

CHANNEL One of an MCA's memory locations for storage of a specific level of energy or division of time.

CHERENKOV RADIATION Photons emitted from polarized molecules when returning to their ground state following excitation by charged particles traveling faster than the speed of light in a transparent medium.

CHI-SQUARE TEST A general procedure for determining the probability that two different distributions are actually samples of the same population. In nuclear counting measurements, this test is frequently used to compare the observed variations in repeat counts of a radioactive sample to the variation predicted by statistical theory.

COINCIDENCE CIRCUIT A circuit with two inputs. The circuit delivers an output pulse if both inputs receive a pulse within a predetermined time interval, usually on the order of milliseconds, but not if just one input receives a pulse. A principle used in pulse height analysis. See also anticoincidence circuit.

COINCIDENCE SUMMING A process where the signal from two or more gamma rays emitted by a single decay of a single radionuclide occur within the resolving time of the detector end up being recorded together as a single event so that the recorded event is not representative of the original decay. Typically causes counts to be lost from the full energy peaks, but may also cause addition to the full energy peaks. Coincidence summing is a function of the sample-to-detector geometry, and the nuclide's decay scheme. It is not a function of the overall count rate.

COLLECT An MCA function that causes storage of data in memory.

COMPTON SCATTERING Elastic scattering of photons in materials, resulting in a loss of some of the photon's energy.

CONFIDENCE FACTOR It is common practice when reporting results to assign them a confidence level: the value plus or minus one standard deviation. radiation protection measurements are usually reported at the 95% confidence level, meaning that the results would be expected to be within plus or minus that range 95 out of 100 times. Also called Confidence Level.

CONTINUUM A smooth distribution of energy deposited in a gamma detector caused by the partial absorption of energy from processes such as Compton scattering or bremsstrahlung.

CONVERSION GAIN The number of discrete voltage levels (or channels) that the ADC's full scale input is divided into.

CONVERSION TIME The time required to change an input signal from one format to another, such as analog to digital, or time difference to pulse amplitude; contributes to dead time.

COSMIC RAYS Radiation, both particulate and electromagnetic, that originates outside the earth's atmosphere.

COUNT A single detected event or the total number of events registered by a detection system.

CRITICAL LEVEL (L_c) The level below which a net signal cannot reliably be detected. See also detection level.

CROSSOVER ENERGY In some efficiency calibration models, the energy at which one calibration curve is changed into a second calibration curve. This is used in the Dual Efficiency Calibration in Genie software.

CURIE [Symbol: Ci] The (approximate) rate of decay of 1 gram of radium; by definition equal to 3.7×10^{10} becquerels (or disintegrations per second). Also, a quantity of any nuclide having 1 curie of radioactivity.

D

DATASOURCE A hardware device or a file which stores data acquisition parameters and spectral data.

DAUGHTER NUCLIDE A radionuclide produced by the decay of a parent nuclide.

DEAD TIME The time that the instrument is busy processing an input signal and is not able to accept another input; often expressed as a percentage. See also live time.

DECAY The disintegration of the nucleus of an unstable atom by spontaneous fission, by the spontaneous emission of an alpha particle or beta particle, isomeric transitions, or by electron capture.

DEFAULT The value of a parameter used by a program in the absence of a user-supplied value.

DERIVED AIR CONCENTRATION (DAC) The concentration (Bq/m^3) of a radionuclide in air that if breathed by Reference Man for a working year (2000 hours) under light activity conditions would result in the annual limit on intake (ALI) by inhalation.

DETECTION LEVEL The level of net signal that can be predicted to be detectable. See also critical level.

DETECTOR A device sensitive to radiation which produces a current or voltage pulse which may or may not correspond to the energy deposited by an individual photon or particle.

DIGITAL STABILIZATION The monitoring of one or two reference peaks in a spectrum, one for gain and one for zero, to correct for drift in the system electronics.

DISCRIMINATOR An electronic circuit which distinguishes signal pulses according to their pulse height or voltage so that unwanted counts can be excluded.

DISINTEGRATION See decay.

DPM Disintegrations per minute. One DPM equals 1/60 becquerel.

DOSE The radiation delivered to the whole human body or to a specified area or organ of the body. This term is used frequently in whole body counting applications.

DOUBLE ESCAPE PEAK See escape peak.

E

EFFECTIVE HALF-LIFE [Symbol: T_{eff}] The time required for a radioactive element in a biological system, such as the human body, to be reduced by one-half as a result of the combined action of radioactive decay and biological elimination. Compare half-life and biological half-life.

EFFICIENCY The fraction of decay events from a standard sample seen by a detector in the peak corresponding to the gamma ray energy of the emission, and stored by a detection system. Also called Peak Efficiency. Used to calibrate the system for quantitative analyses. Also used to specify germanium detectors, where the relative efficiency of the germanium detector is compared to a standard (3 x 3 in.) NaI(Tl) detector. Compare total efficiency.

EFFICIENCY CALIBRATION A function, a lookup table, or series of functions, which correlate the number of counts seen by the detection system in specific peaks with known activity corresponding to such emission energies in a radioactive sample.

ELASTIC SCATTERING See scattering.

ELECTRODEPOSITION A process for coating the surface of samples being prepared for alpha spectroscopy and alpha/beta counting.

ELECTROMAGNETIC RADIATION A general term to describe an interacting electric and magnetic wave that propagates through vacuum at the speed of light. It includes radio waves, infrared light, visible light, ultraviolet light, X rays and gamma rays.

ELECTRON [Symbol: e^-] An elementary particle with a unit negative electrical charge and a mass 1/1837 that of the proton. Electrons surround the positively charged nucleus and determine the chemical properties of the atom.

ELECTRON VOLT [Symbol: eV] The amount of kinetic energy gained by an electron as it passes through a potential difference of 1 volt. It is equivalent to 1.602×10^{-19} joules per second. It is a unit of energy, or work, not of voltage.

ENERGY CALIBRATION A function which correlates each channel in the displayed spectrum with a specific unit of energy. Allows peaks to be identified by their location in the calibrated spectrum.

ESCAPE PEAK A peak in a gamma ray spectrum resulting from the pair production process, the subsequent annihilation of the photons produced, and escape from the detector of the annihilation photons. If both annihilation photons escape, and the rest of the original gamma energy is fully absorbed, a double escape peak is produced at an energy equal to the original gamma ray energy minus 1.022 MeV. If only one of the photons escapes, a single escape peak is produced at an energy equal to the original gamma ray energy minus 511 keV.

EXCITED STATE The state of molecule, atom, or nucleus when it possesses more than its ground state energy. Excess molecular or atomic energy may be reduced through emission of photons or heat. Excess nuclear energy may be reduced through emission of gamma rays or conversion electrons or by further decay of a radionuclide.

eV See electron volt.

F

FACTORS The parameters used by an algorithm for its calculations.

FULL ENERGY ABSORPTION The absorption and detection of all of the energy of an incident photon. May take place as a direct photoabsorption or as a result of multiple Compton scatterings of the incident photons within the resolving time of the detection system.

FULL ENERGY PEAK The peak in an energy spectrum of X-ray or gamma-ray photons that occurs when the full energy of the incident photon is absorbed by the detector.

FWHM (Full Width at Half Maximum) The full width of a peak measured at one-half of its maximum amplitude with the continuum removed. Defines the resolution of a spectroscopy system.

G

GAIN, ADC See conversion gain.

GAIN, AMPLIFIER The ratio of the amplifier's output signal to its input signal.

GAIN CONTROL A control used to adjust the height of a pulse received from the detecting system.

GAMMA RAY [Symbol: γ] A photon or high-energy quantum emitted from the nucleus of a radioactive atom. Gamma rays are the most penetrating of the three common types of radiation (the other two are alpha particles and beta particles) and are best stopped by dense materials such as lead.

GAUSSIAN FIT Calculating the parameters of a Gaussian (or Normal) function to best match a set of empirical data (in spectroscopy, the acquired photopeak histogram). This calculation is typically performed using a least squares method after subtracting the Compton continuum underlying the peak.

GAUSSIAN PULSE SHAPE A pulse shape resembling a statistical bell-curve, with little or no distortion.

GEOMETRY The detector to sample distance, the sizes and shapes of the detector, the sample, and any shielding, all of which affect the radiation seen by the detector. The geometry helps define the efficiency of the detector.

GRAY [Symbol: Gy] The SI unit of absorbed dose, defined as one joule per kilogram of absorbing medium.

GROUND STATE The state of a nucleus, atom or molecule at its lowest energy level.

H

HALF-LIFE [Symbol: $T_{1/2}$] The time in which one half of the atoms of a particular radioactive substance decay to another nuclear form. Half-lives vary from millionths of a second to billions of years.

HISTOGRAM A representation of data by vertical bars, the heights of which indicate the frequency of energy or time events.

I

INELASTIC SCATTERING See scattering.

ION An atom or molecule that has become electrically charged by having lost or gained one or more electrons. Examples of an ion are an alpha particle, which is a helium atom minus its two electrons, and a proton, which is a hydrogen atom minus its single electron.

INDEX An MCA function that jumps the cursor from one region of interest to another.

INPUT/OUTPUT The process of loading data into or copying data from an MCA or computer using a peripheral device, such as a computer, a floppy disk, or a printer.

IN SITU COUNTING Measurement and analysis of radioactivity performed at the sample's location.

INTEGRAL The total sum of counts in the region of interest.

INTENSIFY To change the contrast of a displayed region of interest to set it off from data regions of lesser importance.

INTERACTIVE PEAK FIT The process of refining and verifying the quality of a peak fit. The fitting parameters, such as the centroid location and the way the continuum is defined, can be changed. The change in the quality of the fit is displayed.

INTERFERING PEAK A peak due to background radiation which is produced at the location of a peak in the sample spectrum or due to a peak produced by a radionuclide in the sample at the location of another radionuclide's peak.

IN VIVO COUNTING In vivo counting refers to directly measuring and analyzing radionuclide activity levels in a living body.

IN VITRO COUNTING In vitro counting refers to samples, such as tissue or blood, being analyzed for radionuclide activity levels in an artificial environment (outside of a living body).

I/O See input/output.

IONIZATION The process by which an electrically neutral atom acquires a charge (either positive or negative).

IONIZING EVENT Any process whereby an ion or group of ions is produced. As applied to nuclear spectroscopy, this refers to the passing of radiation through a gas, a crystal, or a semiconductor.

ISOMERIC TRANSITION The de-excitation of an elevated energy level of a nucleus to the ground state of the same nucleus by the emission of a gamma ray or a conversion electron.

ISOTOPE One of two or more atoms with the same atomic number (the same chemical element) but with different atomic weights. An equivalent statement is that the nuclei of isotopes have the same number of protons (thus the same chemical element) but different numbers of neutrons (thus the different atomic weight). Isotopes usually have very nearly the same chemical properties, but somewhat different physical properties. See also nuclide and stable isotope.

K

keV (kiloelectron volt) One thousand electron volts.

KEY LINE Designated in nuclide libraries for reporting purposes only. It is intended to indicate the highest abundance photopeak energy for nuclides with multiple energy lines, or the line that is the least likely to have interferences.

L

LAN Local area network: a network of two or more computers connected together.

L_c See critical level.

LIBRARY DIRECTED PEAK SEARCH Method of designating the location of peaks using all of the lines from the specified nuclide library. All of the nuclide library energies are assumed to have photopeaks present and the peak analysis is typically required to verify or reject each peak. This limits the peak search to the nuclides in the library but allows for greater sensitivity than with typical unknown peak searches. See also second difference peak search.

LIMIT OF DETECTION The minimum amount of the characteristic property being measured that can be detected with reasonable certainty by the analytical procedure being used under specific measuring conditions. If the conditions change, the limit of detection will also change, even if the analytical procedure remains the same. See also lower limit of detection.

LIVE TIME The time that the ADC is not busy processing a signal. See also dead time and real time.

LIVE TIME CORRECTION In an MCA, the process of stopping the live time clock whenever the processing circuits are busy and cannot accept further information. Commonly used to extend the collection time by accounting for the dead time.

LOWER LIMIT OF DETECTION (LLD) The smallest net signal that can reliably be quantified. LLD is a measure of the performance of a system in terms of activity.

LOWER LEVEL DISCRIMINATOR (LLD) An SCA's minimum acceptable energy level. Incoming pulse amplitudes below this limit will not be passed. See also upper level discriminator.

M

MARINELLI BEAKER A standard sample container that fits securely over a detector cryostat's endcap and is used when calibrating voluminous samples (usually soil or water solutions).

MASS NUMBER The sum of the neutrons and protons in a nucleus. It is the nearest whole number to an atom's atomic weight. For instance, the mass number of ^{235}U is 235.

MAXIMUM PERMISSIBLE CONCENTRATION (MPC) The concentration limit for a given radionuclide in air or water in determining possible inhalation, ingestion or absorption for health physics controls.

MCA See multichannel analyzer.

MCS See multichannel scaling.

MDA Minimum detectable activity. See lower limit of detection.

MEAN The average of a group of numbers.

METASTABLE ISOTOPE A long-lived energy state of a particular nuclide that is not its ground state. Some nuclides have more than one isomeric state. An isomeric state has the same mass number and atomic number as the ground state, but possesses different radioactive properties.

MeV (megaelectron volt) One million electron volts.

MIXER/ROUTER See analog multiplexer.

MONITORING, PERSONNEL Periodic or continuous observation of the amount of radiation or radioactive contamination present in or on an individual.

MULTICHANNEL ANALYZER (MCA) An instrument which collects, stores and analyzes time-correlated or energy-correlated events. See also multichannel scaling and pulse height analysis.

MULTICHANNEL SCALING (MCS) The acquisition of time-correlated data in an MCA. Each channel is sequentially allocated a dwell time (a specified time period) for accumulating counts until all the memory has been addressed. MCS is useful for studying rapidly decaying radioactive sources.

MULTISPECTRAL SCALING Also called multiscaling, or MSS. See multichannel scaling.

MULTIPLET Peaks in a spectrum which overlap each other. Compare singlet.

N

NATURALLY OCCURRING RADIOACTIVE MATERIAL (NORM) Radioactivity that is naturally present in the earth.

NEUTRON [Symbol: n] An uncharged elementary particle with mass slightly greater than that of the proton, and found in the nucleus of every atom heavier than hydrogen.

NEUTRON ACTIVATION ANALYSIS (NAA) The process of activating materials by neutron absorption then measuring the emission of characteristic photons on decay to determine the relative abundance of elements in an object.

NID Nuclide Identification, the process of identifying radionuclides by comparing peak energies detected with entries in a nuclide library.

NIM Nuclear Instrumentation Module. A nuclear instrument conforming to the DOE/ER-00457T standard.

NOISE Unwanted signals on or with a useful signal which can distort its information content.

NON-DESTRUCTIVE ASSAY An analysis method that does not destroy the sample. For example: gamma spectroscopy, X-ray fluorescence and neutron activation.

NUCLEAR SAFEGUARDS The general topic of maintaining control and accountability of special nuclear materials.

NUCLEUS The positively charged core of an atom, which contains nearly all of the atom's mass. All nuclei contain both protons and neutrons, except the nucleus of ordinary hydrogen, which consists of a single proton.

NUCLIDE A general term applicable to the isotopes of all elements, including both stable and radioactive forms (radionuclides).

NUCLIDE LIBRARY A file listing nuclides, their names, half-lives, types, energies/lines, and line abundances. These files are used with library directed peak searches, nuclide identification (NID) and as aids in performing calibrations.

O

OFFSET, ADC A digitally performed shift in the ADC's channel zero. Shifts the entire spectrum by the selected amount.

OVERLAP An MCA function allowing one section of memory to be displayed over another.

P

PAIR PRODUCTION Creation of an electron-positron pair by gamma ray interaction in the field of a nucleus. For this process to be possible, the gamma ray's energy must exceed 1.022 MeV, twice the rest mass of an electron.

PARAMETER A variable that is given a constant value for a specific application.

PARENT NUCLIDE A radionuclide that produces a daughter nuclide during decay.

PASSIVE NON-DESTRUCTIVE ASSAY A method that uses radiation emitted by the sample itself, without increasing the emission by bombarding the sample with something, such as neutrons. The sample itself is not changed in any way in the course of passive assay.

PEAK A statistical distribution of digitized energy data for a single energy.

PEAK CHANNEL The channel number closest to the centroid of a peak.

PEAK FIT The optimization of parameters to match an expected model shape to empirical data (see also gaussian fit). This optimization is typically performed using a least squares method.

PEAK-TO-TOTAL RATIO The ratio of the observed counts in a full energy peak to the counts in the entire spectrum, caused by the interaction of radiation with the detector at that emission energy only.

PERCENT SIGMA [Symbol: σ] An expression of the standard deviation as a percentage. It is numerically equal to 100 times the standard deviation divided by the mean.

PHA See pulse height analysis.

PHOTOELECTRIC ABSORPTION The process in which a photon interacts with an absorber atom, the photon disappears completely, and the atom ejects a photoelectron (from one of its bound shells) in place of the photon.

PHOTOELECTRON An electron released from an atom or molecule by means of energy supplied by radiation, especially light.

PHOTOMULTIPLIER TUBE (PMT) A device for amplifying the flashes of light produced by a scintillator.

PHOTON In quantum theory, light is propagated in discrete packets of energy called photons. The quantity of energy in each packet is called a quantum.

PHOTOPEAK See Peak.

PHYSICAL HALF-LIFE See half-life.

POLE/ZERO A method of compensating the preamplifier's output signal fall-time and the amplifier's shaping time constant. Its use improves the amplifier's high count rate resolution and overload recovery.

PMT See photomultiplier tube.

POSITRON[Symbol: β^+] An elementary particle, an "anti-electron"; with the mass of an electron but having a positive charge. It is emitted by some radionuclides and is also created in pair production by the interaction of high-energy gamma rays with matter.

POSITRON ANNIHILATION A process where a positron combines with an electron, producing two annihilation photons of 511 keV each.

PRECISION The degree of agreement between several measurements of the same quantity under specific conditions. See also accuracy.

PRIMORDIAL NUCLIDE A nuclide as it exists in its original state.

PROGENY See daughter nuclide.

PROMPT GAMMA ANALYSIS A form of neutron activation analysis where gammas, emitted during capture of neutrons, are used for analysis instead of gammas of subsequent beta decay.

PROTON An elementary particle with a single positive electrical charge and a mass approximately 1837 times that of the electron. The atomic number (Z) of an atom is equal to the number of protons in its nucleus.

PROTON INDUCED X-RAY EMISSION (PIXE) The emission of X ray when a sample is bombarded by protons. The X rays emitted are characteristic of the elements present in the sample. Used for trace analysis.

PULSE HEIGHT ANALYSIS (PHA) The acquisition of energy-correlated data in the MCA. Each channel, defined as an energy window, is incremented by one count for each event that falls within the window, producing a spectrum which correlates the number of energy events as a function of their amplitude.

PULSE PAIR RESOLUTION The ability to discriminate between two pulses close together in time.

PULSE PILEUP A condition, where two energy pulses arrive at nearly the same time, which could produce false data in the spectrum.

PULSE PILEUP REJECTOR (PUR) An electronic circuit for sensing the pulse pileup condition and rejecting these pulses so that only single pulses are counted.

Q

QUANTUM The unit quantity of energy according to quantum theory. It is equal to the product of the frequency of the electromagnetic radiation and Planck's constant (6.626 x 10^{-34} J/s).

R

RAD A special unit of absorbed dose. Equal to 0.01 gray.

RADIATION The emission or propagation of energy through matter or space by electromagnetic disturbances which display both wave-like and particle-like behavior. Though in this context the "particles"; are known as photons, the term radiation has been extended to include streams of fast-moving particles. Nuclear radiation includes alpha particles, beta particles, gamma rays and free neutrons emitted from an atomic nucleus during decay.

RADIOACTIVITY The emission of radiation from the spontaneous disintegration (decay) of an unstable nuclide.

RADIONUCLIDE A radioactive isotope. See also nuclide.

RANDOM SUMMING A process where the signal from two or more separate decays of the same radionuclide or different radionuclides that occur within the resolving time of the detector end up being recorded together as a single event so that the recorded event is not representative of the original decays. Typically causes counts to be lost from the full energy peaks. Random summing is a function of the overall count rate, or the activity of the sample being measured.

RANDOM SUMMING LOSS The loss of counts from the full energy peaks due to random summing.

RANGE, ADC The full-scale address (number of channels) of the ADC's assigned memory segment.

REAL TIME Elapsed clock time; also called true time. Compare live time.

RECOILING NUCLEUS A nucleus that gains significant kinetic energy from its decay.

REGION OF INTEREST (ROI) A user-defined area of the spectrum which contains data of particular interest, such as a peak.

REM (Roentgen Equivalent Man) A unit of dose equivalency; equal to 0.01 sievert. See also Roentgen.

RESOLUTION The ability of a spectroscopy system to differentiate between two peaks that are close together in energy. Thus, the narrower the peak, the better the resolution capability. Measured as FWHM.

ROENTGEN The Roentgen, the international unit of X radiation or gamma radiation, is the amount of radiation producing, under ideal conditions in one cc ionization of either sign equal to one electrostatic unit of charge.

ROI See region of interest.

S

SCA Single Channel Analyzer. A device which recognizes events (pulses) occurring between the settings of the lower level discriminator and the upper level discriminator. In an MCA, each event within these limits is counted; events outside of these limits are discarded.

SCATTERING A process that changes a particle's trajectory. Scattering is caused by particle collisions with atoms, nuclei and other particles or by interactions with electric or magnetic fields. If there is no change in the total kinetic energy of the system, the process is called elastic scattering. If the total kinetic energy changes due to a change in internal energy, the process is called inelastic scattering. See also backscattering.

SCINTILLATOR A type of detector which produces a flash of light as the result of an ionizing event. See also photomultiplier tube.

SECOND DIFFERENCE PEAK SEARCH A technique for locating photopeaks by calculating the second difference for each channel in a spectrum, then locating areas of negative concavity. See also library directed peak search.

SEGMENTED GAMMA SCANNER A gamma spectroscopy system that analyzes a sample by counting it in discrete segments.

SELF ABSORPTION Absorption of the photons emitted by the radioactive nuclides in the sample by the sample material itself.

SHADOW SHIELD An attenuating enclosure that shields the detector from direct background radiation without being a 4π; shield. Typically used in whole body counting.

SHAPE CALIBRATION The process of establishing a relationship between the expected peak shape and energy. A shape calibration can be established by using two or more peak FWHM/energy (or FWHM/ channel) pairs or by using a least squares fit algorithm.

SIEVERT [Symbol: Sv] The SI unit of dose equivalency (a quantity used in radiation protection). The sievert is the dose equivalent when the absorbed dose of ionizing radiation multiplied by the dimensionless factor Q (quality factor) and N (product of any other multiplying factors) stipulated by the International Commission on Radiological Protection is one joule per kilogram.

SINGLE CHANNEL ANALYZER See SCA.

SINGLE ESCAPE PEAK See escape peak.

SINGLET A single peak in a spectrum, well separated from other peaks. Compare multiplet.

SMOOTHING To decrease the effects of statistical uncertainties in computerized spectrum analysis, the content of each channel is replaced by a weighted average over a number of adjacent channels.

SPECIFIC ACTIVITY The quantity of radioactivity per unit mass; for example, dpm/g or Bq</A>/g.

SPECIAL NUCLEAR MATERIAL (SNM) Material containing fissionable isotopes suitable for nuclear weapons.

SPECTRUM A distribution of radiation intensity as a function of energy or time.

SPECTROMETER A device used to count an emission of radiation of a specific energy or range of energies to the exclusion of all other energies. See also multichannel analyzer.

STABLE ISOTOPE An isotope that does not undergo radioactive decay.

STANDARD DEVIATION [Symbol: σ] A measure of the dispersion about the mean value of a series of observations expressed in the same units as the mean value.

STRIPPING Subtracting a specified fractional part of the data in one section of memory from the data in another section of memory.

SYSTEM BUSY TIME The dead time of an entire spectroscopy system.

T

TOTAL DETECTOR EFFICIENCY All pulses from the detector are accepted, and all interactions (regardless of how low in energy) are assumed counted.

TOTAL EFFICIENCY The ratio of all pulses recorded in the MCA memory (in all channels) to the gamma quanta emitted by the sample. Compare efficiency.

TRANSURANIC (TRU) Possessing an atomic number higher than that of uranium (92).

TRUE COINCIDENCE SUM PEAK A spectral peak, the energy of which equals the sum of the energies of two or more gamma rays or X ray from a single nuclear event.

TRUE TIME See real time.

U

UNCERTAINTY In a nuclear decay measurement, uncertainty refers to the lack of complete knowledge of a sample's decay rate due to the random nature of the decay process and the finite length of time used to count the sample.

UPPER LEVEL DISCRIMINATOR (ULD) An SCA's maximum acceptable energy level. Incoming pulse amplitudes above this limit will not be passed. See also lower level discriminator.

W

WHOLE BODY COUNTING (WBC) In vivo determination of radionuclide activity levels in the human body. Used to determine compliance with the regulations of various governmental bodies regarding radiation exposure.

WINDOW A term describing the upper and lower limits of radiation energy accepted for counting by a spectrometer.

X

X RAY A penetrating form of electromagnetic radiation emitted during electron transitions in an atom to a lower energy state; usually when outer orbital electrons give up some energy to replace missing inner orbital electrons.

Z

ZERO, ADC An ADC control which aligns its zero energy output with a specific channel in the MCA's memory (usually channel zero).

CANBERRA

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