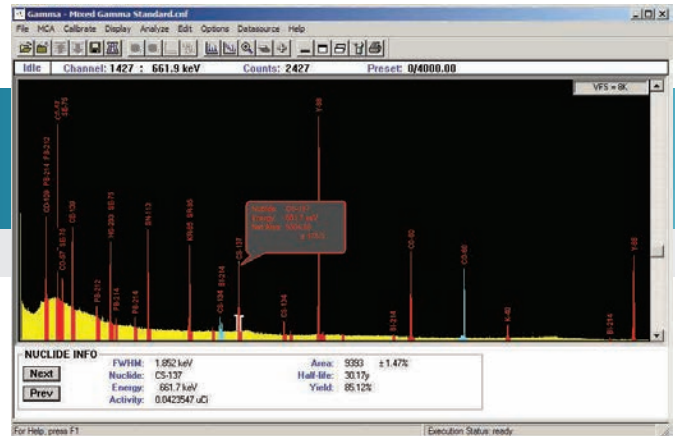




Genie™ 2000

Basic Spectroscopy Software



KEY FEATURES

- Integrated data acquisition and analysis
- Independent support for over 250 detector inputs
- Networking for distributed MCA operation and centralized data management
- Comprehensive and flexible user programming capability
- Compatibility with the full Mirion MCA line
- Wide variety of layered software options available for specialized spectroscopy applications
- Compatible with Windows 7 64-bit, Windows 7 32-bit, and Windows XP 32-bit operating systems, and also Windows Server 2008 32-bit (SP2) and 64-bit (R2 SP1)
- Multi-language support: English, French, German, and Russian

DESCRIPTION

Genie 2000 Basic Spectroscopy Software is a comprehensive environment for data acquisition, display and analysis of gamma and alpha spectrometry data. It provides independent support for multiple detectors, extensive networking capabilities, an intuitive and interactive human interface and comprehensive batch procedure capabilities.

The full multitasking architecture of Genie 2000 software allows the software to run multiple independent count procedures for several detectors simultaneously. No procedure is suspended by the activation of another or caused to slow down excessively by software overhead. With Genie 2000 software, operation is fully independent.

The ability to manage multiple detectors independently and simultaneously is further enhanced by the designed-in network support. Genie 2000 applications on multiple computers can cooperate over a network to allow remote access and multiple access to acquisition hardware and other resources. A lab supervisor can examine a live acquisition taking place in the lab under control of another computer – and perform an analysis – without interrupting the procedure in progress.

In Genie 2000 software, acquisition and analysis capabilities are tightly integrated, providing an intuitive human interface and straightforward operation of the various

applications. Through windowing screen management, graphical spectral display and analysis results can easily be positioned for quick comparisons.

Two human interface environments are provided with Genie 2000 software. The interactive human interface provides fully interactive operation of all system features. It allows the knowledgeable user access to any system function – usually with no more than two or three mouse clicks.

For dedicated, repetitive operation such as routine sample counting, Genie 2000 software supports a user programming environment for custom development and user interfaces. In this environment, the technician level operator can be guided step-by-step through system operations with a security system limiting access to qualified users as determined by the system administrator.

Interactive Graphical User Interface

The Genie 2000 interactive graphical user interface is an intuitive window-style interface that provides the user with straightforward access to system functions. A single window is used to control acquisition and analysis for multiple inputs at the same time.

Continued on next page

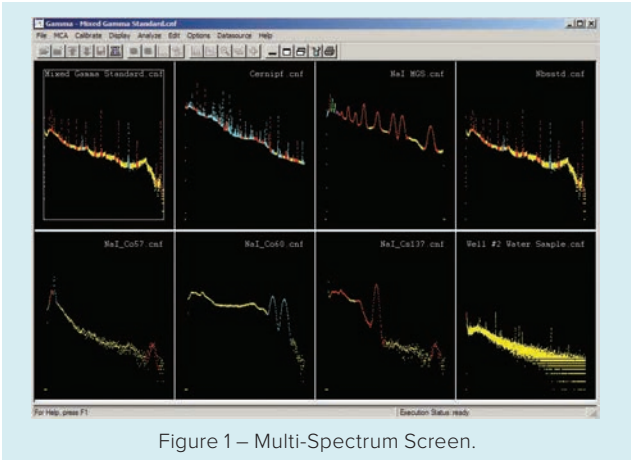


Figure 1 – Multi-Spectrum Screen.

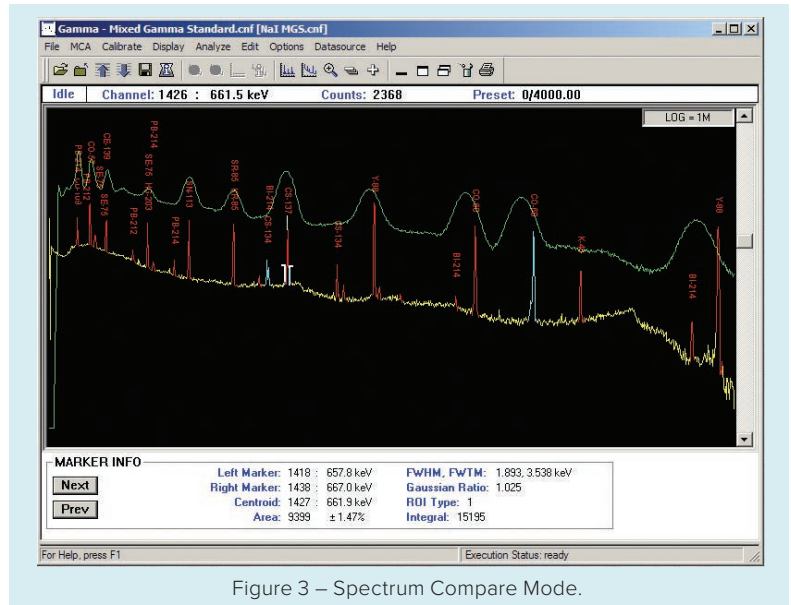


Figure 3 – Spectrum Compare Mode.

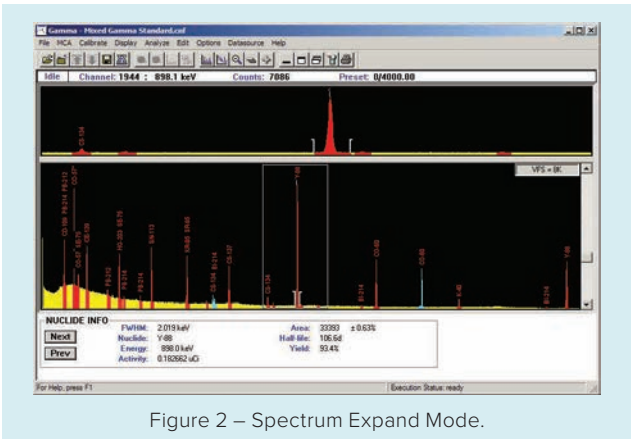


Figure 2 – Spectrum Expand Mode.

The Spectroscopy window provides spectral display and acquisition control for configured detectors as well as spectral display for data files. More than 250 data sources (any combination of detectors and files) can be active in the Spectroscopy window at a time. These can be paged one at a time for detailed review, or up to eight can be displayed simultaneously with live spectral updates (Figure 1).

Comprehensive display manipulation is provided in the Spectroscopy window. This includes spectral EXPAND (Figure 2), COMPARE (Figure 3) of two spectra, regions of interest, markers and cursor.

The Spectroscopy window has an area reserved for “control panel” buttons (as shown in Figure 4). These allow commonly used functions to be accessed directly with the mouse rather than by using the pull down menu dialog. Functions available on the control panel include Acquire On/Off, Expand On/Off, MCA Clear, ROI Index, and Datasource Previous/Next.

A tool bar at the top of the screen gives instant access to frequently used functions. Each tool bar icon has a help text associated with it. The system default tool bar contains about 20 of these icons. Over 50 more icons are available such that the user can easily create one or more custom tool bars duplicating almost all menu selections. A simple user preferences dialog provides icons that can be user-programmed with just a few mouse clicks to initiate analysis sequences or executables for even greater flexibility of operation.

Status pages are provided at the bottom of the MCA window. Up to eight separate status pages may be shown, one at a time, for a detailed listing of MCA/spectral information. The user can review the various selected pages by clicking on the Next and Prev buttons to the left of the status page window.

The control panel, tool bar and/or status pages can be disabled by a display preference to increase the screen area available for spectrum and report display.

The Spectroscopy window provides access to the system’s standard and optional gamma and alpha analysis functions.

Analyses can be performed in a step-by-step manual mode (Figure 4), or a complete analysis sequence can be defined (Figure 5). Note that a few of the selections in Figures 4 and 5 may require other Genie 2000 layered products for nuclide identification or detector quality assurance data processing. However, these selections are automatically and seamlessly added to the menus when the required software packages are installed (typically one or more of the S501 Gamma Analysis, S505 Quality Assurance or S509 Alpha Analysis packages).

In the manual mode, individual analysis modules, such as peak locate or peak area, can be activated by selecting the desired module from a menu. When the module is selected, a setup screen associated with the selected algorithm is presented, thus allowing the user to edit analysis parameters before executing that phase.

The system also has facilities to support multiple analysis algorithms for a given analysis step. For example, the user may select the Unidentified Second Difference Peak Locate algorithm, the User Specified ROI method, one of several library directed peak searches or a peak search based on algorithms available with the Genie-ESP platform. Although these algorithms are each very different from one another, their results feed consistently to subsequent analysis steps such as efficiency correction and/or nuclide identification. This gives the user ultimate flexibility in tailoring analysis sequences for individual applications.

In addition to the manual mode described above, an analysis sequence can be defined using the analysis sequence file editor. The sequence can consist of a series of analysis and reporting steps, complete with their parameter definitions. When a sequence has been created, it can be saved along with a name. That assigned name appears in the Analyze pull down menu and is available for immediate operation. The analysis sequence can also be assigned to a function key or icon for even easier access.

An interactive peak labeling mode allows quick, visual identification of radionuclides in the spectrum right on the spectral display itself. (See page 1.) Also, by placing the cursor on a peak, the nuclide, energy, peak area and activity can be instantly displayed in a “bubble” next to the peak. The results of the peak labeling can either come from a tentative nuclide identification based on a selected nuclide library or from an actual analysis of the spectrum.

An interactive nuclide identification mode provides another way to quickly identify radionuclides from the spectral display. In this mode, the cursor is placed on a peak of interest. The nuclide, energy, abundance and half-life are then instantly displayed in a list box that lets the user manually select alternate nuclides sorted by energy or nuclide name. Optionally, one can view confirming line markers if the nuclide has more than one energy line in order to assist with the nuclide identification (Figure 6).

User Programming Environment

The Genie 2000 user programming environment provides the ability to define highly customized command procedures to fully automate counting and analysis sequences. These procedures are useful in any operation where counting is done according to a specific set of guidelines – as in routine environmental, bioassay, or safeguards measurements.

All of the basic Genie 2000 functions are available as individual component objects which can be executed directly from a user program. The modules are each designed with a set of appropriate command switches or arguments to fully define the function. For example the peak search module accepts arguments for search sensitivity start and stop channels, and other such parameters.

A module is also provided for live spectral display. This module brings up a Spectroscopy window as is used in the interactive environment. Command arguments allow the user to specify the location and arrangement of the window.

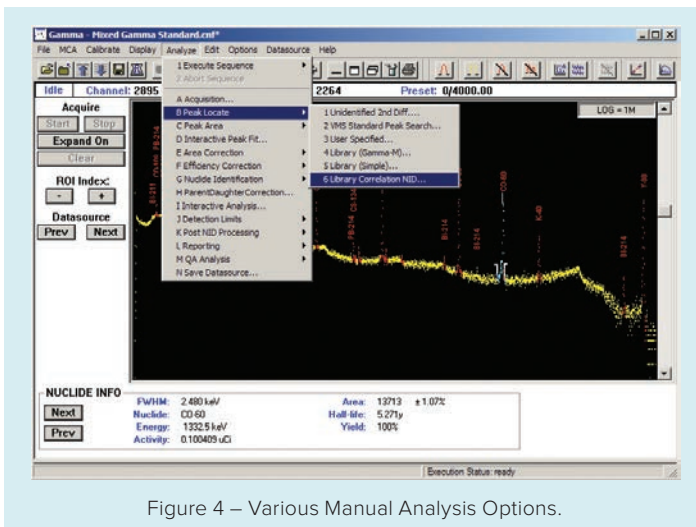


Figure 4 – Various Manual Analysis Options.

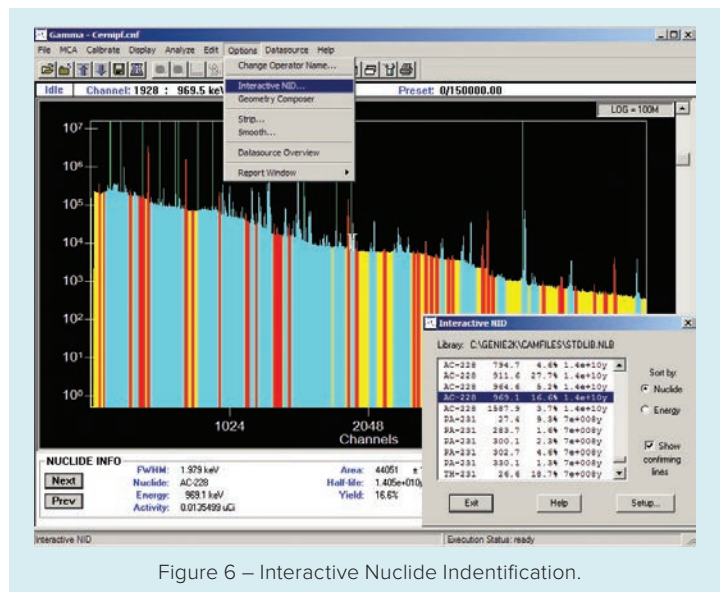


Figure 6 – Interactive Nuclide Identification.

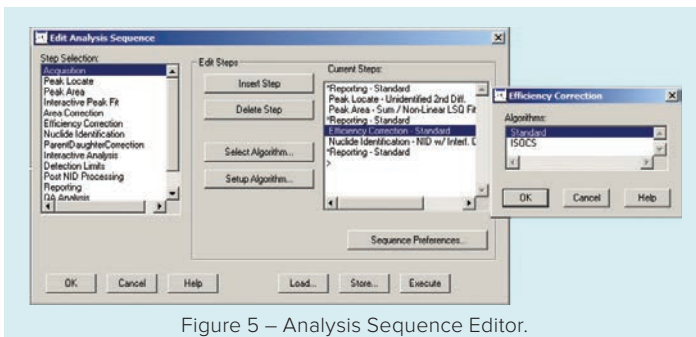


Figure 5 – Analysis Sequence Editor.

Using the Genie 2000 Programming Libraries, the advanced user can develop complete custom applications and user interfaces for Genie 2000 software. Programs can be developed in Visual Basic, C++, and .Net C# programming languages. It is this capability that provides the foundation for all Mirion layered software applications products. The Apex-Gamma™, Apex-InVivo™, Apex-Alpha™ and NDA 2000™ Waste Assay software packages are among many examples of these dedicated application solutions. See the specification sheets on these products for further details.

Scripting Capability for Simple User Programming

The Script Engine in the Basic Spectroscopy Software allows the user to specify a Visual Basic, Java script, or Windows script to execute on a currently opened datasource (file or live spectrum). This feature enables custom operations to be performed on the spectral data in the Genie 2000 Acquisition and Analysis environment. The script can be used in manual analysis of data or it may be inserted into an analysis sequence as one of the analysis and reporting steps for more automated processing.

Information Storage

The advanced methods used for information storage represent one of the unique features of the Genie 2000 product. Rather than using an array of fixed format files for data, calibrations, results, etc., the software uses an extensible single file to store all information pertaining to the system and individual samples. Files are accessed via the Configuration Access Method (CAM) which is internal to the Genie 2000 Basic Spectroscopy Software. Data access in the batch environment is managed by a set of low level commands that read/write CAM data by a defined variable name.

The CAM file structure makes it possible to review and analyze archived spectra just as easily as live counting data. Each file contains sample header information, spectral data, calibration information, analysis parameters, intermediate and

final analysis results, signal processing setup parameters (where programmable components are used) and the analysis library used. With this information available in a single data structure, the user can easily revisit old sample analyses without concern for matching up the correct versions of various supporting files. Quality, integrity and verifiability of the system are maximized.

Acquisition Hardware Support

Genie 2000 software supports a wide range of acquisition hardware for a variety of applications. The software is designed such that the specific acquisition hardware is transparent to the user who simply refers to a given input by detector name without regard to the physical MCA device.

Acquisition support is provided for the following MCAs which are described in their own specification sheets:

- Lynx® Digital Spectrum Analyzer
- Osprey® Digital Tube Base MCA
- Model 556B AIM with ICB NIM
- DSA-1000 Digital Spectrum Analyzer
- InSpector™ 2000 Portable MCA
- Multiport II MCA
- InSpector 1000 Digital Signal Handheld MCA
- Falcon 5000® Portable HPGe-Based Radionuclide Identifier
- Alpha Analyst™ Integrated Alpha Spectrometer

Support for future Mirion MCAs will also be added to the software as they are released.

MCA Input Definition is created with the MID Editor Setup Wizard (Figure 7). This program leads the user through a simple set of selections to define the MCA configuration as can be seen in the example provided for setting up a DSA-1000 Digital Spectrum Analyzer. In most cases, the setup involves answering four to six questions per input. More complex cases, as with multiplexed inputs, are defined using the standard MCA Input Definition (MID) Editor.

Multiple MCA setup definitions can be saved for the same MCA depending on how it will be used in a particular counting

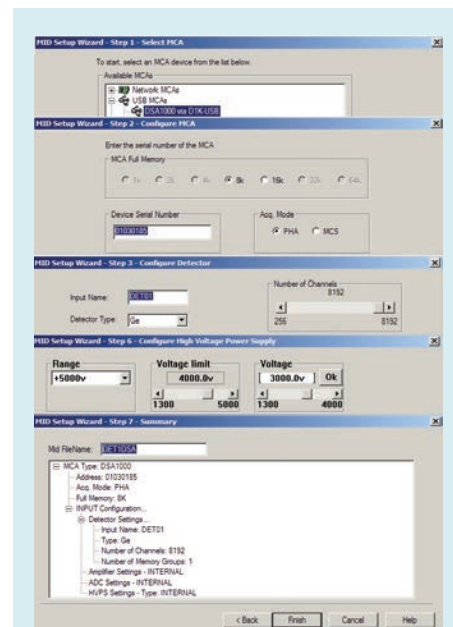


Figure 7 – MID Setup Wizard Steps.

application. This allows the user to define very specific sets of operating parameters that are associated with different types of applications.

Analysis Support

The Genie 2000 Basic Spectroscopy Software includes a set of base spectroscopic analysis algorithms as described in the following paragraphs. Each analysis algorithm can be executed manually, as part of an analysis sequence, or through a batch procedure command. These algorithms provide the ability to locate spectral peaks and calculate peak net areas.

Additionally, a set of spectral manipulation functions are provided for spectral data smoothing and for stripping one spectrum from another. The strip algorithm allows the application of a multiplier which is useful for adding spectra or creating simulated spectra in addition to just subtracting one set of spectral data from another. A more sophisticated environmental background subtraction method is available as part of the S501 Genie 2000 Gamma Analysis Option.

Unidentified 2nd Difference Peak Locate

This algorithm searches the spectrum for peaks above a user specified threshold level and identifies the centroids of found peaks. The resultant list of peak centroids can then be used by peak analysis algorithms for peak area calculations. The algorithm uses a modified 2nd difference computation over a user specified range of channels. Additional features of the algorithm reject Compton edges and other non-peak continuum features.

VMS Standard Peak Search

This peak locate algorithm emulates the popular, time-tested peak search found in the Mirion Genie-VMS spectroscopy platform. It locates all peaks in the search region whose significance is above the Peak Search Sensitivity threshold using a 2nd difference method. The peaks are then fitted using a pure Gaussian fit routine.

User Specified ROI Peak Locate

The User Specified ROI Peak Locate algorithm simply employs user created Region of Interest (ROI) tables to calculate peak centroids. The user may either manually enter ROI limits or may read them in from a CAM file containing ROIs. The resultant list of peak centroids can then be used by peak analysis algorithms for peak area calculations. This method of peak location does not support multiplet deconvolution.

Library (Gamma-M) Peak Locate

A separate algorithm set is available for users whose applications call for a library driven peak search approach. A library-based peak search is recommended for NaI spectroscopy and HPGe applications where only specific nuclides are expected. A library peak search also has advantages in some very low level HPGe spectroscopy applications.

One of these library driven algorithms is based on the Gamma-M approach also available in Genie-VMS spectroscopy systems. The first step in the Gamma-M library locate phase is determination of the continuum background. This is done by an "erosion" process that effectively smooths the spectrum. At the end of this process, the resulting background spectrum is subtracted from the original spectrum to form a net spectrum.

Next, the algorithm builds a table of peak locations from the list of energies in the library. The system will then perform a linear least squares fit of the data, as well as a number of additional tests to determine if, in fact, each peak in the table exists. During this process, the user can enable a "gain shift correction" which takes into account the possibility of deviations between the library energy and the actual centroid energy. If desired, the library peak locate can also be supplemented with an unknown peak search that will find peaks that are not in the library. Those peaks that are confirmed by this process are used to populate a second table that can be used for a later peak area analysis.

Library (Simple) Peak Locate

This peak locate algorithm will assign the peak locations based on the library energies as well. Unlike the Library (Gamma-M) algorithm, there is no erosion of the continuum, gain shift correction or MDA calculations to verify that the peaks are indeed present. All such calculations are delegated to the peak area algorithms.

Peak Area Calculations

Peak area calculations begin with the results of the peak locate algorithms above and compute peak net areas. Those areas may then be used in subsequent analysis and reporting steps. Genie 2000 software provides two algorithms for these area calculations: Sum/Non-Linear Least Squares Fit and Library (Gamma-M).

The first step in the **Sum/Non-Linear Least Squares Fit** is the determination of peak region limits. Here, the system will use either the ROI limits established by the user in the User Specified ROI Peak Locate step, or it will automatically determine limits based upon the results of the other automatic peak locate algorithms. Where automatically established limits are used, the algorithm also makes the determination whether adjacent peaks are going to be analyzed as singlet peaks or multiplets.

Peak areas are calculated differently for singlet peaks and multiplet peaks. For singlets, the algorithm simply sums the gross counts in the peak ROI and subtracts the background continuum. For multiplets, the algorithm performs a non-linear least squares fit to the data, providing the best possible fit to the actual spectral data. The fit model uses both the peak width calibration and, optionally, a low tail shape calibration.

The **Library (Gamma-M)** peak analysis uses the results of the library locate phase to calculate peak areas. The program fits the expected peak model (established by calibration) to each peak in the spectrum. In this process, the algorithm will flag interfering peaks in the spectrum and perform a correction to subtract any interfering peak contribution from the current peak. This process is repeated for all peaks in the spectrum.

Calibration

Genie 2000 software supports energy, width, low-tail and efficiency calibrations. Calibrations may be performed using either the interactive interface or the batch procedure environment depending upon the specific needs of the application. A Peak-to-Total calibration routine is also included as an initial step, if desired, in the correction for cascade summing of coincident peaks in spectra. Full cascade summing correction down to 10 keV is available with the addition of the Gamma Analysis Option. Peak-to-Total calibration is no longer required for this correction, making it a truly sourceless correction.

The calibration process is simplified by the use of certificate files which are created with a graphical Certificate File Editor program. Certificate files essentially duplicate all the information typically furnished with a calibration standard – nuclide, emission rates, uncertainties, and so forth. By matching this information to peaks found in the spectrum after the standard is counted, initial energy/FWHM calibration can be simplified while periodic recalibration can be completely automated. Whether performed in the batch or interactive modes, calibrations are typically done in conjunction with the actual spectral display in the Spectroscopy window. In interactive mode, the user can load a certificate file (which brings in the energies associated with the nuclides in the standard), select an energy with the mouse, and then select the peak directly from the spectral display.

Efficiency calibration is automatic. A peak search algorithm locates and quantifies peaks, then associates them with the known (decay corrected) emission rates for each line to determine an efficiency curve and equation.

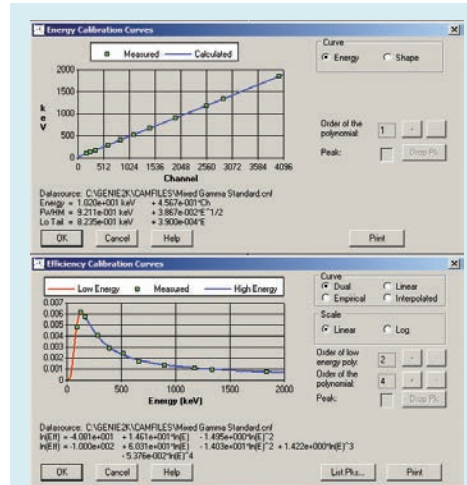


Figure 8 – Typical Calibration Curve Screens.

Interactive calibration plots are provided. These allow the user to view the calibration curves in detail and adjust the order of the curve to achieve the best possible fit to the data (Figure 8). The energy calibration curve may be a 1st, 2nd or 3rd order polynomial. The efficiency calibration may be up to 9th order. Additionally, one of three efficiency calibration algorithms may be selected – dual polynomial, linear polynomial (required by CEA in France) and empirical polynomial. A fourth interpolated method, which connects the data points with straight lines, is also available. This method is ideal when using mathematically determined efficiency data points.

Gain Evaluator and Gain Adjust Options

The Gain Evaluator (Figure 9), which can be used with both file and detector datasources, allows the user to analyze the quality of the current datasource energy calibration and gain settings. It does not perform any MCA electronics hardware adjustments, but provides the ability to assess the impact on NID analysis and to make corrective data adjustments using the File or Auto Gain Adjust options. The Gain Evaluator can be run interactively or as a part of an analysis sequence.

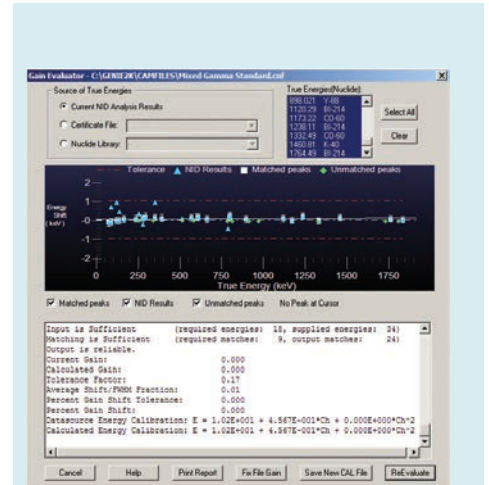


Figure 9 – Gain Evaluator Screen.

File Gain Adjust facilitates matching spectra with different energy calibrations in order to add, strip or compare them. It is available only for file datasources. Executing this routine shifts, or rebins, the current file's spectral data so that it matches the specified "goal" energy calibration of another spectrum instead of the current energy calibration.

The Auto Gain Adjust utility automatically corrects computer-controlled gain/zero to match the current energy calibration. This is implemented by iteratively acquiring a spectrum, matching peaks found by peak search analysis to input certificate file energies, and changing hardware settings based on this peak matching analysis.

Optional Analysis Features

Additional analysis algorithms are available as part of the S501 Genie 2000 Gamma Analysis Option and S509 Alpha Analysis Option packages. These algorithms include efficiency correction, peak net area background subtraction, nuclide identification, automatic interference correction and weighted mean activity, MDA calculation, and more. The Alpha Analysis Option adds other specialized algorithms associated with reagent blanks and tracer/tracerless analysis used in alpha spectroscopy. The S506 Interactive Peak Fit option is also available to view and refine individual peak fits.

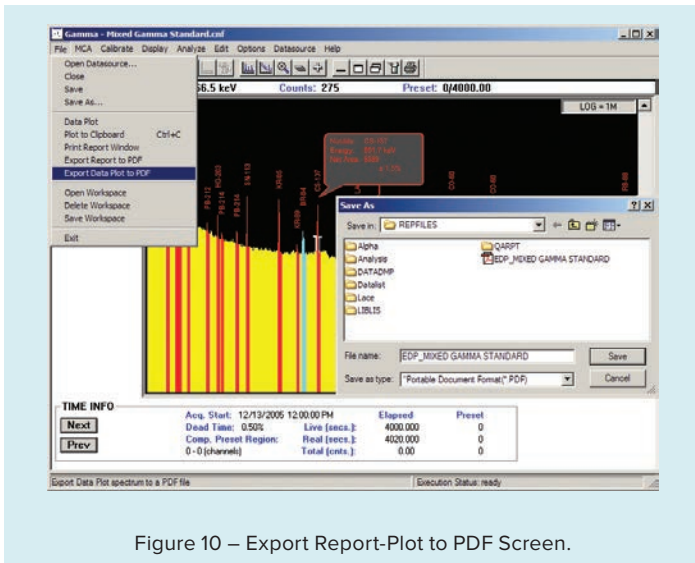


Figure 10 – Export Report-Plot to PDF Screen.

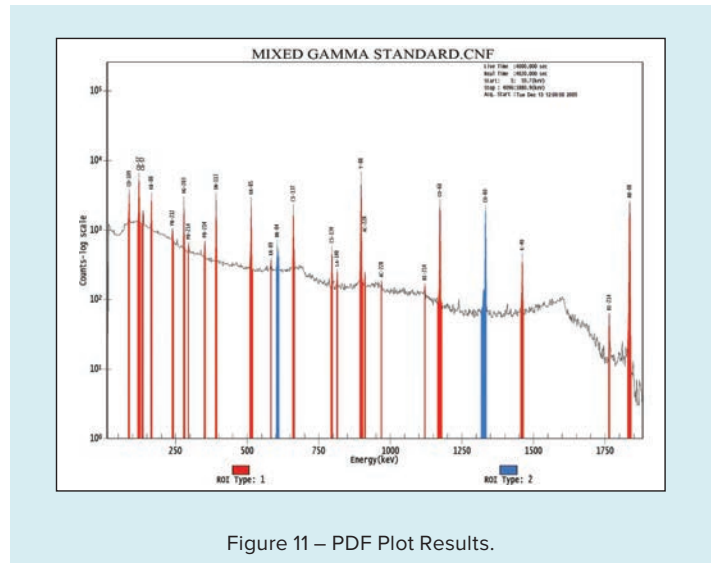


Figure 11 – PDF Plot Results.

Hard Copy Plotting

Hard copy plots may be obtained for spectral data. The plots may also be saved in Adobe Acrobat PDF format with a built-in export utility (Figure 10) for ease of electronic file distribution. Spectral plots are available for the full spectrum (Figure 11) and for the expand region, so the user has the flexibility to output only a certain spectrum range of interest. Various ROI types are delineated by shading or colors, and an x-y grid may be overlaid to assist in determining the energy or number of counts at various points on the plot.

Plots are also available for energy calibration, shape calibration (FWHM and tailing) and for efficiency curves. Spectrum and calibration plots may be called from both the interactive and batch environments.

Report Subsystem

Genie 2000 software allows for the flexible formatting of output data to meet the unique requirements of the application. Report format is controlled by a virtual report engine which contains a set of commands that format the report output.

Features of the report engine include: dynamic setting of the text font, color and other attributes, the ability to create tables, the ability to import graphics files (BMP, JPG, GIF and TIFF) and the ability to execute VB, Java or Windows scripts directly from the report template. Multiple report templates can be created with the report engine for various applications and

then selected at report time during manual sample analysis or as part of an analysis sequence. Also, a set of standard report templates is provided with the software.

This report flexibility gives the Genie 2000 user the ability to output data in a form that can be imported into other packages such as databases and spreadsheets. By defining the report template to produce an ASCII delimited file in a format consistent with the input requirements of other packages, data can easily be exchanged.

Reports are always directed to a data file and optionally to the screen and/or a printer. As with the spectral plots described above, a report can also be exported to PDF format (Figure 10).

Network Support

Network support exists in the Genie 2000 software on several levels. First, the Genie 2000 package supports all Mirion Ethernet network based MCAs. Networked MCAs allow the MCA and associated signal processing electronics to be connected directly to a network, allowing remote data acquisition without relying on intermediary computers

Additionally, multiple Genie 2000 computers can be networked together to share both information and access to MCA resources. This allows an input to be controlled by a computer other than the one to which it is connected. For example, in Figure 12, Genie 2000 #1 can control acquisition and analysis for the Digital Signal Analyzer (DSA) directly connected to Genie 2000 #2.

The physical location of the input is transparent to the operation, and the operation of Genie 2000 #2 is not affected by the remote access except that the DSA input taken by Genie 2000 #1 is not available for it to control. However, Genie 2000 #2 can open the same input in a “Read-Only” mode, allowing live spectral display and analysis, even though the input is “owned” and is being used by the other computer.

This multiple access capability allows a true distributed system to be assembled. Whether the system uses networked or directly computer interfaced MCAs, a supervisor’s computer located in an office can monitor all activity in the lab without affecting lab operation. Acquisition can be monitored remotely and problem samples can be analyzed by the supervisor without leaving the office and without disrupting count room operations in progress.

Specifications on next page

SPECIFICATIONS

System Requirements

Genie 2000 software requires a personal computer with:

- 2.0 GHz Dual Core Pentium highly recommended.
- 2 GB memory, 200 GB hard disk; CD ROM, USB.
- Integrated 10/100 Ethernet interface.
- 1024 x 768 video adapter.
- Windows 7 Professional SP1(32- or 64-bit), Windows XP Professional SP3 (32-bit), Windows Server 2008 SP2 (32-bit), or Windows Server 2008 R2 SP1 (64-bit).

Performance is enhanced with better computer resources. Consult the factory for assistance in configuring a system to the needs of your specific applications.

Ordering Information

Model	Description
S500	Genie 2000 Basic Spectroscopy Software for Multi-Input Applications.
S502	Genie 2000 Basic Spectroscopy Software for Single Input Applications.
S504	Genie 2000 Basic Spectroscopy Software for the InSpector.

Multiple Copy Licenses

Model	Description
S511	1-Input Right to Copy License.

Confers the right to run S502 and base optional layered software on one additional computer. One license is required for each additional computer. Layered software must be purchased on first computer.

Model	Description
S520	Multi-Input Right to Copy License.

Confers the right to run S500 and base optional layered software on one additional computer. One license is required for each additional computer. Layered software must be purchased on first computer.

Optional Layered Software

The following optional software is available for Genie 2000:

- S501 Gamma Analysis Option.
- S509 Alpha Analysis Option.
- S505 Quality Assurance Software.
- S506 Interactive Peak Fit Software.
- S573 In Situ Object Calibration Software (ISOCS™).
- S574 LabSOCS™ Laboratory Calibration Software (LabSOCS).
- S572 IMCA Uranium Enrichment Software.
- S535 Uranium-Plutonium InSpector Software.
- S529C NDA 2000 Integrated Neutron/Gamma Waste Assay Software.
- S507 Multi-Group Analysis for Uranium Software.
- S508 Multi-Group Analysis Software
- Apex-Gamma Lab Productivity Suite.
- Apex-Alpha Spectroscopy Software Suite.
- Apex-InVivo Whole Body Counting Software.

*See individual specification sheets on these optional software packages.

Non-English Language Versions

Genie 2000 software is also available in German, French, Russian and Japanese language versions. Consult your local Mirion office for information on these and on possible future support for other languages.

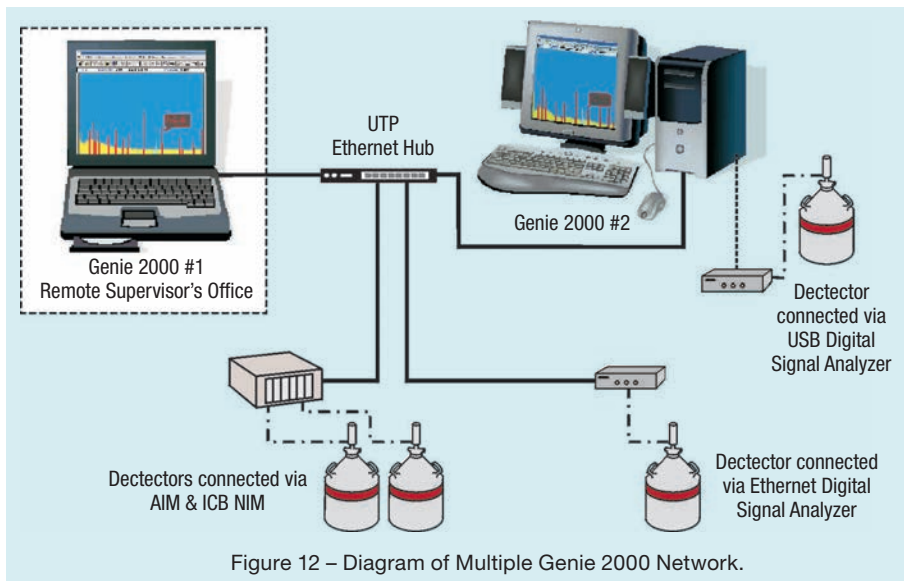


Figure 12 – Diagram of Multiple Genie 2000 Network.



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CANBERRA