

HyperLab 2014
Quick Start Guide for
Main Module



HyperLabs Software

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About this document

For detailed instructions on using the installed Main Module, start reading this *Quick Start Guide*. If you did not install the Main Module yet, refer to *Installation Guide* first. If you want to get finer details about peak evaluation or other HyperLab processes, see the *Reference Guide*.

1. Introduction

This Quick Start Guide contains basic information on HyperLab system, including system overview, and usage instructions. It also details initial steps to fill up a sample database and to carry out most common spectroscopy tasks. We will guide you through a comprehensive tour, where a set of sample spectra will be processed by HyperLab system.

1.1. Purpose of HyperLab

HyperLab is a sophisticated software system, which is intended to greatly ease daily tasks of gamma spectroscopists and scientists with up-to-date techniques and algorithms. It uses novel techniques for reliable **deconvolution** of extremely complex gamma spectra taken with semiconductor detectors. Evaluation of Dual LFC (Loss Free Counting) gamma spectra is also supported for compensating the radioactive decay during measurements.

A high quality **nuclide identification** and minimum detectable activity (MDA) calculation is also available for virtually all nuclei found in common nuclear libraries. Our isotope identification method behaves exceptionally well if isotopes are present with overlapping spectrum peaks.

The software system is also capable of determining your system's various important characteristic functions from multiple measurements taken with multiple radioactive sources:

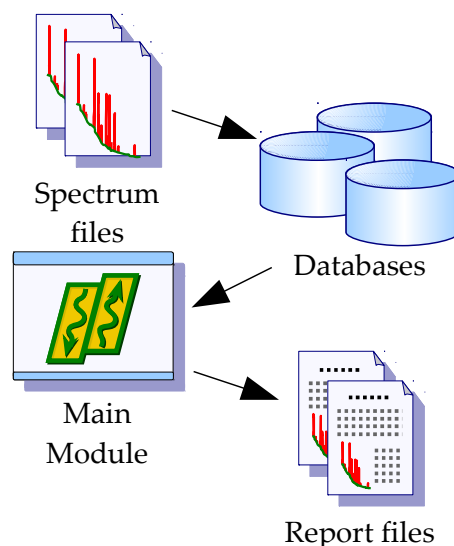
- detector resolution,
- system nonlinearity,
- absolute or relative full-energy detector efficiency,
- peak-to-total ratio.

All of the functions above are determined by numerically stable methods, while providing extremely convenient user interfaces.

1.2. System architecture overview

HyperLab Main Module stores *all* spectroscopic information in relational databases. The next figure illustrates basic system components.

Main module is the application where you will operate various evaluation utilities (peak area evaluator, detector efficiency evaluator etc.) and also the primary interface to information stored in one or more **databases**. Benefits of database systems are described in *Reference Guide*.



1.3. Overview of HyperLab tasks

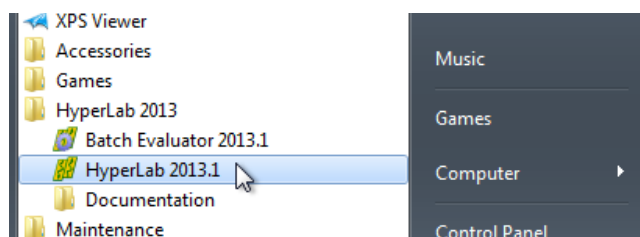
When a gamma spectroscopist starts using HyperLab, usually the following steps are performed:

- Creating one or more databases with Main Module. The new database is “empty” at this point (indeed, it contains nuclear data).
- Defining the measurement setup, and also custom projects. Projects in the database are similar to folders of hard disks, and helps to manage vast amount of information.
- Transferring of existing spectrum files into the database.
- Peak evaluation of spectra; possibly with defining modified energy and FWHM calibration.
- Exporting peak lists for outer evaluation applications.

The resulting peak lists may also be used to perform system *nonlinearity* evaluation, detector *efficiency* or *resolution* determination within Main Module. See *Reference Guide* for details.

2. Getting Started with Main Module

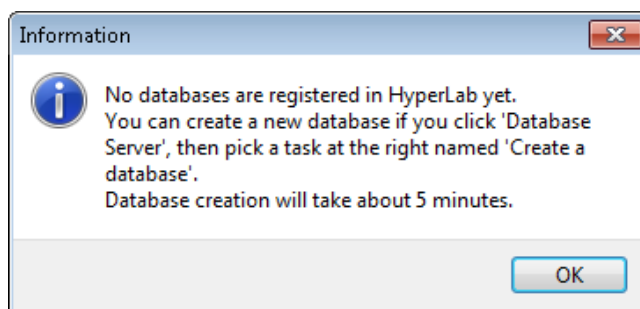
Start HyperLab Main Module by clicking on Start/ Programs/ HyperLab 2014/ HyperLab 2014.1 menu.



A message appears, which warns you about missing databases.

Press Ok.

Main Module window appears now.



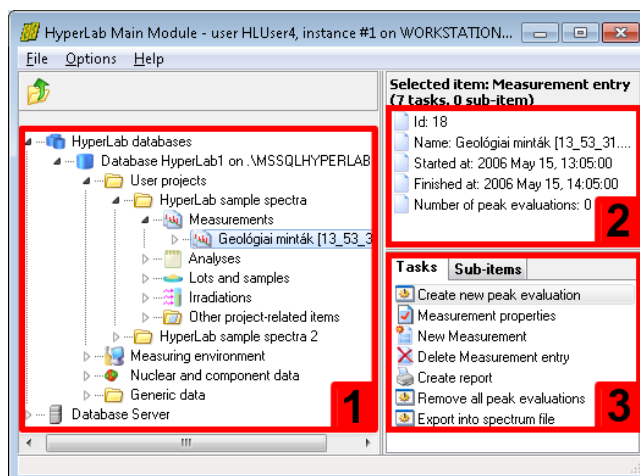
2.1. The Main Module window

This window appears when Main Module is started. Its main parts are the following:

Database browser tree [1] provides hierarchic listing of objects stored in HyperLab databases. The items displayed in this tree are called *nodes*.

Detail lister [2] shows common details for the item which is currently selected in the browser tree.

Tasks and Sub-items panels [3] are refreshing their content according to the data entry you have selected in the database browser tree. *Tasks* provides you operations which may be performed on the selected database entry; whereas *Sub-items* shows special sub-components about it.



Content of the *Tasks* window also appears in a **context menu**, when user right-clicks on a database node.

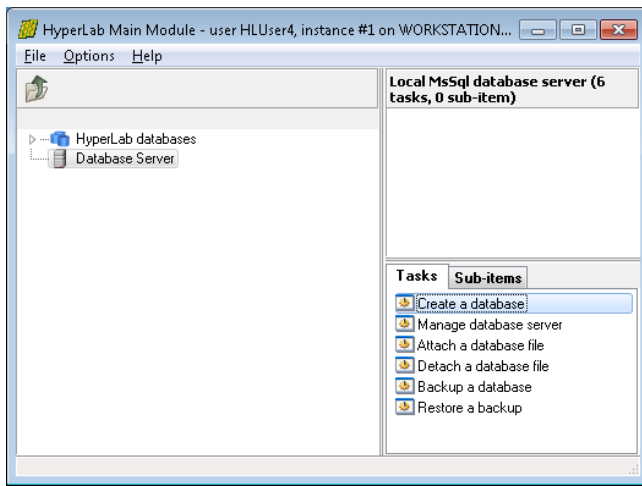
Common **keyboard shortcuts** may help your work: database tree may be walked through by using the *cursor arrow* keys, while the currently selected task may be started by hitting the *Enter* key. *Tab* key switches between the browser tree and the *Tasks* window.

3. Creating a new HyperLab database

In most cases, the initial step of using HyperLab is to create a new local database. First check if your local MSDE database service is running: the icon with the green triangle should be displayed on your system tray.

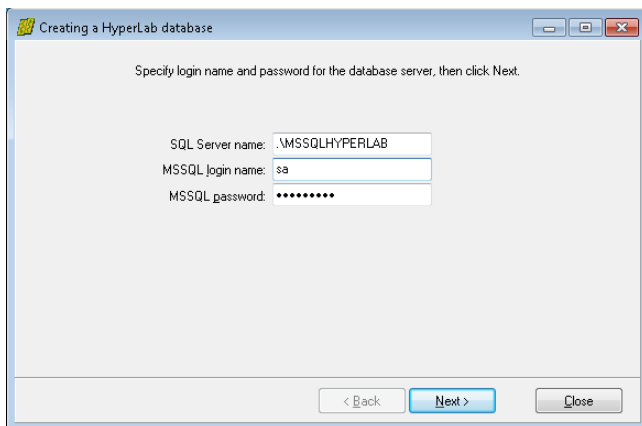
HyperLab is able to use a remote database, that is, to transfer the evaluation data through the computer network from another user's database or from a central SQL server for safe and consolidated data storage. In this case, no local database installation is required, just a registration of the remote database. See *Reference Guide* for details.

3.1. Database creation



Click *Database server* node, then on the task *Create a database*.

The Database creating wizard appears now.

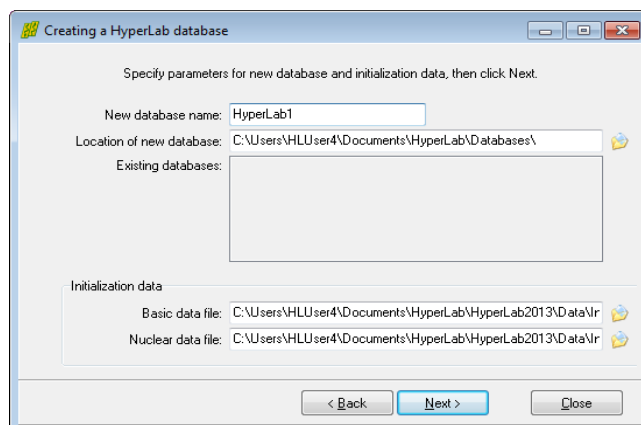


Enter login name **sa** and password **Hlpwd2014** (note it is starting with big **H**) for the database administrator. This is required because the database access is password protected.

Note: in case of an upgrade from a previous HyperLab version, the password remains as is, in other words, it may be hlpwd2002, hlpwd2005, hlpwd2008, hlpwd2009, or Hlpwd2013.

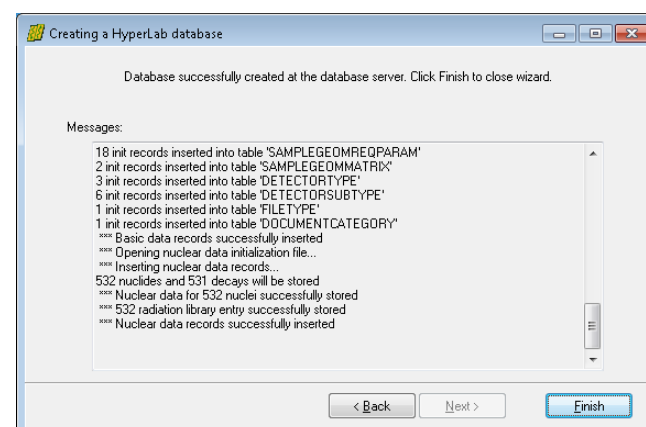
When you are ready, click *Next*.

Specify the name of the new database, then click **Next**.



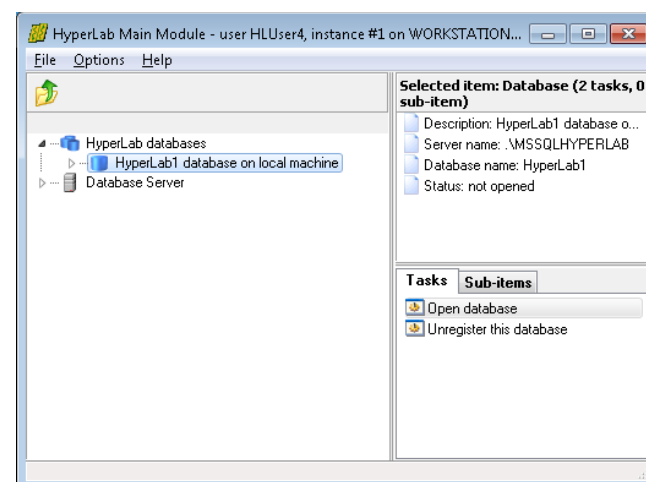
Automatic database creation process starts now, which also incorporates the copying of large amount of nuclear data to the new database.

The process may take several minutes. When the copying process ends, click **Finish**.



After database successfully created, it appears under *HyperLab databases* node. By double-clicking on it, you will be able access its content.

If no such entry appears under *HyperLab databases* node after a successful database creation, refer to *Database registration* section of the *Reference Guide* in order to display it.



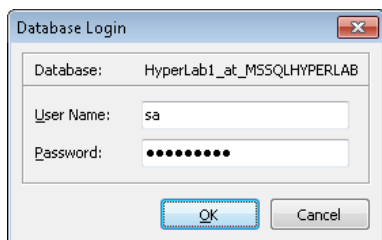
4. Working with databases

If you start Main Module, it will display the newly created and registered databases at the left.

4.1. Opening a database

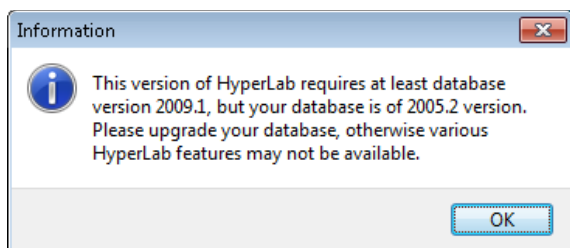
Select a database row at the left, and double-click it to open its content.

Alternatively, you can hit the *Enter* key on the selected database node, which always starts the selected task on the right – in this case, the database opening task.



Specify the database user name and password, then click **OK**.

4.2. Database upgrades



After installation, you may get a notification message about possible database upgrades.

4.2.1. Database upgrade for new installations

In case of a *new installation*, that is, when the database is empty, immediately upgrade the database to the latest version. This way all the new or improved services in newer HyperLab versions will be available. For example, nuclide identification will not work if your database version is less than '2009.1'.

4.2.2. Database upgrade for older HyperLab databases

If you have an older database, which is created and routinely used by an older, proven HyperLab version, there is a tiny chance that the upgrade operation fails, and this affects adversely your previous evaluation data.

As the upgrade of existing HyperLab databases can be undone only by restore the database from a backup, the upgrade decision requires caution.



Before upgrading your database, always make a database backup first!
See the Reference Guide for details.

We suggest to

- Always make a backup before upgrade.
- After backup is ready, upgrade to the latest database version.

If you are especially cautious, you have the possibility to make a copy of your existing database, and restore it immediately under a different name.

This option may be achieved as follows (see the Reference Guide for details):

1. Create a backup of your old database.
2. Restore the backup file into a new, test database.
3. Start using the test database with the newest HyperLab version, and upgrade it, if prompted.
4. Now you can try out the new software version without any risk, as the operations do not affect your original production database in any way.
5. If you are satisfied with the new software version after an extended test period, you can

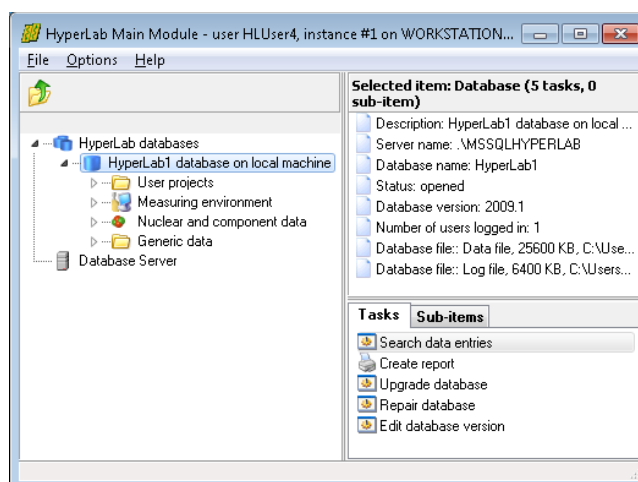
simply upgrade your production database, and uninstall the old HyperLab version.

4.3. Basic database usage

Usually, the database browser tree is displayed at the left, with database details displayed at the top right, while the possible operations listed in the Tasks window.

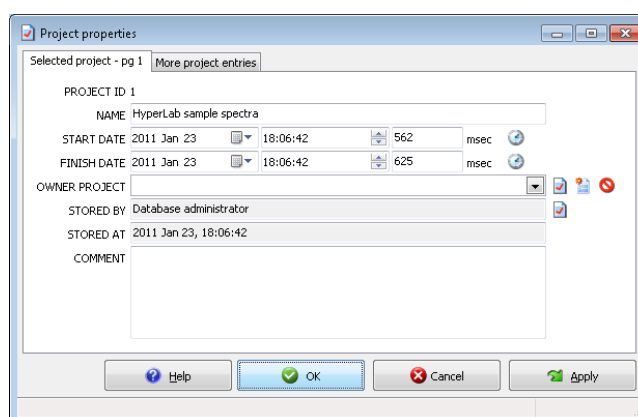
Now you should create a new project for HyperLab sample spectra. Projects are the data organization units for HyperLab, like the directories for a hard disk, and able to hold measurements, peak evaluations, several different kind of analysis and so on, which are related to each other.

To create a new project for the HyperLab's default sample spectra, select *User projects*, then click on “*New project*” task at the right.

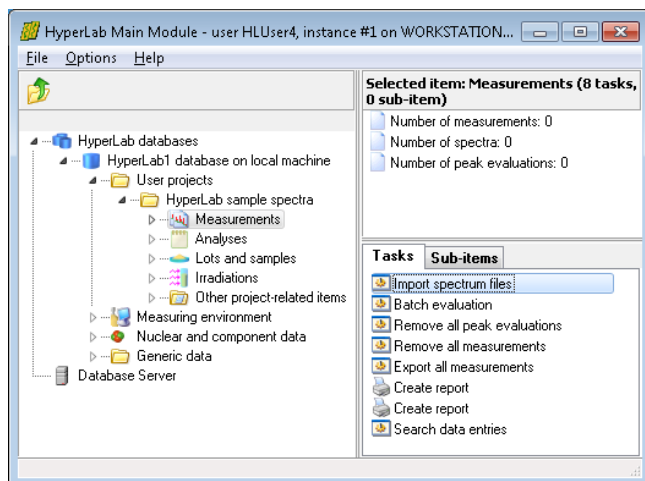


Alternatively, you can use your keyboard: the *arrow keys* can be used to quickly navigate within the database tree, and *Enter* key starts the currently selected task. The *Tab* key switches between the Tasks and the Database tree window.

Now a database entry – or *record* - editor window appears. In this case the details of a new project record may be specified.



Each kind of database entry has different type of editor window, but their basic building blocks are very similar. Now type a project name, say “HyperLab sample spectra”, then click the OK button. Alternatively, you can hit the *Enter* key. *Tab* key will cycle through the editor fields.

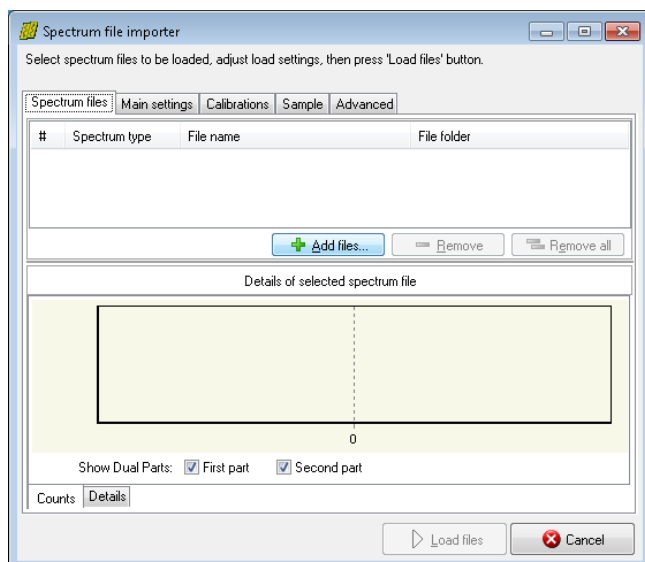


A new user project node appears in the database browser tree now.

As Main Module also stores the count information in databases, you should import your spectrum files to the database before you evaluate them.

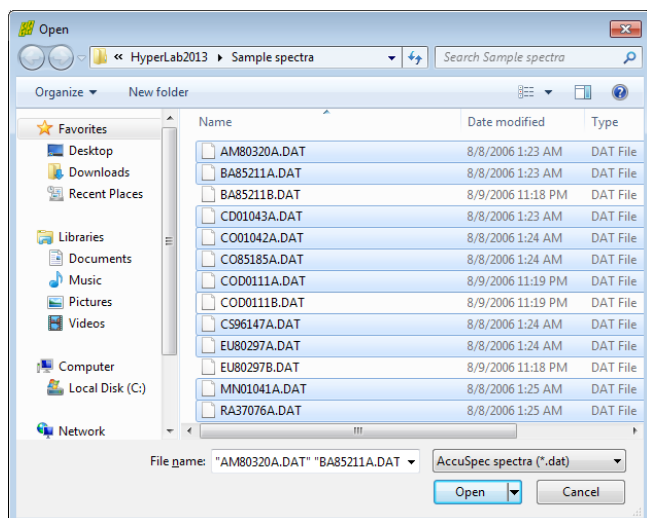
Open your project by a double click. Note that it always has a Measurements node, where its measurements will be listed.

5. Importing spectrum files



Click a project's *Measurements* node, and then select the *Import spectrum files* task from the right pane. A spectrum file importer window appears now.

Click on *Add file...* button to select HyperLab sample spectrum files.



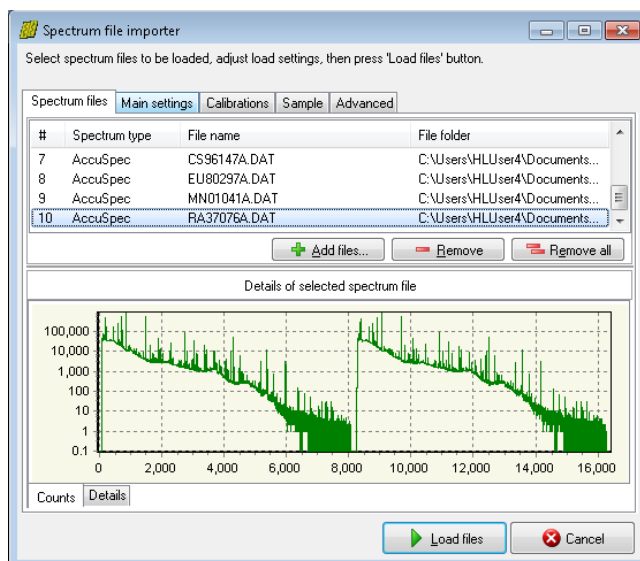
Now a standard file selection dialog appears. Select HyperLab sample spectra from Documents \ HyperLab \ HyperLab2014 \ Sample spectra folder.

Select AccuSpec file type and all AccuSpec spectrum files where the last letter of the file name is "A", then click *Open*. These measurements were taken with 70-3300 keV energy range ("B" ending is used for 50 - 2200 keV range).

The selected files appear on the file importer's list.

As you can see, these are Dual LFC spectra with two similar halves. It is essential to correctly set the spectrum data type before loading, as HyperLab splits up dual spectra and stores their parts separately in the database.

Click on tab *Main settings*.

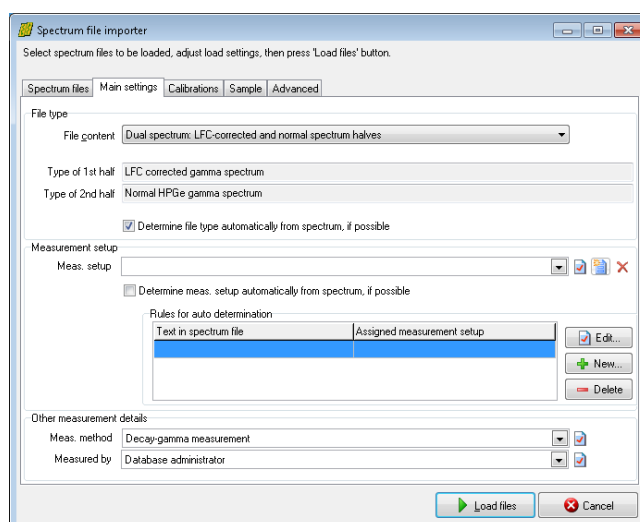


Set *File content* to 'Dual spectrum: LFC'.

Next the measurement setup should be selected from the list to which these measurements will be assigned. This is important, as all calibration curves will be tied to a specific setup, and the automatic selection of the calibration function can be achieved only this way.

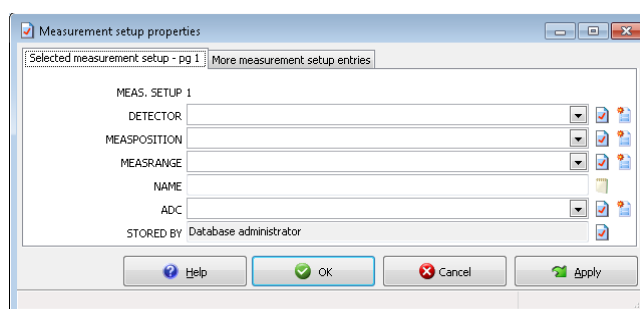
As currently there are no measurement setups defined yet in the new database, the list is empty.

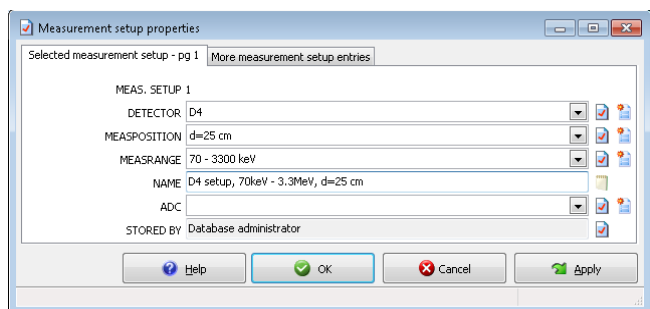
Click the *New record* icon (📄) beside the 'Meas. Setup' list, in order to create a new measurement setup entry.



The record editor window appears for the measurement setup.

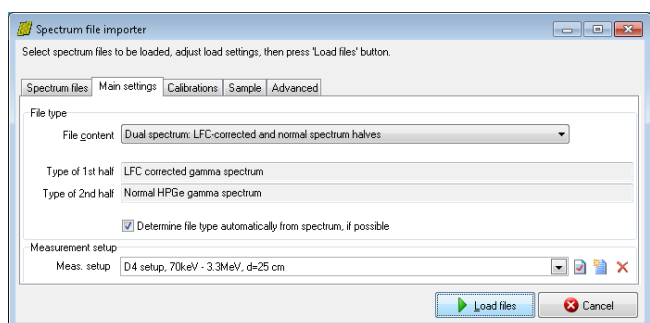
As there are no detector, measurement position and measurement range entries in the database yet, these should also be created by clicking on their corresponding *New record* button (📄) to the right of the combo boxes.



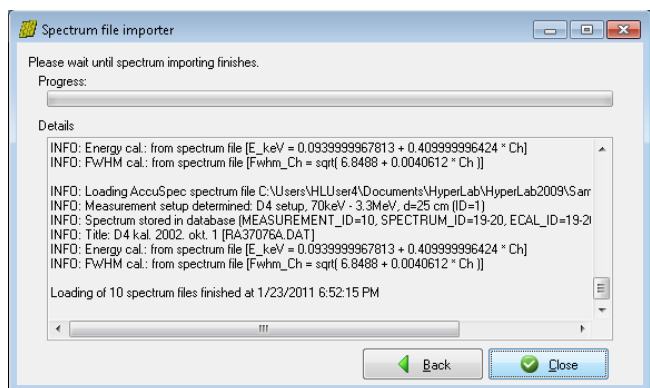


70keV - 3.3Mev, d=25cm' and 'D4 Setup 50keV - 2.2Mev, d=25cm'.

Create the following entries for the HyperLab sample spectrum set: 'D4' detector, 'd=25 cm' measurement position, and two measurement energy ranges: '70-3300 keV' as well as '50-2200 keV'. The two measurement setups are differ only in the applied energy range range, thus should be named as 'D4 Setup



After the measurement setup has been set, check settings under other tabs as well. If you are ready to load spectrum files, click *Load files*.



The spectrum importer now loads all available information from the spectrum file, and stores it in the new database. Click *Close* after loading finished.

After loading, the spectrum files will be displayed under *Measurements* node in the database tree.

Please import similarly the remaining sample spectrum files:

- Those with "B" as the last letter of the file name. These should be assigned to the measurement setup for the 50-2200 keV energy range.
- Spectrum '13_53_31.CNF', which is a Genie-2k spectrum of an irradiated complex geological material. This should be assigned to the measurement setup for the 70-3300 keV energy range. Please switch off '*Automatically determine spectrum type*' during its importing, as this spectrum is of type Dual LFC, but incorrectly states 'PHA+' as its type.

6. Evaluating spectra

In HyperLab system, you have three ways to evaluate your gamma spectra:

- **Spectrum peak evaluator** in Main Module, which has a rich graphical user interface, and provides all tools necessary to modify and fine-tune your fit region by region, if its one-

step automatic deconvolution is not perfect. This is the recommended evaluation method if your spectra are even slightly complicated.

- **Database batch evaluator** in Main Module, which is a special peak evaluation component of HyperLab Main Module. It is capable to automatically evaluate several measurement entries stored in the database, each after the other. This can reduce the human interaction needed for the evaluation, but requires proper FWHM and energy calibration for each spectrum.
- **Standalone 'batch mode' spectrum file evaluator** utility, which operates on a selected group of spectrum files, and does not require usage of databases. Please note that this file-based tool does not support neither manual fit refinement, nor nonlinear energy calibration, so its use is recommended only if you are facing with large amount of extremely simple spectrum files, where the simple evaluation is of paramount importance. For further details, see *Quick Start Guide for Spectrum file batch evaluator* section.

As a rule of thumb, we suggest you that always check the details of fitted regions graphically, as this can help to eliminate trivial problems with the spectrum fit. This can be done by using Spectrum peak evaluator or by RTF reports which may contain the fitted regions graphically. Those versatile RTF reports may also be generated by the batch evaluators.

6.1. HyperLab peak evaluation basics

During the automatic fit, HyperLab first takes the list of suspected peaks, and tries to optimally determine **regions** – range of consecutive channels – around them. These regions contain one or more suspected peaks, which are fitted (deconvoluted) in a nonlinear fitting procedure as a next step.

HyperLab fits several region and peak parameters for each region during the spectrum deconvolution.

Parameters fitted for each region:

- 2nd order polynomial for background
- background step amplitude
- skewed hill in the background under low-energy side of peaks (tail, disabled by default)
- peak skewness slope and amplitude for low-energy side of peaks (left skew)
- peak skewness slope and amplitude for high-energy side of peaks (right skew)
- common peak width (FWHM).

Parameters fitted individually for each peak:

- position of the peak Gaussian
- amplitude of the peak Gaussian.

HyperLab is able to reliably describe the vast majority of gamma spectra with this versatile fitting function set, commonly named as *Common peak width method*.

There is also a *Variable peak width* fitting method, when the peak width are allowed to vary independently of each other within a region – that is, not a common FWHM value used, but it is

fitted for each peak. This may lead to unexpected results for complicated multiplets, so use it only when peak widths truly differ within a region. This is the case, for example for the region around the annihilation peak. HyperLab therefore tries to fit the regions around 511 keV with the *Variable peak width* fitting method by default, thereby making it unnecessary to correct it manually every time.

Moreover, HyperLab tries to eliminate unnecessary fit function parameters after fitting regions, and to automatically remove them, if their use may be questioned. This may lead to 'disappearing' of various fitted parameters. This parameter elimination step is performed in order to increase the stability and reduce the chi-squared value of the final fit and also to reduce the uncertainties of fitted parameters.

See *Reference Guide* for further details of the fitting process.

7. Using of Spectrum peak evaluator

Spectrum peak evaluator is the recommended tool in Main Module to evaluate your spectra in most cases, as it provides you with advanced tools to fine-tune the deconvolution results.

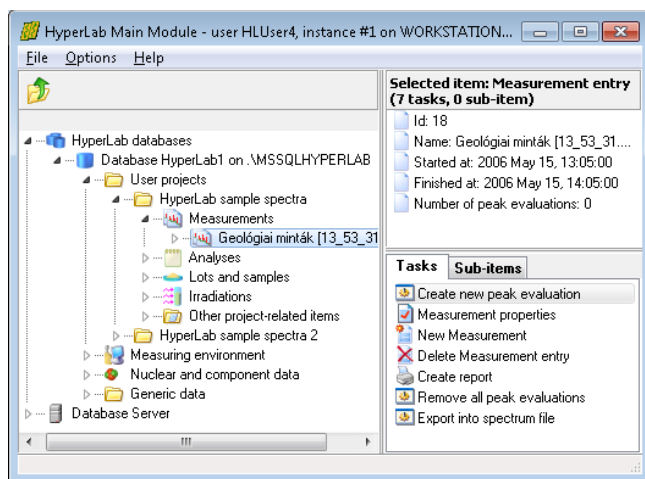
7.1. Quick overview of the evaluation process

A routine gamma spectrum deconvolution in Spectrum peak evaluator module consists of several steps:

- Creating a peak evaluation entry in the database for a measurement
- Starting the evaluator
- Checking measurement's calibrations
- Performing the automatic fit
- Check the resulted regions each after the other, and fine-tuning their fit if necessary
- Saving results into database and report files, as well as exporting data for post-processing.

The following sections will describe these steps in greater detail.

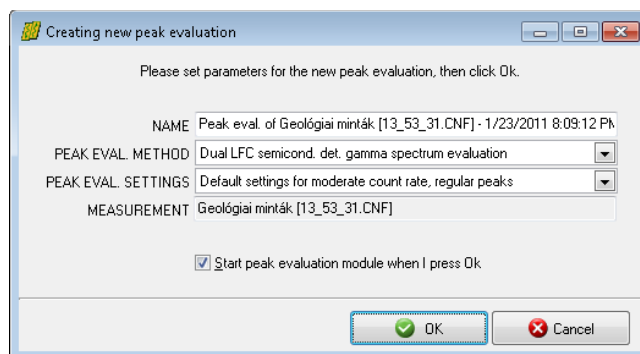
7.2. Starting the evaluator



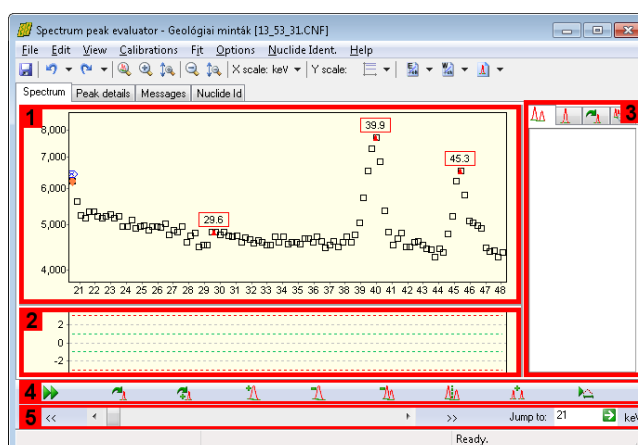
To start using the Peak evaluator, first select your measurement in the database browser tree, then click task *Create new peak evaluation* in the Tasks window.

Alternatively, you can hit the *Enter* key, as it starts the currently selected task.

A new peak evaluation creation window appears now. You can leave defaults in most cases, so just click **OK** for now.

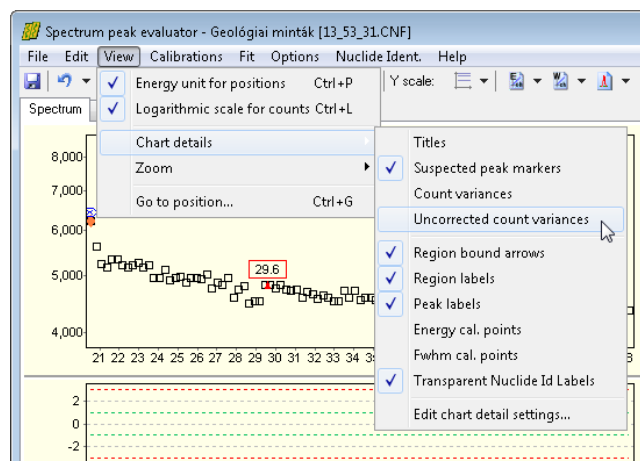


Main window of spectrum peak evaluator appears now. The center of the window is occupied by the **spectrum window** [1] and the **residual window** [2]. The residual window displays the difference between the measured counts and the fitted peak curves. A **region list panel** [3] is placed on the right, while a **fit fine tuning toolbar** [4] and a **navigating toolbar** [5] is at the bottom. List of fitted peaks is displayed under the Peak details tab.

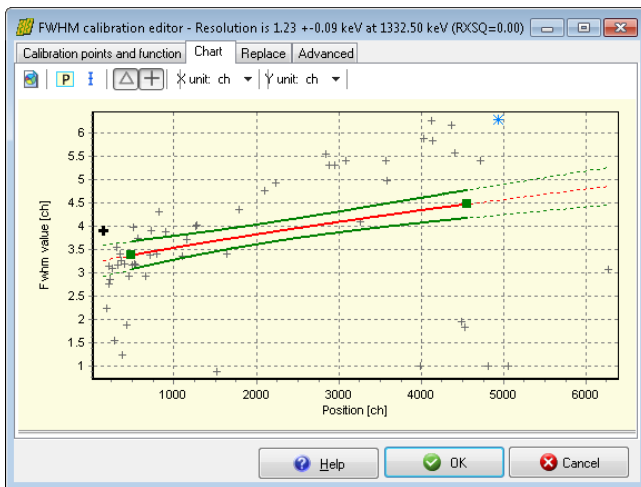


Please note the **red triangles** in the spectrum: these are the positions of the suspected peaks, and their position is determined by the current FWHM calibration. Deconvolution will use these suspected peaks as an initial estimate.

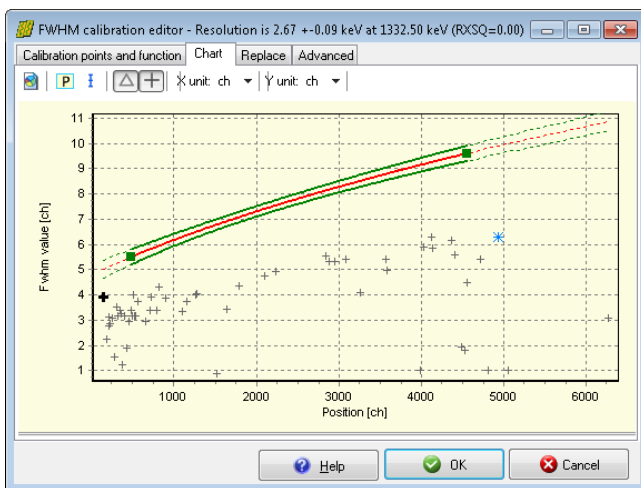
First you should try out how to modify some spectrum display settings. By default, spectrum evaluator displays the counts (black squares) and the suspected peaks. It is also possible to display the corrected variances (gray squares) and uncorrected variances (gray diamonds). The variance correction is for taking account the distorting effect of high count rates. For most users it is advisable to switch off the displaying of these variances via the *View / Chart details* menu.



7.3. Checking FWHM calibration

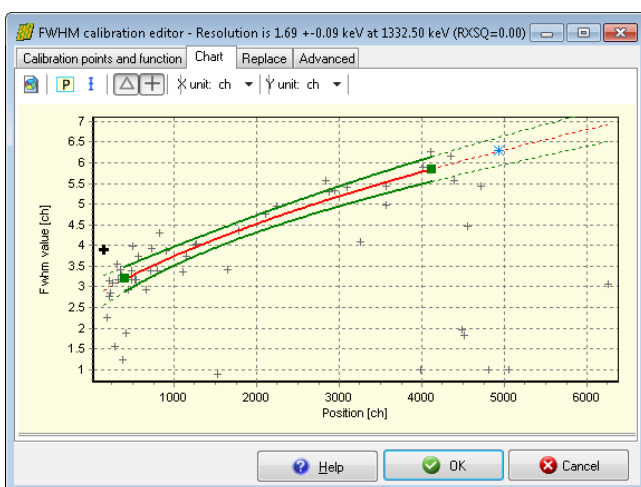


calibration curve displayed here together with filled green squares as FWHM calibration points. HyperLab also estimates the width of the suspected peaks, and displays these values as gray crosses. The figure shows the case when the FWHM calibration provides too low values.



If large deviation found between the current calibration line (red line), and the suspected peaks' FWHM, then a mis-calibrated FWHM may be suspected. In this case, the FWHM and/or the position values of the calibration points should be modified on the *Calibration points* page.

The figure shows the case when FWHM calibration gives higher values than expected.



In case of a proper FWHM calibration, majority of the suspected peaks' estimated FWHM value is in the neighborhood of the calibration curve.

Please note that before the fit large deviations may occur even for a valid calibration, as FWHM values of the peaks are just rough estimations and not fitted values at this time.

Much better agreement is expected after a successful fit, when peaks' FWHM values are fitted and displayed on this chart as gray triangles.

For further details about FWHM calibration editor window, see *Reference Guide*.

7.4. Checking Energy calibration

Exact energy calibration is important for sophisticated tasks, like isotope identification.

However, when only a quick peak list is required for well-known isotopes, a rough energy calibration is enough before fit.

The rough energy calibration is only used during spectrum deconvolution for determining the vicinity of the 511 keV annihilation peak, because HyperLab allows to vary the width of peaks independently of each other.

Your energy calibration is proper for fitting if the annihilation peak is in the 509 – 513 keV range. Otherwise select *Calibration / Energy calibration* menu item, and edit the calibration points' position or energy values in order to correct them.

Note: When the fit completes, a finer energy calibration may be constructed, because exact, fitted peak centroid positions are available.

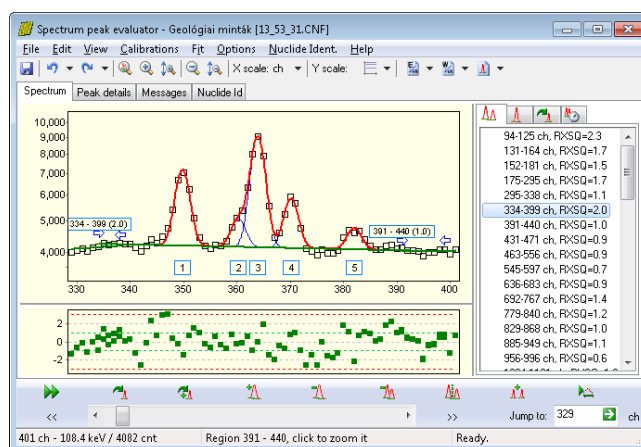
7.5. Performing automatic fit



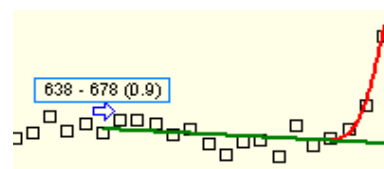
Click the Autofit button or select Fit / Start automatic fitting menu item to initiate a fit for the whole spectrum. A progress window is displayed during the fit, listing the problematic regions, where the reduced Chi-squared of the fit exceeded 3.

After the automatic fit, the counts of the first fitted spectrum region is displayed, along with the fitted curves of the individual peaks (blue lines), sum curves of all fitted peaks (strong red lines), and sum curves of background components (green lines).

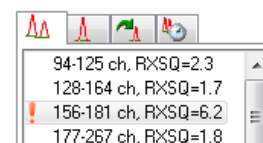
As HyperLab displays all fitted regions which are overlapping over a specific count range, it is common to see several regions, where the background 'wings' of the regions are overlapping. This improves the quality of the fits, as more counts may be utilized for background determination, resulting in more stable fits and lower uncertainties in peak areas.



End points of the regions are designated by blue arrows, which point towards the center of the region. A region label also displayed at the beginning of the regions, which shows the boundaries of the region and also the chi-squared value of the fitted region.



The region list panel at the right contains several pages, from which the list of regions is displayed. Problematic regions are designated with a small, red exclamation mark.



7.6. Navigating fitted regions

Several methods may be used to quickly select a specific region in the Spectrum evaluator. To revise regions one after the other, click double arrow buttons on the Navigation toolbar. To quickly jump to a specific spectrum part, use scrollbar or the Position edit box at the same place. If you are interested in the problematic regions only, click the region with red exclamation mark on the right.

7.7. Refining fitted regions

There are several tools on the Fine tuning toolbar to modify a region's automatic deconvolution.



Re-fits the clicked region. Rarely used, only if you suspect that a sub-optimal unstable fit found, which changes when you repeatedly fit the region.



Re-fits the clicked region with automatic peak insertion. Used when a sub-optimal fit found with a missing peak, but the position of the missing peak is uncertain, and you want to delegate the job of peak position determination to the fitting algorithm.



Insert a peak into the region, at the clicked position. Used when a sub-optimal fit found with a missing peak, and the position of the missing peak is suspected by the user.



Delete a peak from the region, which is located at the clicked position.



Delete the clicked region with all of its peaks.



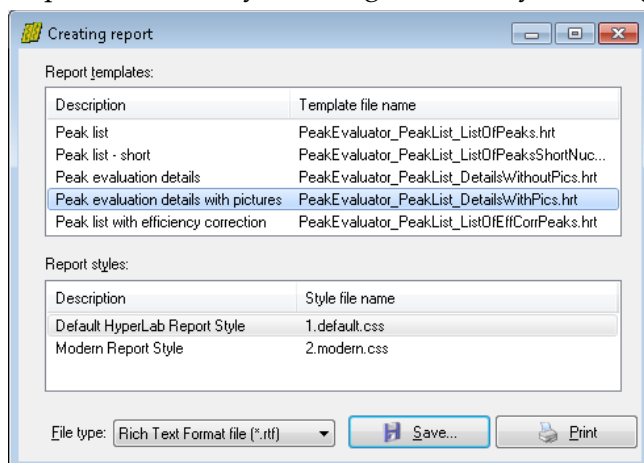
Splits a region at the clicked position into two half regions.



Merges two or more regions. To use this tool, click over the first region and drag the mouse cursor to the last region to be merged (do not release the mouse button).

7.8. Saving the results

When you are ready with the fine-tuning of the spectrum evaluation, select *File / Store* menu item to store the fitting details into the database. If required, a Sampo-90 compatible spectrum and peaklist file may also be generated by selecting the *File / Export to Sampo-90 file* menu.



Select *File / Create report* menu item to create detailed fitting reports.

A report creation window appears now, where you can choose between available report templates, report styles and output file formats.

RTF format reports may contain graphical region fits, and can be loading directly into word processors.

For direct printing of reports, you should have Microsoft Word word processor installed on your computer.

7.9. Further readings

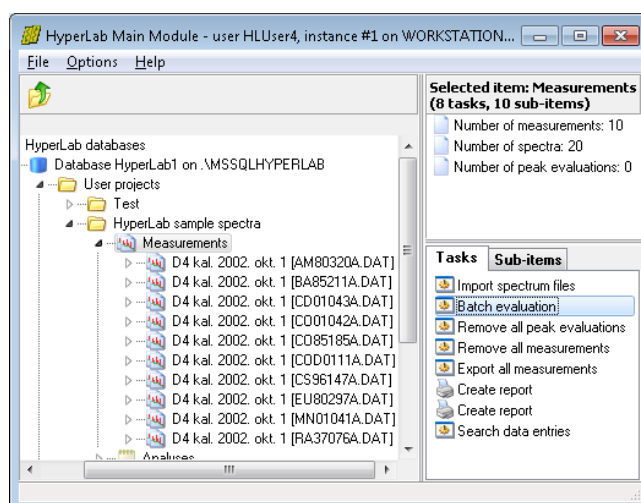
This Guide mentioned only a few from HyperLab's versatile functions. Please read further details in the *Reference Guide*, which deals with:

- FWHM and energy calibration,
- Nonlinearity calibration, which serves much more exact peak positions than it is expected from linear energy calibration;
- Efficiency determination, which may be used to generate efficiency-corrected peak lists;
- Database maintenance utilities for keeping your HyperLab databases in best shape, and much more.

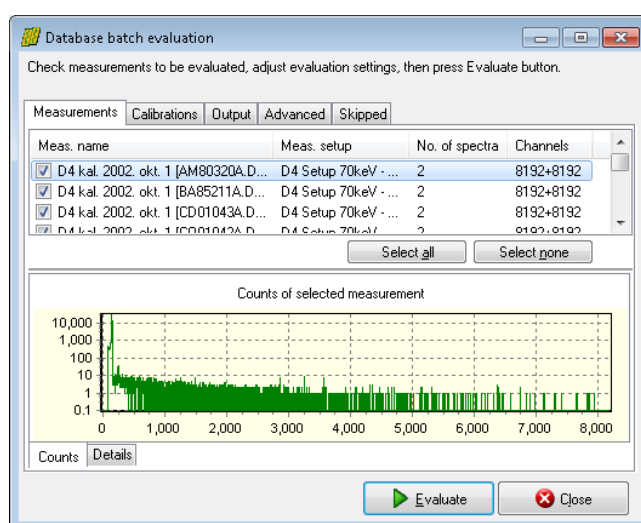
8. Using of the Database batch evaluator

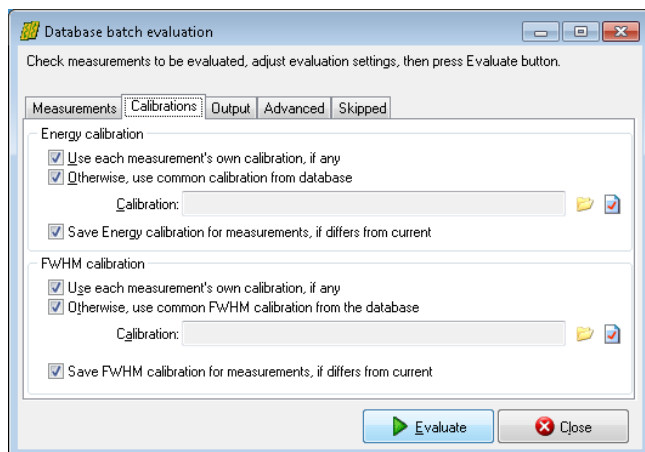
Database batch evaluator is a special peak evaluation component of HyperLab Main Module. It is capable to automatically evaluate several measurement entries stored in the database, each after the other.

To use the Database Batch Evaluator, click on *Measurements* node, then select *Batch evaluation* task.



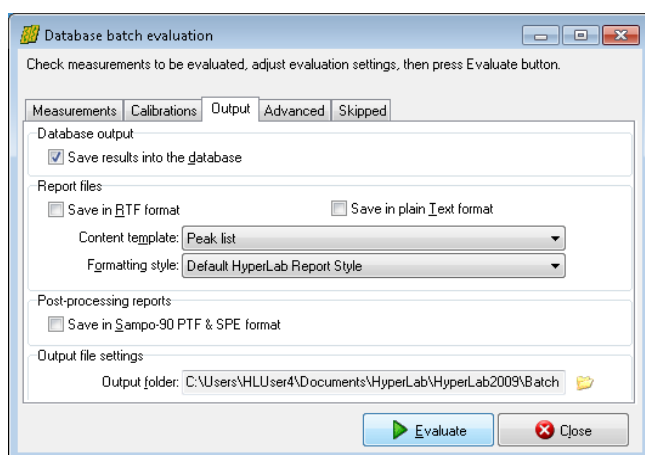
Now an evaluator window appears, listing all measurements assigned to this project. Check the list if it is really required to evaluate all spectra. If a measurement to be skipped, un-check it.





Change to *Calibrations* tab. If necessary, set the source of calibrations according to your measurement environment.

It is possible to use either the measurement's calibration or an arbitrary one from other measurement.

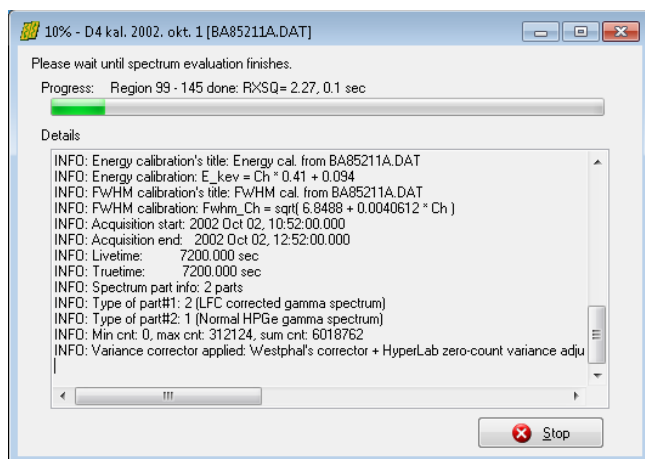


Specify evaluation output options under the *Output* tab.

You can save results into database, generate textual reports or Sampo files for post-processing.

Do not forget to set the folder where your report files will be saved.

You may also specify some other settings under Advanced tab.



Click Evaluate button to initiate the batch evaluation.

A new page appears now, displaying the overall progress of the batch as well as detailed messages for the last few measurement evaluation.

When evaluation finishes, press Close button.

Both the batch evaluation and the regular one-by-one spectrum deconvolution creates a new *Peak evaluation* entry into the database, which contains the fitted peaks and all of their parameters.

To re-open a previous peak fit – for inspection or manual correction – open the measurement node at the left, select the proper peak evaluation entry, then double-click it (or simply hit Enter key).

These peak lists can be easily opened by outer applications, e.g. Microsoft Excel for further data processing.

