MIRION
TECHNOLOGIES

Genie™ Spectroscopy Software Suite

Evolve Your Spectroscopy Operations

Genie Spectroscopy Software Suite empowers laboratories and research teams to achieve new levels of efficiency, accuracy, and confidence in gamma and alpha spectrometry. Genie unifies data acquisition, analysis, and reporting within a single, intuitive platform—enabling teams to focus on outcomes rather than operations.

Its proven reliability, flexible architecture, and robust cybersecurity measures—including encrypted communications, digital code signing, and IPv6 protocol support—make Genie the foundation for modern laboratory operations.

Whether your focus is productivity, compliance, or innovation, Genie adapts to your needs with scalable performance, multi-language support, and a comprehensive ecosystem of modular applications.

Why Choose Genie?

COMPREHENSIVE INTEGRATION

All-in-one platform for acquisition, analysis, and reporting, with layered options for specialized workflows.

DEFENSIBLE RESULTS

Industry-proven algorithms and patented corrections, including Cascade summing and ISO 11929-compliant Minimum Detectable Activity (MDA) calculations.

EFFICIENCY & AUTOMATION

Python® scripting, analysis sequence editor, and streamlined interfaces for high-throughput environments.

SECURITY & COMPLIANCE

Encrypted communications, digital code signing, IPv6 support, and electronic licensing for secure deployment.

COLLABORATION & SCALABILITY

Distributed Multichannel Analyzer (MCA) networking and centralized data management for teams and operations of any size.

QUALITY ASSURANCE

Integrated QA tools, automated checks, and historical data tracking for full traceability.

GLOBAL SUPPORT

Multi-language availability and extensive documentation for a seamless user experience.

Genie Spectroscopy Software Suite

FLEXIBLE MODEL OPTIONS

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.

INTEGRATED ACQUISITION & ANALYSIS

Genie's acquisition and analysis capabilities are tightly integrated, offering real-time spectral updates and straightforward operation for a variety of counting workflows. Users can perform analyses on demand or automate them within multi-step workflows for greater efficiency. Results are viewable either within the integrated screen or in a separate window, making side-by-side spectrum review easy—especially in multi-monitor setups.

INTERACTIVE REPORTING

Reports now feature user-focused interactive tools, transforming the way spectroscopists review and validate data. These enhancements support more transparent, efficient, and dynamic data review processes.

ADVANCED ANALYTICAL ALGORITHMS

Genie provides comprehensive peak and nuclide analysis for gamma ray spectra from any type of gamma detector, as well as advanced algorithms for alpha spectrometry. These methods are built on time-proven, industry-accepted techniques and include patented, innovative analysis and calibration features for defensible, traceable results.

UNIFIED DATA ARCHITECTURE

All analysis execution leverages the Configuration Access Method (CAM) data structures native to Genie Family systems. Results from each algorithm are stored in CAM files, creating a complete, traceable record of every analysis. This unified approach simplifies system administration, data transfer, and archiving, and enables easy reanalysis of archived spectra. Detailed documentation in the Genie Customization Tools manual further supports traceability and independent verification.

Genie User Interfaces/User Experience

CUSTOMIZABLE TOOLBOX FOR LABORATORY OPERATIONS

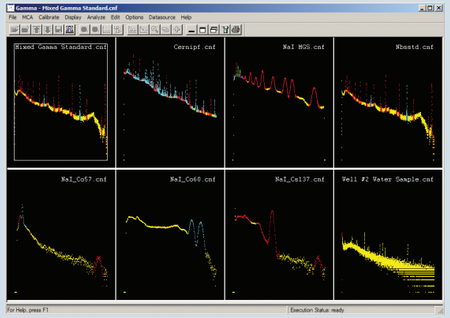
The Genie Spectroscopy Software Suite offers a versatile set of applications, allowing users to tailor workflows to the specific needs of their laboratory. The primary application features a classic window-style interface, providing straightforward access to essential functions such as acquisition control, spectral display, and analysis steps. Users can manage multiple inputs within a single window, streamlining complex operations.

FLEXIBLE DATA HANDLING AND VISUALIZATION

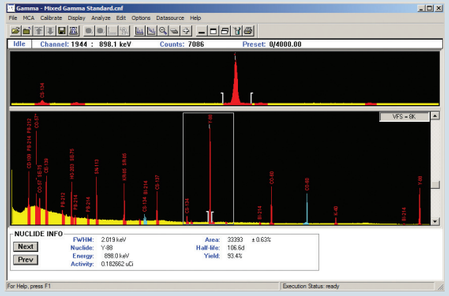
With Genie, more than 250 data sources—including active detector inputs and previously acquired spectral files—can be active in the Spectroscopy window at any time. Users can page through individual spectra for detailed review or display up to eight spectra simultaneously with live updates, making it easy to compare results side by side, especially in multi-monitor environments. The software includes tools such as the EXPAND or Zooming window for focused analysis, and the COMPARE function for overlaying and adjusting the scaling of two spectra. Color-coded regions of interest and dynamic on-screen calculations using markers and cursor placement further enhance the visualization experience.

INTERACTIVE PEAK ANALYSIS AND ROUTINE OPERATIONS

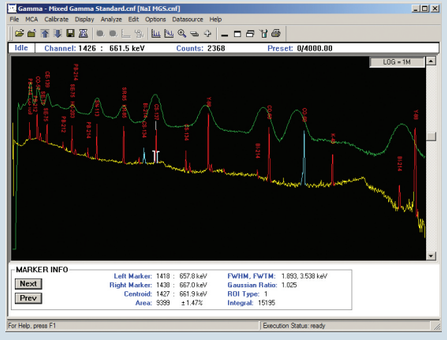
Genie's Interactive Peak Fit (IPF) application enables powerful, peak-by-peak review and fine-tuning of regions of interest, helping users improve the quality of each peak fit. For routine sample counting or screening, the Genie-FieldPro™ application provides a simplified interface, making everyday operations more efficient for technicians and researchers alike.



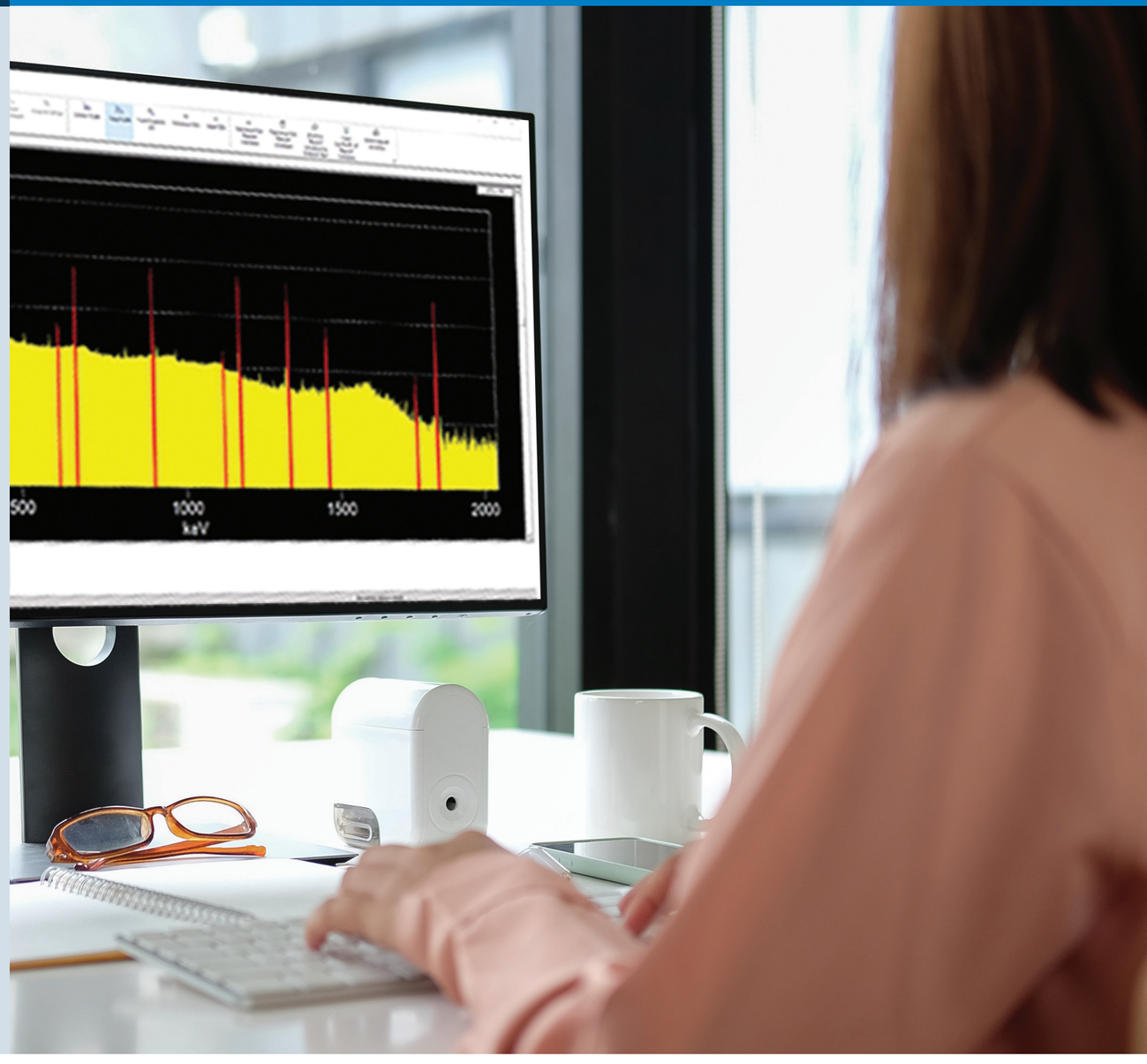
Multi-Spectrum Screen



Spectrum Expand Mode



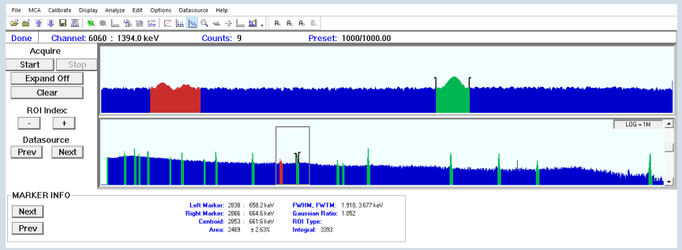
Spectrum Compare Mode



Genie User Interfaces/User Experience

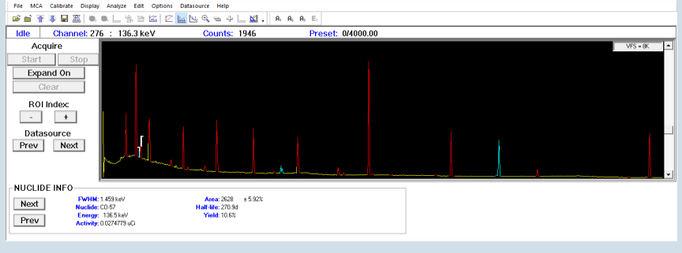
PERSONALIZED CONTROLS AND DISPLAY OPTIONS

To optimize the user experience, Genie allows users to toggle the control panel for quick management of start, stop, and clear functions. The status display provides real-time information about the current data source, including sample details, region of interest parameters, and acquisition statistics. Toolbar icons can be configured for single-click access to complex steps, with optional icon labelling to support easier familiarization and training. The default spectral display uses high-contrast yellow spectrum data on a black background, but users can customize the appearance to suit their preferences.



Example of bright display colors and "Fill" spectral plot mode

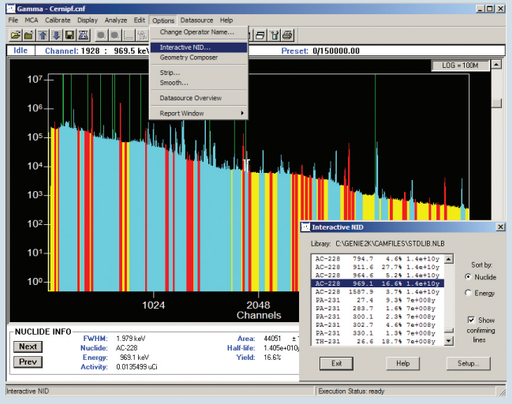
Example of scientific display and "Full" spectral plot mode



Example of high contrast display colors and "Envelop" spectral plot mode

STREAMLINED RADIONUCLIDE IDENTIFICATION

Displaying radionuclide information is straightforward with Genie's Interactive Peak Labelling option, which tags each peak with its associated nuclide from a selected library or full analysis results. Selecting a peak reveals its area, activity, and emission line. The interactive nuclide identification (Interactive NID) mode allows users to place their cursor on a peak of interest and instantly view details such as nuclide, energy, abundance, and half-life. Users can manually select alternate nuclides sorted by energy or name and confirm emission lines to assist with identification.



Interactive Nuclide Identification

EFFICIENT ANALYSIS WORKFLOWS

Analyses can be performed manually, step by step, or automated using complete analysis sequence files (ASF) for routine operations. In manual mode, users can apply individual analysis algorithms, such as peak locate or peak area, by menu selection and edit parameters before execution. The analysis sequence editor enables users to define multi-step workflows, incorporating acquisition controls, analysis algorithms, reporting steps, and scripting hooks for advanced functionality. Saved sequences are easily accessible via the Analyze menu or can be assigned to shortcut keys or icons for single-click operation.

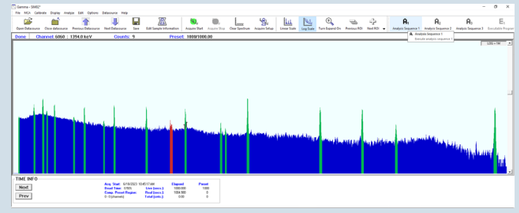


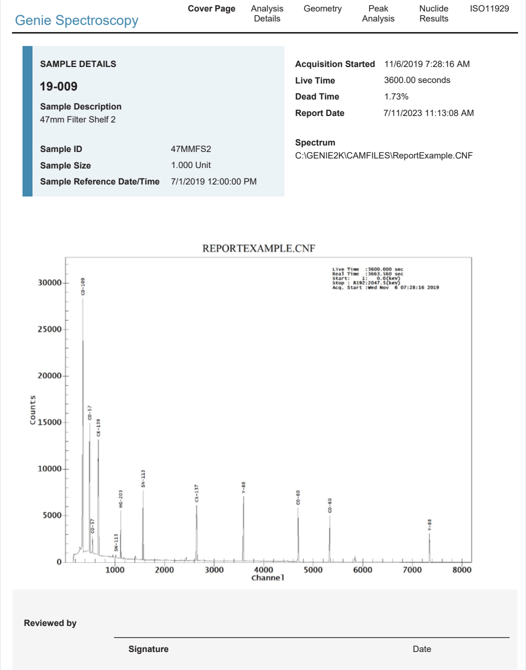
Illustration of launching an Analysis Sequence File from toolbar for single-click operations. Note: The toolbar icons were set to "Large ICONS" mode and toolbar text labels turned on.

Results Review and Reporting

Genie Interactive Reports are designed to provide spectroscopists and laboratory teams with a seamless, efficient data review experience. The clean, intuitive layout ensures that reviewers can validate results, analyze information, and save time with confidence. A key feature is the integration of Interactive Peak Fit displays, accessible directly from any listed energy line in the report, enabling rapid validation of peak quality and fit.

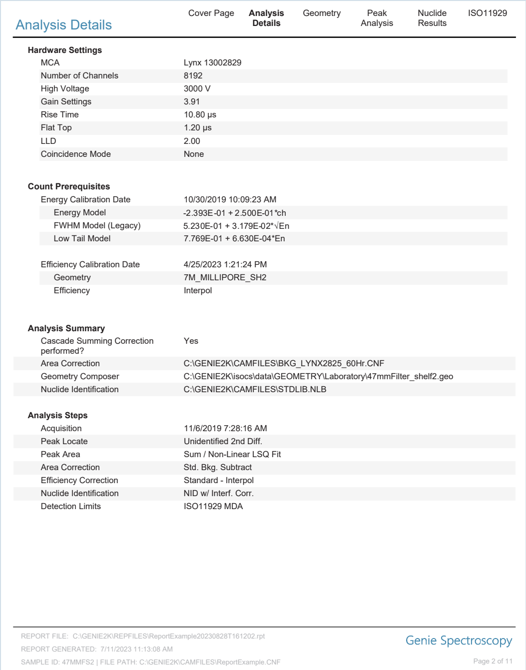
Reports are organized into five key sections:

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



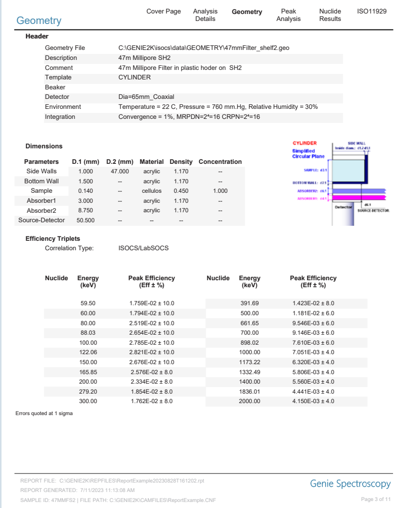
Cover page

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.



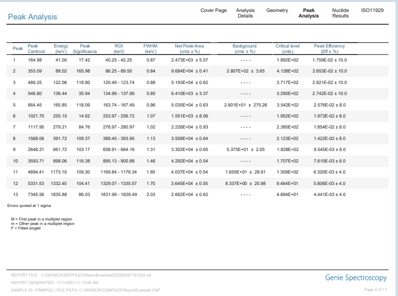
Count and Analysis Details page

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



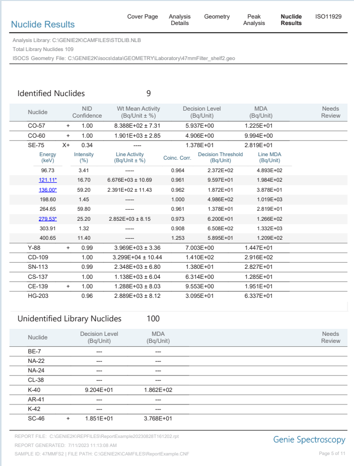
Geometry page

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, Full-Width at Half Maximum (FWHM),, or energy.



Peak Analysis page

Nuclides Results page: Provides a concise summary of nuclide activities and Minimum Detectable Activities (MDAs) for both identified and library nuclides. Expandable entries reveal results for each emission line, supporting high-quality review. Columns can be sorted by any header, and uncertainty results toggled between percent and absolute values. Clicking on any energy launches the Interactive Peak Fit for deeper inspection.



Nuclides Results page

Additional features include a “Review Required” flag that users can mark against any nuclide, and quick links for easy navigation between report sections. Reports can be exported to Excel, Word, PDF, and other third-party formats, and layouts can be customized using the integrated Genie Stimulsoft Engine editor tool. Genie also supports legacy Genie 2000 report templates, ensuring continuity for existing processes and easy integration with other applications.

With Genie, interactive reporting empowers laboratories to validate results quickly, maintain full traceability, and streamline compliance with regulatory standards. The combination of dynamic data exploration, flexible export options, and advanced review tools makes Genie a comprehensive solution for modern spectrometry data management.

Information Storage

One of Genie's core strengths is its unified approach to information storage. Instead of relying on multiple fixed-format files for data, calibrations, and results, Genie uses an extensible single file structure to store all information related to the system and individual samples. This is managed through the Configuration Access Method (CAM), an integral part of the Genie architecture.

The CAM file structure enables users to access, review, and analyze both archived and live spectra with equal ease. Each CAM file contains comprehensive details—including sample headers, spectral data, calibration information, analysis parameters, intermediate and final results, signal processing setup (where applicable), and the analysis library used. Data access in batch environments is streamlined by commands that read and write CAM data by defined variable names.

With all relevant information consolidated in a single data structure, users can revisit previous analyses without worrying about matching up versions of supporting files. This unified approach maximizes quality, integrity, and traceability, ensuring that every analysis is fully documented and easily verifiable.

Acquisition Hardware Support

Genie Spectroscopy Suite and GenieLite applications offer broad compatibility with a wide range of acquisition hardware, making them suitable for diverse laboratory environments. The software is designed for hardware transparency—users simply select inputs by detector name, without needing to manage the specifics of the physical MCA device.

Genie supports Pulse Height Analysis (PHA) and Multi-Channel Scaling (MCS) acquisition for the following Mirion MCAs:

- Lynx-II® 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

Advanced capabilities such as coincidence/anti-coincidence counting modes, sample changer control, and other specialized features are also available where supported. For further details, please refer to the individual device specification sheets.

To streamline setup and communication with detector systems, Genie provides a dedicated utility for initial MCA input configuration. Users can save multiple setup definitions for the same MCA, allowing for precise operating parameters tailored to different applications and workflows.

Network Support

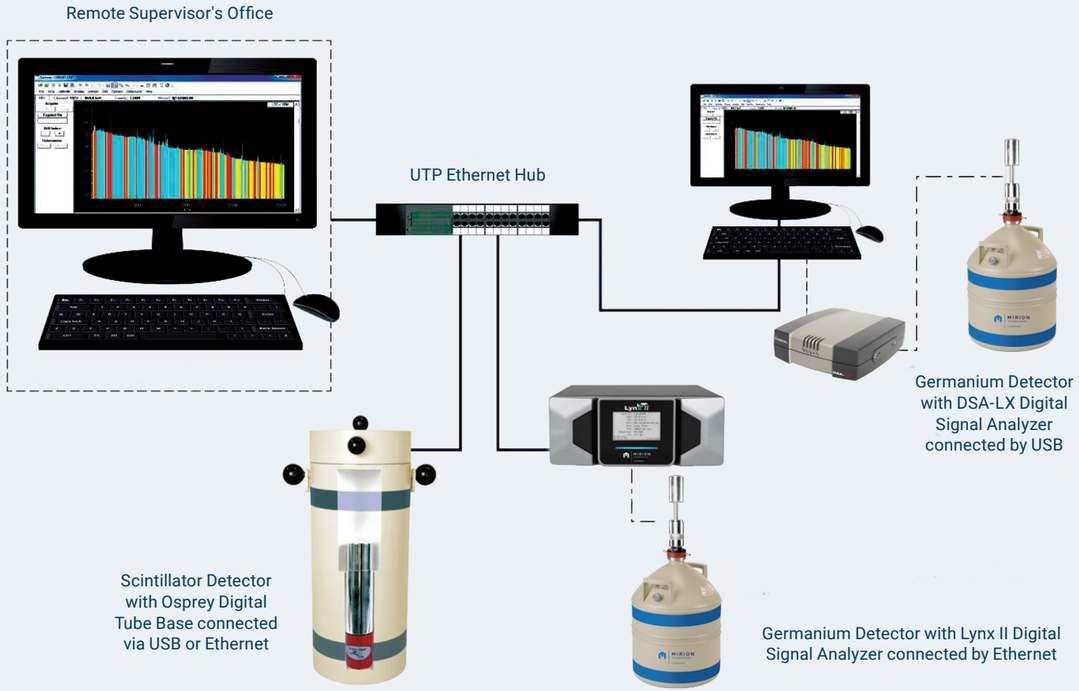


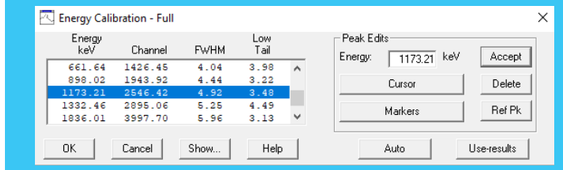
Illustration of network connectivity capabilities for Genie applications

Genie software offers robust network connectivity at multiple levels, enabling seamless integration with supported MCAs via both Ethernet and USB. Ethernet-enabled MCAs can be connected directly to laboratory networks, allowing remote data acquisition and signal processing without the need for intermediary computers.

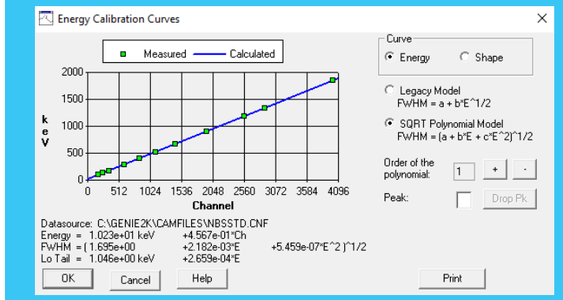
Genie applications can also be networked across multiple computers, facilitating shared access to MCA resources and information. This means that detector inputs can be controlled from any connected workstation, regardless of their physical location.

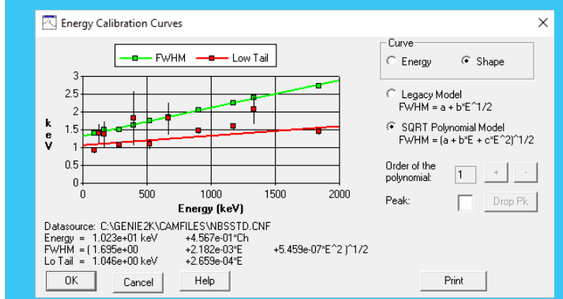
For example, see on page 14, Genie System #1 can control acquisition and analysis for the MCA directly connected to Genie System #2.

This multi-access capability allows supervisors to monitor all laboratory activity from their office-based computers, without disrupting ongoing lab operations. Acquisition and analysis can be overseen remotely, and problem samples can be reviewed without the need to physically enter the count room.



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





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.

Calibrations

ENERGY & RESOLUTION CALIBRATION

Genie Spectroscopy Suite and GenieLite software provide robust capabilities for energy versus channel calibration, resolution or "Full-Width at Half Maximum" (FWHM) calibration, and peak low-side tailing calibration. For FWHM calibration, users can choose between a legacy fitting option and a high-fidelity model, ensuring the best match for their detector's resolution curve.

EFFICIENCY CALIBRATION METHODS

Efficiency calibration is a core feature, with multiple algorithms available:

- Dual polynomial (with user-defined crossover points)
- Linear polynomial
- Empirical polynomial
- Interpolated method (ideal for mathematically determined efficiency data points)

A Peak-to-Total calibration routine is also included for legacy support, though it is no longer required for cascade summing corrections.

CERTIFICATE FILES & AUTOMATED CALIBRATION

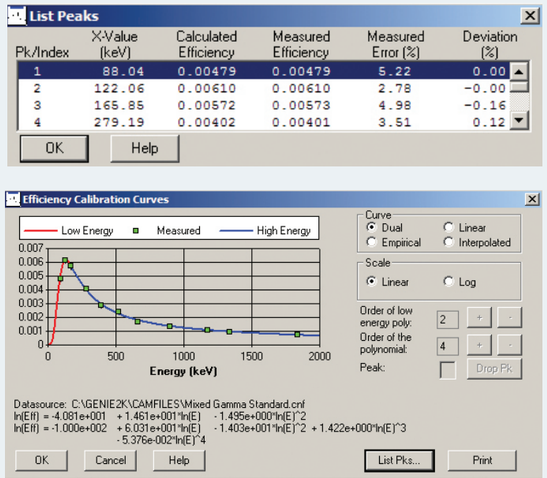
The calibration process is streamlined using certificate files created with the Certificate File Editor. These files contain all relevant calibration standard information—such as nuclide, emission rates, and uncertainties—making both initial and periodic recalibration straightforward and automatable. Genie's automatic peak search algorithm locates and quantifies peaks, then associates them with decay-corrected emission rates to generate efficiency curves and equations.

ADVANCED CALIBRATION CONTROL

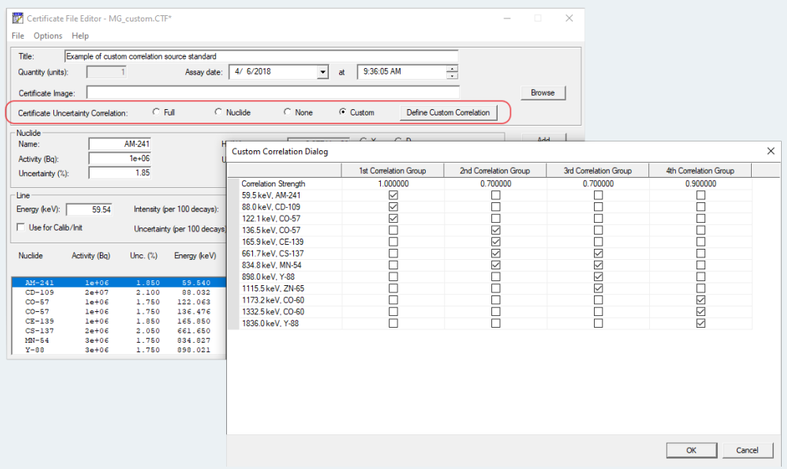
Genie offers interactive calibration plots that enable users to inspect curves in detail and adjust their order for optimal data fitting, see on page 17. Energy calibration supports 1st, 2nd, or 3rd order polynomials, while efficiency curves can extend up to 9th order.

Four efficiency calibration algorithms are available: dual polynomial with a user-defined crossover point, linear polynomial (required by CEA in France), empirical polynomial, and an interpolated method that connects data points with straight lines—ideal for mathematically derived efficiency data.

Dual and linear polynomial models use least squares fitting to calculate uncertainty, and with Genie 4.0, these models now support correlation handling during fitting routines. Users can define correlations in the certificate file editor by marking calibration points as fully correlated by nuclide, or independent, and can even create a custom correlation matrix for advanced control, see on page 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.



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.

Peak Locate and Peak Area Analyses

The Genie Spectroscopy Suite offers a comprehensive set of tools to locate spectral peaks and calculate peak net areas for both basic and advanced spectroscopic analysis. A wide range of algorithms provides the flexibility to tailor your approach to the specific requirements of each application. Analyses can be performed manually, integrated into an automated sequence, or executed via batch commands for high-efficiency workflows. These algorithms are also available in GenieLite for essential spectroscopy tasks.

UNIDENTIFIED 2ND DIFFERENCE PEAK LOCATE

Ideal for detecting unknown nuclides, this algorithm identifies peaks above a user-defined threshold and calculates their centroids. It uses a modified second-difference method across a specified channel range, rejecting Compton edges and other non-peak continuum features. The resulting peak list can be used for area calculations.

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 second 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 multiple 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

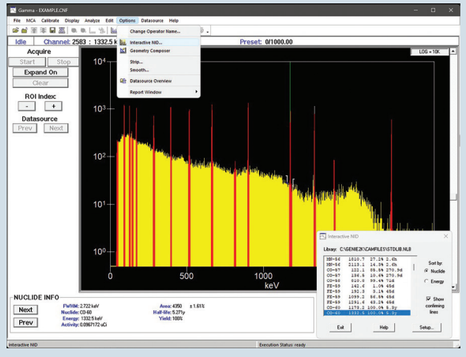
A library-based peak search may be recommended for NaI spectroscopy and HPGe applications where only specific nuclides are expected, or with some very low level HPGe applications.

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.”



Interactive NID

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.

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.

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

Genie Spectroscopy Suite Analysis Algorithms

For comprehensive spectroscopy analysis, the Genie Spectroscopy Suite delivers advanced algorithms designed to provide the highest level of accuracy.

Please note: These algorithms are exclusive to the Genie Spectroscopy Suite and are not included with the GenieLite Basic Spectroscopy product.

INTERACTIVE PEAK FIT

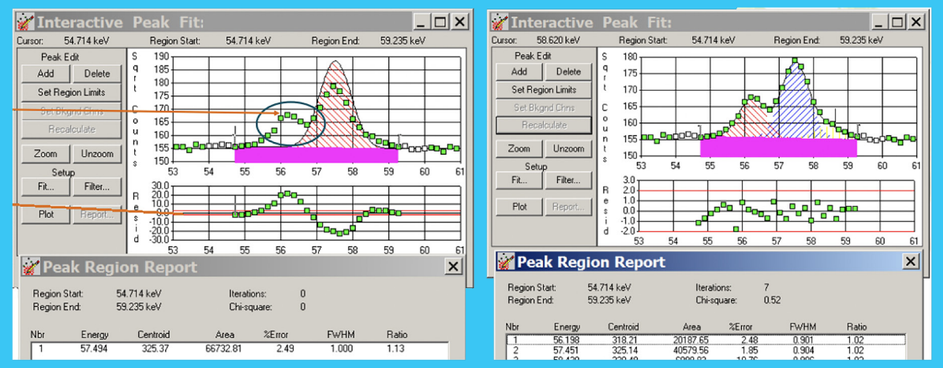
An advanced feature of the Genie Spectroscopy Suite, **Interactive Peak Fit (IPF)** enables detailed review and adjustment of specific Regions of Interest (ROI) for precise spectral analysis.

IPF allows analysts to examine the quality of the peak fit within a chosen ROI and make adjustments limited to that region. Possible adjustments include adding or deleting peaks, changing ROI limits, and modifying the peak fit or continuum model. This capability is particularly useful for complex spectra or when reviewing unusual or anomalous results, and it supports thorough validation of analysis outcomes.

IPF is typically executed after the peak locate and peak analysis phases. Filters can be applied to zoom directly to specific ROIs—for example, targeting by energy or nuclide or requiring review of any region where the Chi-Square value exceeds a set threshold. These options simplify integration of IPF into routine sample counting procedures.

The IPF display provides:

- Channel data (green squares)
- Fitted peak area (dashed shaded regions)
- Continuum values under the peak (solid magenta)
- Channels used to determine continuum height (white squares)
- A residual plot comparing fitted peak area to channel data (see Figure below)



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.

EFFICIENCY CORRECTION

The efficiency correction process calculates a peak efficiency and its uncertainty for each detected peak based on the efficiency calibration. During this step, the system determines which of the four calibration fits—dual, linear, empirical, or interpolated—to apply for the analysis.

With **Genie**, the efficiency correction propagates the uncertainty correlation matrix throughout the analysis, enhancing accuracy.

When using the **ISOCS efficiency calibration option**, the "Efficiency Correction by ISOCS" step calculates efficiency directly from the ISOCS or LabSOCS model at the peak search results. This eliminates the need to provide an efficiency calibration prior to analysis.

NUCLIDE IDENTIFICATION AND QUANTIFICATION

The nuclide identification algorithms consider all energy lines of a nuclide defined in the analysis library, including their correct line abundances and the nuclide's half-life.

For a positive identification:

- At least one gamma energy must fall within the user-selected energy tolerance of an observed peak in the spectrum.
- A sufficient number of the other energies (if present) must also match peaks in the spectrum. This is determined by comparing the sum of line abundances for matching peaks against those without matches.
- The decay time of the measured spectrum must not be excessive relative to the nuclide's half-life.

Nuclides that meet these criteria and exceed the user-selected confidence index threshold are classified as identified. For each identified nuclide, the algorithm calculates:

- The confidence index value.
- A decay-corrected activity per unit volume (or mass) for each energy with a matching peak.

If applicable, decay correction automatically accounts for:

- Decay during acquisition.
- Decay from the sample date to the start of acquisition.
- Additional correction for samples collected or accumulated over a finite period (e.g., air filters, air cartridges, activation samples).

MEAN ACTIVITY CALCULATIONS

After standard nuclide identification, the spectrum can be analyzed for **interference sets**—two or more nuclides sharing at least one common energy peak that has not been resolved by peak location and area calculation. The activities of these nuclides are determined by solving a linear least squares equation, see figure on right.

The algorithm automatically identifies nuclides with interferences—no special library is required. However, energies can be flagged in the library for exclusion from weighted mean activity calculations.

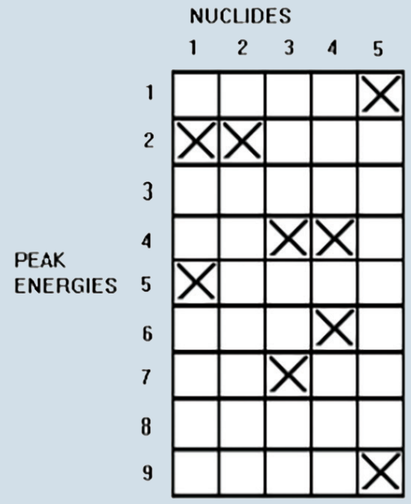
For nuclides without interference:

- If multiple peaks exist, activity is calculated as a weighted average of the activities for each peak.
- If only one peak exists and there is no interference, activity is calculated directly from that peak.

Weighting factors include:

- Efficiency
- Peak area
- Efficiency uncertainty
- Branching ratios of the peaks

To improve accuracy, the **"NID with Correlations"** engine can now be used, incorporating correlations into weighted mean activity uncertainties for more rigorous results.

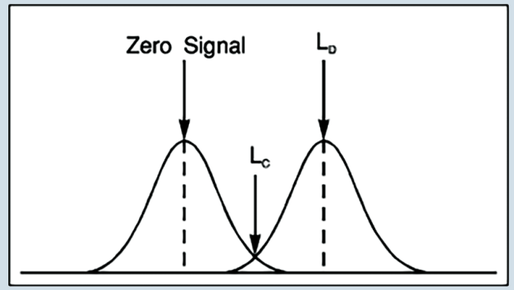


Identification matrix of peak energies to corresponding nuclides. Note Peak Numbers 2 and 4 have multiple potential nuclide matches. An interference correction is used to resolve the identification.

Genie Spectroscopy Suite Analysis Algorithms

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.



Illustrating the Critical Level (L_C) and Decision Level (L_D) concepts

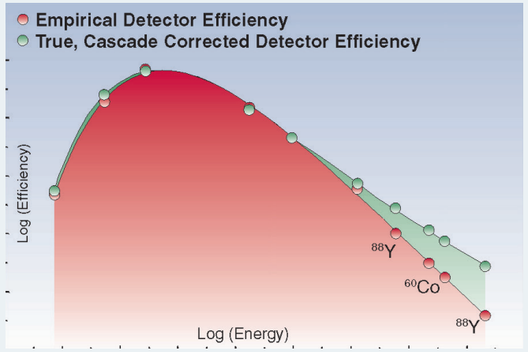
Corrections

TRUE COINCIDENCE (CASCADE) SUMMING CORRECTION

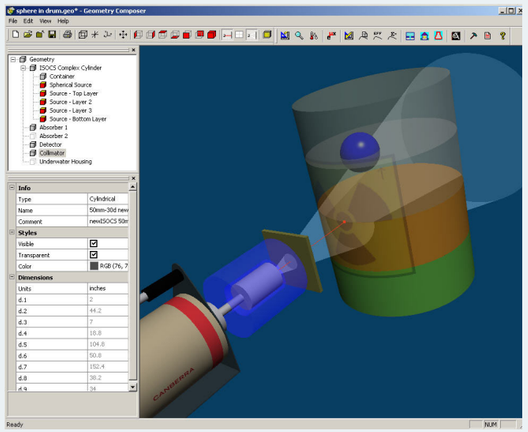
The Mirion unique and patented Cascade Summing Correction feature* corrects your entire spectrum, from 10 keV to 7 MeV, against loss or gain of observable peak area as a function of nuclide decay scheme and geometry. True coincidence summing can cause systematic peak area errors of 30% or more with certain nuclides and geometries, see below. 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.



Comparison of Cascade Corrected to Empirical Efficiency



Geometry Composer

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

GEOMETRY COMPOSER

Accurate sample geometry is essential for the Cascade Summing Correction algorithm and for calibration using the optional ISOCS/LabSOCS software. The Geometry Composer, see below, is a powerful tool that enables interactive definition and real-time 3D visualization of all geometry-related parameters, including, detector properties, sample dimensions and densities as well as distances and shielding between the detector and sample.

The tool renders the geometry in three dimensions, providing immediate visual feedback for quick error detection.

Additional features include:

- Custom beaker creation (with or without absorbers)
- Object isolation for focused design
- Transparency for viewing internal components
- Zooming and other interactive controls

PARENT/DAUGHTER DECAY CORRECTION

Gamma spectra often include peaks from both a nuclide's ground state and its progeny. When the parent nuclide and its daughters are not in equilibrium, a correction is required to ensure accurate activity reporting. The Genie Parent/Daughter Decay Correction algorithm applies this adjustment 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 subtraction algorithm removes environmental background peaks from sample spectra. Before execution, the background spectrum must be analyzed separately for its peak locations and associated areas. When applied, the algorithm automatically scales its results to match the acquisition time of the sample, and users can specify an energy tolerance for matching peaks between the sample and background spectra.

Reference peak correction normalizes the areas of all other peaks in the spectrum using a reference peak of known count rate. The reference source can be an electronic pulser or an external stationary source.

Both corrections—background subtraction and reference peak adjustment—can be applied to the same sample spectrum if required.

GAIN EVALUATOR AND GAIN ADJUSTS

Three utilities are available to manage changes in gain from a calibrated spectrum:

Gain Evaluator - analyses the quality of the current data source's energy calibration and gain settings, allowing users to assess the impact on nuclide identification (NID) analysis.

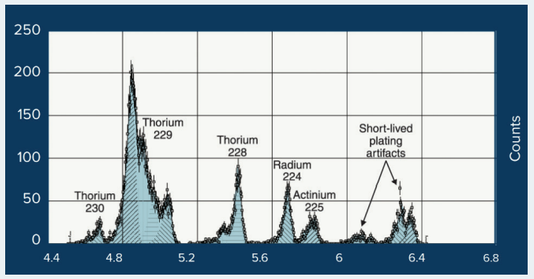
File Gain Adjust - enables matching of previously acquired spectra with different energy calibrations for comparison, addition, or stripping. This routine shifts, or rebins, the current file's spectral data to match the specified "goal" energy calibration of another spectrum rather than its original calibration.

Auto Gain Adjust - automatically adjusts the MCA gain of a live data source to match the current energy calibration. It works by iteratively acquiring a spectrum, matching peaks found by peak search analysis to input certificate file energies, and adjusting hardware settings based on this peak matching.

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.

Analysis steps such as Peak Locate, Peak Area, Background Subtraction, Nuclide Identification, and Minimum Detectable Activity (MDA) can be performed individually or integrated into an analysis sequence file. The following sections describe these algorithms and their application to alpha spectroscopy.



Example of alpha spectrum

PEAK LOCATE SCHEMES

Traditionally, manually defined ROIs have been a sufficient peak locating mechanism for alpha spectroscopy. This approach is supported with the User Specified Peak Locate engine, which can use the current ROIs defined in the spectral window or pull from a pre-defined ROI file.

For advanced analysis requiring deconvolution of complex alpha spectra, the generalized second difference method is available. This method is particularly useful when ROI-based peak location is inadequate due to interfering peaks, variable tailing, or when re-preparation of the sample is not feasible.

Both peak locate schemes can be used individually or combined, with their results summed for improved accuracy.

PEAK AREA CALCULATION SCHEMES

Peak areas can be calculated either by summing the counts within a Region of Interest (ROI) or by fitting the data using a modified Gaussian function.

Summing counts is particularly useful when spectra have poor statistics, lack clear peak shapes, or when resolution does not allow multiplet fits—a common situation in alpha spectroscopy.

The fitting option supports both singlets and multiplets and allows Full Width at Half Maximum (FWHM) and tail parameters to remain fixed to calibrated values or vary for the best fit. This approach is most effective when spectra have good statistics and sample preparation has produced high-resolution results.

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. After subtraction, a critical level test can be applied to every peak to ensure accuracy.

NUCLIDE IDENTIFICATION

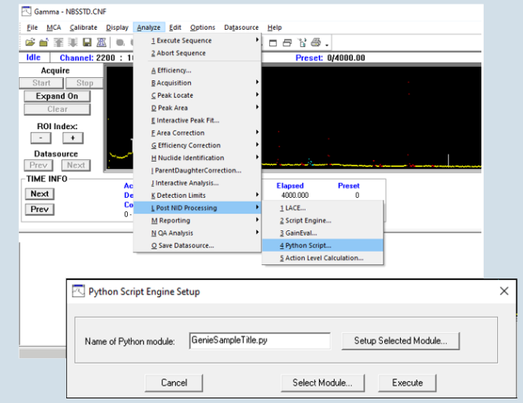
The Nuclide Identification algorithms offer flexible tools that can be customized for specific applications. Nuclide identification is based on operator-selected libraries of alpha emitters. The performance of the algorithm can be fine-tuned by adjusting a confidence threshold as well as the identification 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.

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, see below.




```
def execute(chan, step):
    ds=Datasource(chan)
    f = open("c:/temp/geniecam.txt", "a")
    f.write("sample title: " + str(ds.getParameter(ParameterCodes.CAM_T_STITLE)))
    f.close()
    return 0

def setup(chan, step):
    return 0
```

Launching a Python script from the Post NID processing step in Genie software applications

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 considered best practice. These checks help identify issues with the measurement system, and flag discrepancies 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 monitoring and recording of parameters such as peak centroid, FWHM, nuclide activities, backgrounds, and MDA, etc. Non-Genie parameters can also be integrated 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 invalid results or correct data.

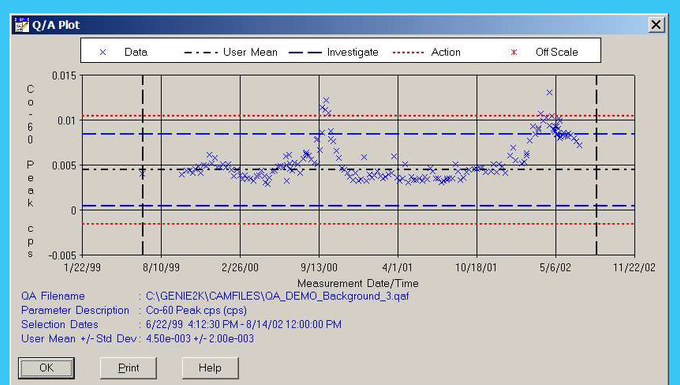
For each tracked parameter, statistical analysis rules (described in detail below) are configured to indicate if a QA count has acceptable results or if action is needed.

The data and results are displayed as:

Scatter charts - showing parameter limits over time or comparing multiple parameters.

Reports - using two templates:

- **Full Report:** Complete parameter history.
- **Last Measurement Report:** Highlights the most recent QA count.



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

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.

INTERACTIVE SPECTRAL ANALYSIS

The Interactive Analysis utility enables detailed review, exploration, and refinement of spectral analyses with real-time visual feedback. When launched, it displays the current data and analysis results, including options to visualize peak significance, peak correlation, peak residuals, and nuclide residuals.

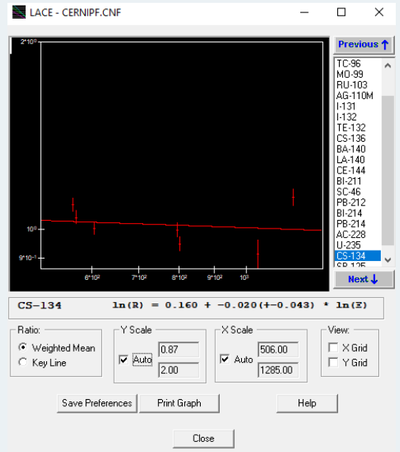
Expert users can interactively add, edit, or delete peaks and peak regions based on detailed spectral information. Calibrations and nuclide libraries can also be reviewed and updated directly within this module, ensuring accurate and customized analysis.

Genie-FieldPro Application

LINE ACTIVITY CONSISTENCY EVALUATOR

The Line Activity Consistency Evaluator (LACE), shown on right, helps assess the quality of gamma analysis by evaluating the consistency of line activities calculated for multi-line radionuclides. It compares individual line activities to either the key line activity or the weighted mean activity, as selected 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]		

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.

Genie-FieldPro provides a streamlined, user-friendly interface for gamma spectroscopy sample counting, designed for maximum usability by field technicians regardless of their spectroscopy expertise. It enables quick, confident analysis of samples for gamma radiation.

SIMPLIFIED SETUP

Sample geometry is selected using two customizable drop-down menus: Geometry and Contents/Matrix. A reference image is displayed to confirm the selection. Count time, calibration, and analysis parameters are automatically linked to the chosen geometry and executed with the count.

TRACEABILITY AND CONFIDENCE

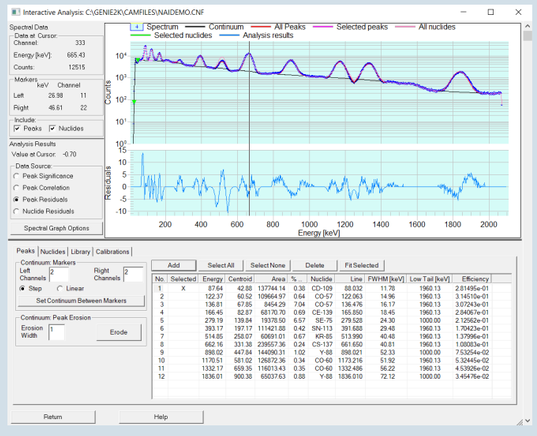
At the end of each count, users are prompted to take a photo of the sample, which is saved alongside the spectrum file. Each count runs a Genie analysis sequence and checks for specific nuclides. Results are summarized in an automatically generated report indicating CLEAR, EXCEEDS LIMITS, or MDA NOT MET, based on user-defined limits.

BUILT-IN QA CONTROLS

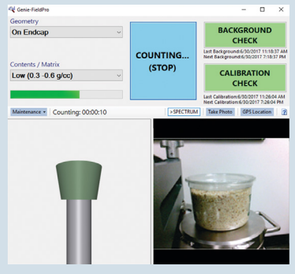
The interface includes calibration and background check functions. If a check fails, the system locks further sample counting until resolved. The software also tracks when checks are due and prevents counts if overdue.

ADDITIONAL FEATURES

- “Count to MDA” option
- Password-protected configuration file and audit log
- GPS integration
- Auto-export/import for transferring results to a remote Apex-Gamma™ system



Interactive Analysis Application



Genie-Fieldpro provides a simplified user counting interface for screening applications.

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.

System Requirements

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

ORDERING TABLE

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.
GenieReview	GenieReview Data Review Application

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.
GenieReview **GenieReview-1yr** **GenieReview-3yr**	GenieReview Perpetual License GenieReview 1yr License GenieReview 3yr License

Genie supports a wide range of Mirion MCAs and is fully compatible with major Windows operating systems, including Windows 11, Windows 10, Windows Server 2022, and Windows Server 2019. This ensures flexible deployment across diverse IT environments.

Genie software utilizes electronic software licensing technology, eliminating the need for physical dongles. Each computer requires a one-time activation, with modes supported for both internet-connected and isolated systems, ensuring secure and flexible license management.

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
- GenieReview – dedicated application for efficient post-acquisition spectrum review, reanalysis, and quality assurance. It supports multiple peak searches, background subtraction, energy and efficiency calibration, nuclide identification with interference correction, cascade summing correction, weighted mean activity calculations, MDA assessment, alpha analysis, and interactive peak fit.

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

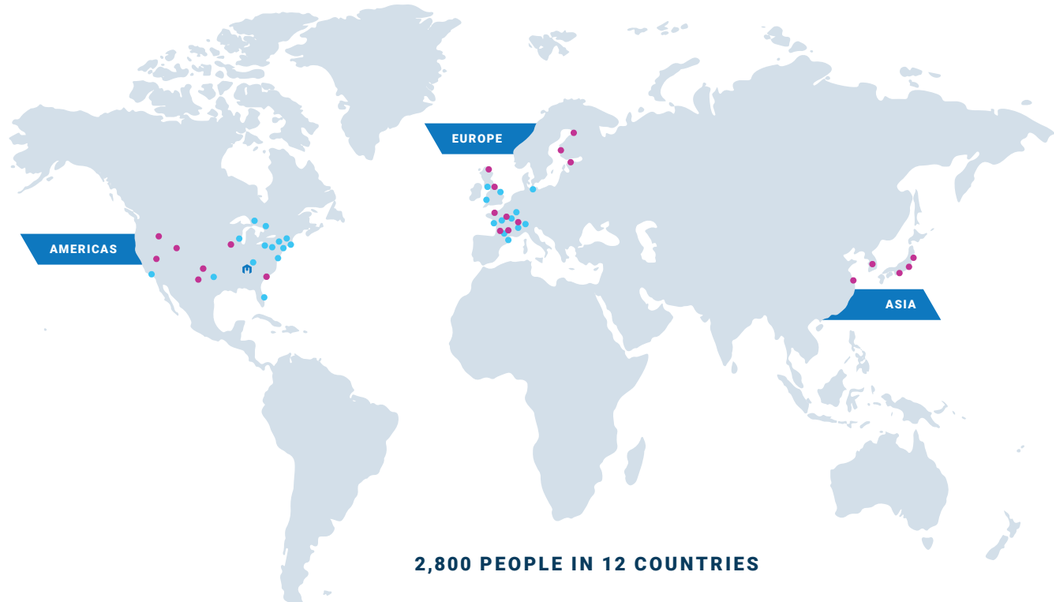
Genie is available in German, French, and Japanese language versions. For information on additional language support, consult your local Mirion office.

Empowering Progress Across Continents

Mirion Technologies combines innovative radiation safety technologies with unrivaled expertise, cultivated over decades of collaboration with reactor manufacturers and operators, nuclear fuel facilities, regulators, national labs (such as the U.S. DOE), nuclear institutes, universities, and national military/security organizations worldwide.

Trust us to provide the solutions and support you need to safeguard your valuable assets and ensure a secure and sustainable future.

CORPORATE HQ (ATLANTA, GA) MANUFACTURING SITES SERVICE & SALES CENTERS



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