HyperLab 2005
Quick Start Guide for
Main Module

HyperLabs Software
Budapest, Hungary

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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

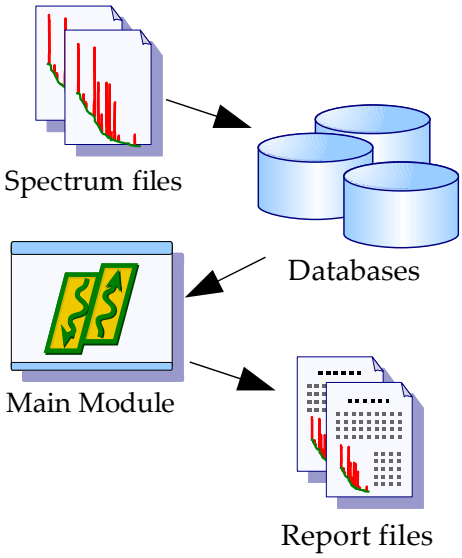
This Quick Start Guide contains basic information on HyperLab system, including system overview, and usage instructions. It also details initial steps to fill up a sample database and to carry out most common spectroscopy tasks. We will guide you through a comprehensive tour, where a set of sample spectra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

1.1. What is 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 to reliably evaluate extremely complex gamma spectra taken with semiconductor detectors. Evaluation of Dual LFC (Loss Free Counting) gamma spectra is also supported.
The software system is capable of determining your system's absolute or relative full-energy detector efficiency functions, as well as system nonlinearity function from multiple measurements taken with multiple sources. It is also capable of investigating the detector resolution versus energy function for arbitrary isotopes.

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 **database**s. Benefits of database systems are described in *Reference Guide*.



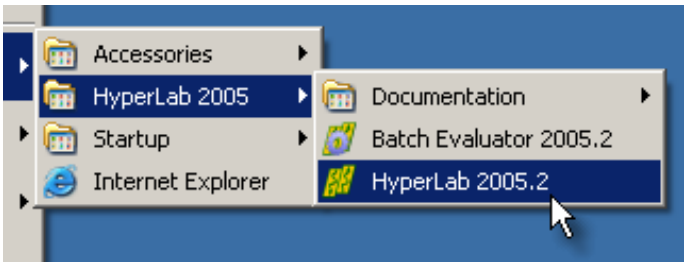
1.3. Overview of HyperLab tasks

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

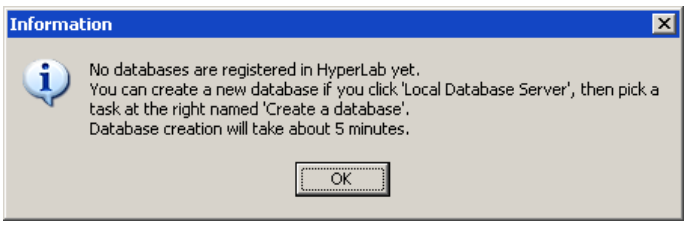
- Creating one or more databases with Main Module. The new database is “empty” at this point (indeed, it contains nuclear data).
- Defining the measurement setup, and also custom projects. Projects in the database are similar to folders of hard disks, and helps to manage vast amount of information.
- 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



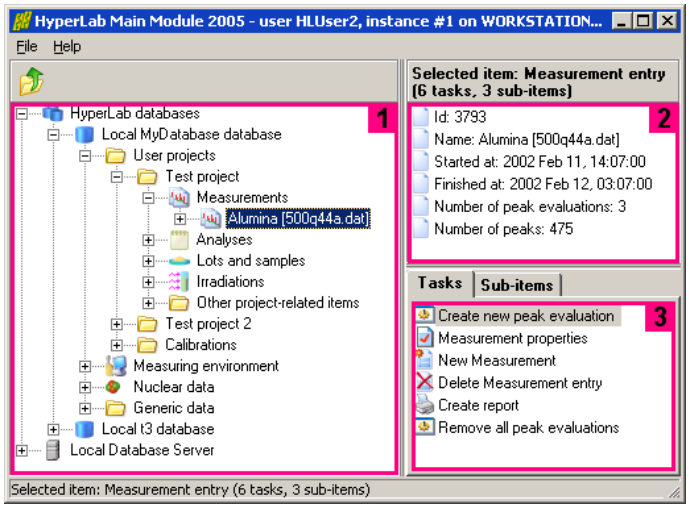
Start HyperLab Main Module by clicking on `Start/ Programs/ HyperLab 2005/ HyperLab 2005.2` menu.



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.

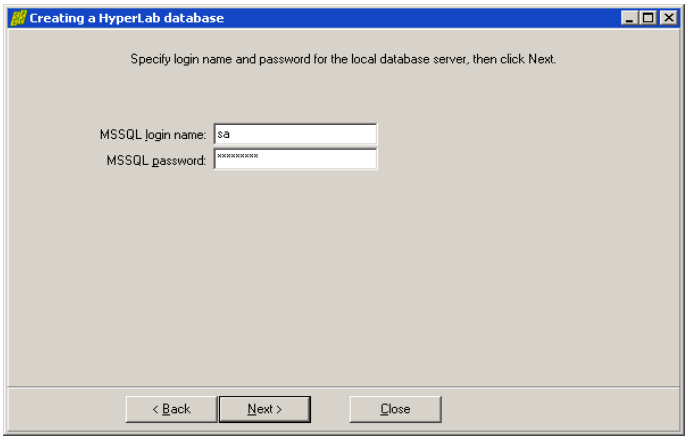
Common **keyboard shortcuts** may help your work: database tree may be walked through by using the *cursor arrow* keys, while the currently selected task may be started by hitting the *Enter* key. *Tab* key switches between the browser tree and the *Tasks* window.

3. Creating a new HyperLab database

In most cases, the next step is to create a new local database. First check if your local MSDE database service is running: the familiar green triangle should be displayed on your system tray. Starting with version 2005, HyperLab is able to use a remote database, that is, to transfer the evaluation data through the computer network from another user's database. In this case, no local database or database server installation is required, just a registration of the remote database. See *Reference Guide* for details.

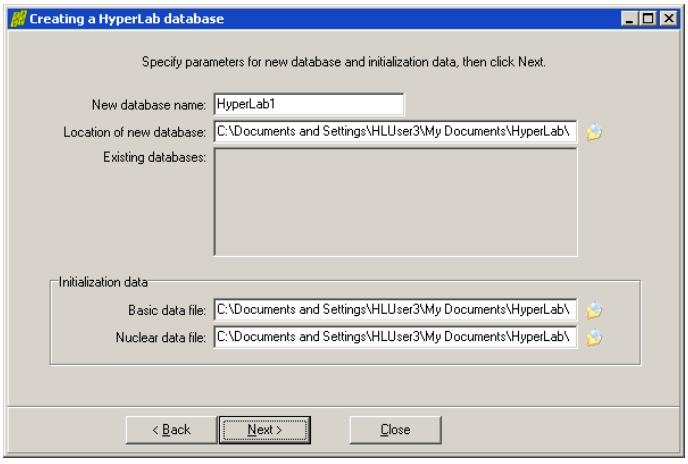
3.1. Database creation

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



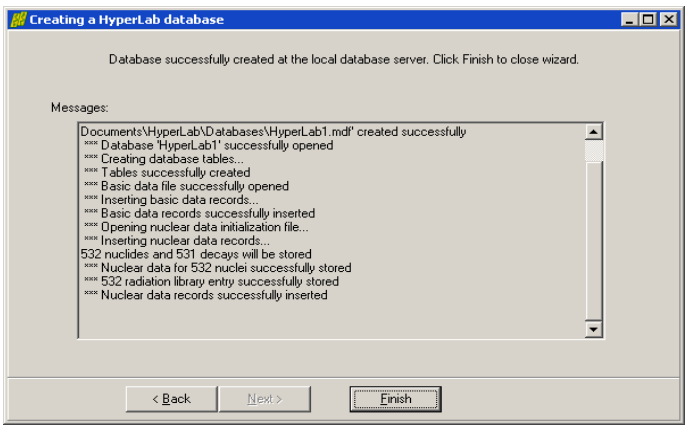
Database creating wizard appears now. Enter login name **sa** and password **hlpwd2005** for the database administrator. This is required because the database access is password protected.

When you are ready, click `Next`.



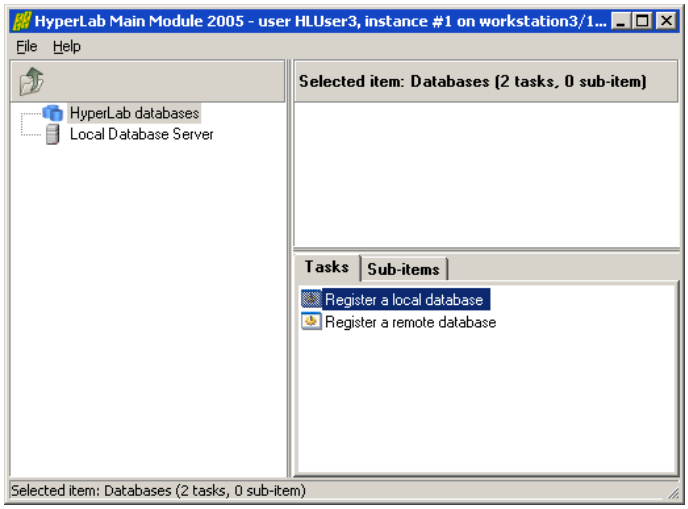
Specify the name of the new database, then click `Next`.

An automatic database creation process is started, which also incorporates the copying of large amount of nuclear data. The process may take several minutes. When the copying process ends, click `Finish`.



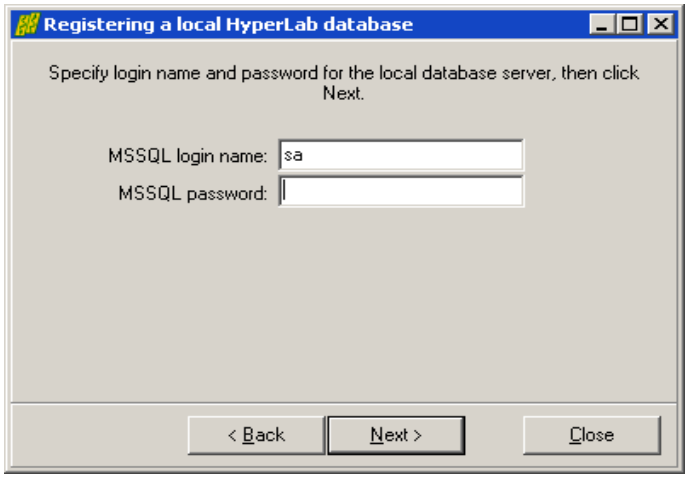
3.2. Database registration

When you create a new HyperLab database, MSDE database server will be its owner. However, HyperLab will not be aware of this new database without *registering* it. During registration, a simple entry created in a text file, which will direct HyperLab to display the database in the Main Module's database browser tree, under 'HyperLab databases' node. In order to register a newly created local database, follow the steps detailed below.

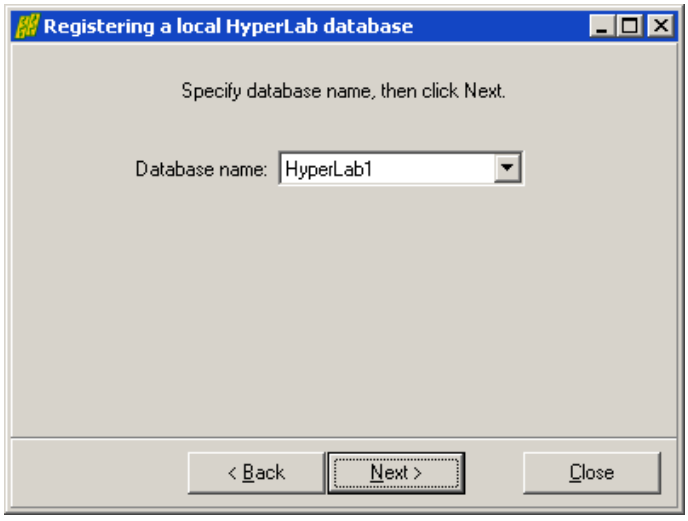


Click on the *HyperLab databases* root node in the database browser tree of the Main Module.

Click *Register a local database* task from the Tasks window.



The local database registering wizard appears now. Enter a valid database user name and password, then click *Next*.

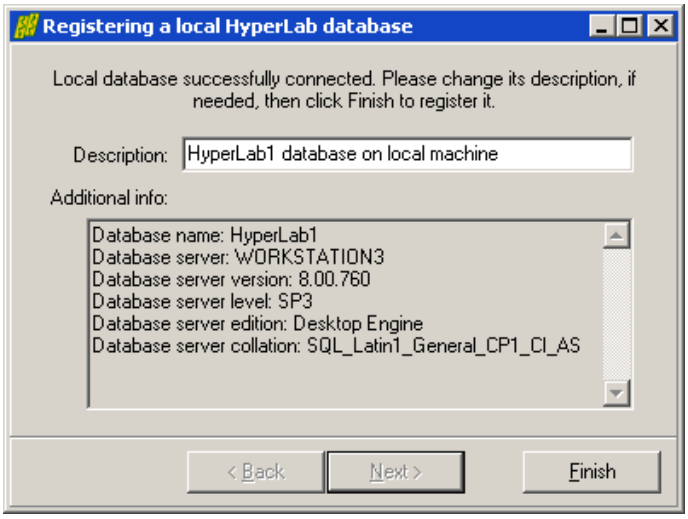


Select a local database which is currently not registered, then click next.

If the selected database is accessible on the local database server, then you can specify a description for the database. This description will be displayed in Main Module's database browser tree, under *HyperLab databases* node.

Also some attributes of the local database server is displayed.

When you are ready, click Finish.

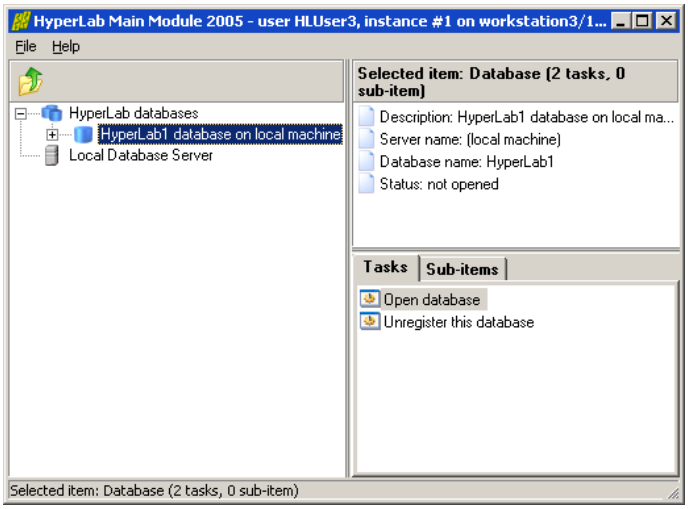


4. Using databases

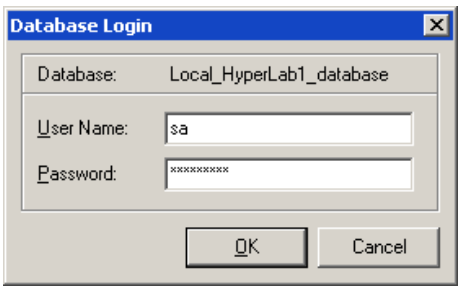
If you start Main Module, it will display the newly created database now.

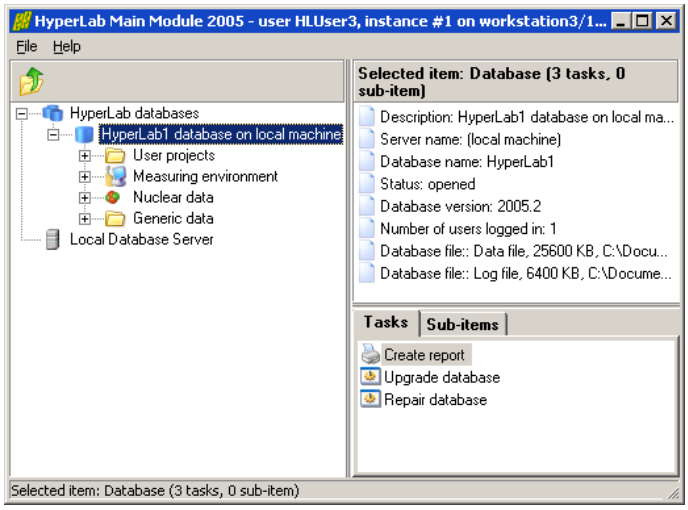
Click on the [+] sign beside the database to start working with it.

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



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

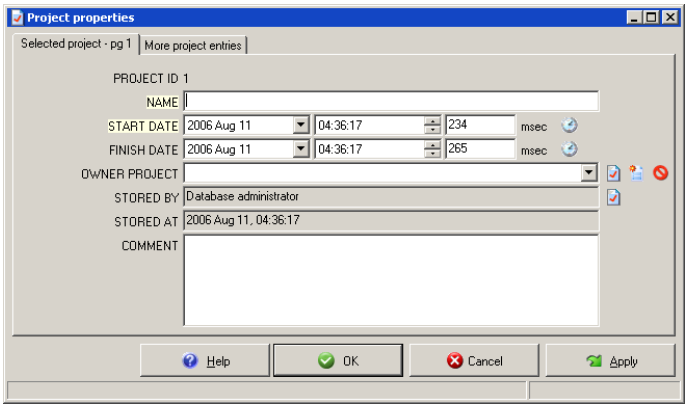




Usual database browser tree displayed at the left, with database details displayed at the top right, while the possible operations listed in the Tasks window.

Now you should create a new project for HyperLab sample spectra. Click on *User projects*, and on the task "*New project*".

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.

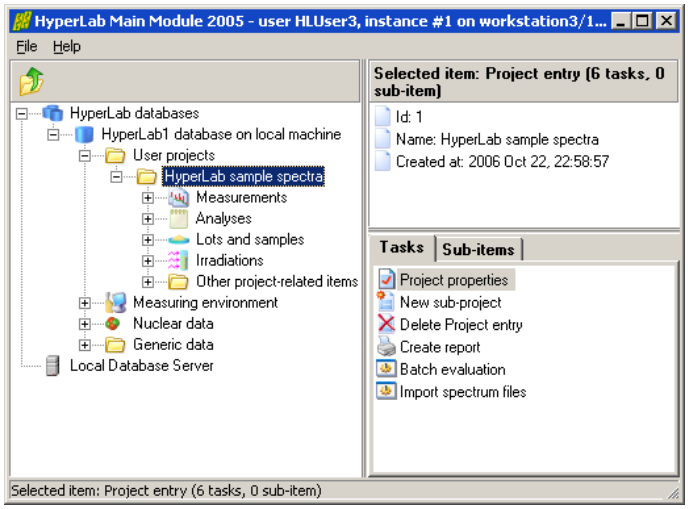


Now a database entry – or *record* - editor window appears. In this case the details of a new project record may be specified.

Different window belongs to each kind of database entry, but their basic building blocks are very similar.

For detailed description of record editor pages, see the *Reference Guide*.

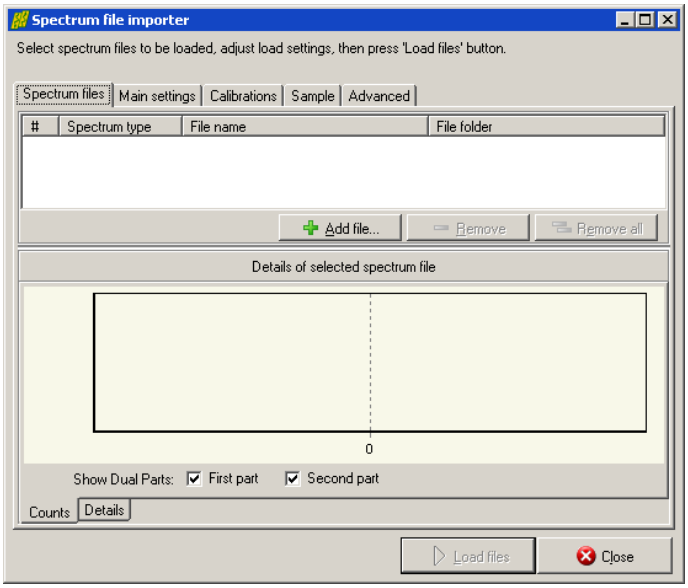
Now type a project name, say "HyperLab sample spectra", then click the OK button. Alternatively, you can hit the *Enter* key. *Tab* key will cycle through database editor fields.



A new user project appears in the database browser tree.
Open it, and click on *Measurements* node, then initiate the *Import spectrum files* task: simply click on it once in the Tasks window.

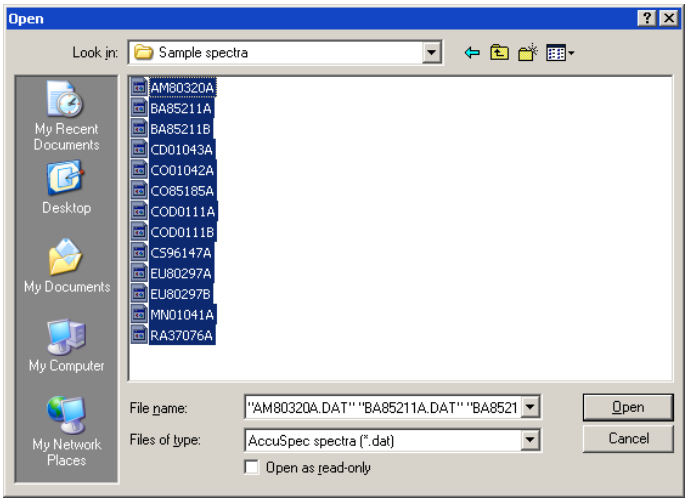
5. Importing spectrum files

As Main Module stores also the count information in databases, you should import your spectrum files to the database in order to evaluate them.
Click a project's *Measurements* node, and then select the *Import spectrum files* task.
A spectrum file importer window appears now.
Click on *Add file...* button to select HyperLab sample spectrum files.



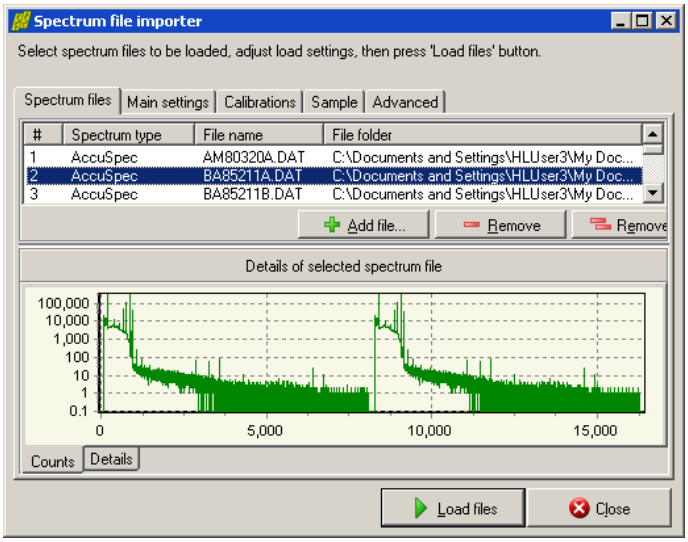
Now a standard file selection dialog appears. Select HyperLab sample spectra from folder `My Documents \ HyperLab \ HyperLab2005 \ Sample spectra`.

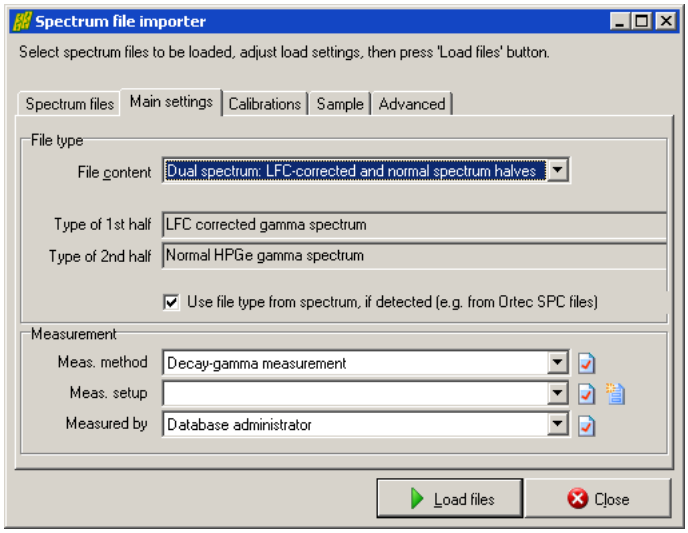
Select AccuSpec file type and all AccuSpec spectrum files where the last letter of the file name is “A”, then click *Open*. These measurements were taken with 70-3300 keV energy range.



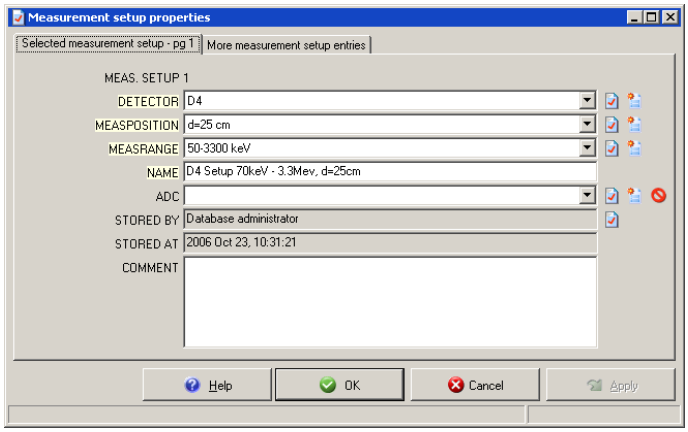
The selected files appear on the file importer's list.
As you can see, these are Dual LFC spectra with two similar halves. It is essential to correctly set the spectrum data type before loading, as HyperLab splits up dual spectra and stores their parts separately in the database.

Click on tab *Main settings*.



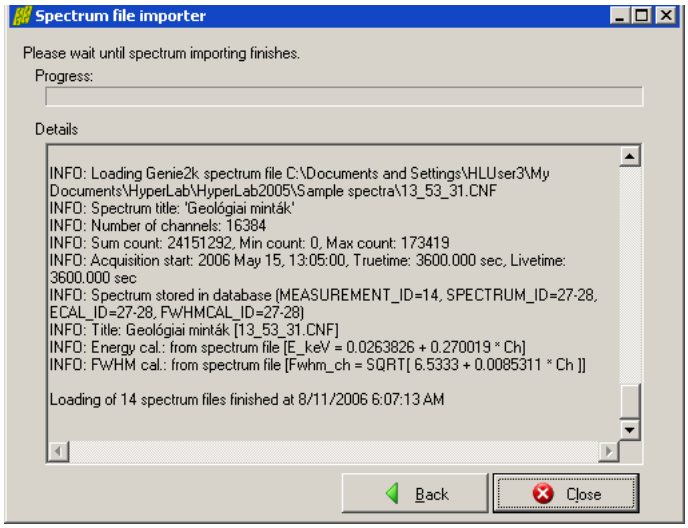


Set *File content* to Dual LFC.
Now the measurement setup should be selected from the list.
As currently there are no measurement setups defined yet in the new database, the list is empty. Create a new measurement setup entry by clicking on the *New record* icon:



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.

Create the following entries for the HyperLab 2005 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 70keV - 3.3Mev, d=25cm**' and '**D4 Setup 50keV - 2.2Mev, d=25cm**'.
After this setting is appropriate, 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.
The spectrum files will be displayed under *Measurements* node in the database tree now.
Do not forget to import also the spectrum files with “B” as the last letter of the file name. These should be assigned to the measurement setup 50-2200 keV energy range.

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.
- **Standalone spectrum file evaluator** utility, which operates on a batch 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 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.

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:

– 2^{nd} 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 – 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.

Moreover, HyperLab tries to eliminate unnecessary fit components after fitting regions, and to automatically remove them. 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.

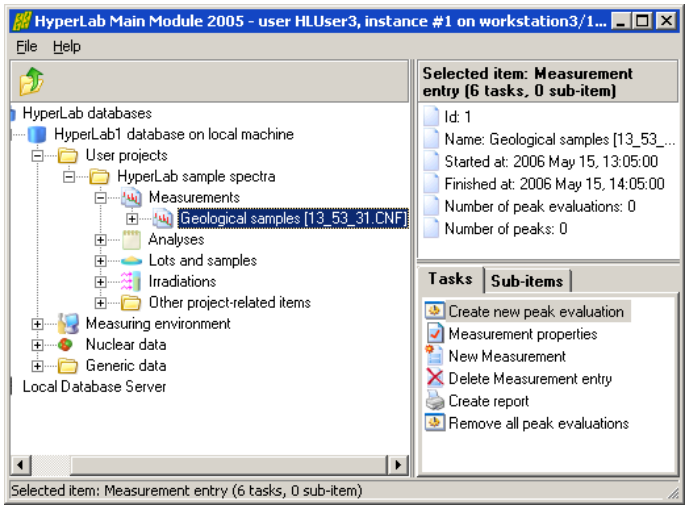
7.1. A bird's eye view of the evaluation process

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.

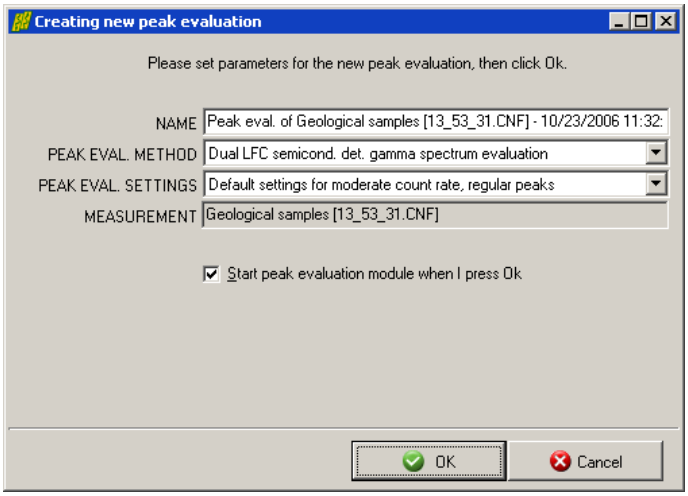
7.2. Starting the evaluator



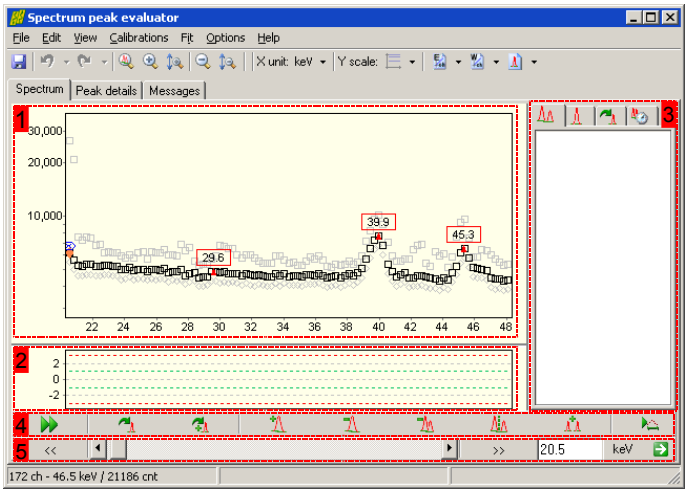
To start using the Peak evaluator, first select your measurement in the database browser tree, then click task *Create new peak evaluation* in the Tasks window.

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

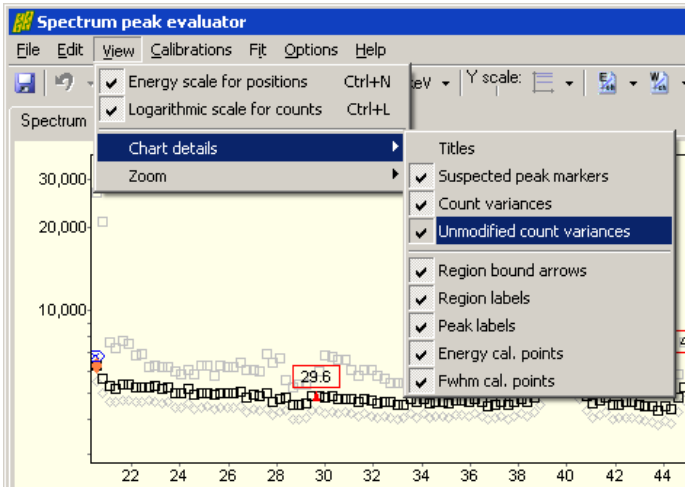
A new peak evaluation creation window appears now. You can leave defaults in most cases, so just click *OK* for now.



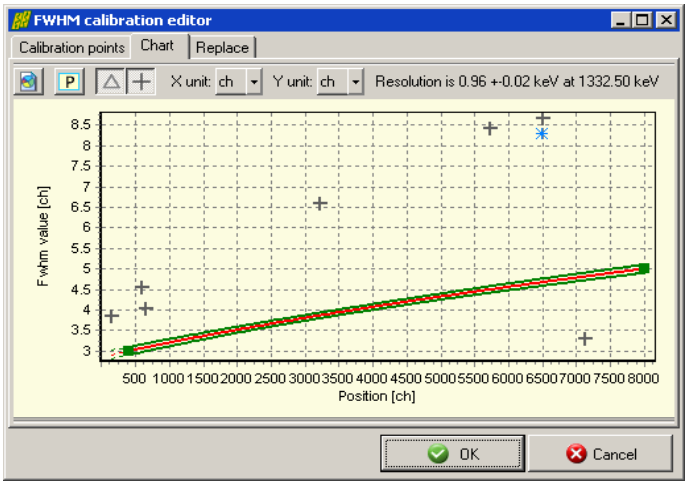
Main window of spectrum peak evaluator appears now. The center of the window is occupied by the **spectrum window [1]** and the **residual window [2]**. The residual window displays the difference between the measured counts and the fitted peak curves.
A **region list panel [3]** is placed on the right, 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 **suspected peaks**, whose position is determined by the current FWHM calibration. Deconvolution will use these suspected peaks as an initial estimate.



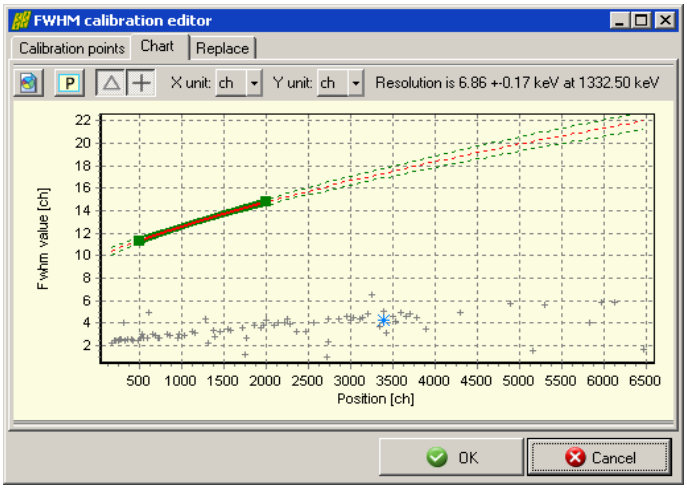
First you should modify some spectrum display settings. By default, spectrum evaluator displays the counts (black squares) together with the corrected variances (gray squares) and uncorrected variances (gray diamonds). The variance correction is for taking account the distorting effect of high count 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

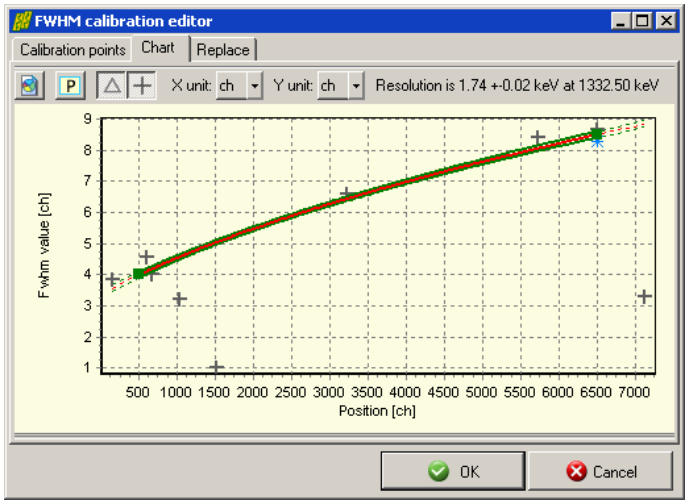


HyperLab's nonlinear spectrum deconvolution algorithm requires only a rough peak width (FWHM) calibration to start working. For exact peak positions, a valid energy calibration is also required. Therefore it is advisable to check first the validity of the FWHM calibration.
To display current FWHM calibration, select *Calibration / FWHM* calibration menu item. Now the FWHM calibration editor window appears.
For a quick calibration check, click *Chart* tab at the top. Currently used FWHM 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 serves 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 FWHM calibration points should be modified on the *Calibration points* page.

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



In case of proper FWHM calibration majority of the suspected peaks' estimated FWHM value is in the neighborhood of the calibration curve.
Please note that large deviations may occur even for valid calibration, as peaks' FWHM values 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*.

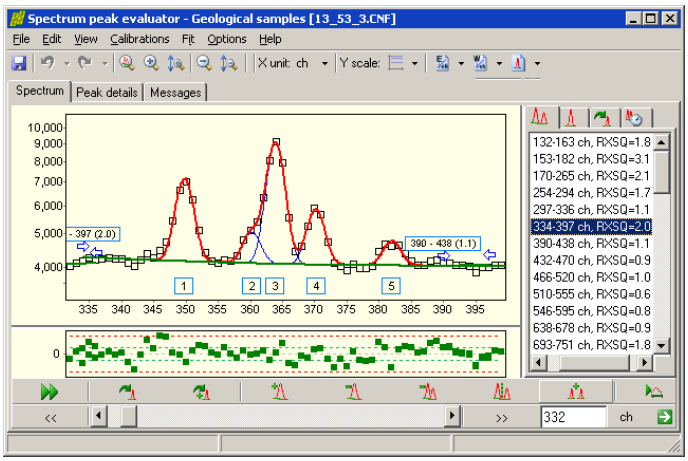
7.4. Checking Energy calibration

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.

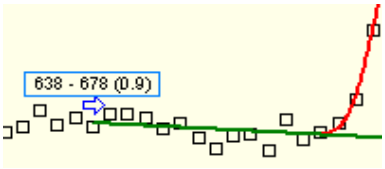
Note: When the fit completes, a finer energy calibration may be constructed, because exact, fitted peak centroid positions are available.

7.5. Performing automatic fit

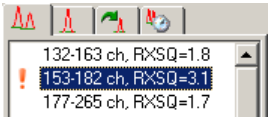
Click the Autofit button or select Fit / Start automatic fitting menu item to initiate a fit for the whole spectrum. A progress window is displayed during the fit, listing the problematic regions, where the reduced Chi-squared of the fit exceeded 3.



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.



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.

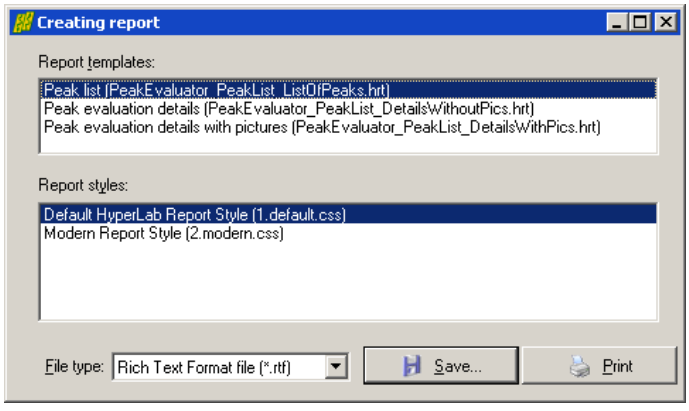
Delete the clicked region with all of its peaks.

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 2000 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:

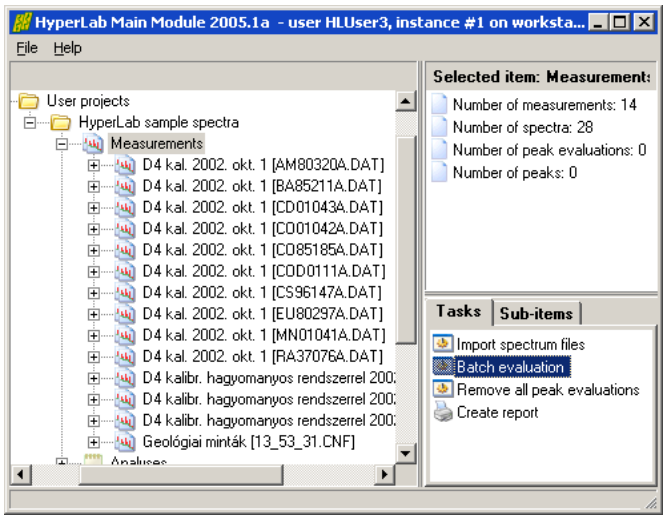
- FWHM and energy calibration,
- Nonlinearity calibration, which serves much more exact peak positions then it is expected from linear energy calibration;
- Efficiency determination, which may be used to generate efficiency-corrected peak lists;
- Database maintenance utilities for keeping your HyperLab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

and much more.

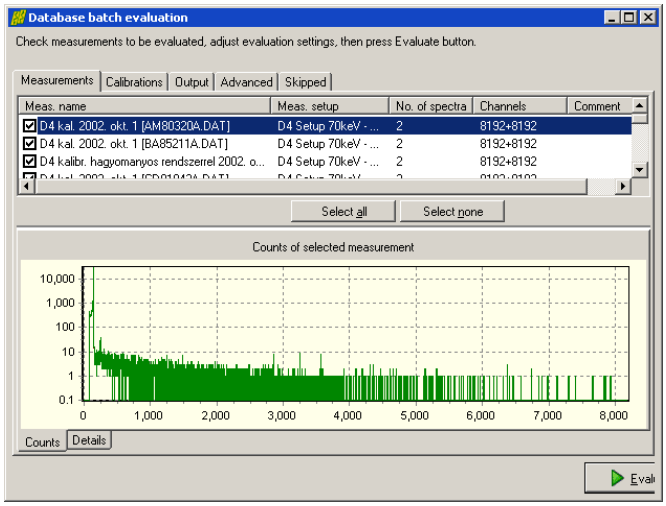
8. Using of the Database batch evaluator

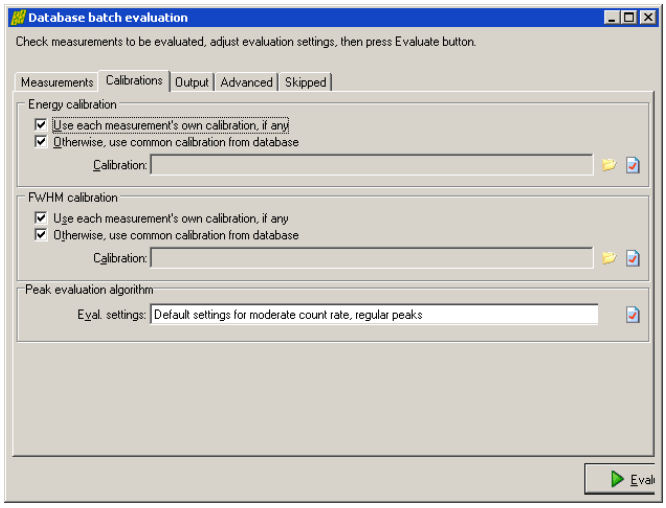
Database batch evaluator is a special peak evaluation component of HyperLab Main Module. It is capable to automatically evaluate several measurement entries stored in the database, each after the other.

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

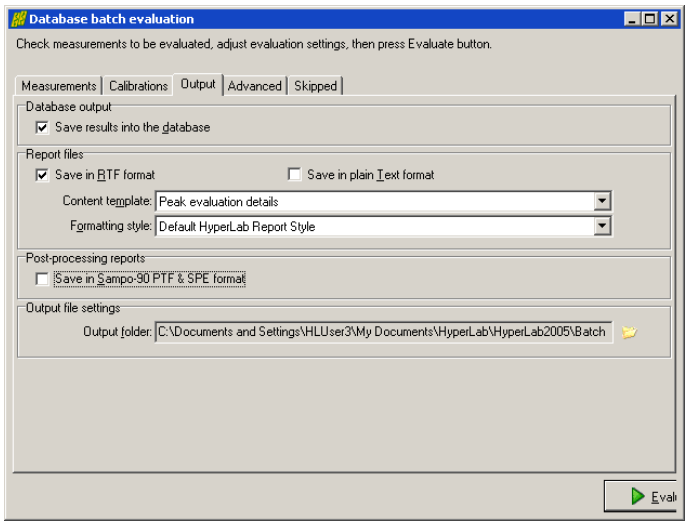


Now an evaluator window appears, listing all measurements assigned to this project.
Check the list if it is really required to evaluate all spectra. If a measurement to be skipped, un-check it.



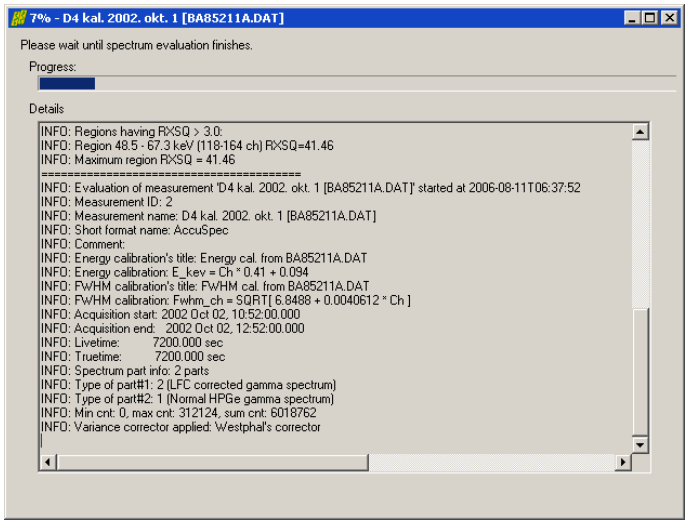


Change to Calibrations tab. Set the source of calibrations according to your measurement environment.
It is possible to use either the measurement's calibration or an arbitrary one from other measurement.



Specify evaluation output options under 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.