



COMPREHENSIVE & CUSTOMIZABLE

Genie™

Spectroscopy Software Suite



The Genie Spectroscopy Software Suite provides the core software functionality for a comprehensive, high quality, and defensible gamma or alpha spectrometry system.

The suite includes robust data acquisition, interactive spectral display and results reporting, and industry-proven analysis algorithms for defensible radionuclide activity and decision limits results.

The Genie Spectroscopy suite and GenieLite™ software are available in single-input and multi-input models. The multi-input models provide independent support for multiple detector systems, allowing users to run independent counting on several detectors simultaneously. Acquisition and analysis capabilities are tightly integrated, providing a real-time spectral update display and straightforward operation of various counting operations. These operations can be performed on demand or incorporated into automatically executed workflows. Analysis results are viewable either in the integrated screen or a separate window (ideal for multi-monitor systems), allowing for side-by-side review of the spectrum while scrutinizing reported results. Reports now include user-focused interactive features, which will evolve the way spectroscopists perform data review.

FEATURES

- ✓ Integrated data acquisition and analysis
- ✓ Independent support for over 250 detector inputs
- ✓ Distributed MCA (Multichannel Analyzer) networking with centralized data management
- ✓ Layered software options available for specialized spectroscopy applications
- ✓ Qualified with Windows 11, Windows 10, Windows Server 2022, and Windows Server 2019
- ✓ Full gamma and alpha spectrum analysis, including:
 - Energy, Shape, and Efficiency Calibrations
 - Background subtraction, reference peak correction, and tracer peak
 - Nuclide identification, Interference correction, and weighted mean activity calculations
 - Patented true coincidence (Cascade) summing correction
 - 3-Dimensional Geometry Composer for interactive definition and visualization of sample, detector, and absorber parameters
 - Minimum Detectable Activity (MDA) calculations, including ISO 11929 compliance
- ✓ Interactive reports for dynamic data review
- ✓ Ability to review, adjust, or add/delete peaks in specific Regions of Interest
- ✓ Parameter tracking, reporting, and limits evaluation with statistical tests for QA/QC counts
- ✓ Python® Scripting Integration for increased automation
- ✓ Additional simplified counting interface for screening applications with Genie-FieldPro™ software

The analysis algorithms of the Genie Spectroscopy suite provide complete peak and nuclide analysis capability for gamma ray spectra obtained from any type of gamma detector. Additionally, alpha spectrum analysis algorithms are included for advanced alpha spectrometry. Genie analysis algorithms are based on time proven methodologies with a long history of acceptance and refinements, and include patented, groundbreaking analysis and calibration techniques.

Analysis execution utilizes data resident in the Configuration Access Method (CAM) data structures native to all Genie Family systems. Results from each algorithm are also stored in CAM files, making the resultant data file a complete record of the entire analysis. This unique method of data storage greatly simplifies system administration, data transfer, data archiving, and any necessary reanalysis of archived spectra at a later date. Additionally, each algorithm is documented in detail in the Genie Customization Tools manual, easing traceability and independent verification of results.

GENIE USER INTERFACES / USER EXPERIENCE

The Genie Spectroscopy Software Suite is truly a toolbox of applications that allow users to customize the experience for their operations. The primary application uses a classic window-style interface that provides straightforward access to system functions such as acquisition control, spectral display, and analysis steps. A single window is used to control acquisition and analysis for multiple inputs at the same time.

More than 250 data sources (any combination of active detector inputs and previously acquired spectral 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). Spectral display can be interrogated with a secondary EXPAND or Zooming window, ability to overlay and adjust scaling of two spectra with the COMPARE function, color-coded creation of regions of interest, and dynamic on-screen

calculation of spectrum details via markers and cursor placement. With Genie Spectroscopy suite, the Interactive Peak Fit (IPF) application provides powerful peak-by-peak review of regions of interest, providing the ability to fine-tune and improve the quality of each peak fit. The Genie-FieldPro application, now available with the Genie Spectroscopy suite, provides a simplified interface for routine sample counting or screening applications.

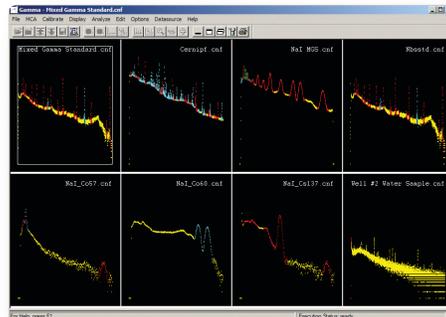


Figure 1 – Multi-Spectrum Screen

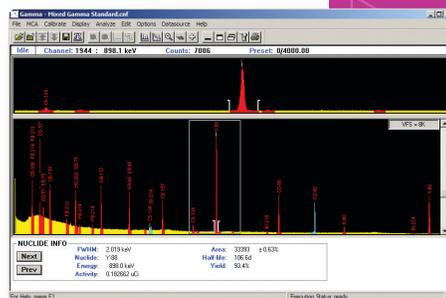


Figure 2 – Spectrum Expand Mode

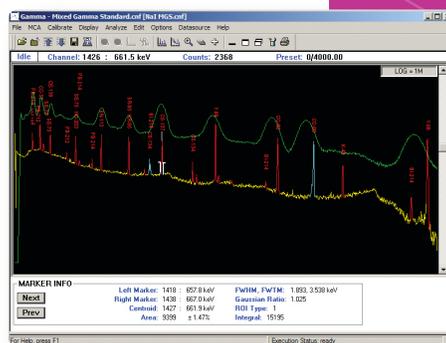


Figure 3 – Spectrum Compare Mode

To optimize the Genie application experience, users can toggle on/off the control panel (for quickly managing start/stop and clear functions), the status display (to provide real-time information of the current data source, whether this is sample information, region of interest parameters, or acquisition count time statistics), and toolbar icons. The toolbar icons can be configured to provide single-click operations of complex steps or expose icon labeling for easier familiarization and training. The spectral display by default is a high-contrast yellow spectrum channel data over a black background, that can be customized per user.

To display radionuclide information on the spectral window, the Interactive Peak Labeling option can be enabled to tag each peak with the associated nuclide from a tentative nuclide identification from a selected nuclide library, or from full spectral analysis results. Selecting the peak exposes the peak area, activity, and emission line. Alternately, with the interactive nuclide identification (Interactive NID) mode, the user can place their cursor on a peak of interest and nuclide, energy, abundance, and half-life are then instantly displayed. A list box lets the user manually select alternate nuclides sorted by energy or by nuclide name. One can view confirming emission lines (if existing) to assist with the nuclide identification (Figure 7).

Analyses can be performed in a step-by-step manual mode, or a complete analysis sequence file (ASF) can be defined and executed for routine operation. In manual mode, individual analysis algorithms, such as peak locate or peak area, can be applied to the spectrum by menu selection. The setup screen associated with the selected algorithm is presented, thus allowing the user to edit analysis parameters before executing that phase.

The analysis sequence editor is used to define an analysis sequence. The sequence can consist of a series of acquisition controls, analysis algorithms and reporting steps, complete with their parameter definitions and analysis settings. It can also incorporate scripting hooks for functionality beyond standard Genie operations. When the analysis sequence is saved, it appears in the Analyze pull down menu and is available for immediate operation. The analysis sequence can also be assigned to a shortcut key or icon for single-click operation (Figure 8).

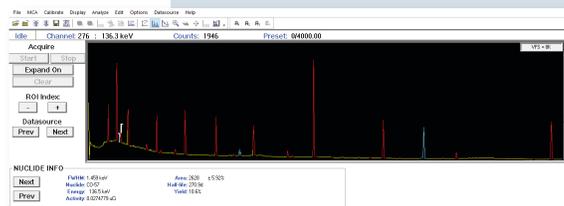


Figure 4 – Example of high contrast display colors and "Envelop" spectral plot mode.

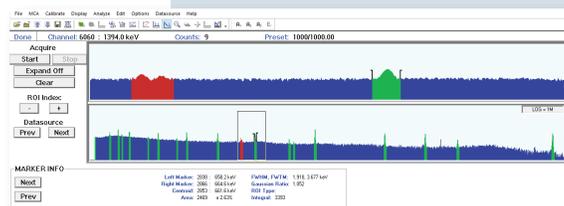


Figure 5 – Example of bright display colors and "Fill" spectral plot mode.

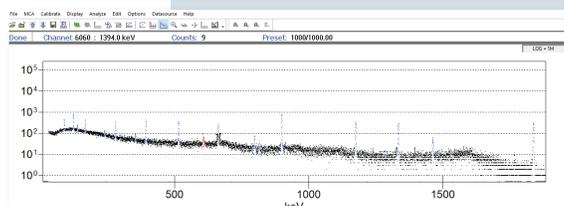


Figure 6 – Example of scientific display and "Full" spectral plot mode.

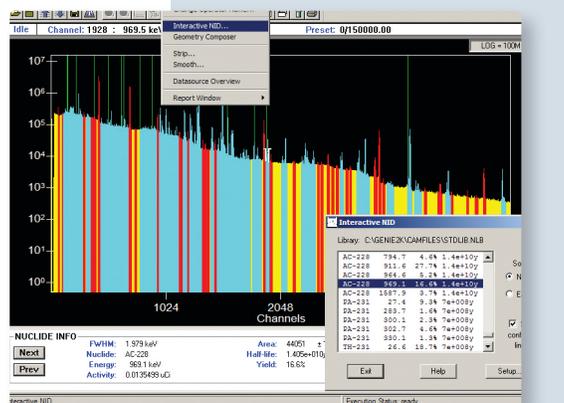


Figure 7 – Interactive Nuclide Identification



Figure 8 – Illustration of launching an Analysis Sequence File from toolbar for single-click operations. Note: The toolbar icons were set to "Large ICONS" mode and toolbar text labels turned on.

RESULTS REVIEW AND REPORTING

New with Version 4.0, Genie Interactive Reports are developed with spectroscopists in mind. These reports feature a clean, easy-to-read style and layout, ensuring a seamless experience for data reviewers and scientists using the reports to validate results, analyze information, and save time. The most exciting feature is the integration of Interactive Peak Fit display, accessible directly from the listed energy line on the report, providing a fast way for users to validate the quality of the peak fit.

Reports are organized into five key sections:

1) Cover page: Provides sample information, a spectral image for visual evidence of count, and an optional signature field.

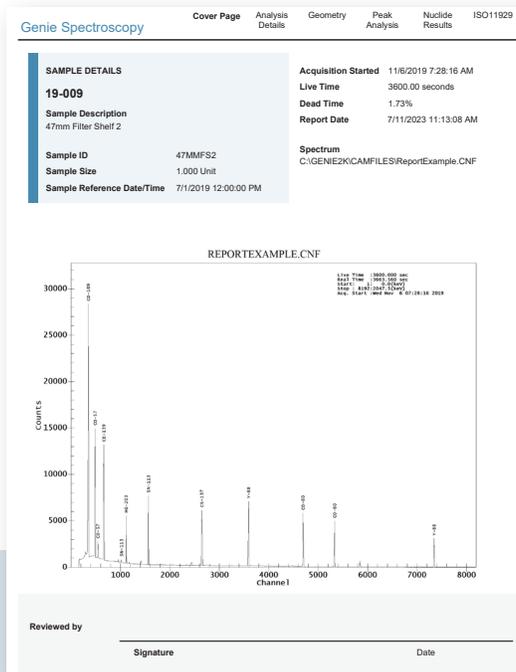


Figure 9 – Cover page

2) Count and Analysis Details page: Provides a record of MCA settings, calibrations applied, libraries used, and analysis algorithms executed, providing traceability of a sample count and analysis performed.

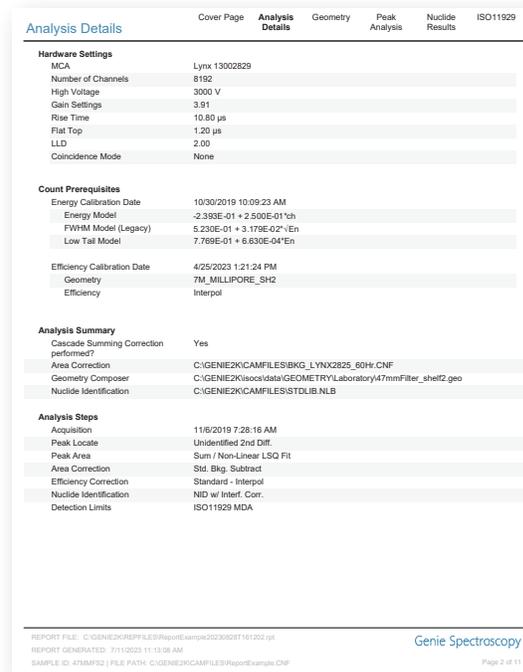


Figure 10 – Count and Analysis Details page

3) Geometry page: Includes a schematic of the ISOCS™ or LabSOCS™ template (if cascade summing or ISOCS efficiency was performed) and the efficiency triplets associated with the analysis.

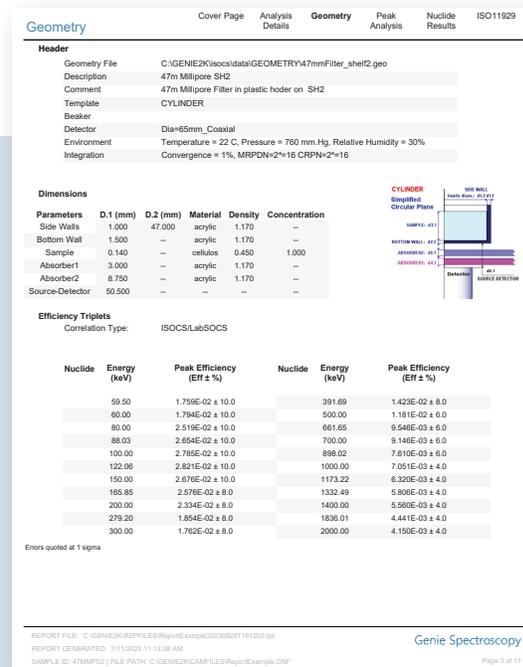


Figure 11 – Geometry page

4) Peak Analysis page: Lists values including Region of Interest, FWHM, peak area and uncertainties, background subtracted counts, and the decision threshold. The decision threshold is a key parameter, as it provides the minimum number of counts for a peak in the Region of Interest to be statistically significant. Columns can be dynamically sorted by the column header, enabling users to sort by peak area, FWHM, or energy.

Peak	Peak Centroid	Energy (keV)	Peak Significance	ROI (keV)	FWHM (keV)	Net Peak Area (cts ± %)	Background (cts ± %)	Critical level (cts)	Peak Efficiency (Eff. %)
1	164.98	41.00	17.42	40.25 - 42.25	0.87	2.473E+03 ± 5.07	1.892E+02	1.799E-02 ± 10.0
2	353.09	88.02	165.98	86.25 - 89.50	0.84	9.684E+04 ± 0.41	2.807E+02 ± 3.65	4.128E+02	2.653E-02 ± 10.0
3	489.25	122.06	118.80	120.49 - 123.74	0.88	5.193E+04 ± 0.62	3.717E+02	2.821E-02 ± 10.0
4	546.80	136.44	35.94	134.99 - 137.99	0.85	6.410E+03 ± 3.37	3.295E+02	2.742E-02 ± 10.0
5	664.45	165.85	118.09	163.74 - 167.49	0.96	5.035E+04 ± 0.63	2.601E+01 ± 275.26	3.542E+02	2.576E-02 ± 8.0
6	1021.70	255.15	14.62	253.97 - 256.72	1.07	1.651E+03 ± 9.06	1.952E+02	1.973E-02 ± 8.0
7	1117.95	279.21	84.76	276.97 - 280.97	1.02	2.228E+04 ± 0.53	2.385E+02	1.854E-02 ± 8.0
8	1568.06	391.72	109.37	389.45 - 393.95	1.13	3.559E+04 ± 0.64	2.123E+02	1.422E-02 ± 8.0
9	2648.21	661.72	103.17	658.91 - 664.16	1.31	3.302E+04 ± 0.65	5.373E+01 ± 2.05	1.828E+02	9.545E-03 ± 6.0
10	3593.71	898.06	116.38	895.13 - 900.88	1.46	4.292E+04 ± 0.54	1.707E+02	7.610E-03 ± 6.0
11	4694.41	1173.19	109.30	1169.84 - 1176.34	1.65	4.037E+04 ± 0.54	1.655E+01 ± 28.91	1.308E+02	6.320E-03 ± 4.0
12	5331.53	1332.45	104.41	1329.07 - 1335.57	1.70	3.645E+04 ± 0.55	8.337E+00 ± 25.98	9.454E+01	5.806E-03 ± 4.0
13	7345.96	1835.88	86.03	1831.99 - 1839.49	2.03	2.682E+04 ± 0.62	4.694E+01	4.441E-03 ± 4.0

Figure 12 – Peak Analysis page

Additional features include a “Review Required” flag that users can mark against any nuclide, and quick links to easily navigate through sections. The reports can be exported to Excel, Word, PDF, and other third-party applications from the menu bar, and customized using the integrated Genie Stimulsoft Engine editor tool.

Genie 4.0 will continue to support legacy Genie 2000 report templates, which have been used for thousands of analyses. These report templates produce an ASCII delimited file that is easy to read and parse into other applications, or to print to PDF or a physical printer.

5) Nuclides Results page: Provides a concise summary of nuclides activities and MDAs for both identified and library nuclides. Nuclide entries can be expanded to reveal results associated with the respective emission lines, providing the most relevant data for a high-quality review of reported results. Each column can be sorted by any header, and uncertainty results can be toggled between percent and absolute uncertainties. Users can inspect any emission line (whether identified or not found) by clicking on the energy in the report, directly launching the Genie Interactive Peak Fit at the selected energy.

Nuclide	NID Confidence	Wt Mean Activity (Bq/Unit ± %)	Decision Level (Bq/Unit)	MDA (Bq/Unit)	Needs Review
CO-57	+	1.00	8.388E+02 ± 7.31	5.937E+00	1.225E+01
CO-60	+	1.00	1.901E+03 ± 2.85	4.906E+00	9.994E+00
SE-75	X+	0.34	1.378E+01	2.819E+01
96.73	3.41	0.964	2.372E+02	4.893E+02
121.111	16.70	6.676E+03 ± 10.69	0.961	5.957E+01	1.984E+02
136.02	59.20	2.391E+02 ± 11.43	0.962	1.872E+01	3.878E+01
198.60	1.45	1.000	4.986E+02	1.019E+03
264.65	59.80	0.961	1.378E+01	2.819E+01
279.52	25.20	2.852E+03 ± 8.15	0.973	6.200E+01	1.266E+02
303.91	1.32	0.908	6.508E+02	1.333E+03
400.65	11.40	1.253	5.895E+01	1.209E+02
Y-88	+	0.99	3.969E+03 ± 3.36	7.003E+00	1.447E+01
CD-109	1.00	3.299E+04 ± 10.44	1.410E+02	2.916E+02	
SN-113	0.99	2.348E+03 ± 6.80	1.380E+01	2.827E+01	
CS-137	1.00	1.138E+03 ± 6.04	6.314E+00	1.285E+01	
CE-139	+	1.00	1.288E+03 ± 8.03	9.553E+00	1.951E+01
HG-203	0.96	2.889E+03 ± 8.12	3.095E+01	6.337E+01	

Nuclide	Decision Level (Bq/Unit)	MDA (Bq/Unit)	Needs Review
BE-7	
NA-22	
NA-24	
CL-38	
K-40	9.204E+01	1.862E+02	
AR-41	
K-42	
SC-46	+	1.851E+01	3.768E+01

Figure 13 – Nuclides Results page

INFORMATION STORAGE

The unique methods used for information storage represent one of the strengths of the Genie platform. 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 architecture. Data access in the batch environment is managed by a set of 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 Spectroscopy suite and GenieLite applications support a variety of acquisition hardware for a wide range 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.

PHA and MCS acquisition support is provided for the following Mirion MCAs:

- Lynx-II® and Lynx® Digital Spectrum Analyzer
- Osprey® Digital Tube Base MCA
- InSpector™ 2000 Portable MCA
- Multiport II™ MCA
- Aegis™ Portable HPGe Spectrometer
- Falcon 5000® Portable HPGe-Based Radionuclide Identifier
- Alpha Analyst™ Integrated Alpha Spectrometer

Where applicable, coincidence/anti-coincidence counting modes, sample changer control, and other advanced capabilities are also supported. Please reference individual device specification sheets for more details.

A separate utility is used to initially identify and configure the MCA input for ease of communication with the detector system. Multiple MCA setup definitions can be saved for the same MCA depending on its use within a particular counting application. This allows the user to define very specific sets of operating parameters associated with different types of applications.

NETWORK SUPPORT

Network support exists in the Genie software on several levels. Genie software connects to the supported MCAs both over the Ethernet and via USB. The Ethernet 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, Genie applications on multiple 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 14, Genie System #1 can control acquisition and analysis for the MCA directly connected to Genie System #2.

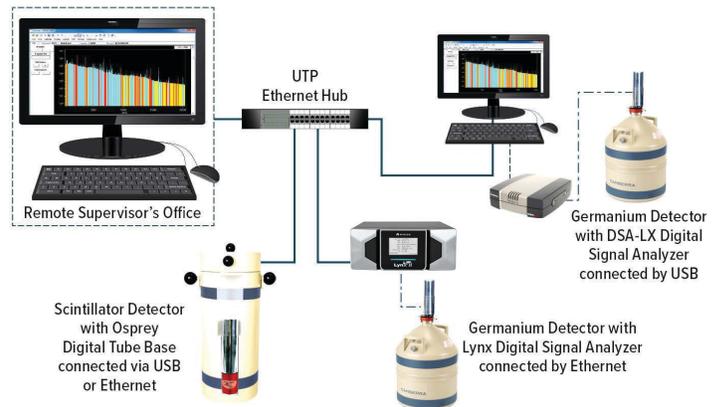


Figure 14: Illustration of network connectivity capabilities for Genie applications

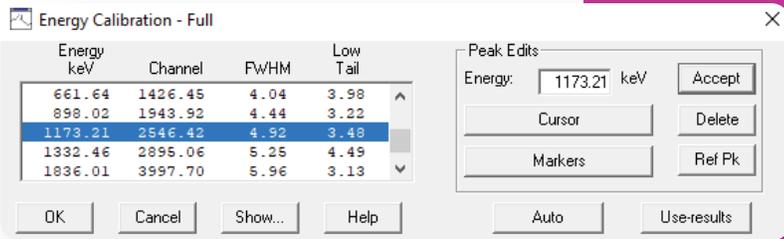


Figure 15 – Auto-calibration utility for associating calibration spectrum channel data with energy and resolution.

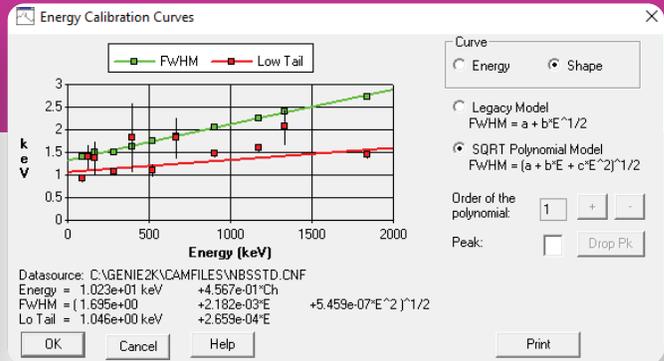
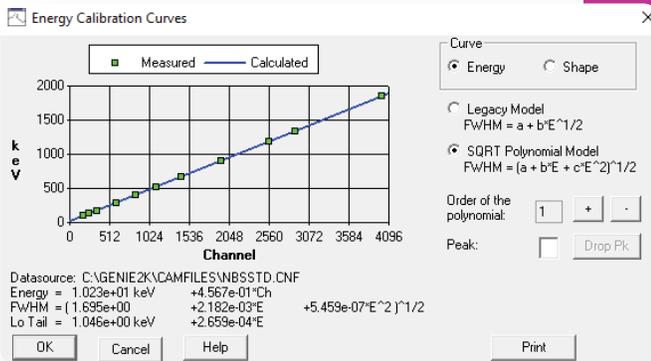


Figure 16 – Screens for reviewing and refining calibration fits for energy vs channel and shape (FWHM) vs energy. Note the ability to toggle between to fitting modes for FWHM.

This multiple access capability allows a true distributed system to be assembled. Whether the system uses networked or locally-connected MCAs, a supervisor's office-based computer 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.

CALIBRATIONS

Both the Genie Spectroscopy suite and GenieLite software provide capabilities for Energy verse channel calibrations, Resolution or "Full-Width at Half Maximum" (FWHM) calibrations, and peak low-side tailing calibrations. With Genie 4.0, the user now has the choice of two models for the FWHM calibration: a legacy fitting option and a newer option that has been shown to have best fidelity to detector resolution curves. The Genie Spectroscopy suite provides multiple options for efficiency calibrations, which are necessary

to determine nuclide activities. A Peak-to-Total calibration routine is also included, which is for legacy support and is no longer required to implement cascade summing corrections in Genie software.

The calibration process is simplified using certificate files created with the Certificate File Editor program. Certificate files essentially duplicate all information typically furnished with a calibration standard – nuclide, emission rates, uncertainties, etc. 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.

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. This is the "Certificate File" driven Efficiency Calibration option.

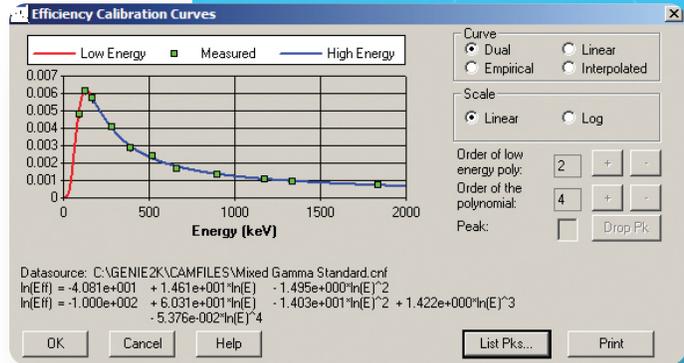
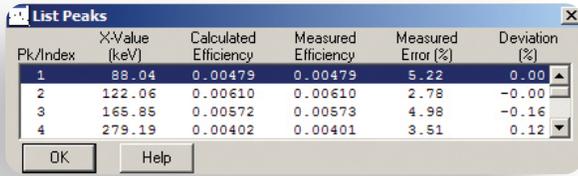


Figure 17 – Screen for reviewing and refining the efficiency calibration fitting. Note ability to select four different efficiency calibration options, adjust the order of the polynomial, and view the efficiency values for each efficiency calibration peak.

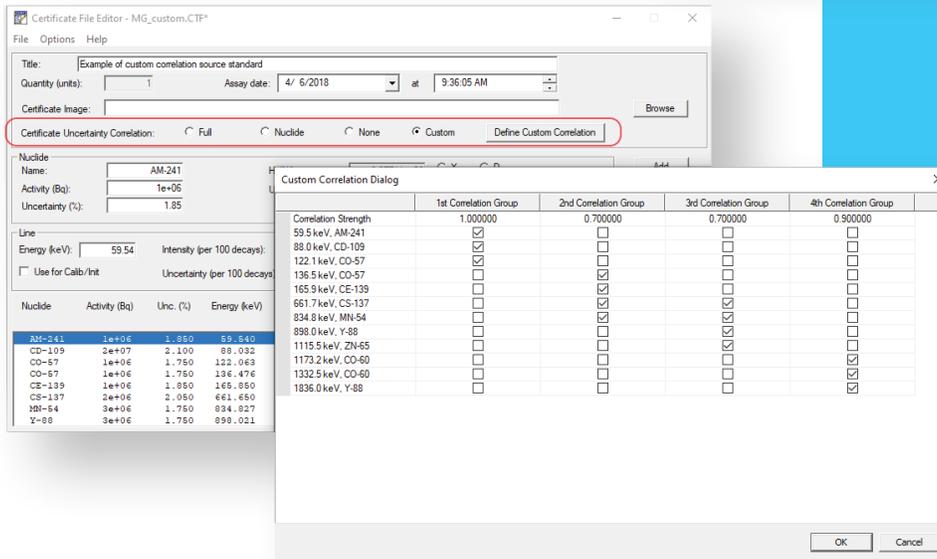


Figure 18 – Genie Certificate File Editor, which provides reference information of calibration sources for use by Genie calibration engines. Note the ability to define the correlation type of a calibration source, including an option to define custom correlation groups if known.

Interactive calibration plots are provided. These allow the user to view calibration curves in detail and adjust the order of the curve to achieve the best possible fit to the data (Figure 17). The energy calibration curve may be a 1st, 2nd or 3rd order polynomial. The efficiency curves may be up to 9th order.

Four efficiency calibration algorithms may be selected – dual polynomial (with a user-defined crossover point), linear polynomial (required by CEA in France), and empirical polynomial. The fourth interpolated method, which connects the data points with straight lines, is also provided. This method is ideal when using mathematically determined efficiency data points.

The dual and linear polynomial models use a least squares fitting methodology to determine the uncertainty of efficiency calibration, and now with Genie 4.0 these models support correlations during the fitting routines. The user defines the correlations in the certificate file editor by identifying the calibration data points from each emission line to be either fully correlated, correlated by nuclide, or independent. The user also has the option to define a custom correlation matrix (Figure 18).

Peak Locate and Peak Area Analyses

The Genie Spectroscopy suite includes many options for locate spectral peaks and calculate peak net areas needed for basic and advanced spectroscopic analysis. The range of algorithms allow flexibility to tailor your analysis to the unique requirements of each application. Each analysis algorithm can be executed manually, as part of an analysis sequence, or through a batch procedure command. These algorithms are also available with the GenieLite applications for basic spectroscopy.

UNIDENTIFIED 2ND DIFFERENCE PEAK LOCATE

Ideal to locate any unknown nuclides in the spectrum, this algorithm evaluates 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 time-tested peak search found in the historical 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 stored file. 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 (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.

LIBRARY (GAMMA-M) PEAK LOCATE/PEAK AREA

A library-based peak search may be recommended for NaI spectroscopy and HPGe applications where only specific nuclides are expected, or with some very low level HPGe applications.

The Library Gamma-M Peak Locate approach (comparable to the Gamma-M in the historical Genie-VMS applications) first uses an erosion technique to strip the continuum from the spectrum. The spectrum is then evaluated against the expected peaks from a library using a linear least squares fit to determine the presence of these peaks. Additional capabilities are corrections for gain shifts and combining with unknown peak search algorithms for more flexibility. The Library (Gamma-M) peak analysis also calculates peak areas by fitting the expected peak model (established by calibration) to each peak in the spectrum. The algorithm will flag interfering peaks in the spectrum and perform a correction to subtract any interfering peak contribution from the current peak.

SUM/NON-LINEAR LEAST SQUARES FIT FOR PEAK AREA CALCULATIONS

Using the peak centroid results of the previously executed Peak Locate step, the Sum/Non-Linear Least Squares Fit automatically determines the limits for each Region of Interest (ROI). If adjacent peaks are detected, it will extend the ROI to include additional peaks and the ROI will be analyzed as a "Multiplet." Note: If the User Specified ROI Peak Locate step was used, the limits from this algorithm will be used instead. Next, the peak areas and peak area uncertainties for each region are determined. Unless the "fit singlets" option is selected, the peak area calculation for non-multiplet peaks is simply the gross counts in the peak ROI with the continuum subtracted. For multiplets and fitted singlets, the algorithm assumes a Gaussian peak shape and performs a non-linear least squares fit to the data, providing the best possible fit to the actual spectral data.

The user has the option to optimize the continuum model (Linear, Step, or None) and adjust the number of adjacent channels used to define the continuum for a given ROI. Additionally, users can fine-tune how multiplets are determined and deploy tests to reject peaks that fail certain criteria, such as the "95% critical level test."

LIBRARY CORRELATION NID PEAK LOCATE

The Library Correlation NID Peak Locate analysis engine is designed for compatibility with the ANSI N42.34^{***} standard. Beyond peak location and peak fitting, the Library Correlation NID engine also provides tentative nuclide identification and activity estimation results. Benefits include the ability to accurately locate minor peaks, especially those hidden in multiplets, while also being able to correct calibration errors that might otherwise impair later nuclide identification analyses. This preliminary nuclide identification capability can be useful for applications in which a quick identification of the nuclides present in a sample is more important than a precise activity determination. Included in this engine is a background compensation option that is very useful for applications using LaBr₃ detectors, where the intrinsic background can be rebinned and subtracted out on a channel-by-channel basis.

***ANSI N42.34 Performance Criteria for Hand-held Instruments for the Detection and Identification of Radionuclides.

SPECTRUM STRIPPING AND SMOOTHING ALGORITHM

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. This is separate from the Background Subtraction Correction algorithm, which fits peak areas in a background measurement and subtracts the peak area counts (normalized for differences in count times) from corresponding peaks in the primary spectrum.

Genie Spectroscopy Suite Analysis Algorithms

For complete spectroscopy analysis, Genie Spectroscopy suite provides a series of sophisticated algorithms to yield the most accurate results.

Note: These algorithms are only available with Genie Spectroscopy suite. They are not provided with the GenieLite Basic Spectroscopy product.

INTERACTIVE PEAK FIT

An exciting feature of Genie Spectroscopy suite is the Interactive Peak Fit (IPF). This feature allows detailed review of a specific Region of Interest (ROI), including the quality of the peak fit, and enables peak fitting adjustments that are limited to the individual ROI. Possible adjustments include adding or deleting peaks within the ROI, adjusting the limits, and changing the model of the peak fit or continuum. This capability is particularly useful where complex spectra are encountered. It is also used in any application where an analyst must review either all analysis results or any unusual or anomalous results.

IPF is typically executed directly after the peak locate/peak analysis phases of spectral analysis and can use filters to zoom directly to specific Regions of Interest. For example, users can apply a filter on energy or nuclide to target review of a particular region or require that any multiple of area exceeding a particular Chi-Square value be reviewed. This simplifies integrating IPF into data review procedures for routine sample counting operations.

The display allows the user to determine channel data (green squares), fitted peak area (dashed shaded regions), continuum values under the peak (solid magenta color), channels used to determine the continuum height (white squares), and a residual plot of the fitted peak area to the channel data (Figure 19).

EFFICIENCY CORRECTION

The efficiency correction calculation involves calculating a peak efficiency and its uncertainty for each of the found peaks from the efficiency calibration. The efficiency correction step identifies which of the four calibration fits (dual, linear, empirical, or interpolated) to use for the analysis. With Genie 4.0, the efficiency correction step now propagates the uncertainty correlation matrix during the analysis.

Available with the ISOCS efficiency calibration option, the "Efficiency Correction by ISOCS" step will calculate the efficiency at the peak search results directly from the ISOCS or LabSOCS model, removing the need to provide an efficiency calibration prior to analysis.

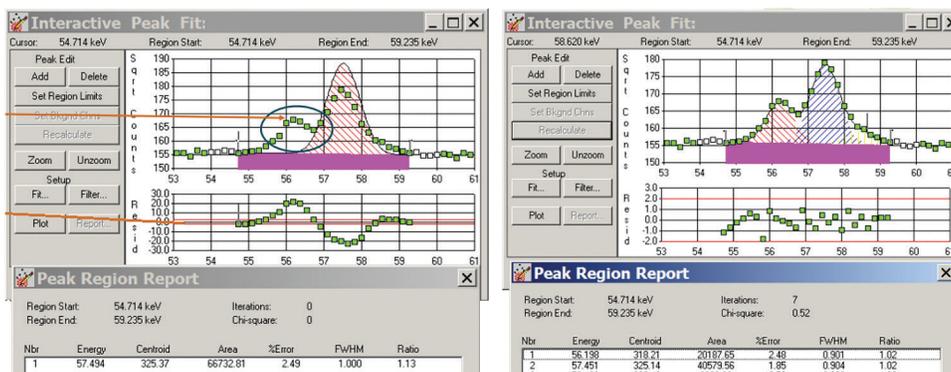


Figure 19 – Genie Interactive Peak Fit application. Shown here on left is example of a missing peak in a Region of Interest and on right the result of adding the peak manually to the ROI. This is done with the "Add" peak edit button on the left menu.

NUCLIDE IDENTIFICATION AND QUANTIFICATION

The nuclide identification algorithms take into account all energy lines of a nuclide defined in the analysis library with their proper line abundances, as well as the half-life of the nuclide. For a positive identification, a nuclide must have at least one gamma energy within the user-selected energy tolerance of an observed peak in the spectrum.

Furthermore, a sufficient number of the other energies of the nuclide (if there are other energies) must also have matching peaks in the spectrum. The number of peaks that must be seen is determined by the sum of the line abundances of the peaks with matching spectrum peaks as compared to the sum of the line abundances of the peaks without matching spectrum peaks. Finally, the decay time of the measured spectrum must not be excessive compared to the half-life of the nuclide.

Nuclides that pass these tests with a confidence index greater than the user selected threshold will be classified as identified. For all identified nuclides, the algorithm calculates the value of the confidence index and a decay corrected activity per unit volume (or mass) for each energy with a matching peak in the spectrum.

If applicable, the decay correction automatically includes a correction for decay during the acquisition as well as for decay from the sample date to the start of the acquisition. An additional decay correction is automatically provided for samples where the sample material is collected or accumulated over a finite period of time. Such samples include air filters, air cartridges and activation samples.

MEAN ACTIVITY CALCULATIONS

After standard nuclide identification, the spectrum can be analyzed for interference sets. An interference set is defined as two or more nuclides with at least one common energy; that is, a peak that has not been resolved into separate peaks by the peak locate and area calculation. The activities of such nuclides are calculated as a solution to a linear least squares equation (Figure 20).

The algorithm automatically finds the nuclides that have interferences – no special library is required. However, energies for nuclides can be marked in the library for exclusion from weighted mean activity calculations. The activity of a nuclide which is not part of an interference set is automatically calculated as a weighted average of the activities calculated for each of its peaks. The activity of a nuclide with only one peak and no interference from other nuclides is automatically calculated from its peak. Factors taken into account in the weighting of the peak activities include efficiency, area and efficiency uncertainty, and the branching ratios of the various peaks.

To include the impact of correlations in the weighted mean activity uncertainties, the “NID with Correlations” engine can now be used. This will provide more rigorously accurate results.

		NUCLIDES				
		1	2	3	4	5
PEAK ENERGIES	1					X
	2	X	X			
	3					
	4			X	X	
	5	X				
	6				X	
	7			X		
	8					
	9					X

Figure 20 – Identification matrix of peak energies to corresponding nuclides. Note Peak Numbers 2 and 4 have multiple potential nuclide matches. An interference correction is used to resolve the identification.

MINIMUM DETECTABLE ACTIVITY (MDA) CALCULATIONS

A Minimum Detectable Activity (MDA) can be calculated for both the radionuclides which have and have not been found in the spectrum. The MDA algorithms can perform Currie, KTA, or ISO 11929 MDA and Lower Limit of Detection (LLD) calculations. If applied to a spectrum collected with a blank sample, or in an empty shield, the MDA calculation is equivalent to a LLD calculation. The MDA confidence factor and constants are user-selectable. Also, the user can elect to apply variable ROI widths and cascade summing corrections to the MDA calculations.

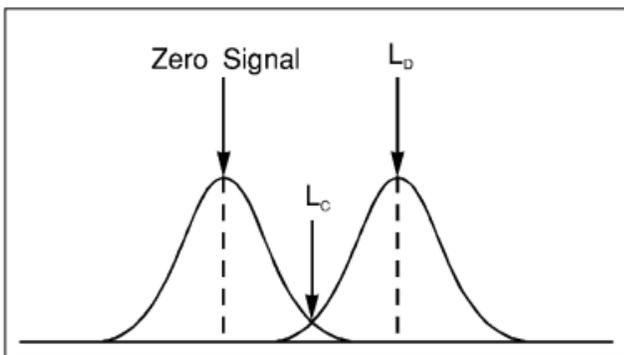


Figure 21 – Illustrating the Critical Level (L_c) and Decision Level (L_d) concepts.

Corrections

TRUE COINCIDENCE (CASCADE) SUMMING CORRECTION

The Mirion unique and patented Cascade Summing Correction feature* corrects your entire spectrum, from 10 keV to 7 MeV, against loss or gain of observable peak area as a function of nuclide decay scheme and geometry. True coincidence summing can cause systematic peak area errors of 30% or more with certain nuclides and geometries (Figure 22). Mirion cascade summing correction takes into account a wide range of scenarios, including gamma-gamma, X-ray-gamma, and positron annihilation-gamma summing effects.

The Genie Cascade Summing Correction method uses ISOCS/LabSOCS technology and the Genie 3D Geometry Composer to precisely describe the sample/detector geometry without the need for expensive

and time-consuming calibration using radioactive standards. A generic selection of germanium detector characterizations ensures that Cascade Summing Correction can be carried out for the majority of detector sizes without prior LabSOCS/ISOCS detector characterization. However, these characterizations, including more specific detector data, may be used if available for even higher accuracy. Cascade Summing Correction is now also available for SAGE™ Well detectors when combined with model ISOXCAL ISOCS Detector Characterization.

Note: This feature does not require a peak-to-total calibration and is available without the ISOCS/LabSOCS software option.

GEOMETRY COMPOSER

The Cascade Summing Correction algorithm described above and the calibration algorithms in the optional ISOCS/LabSOCS calibration software require an accurate description of the counting geometry for each sample.

The Geometry Composer (Figure 23) is a powerful tool allowing the interactive definition and 3D visualization of all geometry-related parameters including detector properties, sample dimensions and densities, and distances shielding between the detector and sample. The tool renders the geometry real-time in 3-dimensional space providing immediate visual feedback and allowing for quick error detection. Additional features include custom beaker creation with or without absorbers, object isolation for focused design, object transparency for viewing of internal items, zooming, and more.

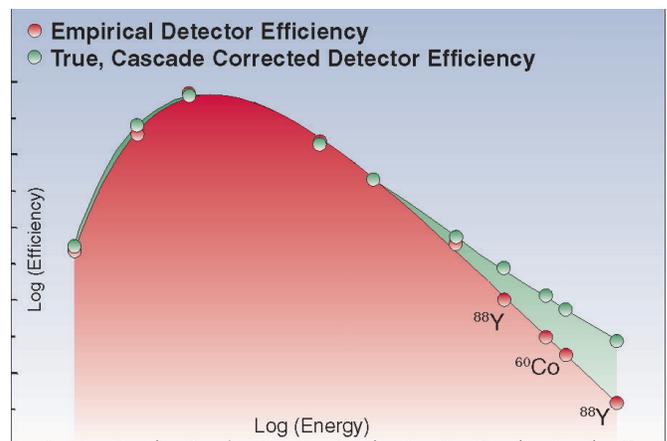


Figure 22 – Comparison of Cascade Corrected to Empirical Efficiency

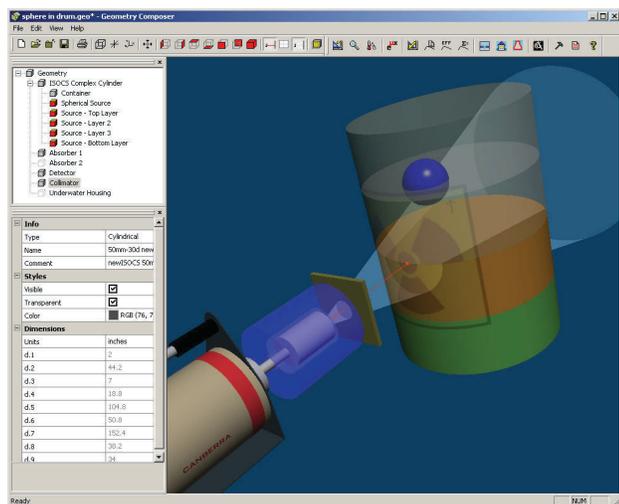


Figure 23 – Geometry Composer

PARENT/DAUGHTER DECAY CORRECTION

The peaks observed in gamma spectra often originate from a nuclide’s ground state and its progeny. When the parent nuclide and its daughters are not in equilibrium, a correction must be applied to report proper nuclide activities. The Genie Parent/Daughter Decay Correction algorithm applies such a correction based on sample time, acquisition start time, elapsed acquisition live time and nuclide Parent/Daughter information contained in the nuclide library used for the analysis.

BACKGROUND SUBTRACTION AND REFERENCE PEAK CORRECTION

The background subtract algorithm allows the subtraction of environmental background peaks from sample spectra. The background spectrum must first be analyzed separately for its peak locations and associated areas. At the time of execution, the background subtract algorithm automatically scales its results to be proportional to the acquisition time of the sample. An energy tolerance to match the peaks in the sample and background spectra can be specified by the user.

The purpose of a reference peak correction is to use a reference peak in the spectrum (of a known count rate) to normalize the areas of all other peaks in the spectrum. The reference source can be either an electronic pulser or an external stationary source.

Both a reference peak correction and an environmental background subtract can be applied to the same sample spectrum if desired.

GAIN EVALUATOR AND GAIN ADJUSTS

Three utilities are available to manage changes in gain from a calibrated spectrum. The Gain Evaluator allows the user to analyze the quality of the current datasource energy calibration and gain settings, providing the ability to assess the impact on NID analysis. The File Gain Adjust facilitates matching previously acquired spectra with different energy calibrations in order to add, strip or compare them. 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 adjusts the MCA gain of a live datasource 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.

Alpha Analysis

The Genie Spectroscopy suite provides alpha spectroscopists with a powerful set of tools to complete advanced spectrum analysis. The algorithms permit a variable tail component typical of peaks found in alpha spectra. Tentative peak shapes are established during energy calibration and used during efficiency calibration and peak locate and area calculations. The Peak Locate, Peak Area, Background Subtraction, Nuclide Identification, and MDA analysis steps each can be performed individually or integrated into an analysis sequence file. The algorithms and their applications to alpha spectroscopy are described below:

PEAK LOCATE SCHEMES

Traditionally, manually defined ROIs have been a sufficient peak locating mechanism for alpha spectroscopy. This is supported with the “User Specified Peak Locate” engine, which can use the current ROIs

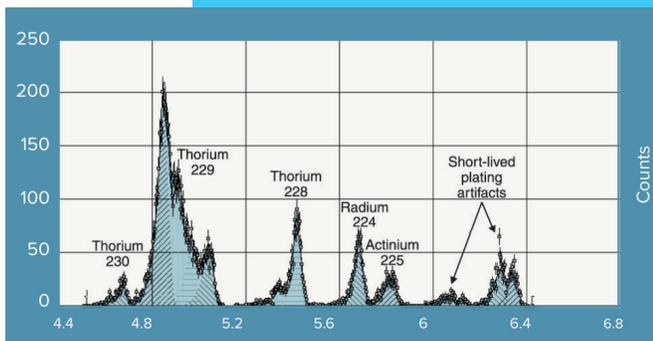


Figure 24 – Example of alpha spectrum

defined in the spectral window or pull from a pre-defined ROI file. For advanced spectrum analysis that requires de-convoluting difficult alpha spectra, the generalized second difference method is available. This may be required when a ROI peak locate is not acceptable due to interfering peaks and variable tailing and re-preparation of the sample is not feasible or desired. These peak locate schemes can be used individually or with their results summed together.

PEAK AREA CALCULATION SCHEMES

Peak area calculations can be performed either by summing the counts in a Region of Interest, or by performing a peak fit to the data using a modified Gaussian function. The summing of the counts is particularly useful when the spectra exhibit very poor statistics with no clear peak shapes or when the peak resolution does not permit multiplet fits, a situation that is quite common in alpha spectroscopy. The fitting option permits fitting singlets as well as multiplets, and allows the FWHM and tail parameters to either stay fixed to the calibrated values or vary for best fit to the data being analyzed. The fitting options are particularly useful when the statistics in the spectrum are quite good, and the sample preparation and mounting techniques have resulted in very good resolution spectra.

BACKGROUND SUBTRACT

Although alpha spectroscopy backgrounds are normally quite low, precision often requires subtraction of some background components in the spectrum. The background subtraction algorithm uses an operator-selected background file to subtract the sum of the counts in the equivalent ROI in the background spectrum from the counts in the sample spectrum. Alternatively, the operator may set a tolerance for matching the peaks in the sample spectrum with those in the background file. A critical level test can be applied to every peak after the background has been subtracted.

NUCLIDE IDENTIFICATION

The Nuclide Identification algorithms provide a variety of tools that can be customized to the application. Nuclide identification is based on operator-selected libraries of alpha emitters. The performance of the algorithm can be fine-tuned by adjusting a confidence threshold as well as the identification tolerance, conveniently based on energy or full width at half maximum. For precise work or where chemistry has not significantly reduced interfering peaks, the Nuclide Identification algorithm can automatically perform an interference correction.

DETECTION LIMITS

The Alpha Analysis software provides the spectroscopist with a choice of formalisms for calculating the “Minimum Detectable Activity” (MDA), including an ISO 11929 compliant option. The MDA is calculated for both the nuclides which have been found in the spectrum as well as those which have not been found.

Additional Features

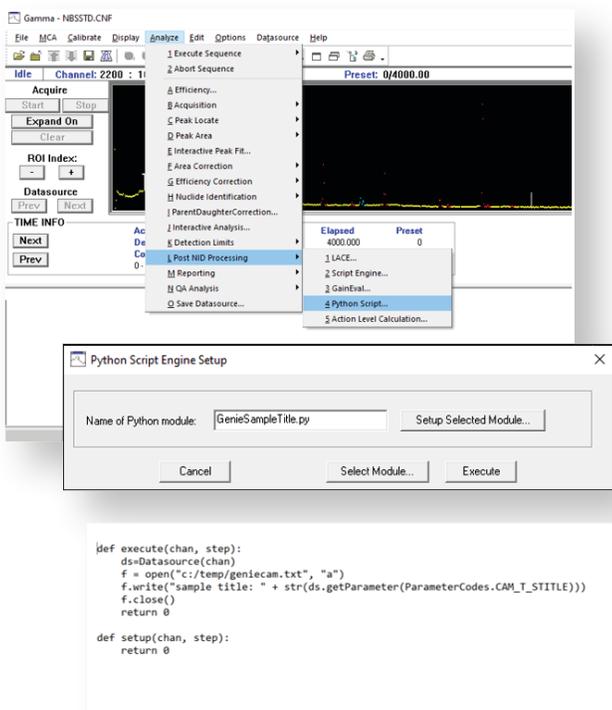


Figure 25 – Launching a Python script from the Post NID processing step in Genie software applications.

INTEGRATION OF PYTHON SCRIPTS FOR SIMPLE USER PROGRAMMING

An extremely powerful feature is the scripting interface in Genie Spectroscopy software, which now supports Python® Scripting, along with Visual Basic, and Java. Using the power of the CAM data structure, easy-to-develop scripts can be written to extract and manipulate data from the Genie data source. These can be operated outside the Genie interface or integrated into an Analysis Sequence File for automatic operation. Scripts are commonly used to perform custom calculations, export results to a CSV file or other third-party applications (such as results databases or LIMS systems), or to perform validation and verification comparisons (Figure 25).

QUALITY ASSURANCE

The Genie Quality Assurance application provides the critical capabilities required to monitor the performance of the spectroscopy system and ensure the validity of sample measurement results.

Regular execution of QA checks is mandatory in many applications and a best practice in general. A QA check indicates if there is an issue with the measurement system, and can flag if there is a discrepancy between calibration settings and system performance. Maintaining a history of QA data is also highly recommended: Even many years after a sample is counted and analyzed, the spectroscopist may be called upon to prove the system was functioning properly at the time of measurement or need to investigate discrepancies of results.

With the Genie Quality Assurance application, users can configure the application to monitor and record parameters such as peak centroid, FWHM, nuclide activities, backgrounds, MDA, etc. Users also can integrate non-Genie parameters through manual entry. This data is stored in a Genie CAM style format, which stores, displays, and reports data for a particular detector system over the lifetime of the system.

QA Count parameter data is transferred from live detectors or previously stored CAM files through a menu selection, integrated with an Analysis Sequence File, or automatically through batch procedure commands where QA information is recorded as part of a count room procedure. If needed, the “edit results” function allows users to reject results that are known to be invalid or to correct results.

For each tracked parameter, statistical analysis rules (described in detail below) are configured to indicate if a QA count has acceptable results or if action is needed. The data and results are displayed either through a scatter chart or via one of two report templates, which can be automatically printed at the end of a count. The scatter plot can display a parameter and its limits over time, or compare multiple parameters. The two standard report templates are the “Full” report with complete parameter history or the “Last Measurement” report, highlighting the results of the last QA count.

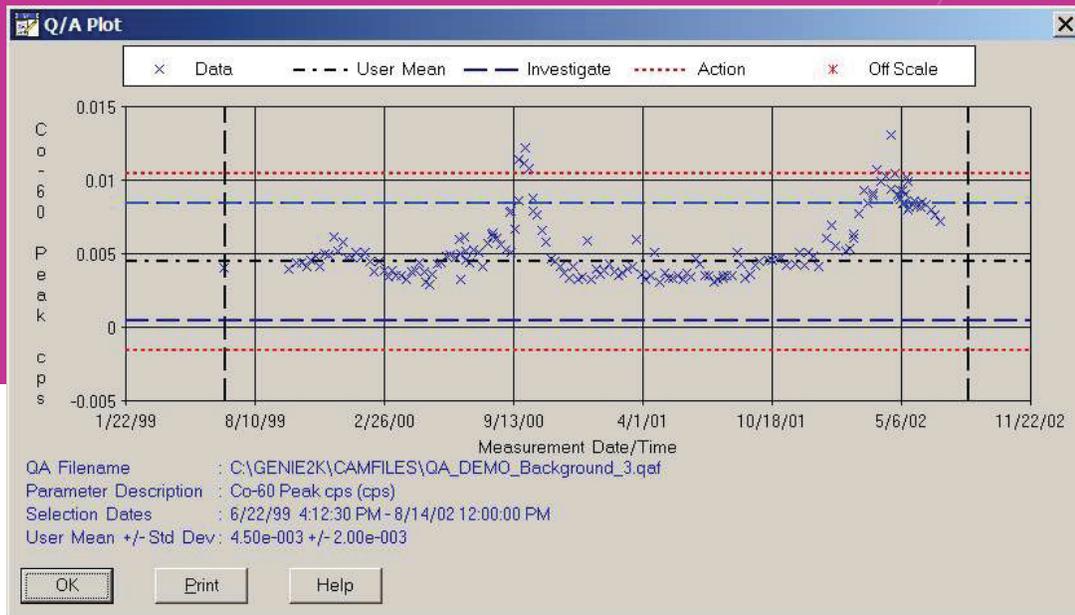


Figure 26 – Representative quality assurance control chart for Co-60 peak area count rate over 3 years. Note the mean, investigate, and action levels displayed.

N-Sigma Test: The N-Sigma Tests employ user-defined multipliers of the standard deviation to determine Investigate and Action limits for a specific QA Count parameter. The Sample Driven N-Sigma test calculates mean and standard deviation, also known as “sigma,” from the full parameter history or a subset of the parameter history with start and stop dates defined by the user. The Bias N-Sigma Test uses a user-entered “true” known value for the mean, for example when the parameter value is known information (i.e., ⁶⁰Co energy at 1332.5 keV). The User Driven N-Sigma Test has both the mean and standard deviation entered by the user, helpful for when the user has recently purged historical data from the system and is beginning a new file.

Boundary Test: In the Boundary Test, the user specifies absolute conditions for alarm testing. For example, if a peak centroid is expected in channel 1000, the user may wish to alarm at channel 1005 or 995, regardless of long-term means and trends.

Trend Tests: In Trend Tests, the user specifies a number of consecutive samples on one side of the mean (above or below) to indicate an alarm. The user can also specify a number of samples trending in the same direction to indicate an alarm.

CUSTOM ACTION/ALARM LEVELS

The Action/Alarm Level calculations can be enabled to provide alerts if activities or concentrations in samples (or whole body counts) have exceeded limits established by the user. Up to two alarm settings are available, and the limit values for the nuclides of interest are stored in the nuclide library.

LINE ACTIVITY CONSISTENCY EVALUATOR

The Line Activity Consistency Evaluator (LACE), as shown in Figure 5, can assist the user in evaluating the quality of the gamma analysis. LACE assesses the consistency between line activities calculated by the gamma assay for multi-line radionuclides. The individual line activities are compared to the key line activity or weighted mean activity (as chosen by the user) for each multi-line nuclide in the sample. A graph of these ratios along with the resulting equation allows the user to identify possible discrepancies between the efficiency calibration and the actual sample counted. For example, a sample of higher density than the one used for calibration will result in a low reported activities bias, and the bias will be more pronounced at lower energies.

Nuclide Name	Energy (keV)	Activity (uCi/)	Activity %Uncert*	WM Activ [%Uncert]	Ratio[%Uncert]	A	B [uncert]
CS-134	563.2	3.909E-02	2.262	3.566E-02	1.096[2.542]	0.16	-0.020
	569.3	3.728E-02	2.248	[1.159]	1.045[2.529]		[0.043]
	604.7	3.580E-02	2.106		1.004[2.403]		
	795.8	3.556E-02	2.421		0.997[2.684]		
	801.9	3.381E-02	2.495		0.948[2.751]		
	1038.6	3.258E-02	5.015		0.914[5.147]		
	1167.9	4.012E-02	2.910		1.125[3.132]		

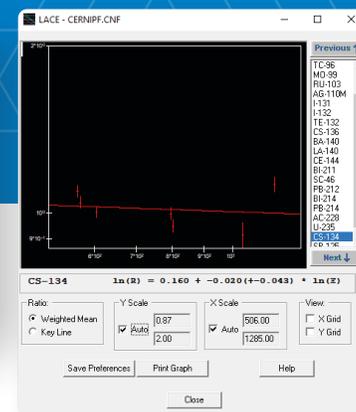


Figure 27 – Line Activity Correction Evaluator (LACE) provides valuable data quality information about the self-consistency of line activities. Deviations from ratios of unity may indicate an error or inconsistency in measurement data or analysis.

INTERACTIVE SPECTRAL ANALYSIS

Interactive Analysis is a utility that facilitates the review, exploration and refinement of spectral analyses while providing direct visual feedback. When initially launched, the current data and analysis results are graphed, including options to visualize the peak significance, peak correlation, peak residuals, and nuclide residuals. An expert user then can modify analysis results by interactively adding, editing, and deleting peaks and peak regions based on the detailed spectral information that is provided. Calibrations and nuclide libraries can also be reviewed and updated, if necessary, from this software module.

GENIE-FIELDPRO APPLICATION

Genie-FieldPro software provides a powerful user interface for streamlined and simplified gamma spectroscopy sample counting. Genie-FieldPro software is designed for maximum usability by field technicians to quickly and confidently analyze samples for gamma radiation, regardless of their spectroscopy knowledge level. A sample geometry is determined by two customizable drop-down selections, “Geometry” and “Contents/Matrix.” This also displays a picture file as an additional reference for the user to confirm their selection. The count time, calibration, and analysis parameters are linked to the selection of the geometry and are automatically executed with the count.

To improve traceability and confidence, the user is prompted to take a photo of the sample at the conclusion of the count, which is saved alongside the spectrum file. Each count executes a Genie analysis sequence and evaluates for the presence of particular nuclides. A report is automatically generated that will indicate “CLEAR,” “EXCEEDS LIMITS” or “MDA NOT MET” based on the results of the analysis and the user-defined limits.

The user interface is completed with a calibration check function and background check function. Failure will lock the system from further sample counting until the check is successfully passed. The software also maintains a schedule of when the calibration or background check is next due and will lock the system for sample counts if a check is overdue. Additional features include a “count to MDA” option, password protected configuration file and audit log, GPS integration, and auto-export/import abilities to transfer results to a remote Apex-Gamma™ system.

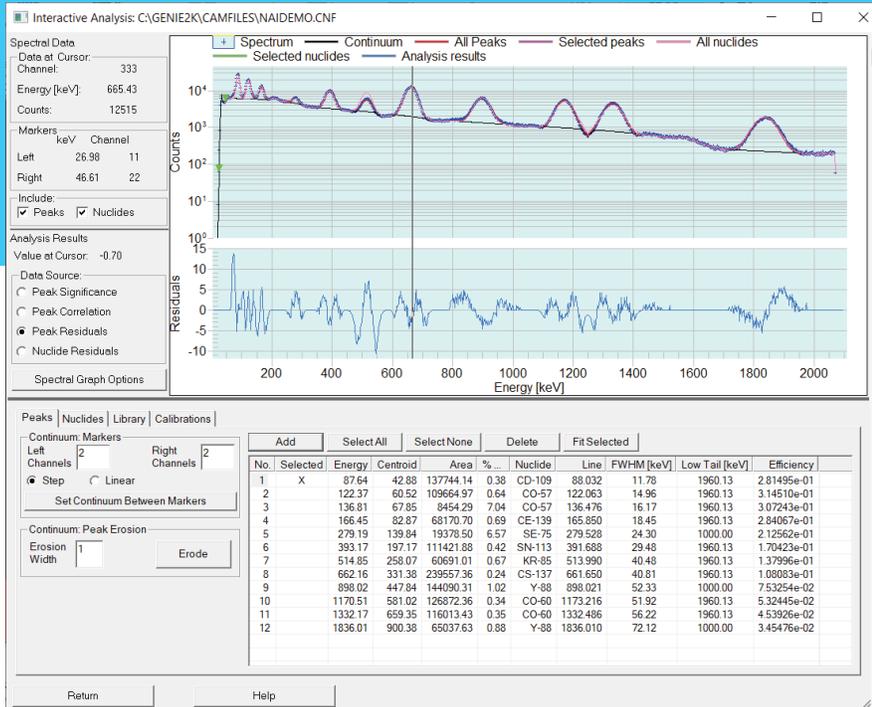


Figure 28 – Interactive Analysis Application.

Specifications

SYSTEM REQUIREMENTS

Please reference the current Genie compatibility matrix for most up-to-date information.

ORDERING INFORMATION	
BASE MODEL	DESCRIPTION
Genie-Multi	Genie Spectroscopy Suite for Multi-Input Applications
Genie-Single	Genie Spectroscopy Suite for Single Input Applications
GenieLite-Multi	Genie Basic Spectroscopy for Multi-Input Applications
GenieLite-Single	Genie Basic Spectroscopy for Single-Input Applications
Genie-Doc-Kit	Optional Printed User Manuals for Genie Spectroscopy Suite and GenieLite Software. (PDF manuals are included with software distribution.)
Genie_CD	Optional physical media for Genie applications (Genie Spectroscopy Suite is delivered by electronic download). Does not include license to operate Genie software.
GenieLite_CD	Optional physical media for GenieLite application (GenieLite Software is delivered by electronic download). Does not include license to operate GenieLite software.

LICENSE OPTIONS	
MODEL	DESCRIPTION
Genie-Multi-1yr Genie-Single-1yr GenieLite-M-1yr GenieLite-S-1yr	1 YEAR SUBSCRIPTION Right to use the software for 1 year, plus updates as released and Premium local service offerings.
Genie-Multi-3yr Genie-Single-3yr GenieLite-M-3yr GenieLite-S-3yr	3 YEAR SUBSCRIPTION Right to use the software for 3 years, plus updates as released and Premium local service offerings.
Genie-Multi Genie-Single GenieLite-M GenieLite-S	ONE-TIME PURCHASE Non-expiring license for perpetual use. Does not include updates or Premium local service offerings.

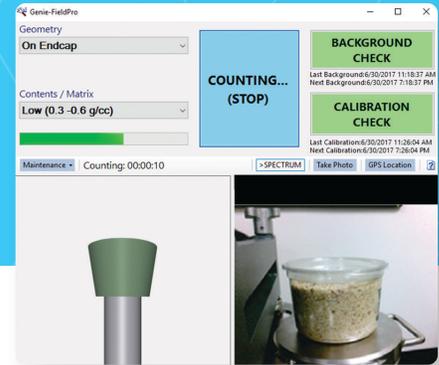


Figure 29 – Genie-FieldPro provides a simplified user counting interface for screening applications.

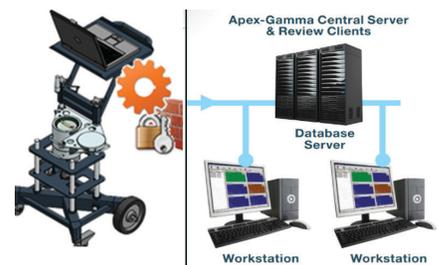


Figure 30 – Example application of Genie-FieldPro to auto-transfer sample spectra and results to a remote Apex-Gamma application for post processing, reanalysis, and data storage.



Genie and GenieLite products use electronic software licensing technology. No USB dongle is required or supported. The electronic licensing is unique to each computer. A one-time activation is required for each computer licensed. Activation modes are supported for both internet-connected and isolated computers.

OPTIONAL LAYERED SOFTWARE

The following optional software is available for Genie Spectroscopy Suite:

- ISOCS™ Option: ISOCS/LabSOCS™ Mathematical Efficiency Calibration Software
- MGAU™ Multi-Group Analysis for Uranium Software
- MGA™ 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.*

Genie documentation is provided electronically with software distribution. Printed user manuals are available on request.

RELEVANT SPECIFICATION SHEETS AND MANUALS

- Genie Operations Manual
- Genie Customization Tools Manual
- Genie Coincidence Summing Library Reference Manual
- Geometry Composer User's Manual

NON-ENGLISH LANGUAGE VERSIONS

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



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