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Brief Operating Instruction
ENERSIC600

Software Manual

Endress+Hauser
People for Process Automation

Described product
Product name: ENERSIC600

Manufacturer
Endress+Hauser SICK GmbH+Co. KG.
Bergener Ring 27
01458 Ottendorf-Okrilla
Germany

Legal information

Original document
This document is an original document of Endress+Hauser SICK GmbH+Co. KG.

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Table of Content

1 About this document

1.1 Function of this document

This document describes the use of the dedicated PC software for the ENERSIC600.

1.2 Scope of application

These User Instructions are only applicable for the device described in the product identification.

They are not applicable for other Endress+Hauser devices.

The standards referred to in these User Instructions are to be observed in the respective valid version.

1.3 Target groups

This Manual is intended for persons commissioning and operating the device.

Commissioning and operation

The software may only be used by qualified persons who, based on their device-specific training and knowledge as well as knowledge of the relevant regulations, can assess the tasks given and recognize the hazards involved.

1.4 Further information

- Operating Instructions ENERSIC600

2 Product description

2.1 Product identification

Product name	ENERSIC600
Manufacturer	Endress+Hauser SICK GmbH+Co. KG. Bergener Ring 27 · D-01458 Ottendorf-Okrilla · Germany
Type plate	Bottom, beneath gas ports

2.2 Product characteristics

The ENERSIC600 software is dedicated to remote control ENERSIC600 on-line gas composition analyzers via a Windows PC. It also provides both data handling facilities and instrument control.

3 Introduction

3.1 System requirements

The ENERSIC600 software has the minimum system requirements as follows:

Processor: Pentium III/Celeron 866 MHz (or equivalent) or later (32-bit), Pentium 4 G1 (or equivalent) or later (64-bit)

RAM: 4 GB

Minimum screen resolution: 1024 x 768 pixels

Minimum disk space: 620 MB

Operating system: Windows 10/8.1/7 SP1, Windows Server 2012 R2, Windows Server 2008 R2 SP1

3.2 Communication

The communication between the analyzer and PC is via a (wired) LAN connection.

3.3 Installation

Running the ENERSIC600 installer which is supplied by Endress+Hauser allows to install the ENERSIC600 software on the system. The user must respond to the dialog windows during installation. The system must be restarted when installation is completed. The ENERSIC600 application requires the LabVIEW 2016 run-time engine, which is installed if necessary.

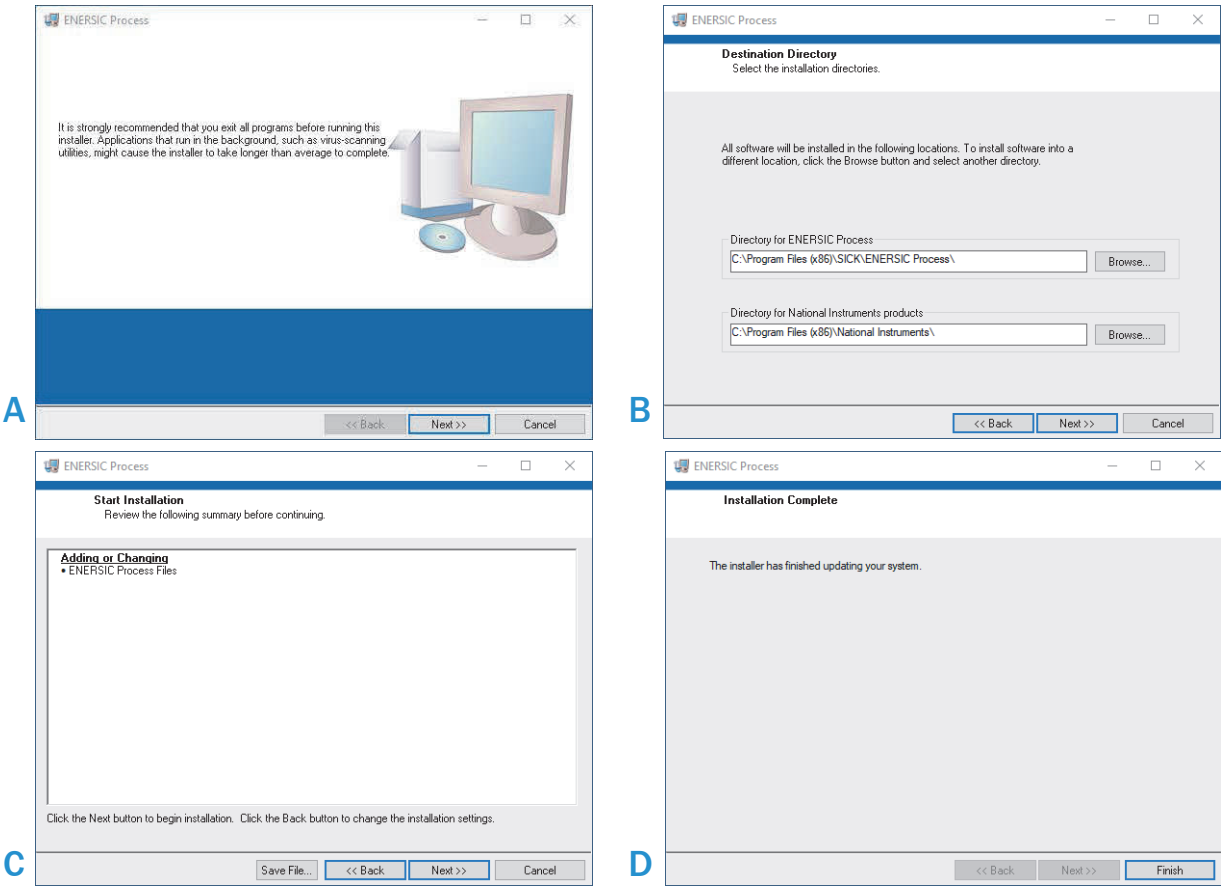


Fig. 1: ENERSIC600 software installation steps

3.4 Running multiple instances

It is possible to run multiple instances of the ENERSIC600 software.

- Each instance requires its own executable. This can be achieved by selecting a different directory for each ENERSIC600 instance during the installation process (see step B in Figure 1).
- Each instance requires its own application data location. This can be set in the Application preferences (see Chapter 5.1.2).

Note that the Application data folder setting itself is stored in the default storage location (My Documents\ENERSIC Explorer\GC control). This folder should therefore not be deleted after the data location has been changed.

4 Quick start guide

4.1 Start and Login

When the ENERSIC600 software is started, the login screen appears.

Instruments on the local network can be detected by clicking the “magnifying glass”. When multiple instrument addresses are available, the instrument can be selected from the drop-down list according to the analyzer serial number. The serial number can be found on the label of the instrument. The list can be cleared via right click option on the list. It is also possible to use the software without communication with an analyzer. In this case, “Offline” option must be chosen.

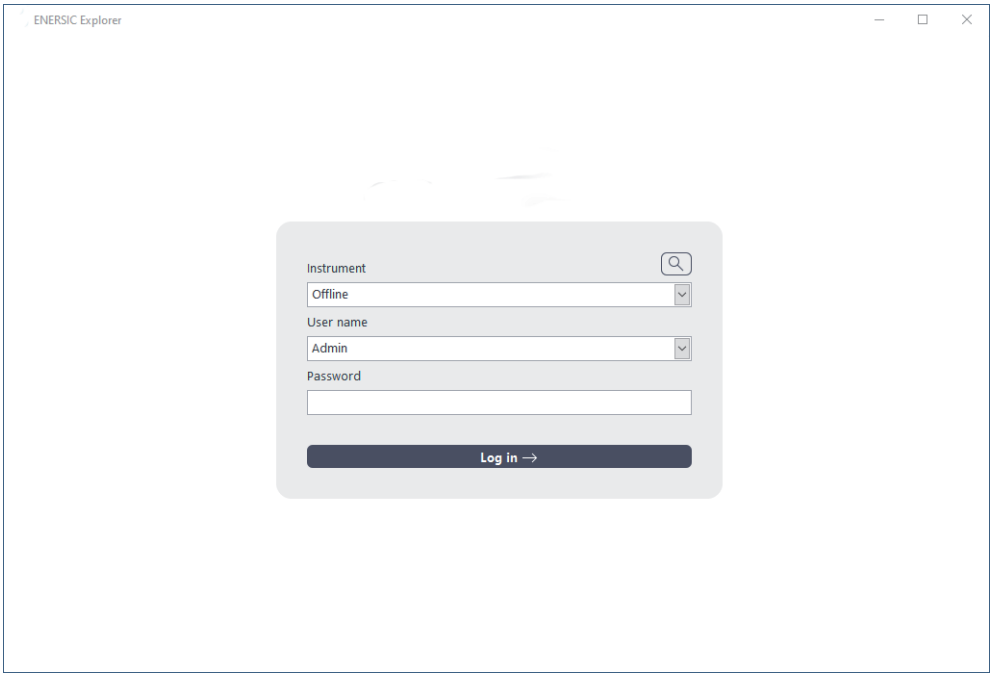


Fig. 2: Login screen

When the user name and password (if required) are entered, the main user interface appears and the software is ready to use. The user credentials can be managed by admin level users (see Chapter 5.1.1).

The ENERSIC600 software supports the languages English, German, French, Dutch and Portuguese. The language setting can be changed by admin level users. The default selection is based on the native language of the installed operating system. The default is English, when the operating system does not match any of the available languages (see Chapter 5.1.2).

The main user interface (UI) (Figure 3) consists of a menu bar (Application, Instrument, Sequence, Method, Data, Info) and fields (Instrument control, Instrument status, Live view, Result view, Trend view) on the view selector which is on the left hand side of the main window. Instrument control, Instrument status, Live view fields and Instrument menu on the menu bar are available only when the software is connected to an analyzer (online). The status bar at the bottom shows instrument current date - time, instrument status, current user, progress indicator and connection status.

The main user interface is explained in detail in Chapter 4.3.

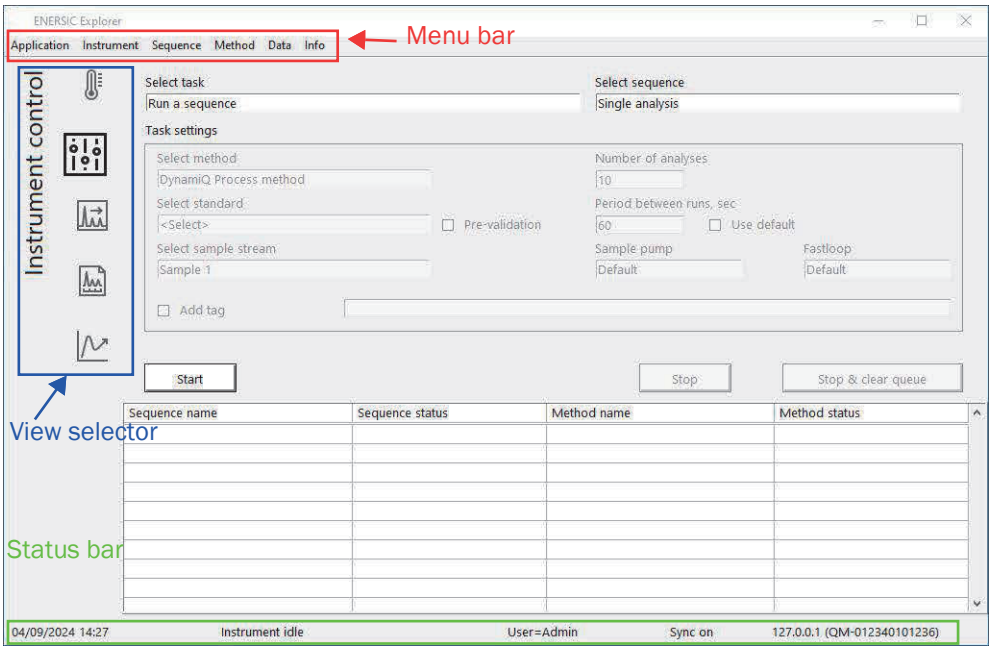


Fig. 3: Main user interface (UI) (online view)

4.2 Method setup

In order to run an application, an analysis method must be defined (see also Chapter 5.1). This can be achieved via the Method editor wizard. It consists of multiple windows and allows to set up the method step-by-step. The right click on Previous or Next on the Method editor windows allows to open the desired Method editor window directly.

Method-> Method editor (F9)

The Method editor wizard can be used in combination with the Method preview tool to show the effect of a change in the method settings on the existing results (see Chapter 5.1).

The method to be edited should be chosen via the Method selection window (Figure 4). The following options are available:

New method (online) creates a blank method adapted to the connected instrument.

Existing method (online) loads an existing method residing on the connected instrument.

Saved method (offline) loads an offline method saved locally on the PC. In case the software is connected to an instrument, the method is adjusted (if possible) to match the configuration of the connected instrument.

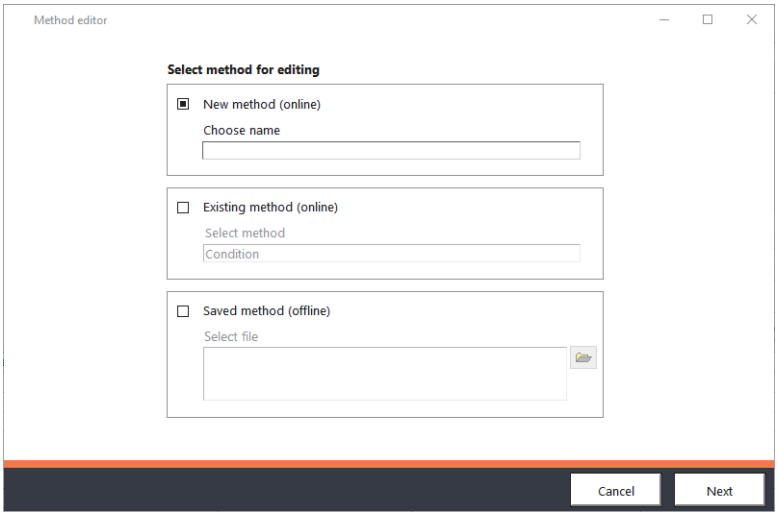


Fig. 4: Method editor, Method selection window

4.2.1 Instrument settings

After selecting the method to be edited, the next step is Instrument settings (Figure 5).

The Instrument settings window consist of two parts: the left part gives an overview of all method settings, the right part allows defining a setpoint profile for the parameters supporting this (which are highlighted in grey), e.g. column temperature, carrier pressure, etc. Selecting such a setpoint enables the Profile Table and graph on the right and allows to define a profile. The items can be expanded/collapsed by right click.

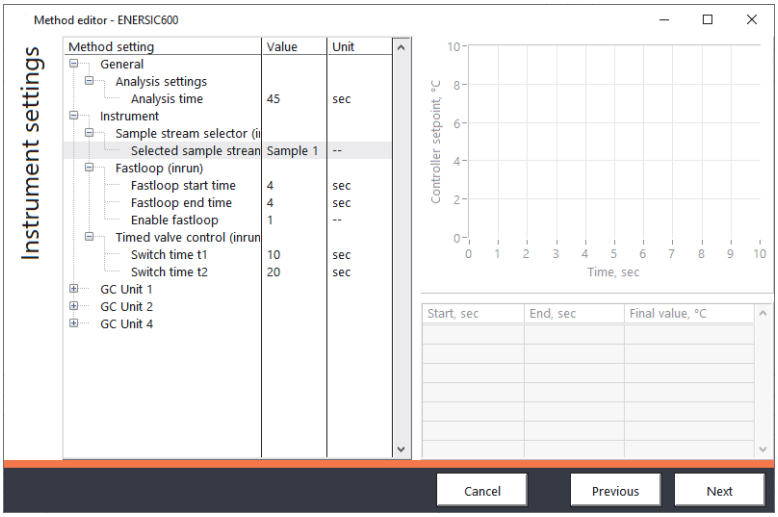


Fig. 5: Method editor, Instrument settings

Run settings are under General and allow to set run time per analysis in seconds where t=0 is the start of the injection.

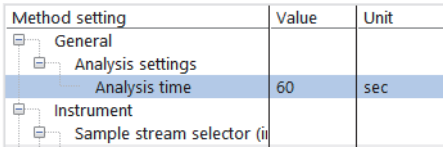


Fig. 6: Instrument settings, Run settings

Instrument settings allow to adjust instrument related devices setup e.g. sample gas pump, stream selector, fastloop (Figure 7). Which devices are listed depends on the specific configuration of the instrument. Sample gas pump 1 and Fastloop (inrun) can be enabled by entering value “1” and disabled by entering value “0”. The stream must be selected from the drop-down list. See your instrument’s Operating instructions for further details about the instrument devices.

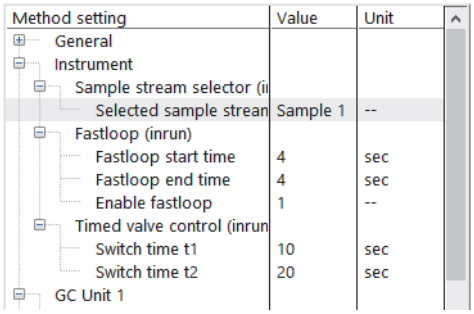


Fig. 7: Instrument settings, Instrument settings

Channel settings allow to adjust the injector and detector temperature, column temperature, carrier pressure, foreflush and backflush timing for each individual channel.

The temperature of the injector and the detector cannot be controlled separately since both elements are located on a single micro-chip. The recommended range is between 100-120 °C.

The recommended range for the column temperature is between 50-180 °C and between 50-270 kPa for the carrier pressure.

The injection time is the duration of the injection in milliseconds. The backflush time is the amount of time between the injection and the switch to the backflush state in seconds. The foreflush time is the amount of time between the injection and the switch to the foreflush state in seconds. The foreflush time should be set to at least 2x backflush time to ensure to remove sample from the pre-column before switching back to foreflush. A negative value can be set, indicating that the injector is switched to foreflush before injection. Prerun backflush on can be enabled by entering the value “1” and then the run starts in the backflush state. In this case a negative foreflush time should be set to ensure that the injector is in foreflush during the injection and so that the sample is injected, e.g. when the foreflush time is set to -10 sec., the injection will occur 10 seconds after the run start. See your instrument’s Operating instructions for further details about foreflush and backflush.

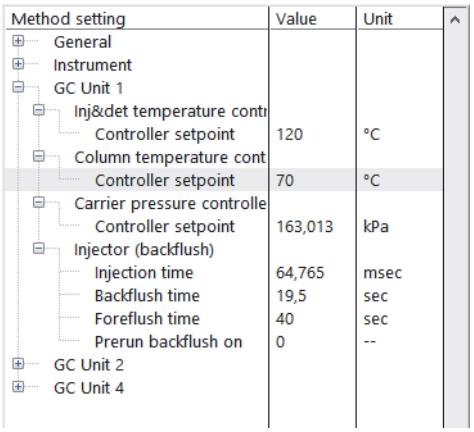


Fig. 8: Instrument settings, Channel settings

After the instrument settings are adjusted, the next step is to select the detectors to be included to the analysis (Figure 9). The Select detectors window shows all detectors available on the instrument and allows selection.

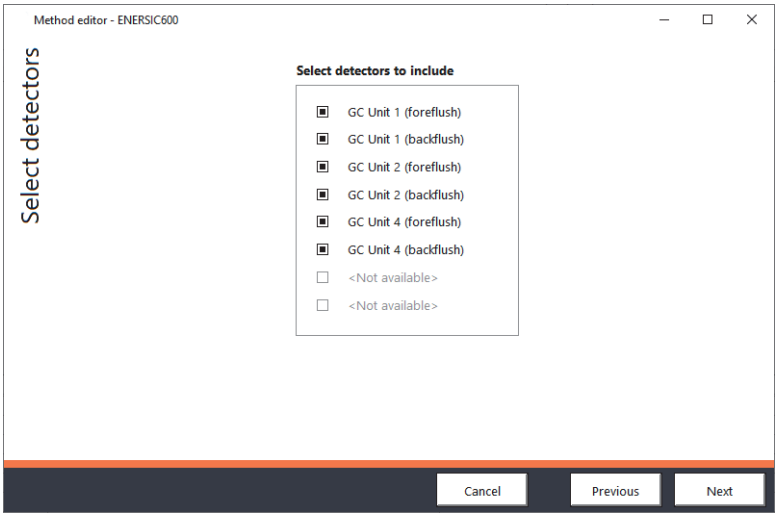


Fig. 9: Method Editor, Select detectors

After selecting the detectors to be included to the analysis, a pilot chromatogram can be created in the next step.

A pilot run can be run by clicking the Start button (online only). This will start a run using the settings defined in the previous steps (Figure 10). The acquired pilot chromatogram allows to optimize the integration and identification of the peaks in the next steps. The appearance of the chromatogram can be adjusted using the zoom palette (see Chapter 7.1) or by right clicking to change preferences.

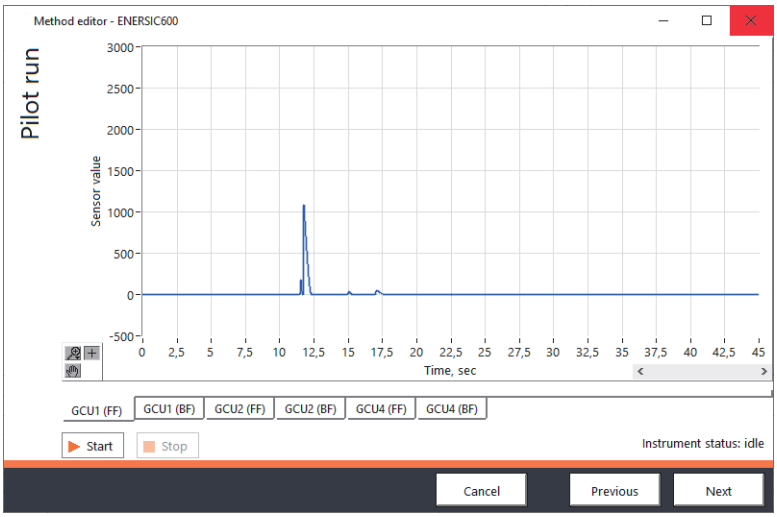


Fig. 10: Method editor, Pilot run

4.2.2 Integration

The next step is integration of the peaks. The Method editor integration window shows the pilot run and the Integration Table (Figure 11).

The peaks are integrated using an automatic built-in algorithm. The integration events allow the user to fine-tune the algorithm by overriding default parameters.

The Integration Table allows to set integration events for each available peak. A right click on the table shows options for the table and left click on the values allows to edit these. Peak tracking can be enabled/disabled for each event (see Chapter 4.2.5).

Integration events are applied in the given order - starting from the top of the table. The overlapping events of the same type override each other, i.e. for similar events in the same time section, the last event in the list is used.

The chromatogram appearance can be adjusted via the zoom palette (see Chapter 7.1) or by right clicking to change preferences.

See Chapter 7.2 for tips and tricks to setup integration events.

The integration events can be classified as detection events, filtering events, baseline selection events and baseline skimming events. Brief explanations for the available integration events are listed below.

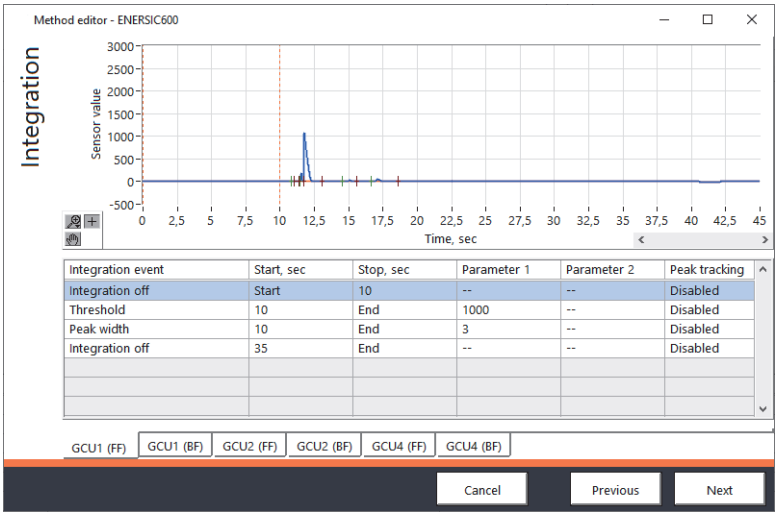


Fig. 11: Method editor, Integration

Peak detection

Threshold influences the sensitivity of the peak detection. Decreasing this value not only increases detection sensitivity, but also the rate of false identifications. If many false peaks are present, the threshold should be increased (Default = 1000).

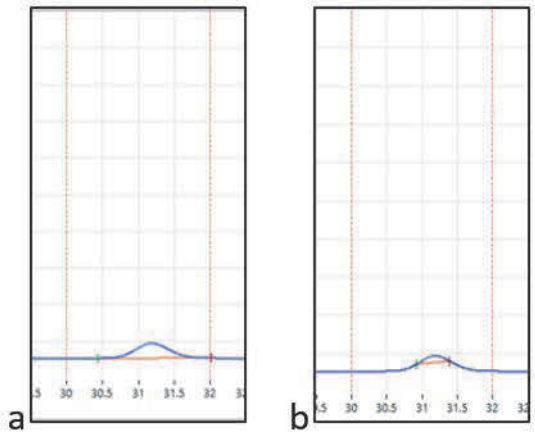


Fig. 12: Changing Threshold value from 10 (a) to 1000 (b)

Peak width influences the sensitivity of the peak detection. It should typically be equal to 1-2 times of the width of the peak to be detected (Default = 1 sec.).

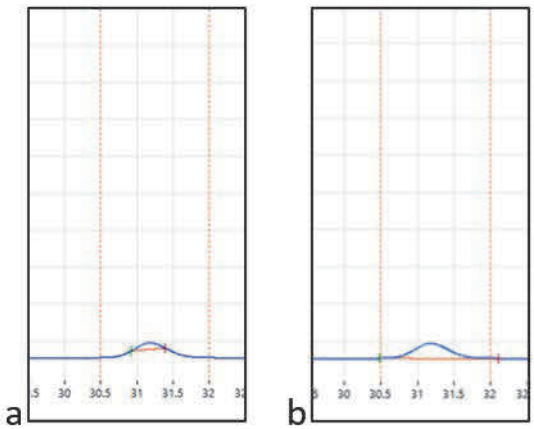


Fig. 13: Changing Peak width value from 1 (a) to 10 (b)

Negative peaks allows to integrate only the negative peaks in a specific area in the chromatogram. If negatives peaks are to be integrated, the start and stop points should be set around the negative peak.

All peaks allows to integrate both the negative and positive peaks in a specific area of the chromatogram.

Peak filtering

The peak filtering events filter out unwanted peaks from the result set.

Integration off filters out all the peaks in a specific area of the chromatogram.

Minimum area allows not to integrate all peaks with an area below the chosen value.

Minimum height allows not to integrate all peaks below a chosen height in a specific area of the chromatogram (default = 0).

Minimum width allows not to exclude all peaks below a minimum width a specific area of the chromatogram.

Baseline selection

The baseline selection events allow local adjustments to the baseline. The events valley-to-valley and common baseline affect the baseline only when they are applied to the groups of partially separated peaks. The other baseline selection events can also be applied to the individual peaks.

Valley to valley draws the baseline from the beginning of the first peak to the lowest point between the first peak and the second peak, and from that point to the ending of the second peak.

Common baseline draws a baseline from the peak start to the peak stop. This is the default method to draw the baseline.

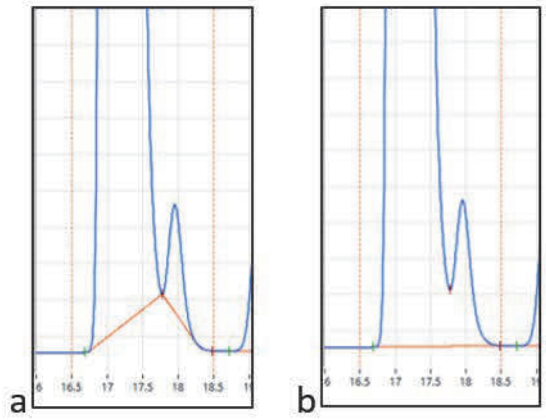


Fig. 14: (a) Valley to valley, (b) common baseline

Forward horizontal draws the baseline as horizontal line from the start of a peak.

Backward horizontal draws the baseline as a horizontal line from the end of a peak.

Lowest point horizontal draws the baseline as horizontal line from the side that is lowest, which can be either the right or the left side of the peak.

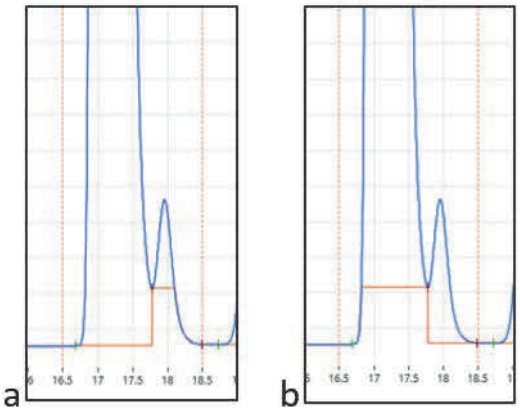


Fig. 15: (a) Forward horizontal, (b) backward horizontal

Baseline skimming

Baseline skimming events allow to adjust the baseline and/or handling of shoulder peaks. By default, partially separated peaks are calculated using a drop-down perpendicular. This may be changed by applying skimming. These events redistribute the peak area by adding the area below the shoulder peaks to the main peak. The set value denotes the ratio between the peak heights, for which the rule is applied. It is only useful to apply this event if the peak is on the tail or front of a much larger peak. If the set value is lower than the default value, the event is not applied.

Front tangent draws a straight line with a certain slope from the ending (valley) of a peak to a point on the baseline backwards in time to simulate the starting of the peak (Default = 5).

Tail tangent draws a straight line with a certain slope from the ending (valley) of a peak to a point on the baseline forwards in time to simulate the ending of the peak.

Front exponential draws an exponential line with a certain shape from the ending (valley) of a peak to a point on the baseline backwards in time to simulate the starting of the peak (default = 5, default parameter 2 = 50)

Tail exponential draws an exponential line with a certain shape from the ending (valley) of a peak to a point on the baseline forwards in time to simulate the ending of the peak.

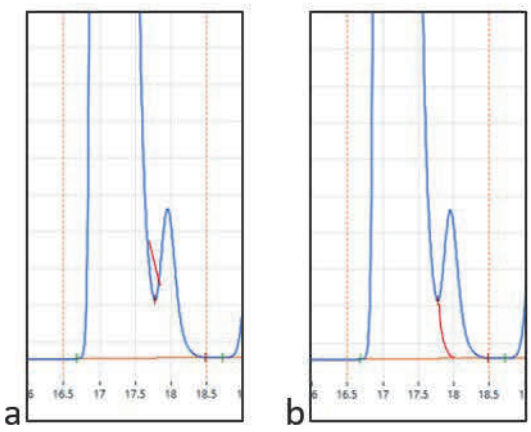


Fig. 16: (a) Tail tangent, (b) tail exponential

4.2.3 Identification

After the integration events are set, the next step is identification of the peaks. The Method editor identification window shows the pilot run and the Identification Table (Figure 17).

The appearance of the chromatogram can be adjusted via the zoom palette (see Chapter 7.1) or by right clicking to change preferences.

The Identification Table allows to identify the integrated peaks. The right click on the table shows options for the table and left click on the values allows to edit them.

Apart from the compound name and the Identification window, the identification type (Peak or Group) must be chosen. Peak tracking can be enabled/disabled for each compound (see Chapter 4.2.5).

Once a peak is identified, it cannot be identified again. Identification rules are applied in the given order - starting from the top of the table. The order may be changed using the Table context menu.

The applied order allows (as explained below) for overlapping Identification windows.

If multiple peaks are found within an Identification window, either the peak with the largest area is identified (Peak identification) or all peaks within the window are identified (Group identification). If some peaks in the window are desired to be excluded from the group, they must be identified before the group is identified.

It is possible to define overlapping Identification windows. In this case the peak with the largest area is identified first and then the one with the second largest area and so on.

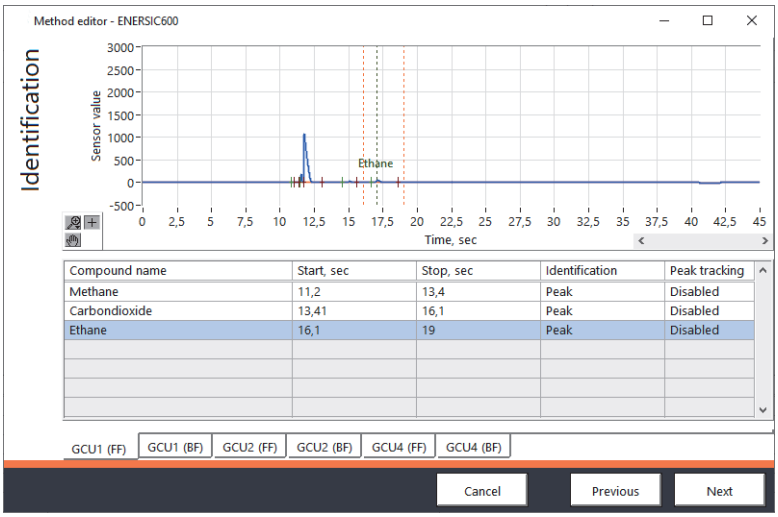


Fig. 17: Method editor, Identification

4.2.4 Calibration

After the peaks are identified, the next step is adjusting the calibration settings and specifying the calibration standards. The Method editor calibration window consists of the following tables (Figure 18):

Standard Table (red box on Figure 18) allows to add/remove calibration standards. A right click on the table shows options for the table and left click on the values allows to edit them. Standards can be imported/exported from/to the standard database using the context menu of the standard list (see Chapter 5.4.6). It must be chosen in this table when the added standard is included in the calibration. Non-included standards can be used to update response factors without changing the response curve in case of Calibration (update), and can be used to update the response factors and scale the response curve in case of Calibration (scale). Both included and non-included standards can be used to validate the response curve (see Chapter 4.3.1).

Composition Table (blue box on Figure 18) allows to specify the composition of the calibration gases. The certified quantity of the used standard must be specified for each compound. The total summed quantity can be seen at the bottom. The right click on the table shows options for the table and left click on the values allows to edit them. The values of the Response column can be left at zero, this will be determined by running a calibration.

Calibration Table (green box on Figure 18) shows the identified compounds in the previous step (Identification) and allows to adjust calibration settings. This can be done by left clicking on the columns and selecting the value from a drop-down list for each identified compound. The Standards column links the compound in the Calibration Table to a compound in the defined standard (i.e. the Composition Table); a compound in the Calibration Table may be linked to multiple standards, each link effectively adding a point to the calibration curve. The right click on the table allows to open the Calibration viewer (see Chapter 4.3.6) or to export data to the clipboard.

The calibration curve should be linear but may be somewhat non-linear due to e.g. peak overloading or TCD non-linearity. The curve can be modeled using a polynomial of max. 3rd order. Different compounds may require different polynomial orders and regression

analysis (ISO 10723) may be used to determine the required polynomial order. The number of calibration points should be sufficient for the selected regression, e.g. a quadratic model requires more points (3) than linear through zero (1).

After choosing the calibration model, the regression mode should be chosen the for each component. There are 3 different modes for the regression: Standard, weighted, manual.

Standard regression mode uses a standard polynomial regression to determine the calibration function.

Weighted regression mode uses a weighted polynomial regression to determine the calibration function in which the points of the regression are weighted using the inverse of the certified concentrations. This gives more weight to lower concentration calibration points and in some cases may result in a more representative regression. To avoid a disproportionate influence of low-concentration calibration points, the weight factors have an upper limit of (the inverse of) 100ppm.

Manual coefficients mode does not use a regression, but uses the coefficients entered manually in the top-right table (orange box on Figure 18). The number of coefficients depends on the selected polynomial model. In this case only the single-point calibration scale method should be used, other calibration methods (update and scale by response) do not affect the polynomial (see Chapter 4.3.1) .

The calibration curve can be viewed via the Calibration viewer (see Chapter 4.3.6).

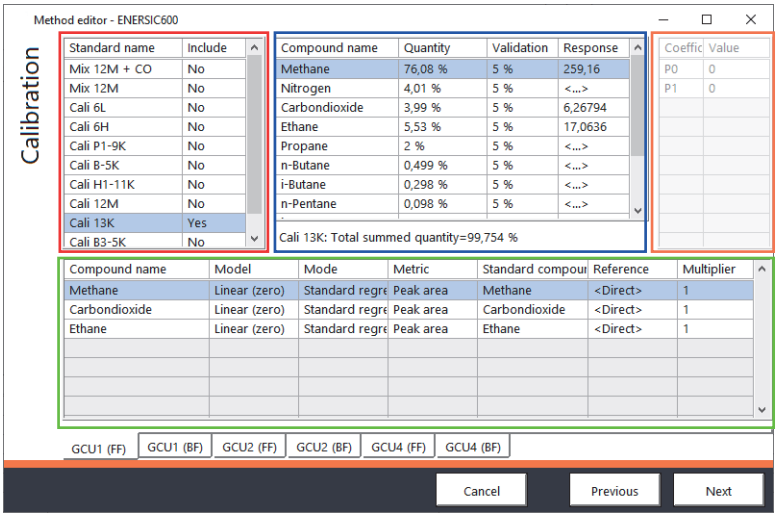


Fig. 18: Method editor, Calibration

4.2.5 Peak tracking

Peak tracking allows automatic adjustment of integration and identification timing to compensate for retention time drift which may occur due to e.g. column degradation or changes in ambient conditions. The Peak tracking window consists of the following parts:

Standard Table and Composition Table allow to select a standard and showing the available compounds in the standard. Note that the standard list and composition are the same as those defined on the Calibration window and can only be edited in the Calibration window (see Chapter 4.2.4).

The *Peak tracking Table* allows to select marker (Peak tracking) compounds for the selected standard and viewing or setting the stored retention times. A minimum of two marker peaks is required to accurately model the retention time shift. More peaks may be used to improve the accuracy of the correction.

Peak tracking options allow to enable/disable peak tracking for all integration and identification events.

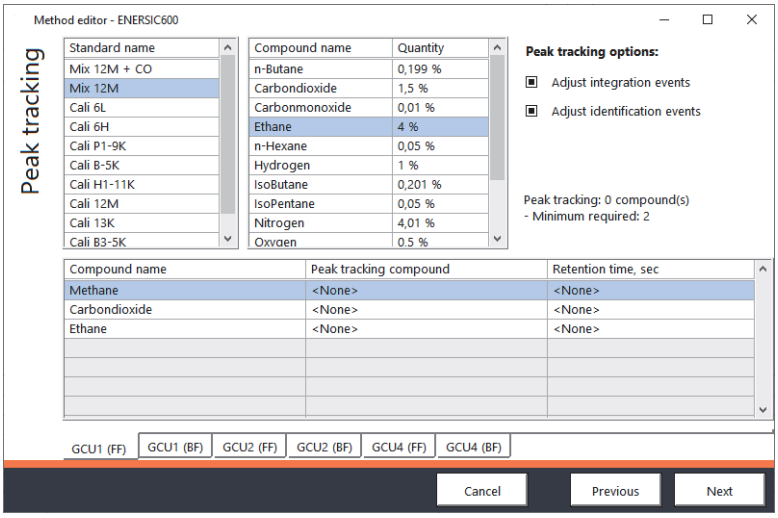


Fig. 19: Method editor, Peak tracking

4.2.6 Post-calculation

The Post-calculation window consists of 3 tabs which are explained below.

Post-calculation allows to activate normalization (normalize total concentration to 100%), select which compound concentrations to be included in the calculation of the total unnormalized sum and to specify custom equations, e.g. calculation of the ratio between specified peak areas. Right click on the Expression Table to add/remove expressions.

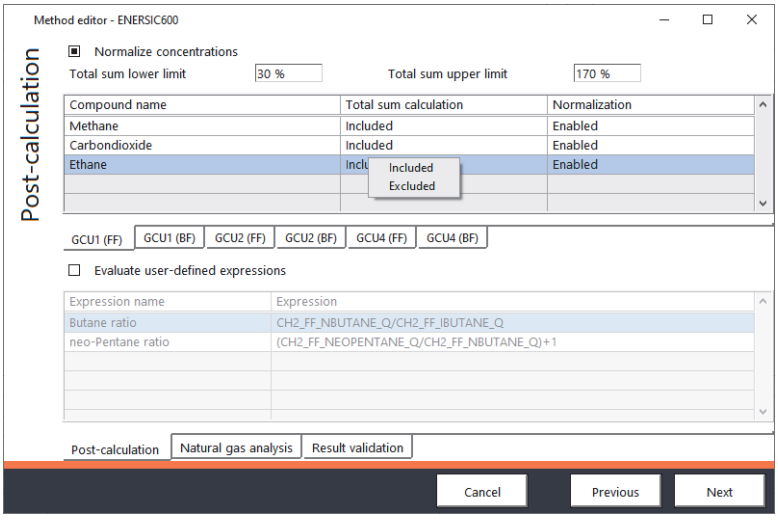


Fig. 20: Method editor, Post-calculation

Natural gas analysis allows to calculate the natural gas combustion heating values based on a calculation standard, e.g. ISO-6974.

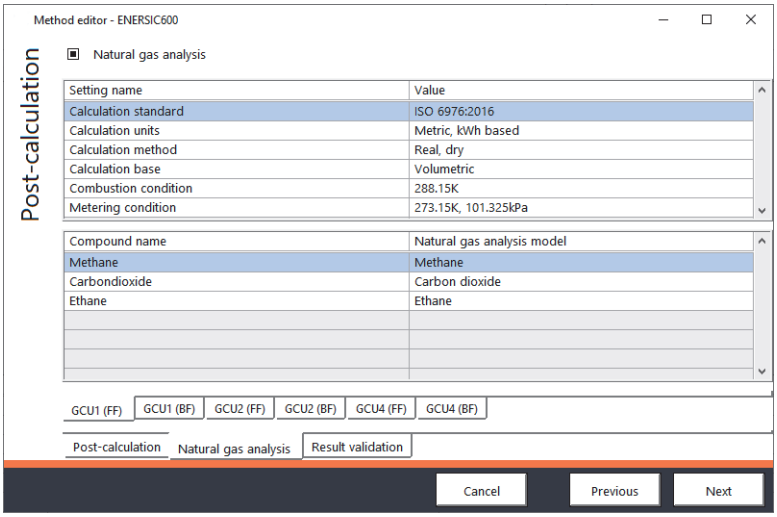


Fig. 21: Method editor, Post-calculation, natural gas analysis

Result validation allows to define a set of test criteria to determine if a result is valid, e.g. the methane concentration should be in the range 75-100%. The items can be selected by using Drag & Drop.

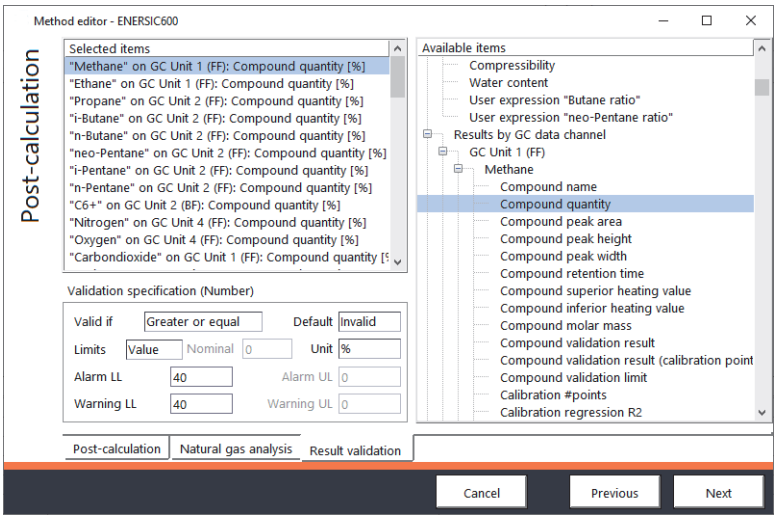


Fig. 22: Method editor, Post-calculation, result validation

4.2.7 Save method

The last step is saving the method. The following options are available (Figure 23):

Create new method (online) saves the method as a new method on the instrument.

Update existing method (online) replaces an existing method residing on the connected instrument.

Save locally (offline) saves the method in a directory on the local computer.

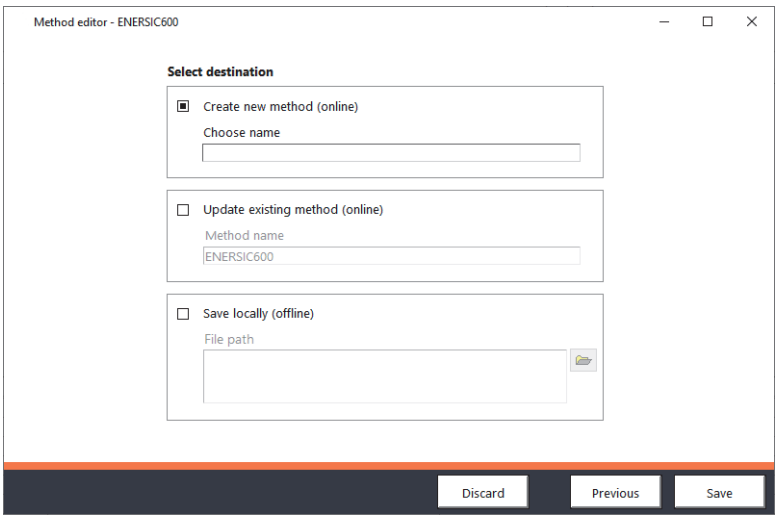


Fig. 23: Method editor, save method

After storing a method on the instrument, it can be used to run an analysis. This requires to start a task, which can be done on the Instrument control window of the main UI, as explained in the next Section (see Chapter 4.3).

4.3 Main user interface (UI)

The main user interface (UI) (Figure 3) consists of a menu bar (Application, Instrument, Sequence, Method, Data, Info) and fields (Instrument control, Instrument status, Live view, Result view, Trend view) on view selector which is on the left hand side of the main window. Instrument control, Instrument status, Live view fields and Instrument menu are only available on the menu bar when the software is in communication with an analyzer (online). The status bar at the bottom shows instrument current date- time, instrument status, current user, progress indicator and connection status.

4.3.1 Instrument control (online only)

The Instrument control field allows the user to perform a selected task online. The task can be selected from a drop-down list and then the related task settings become active and can be selected from the drop-down list. It is also possible to queue multiple tasks which are executed in queue sequence. Running a task automatically generates and/or starts a sequence. For further details about the sequence, see Chapter 5.3. The sequence queue is shown as a list in the bottom part of the UI. The start and stop buttons are used to start and stop the selected task.

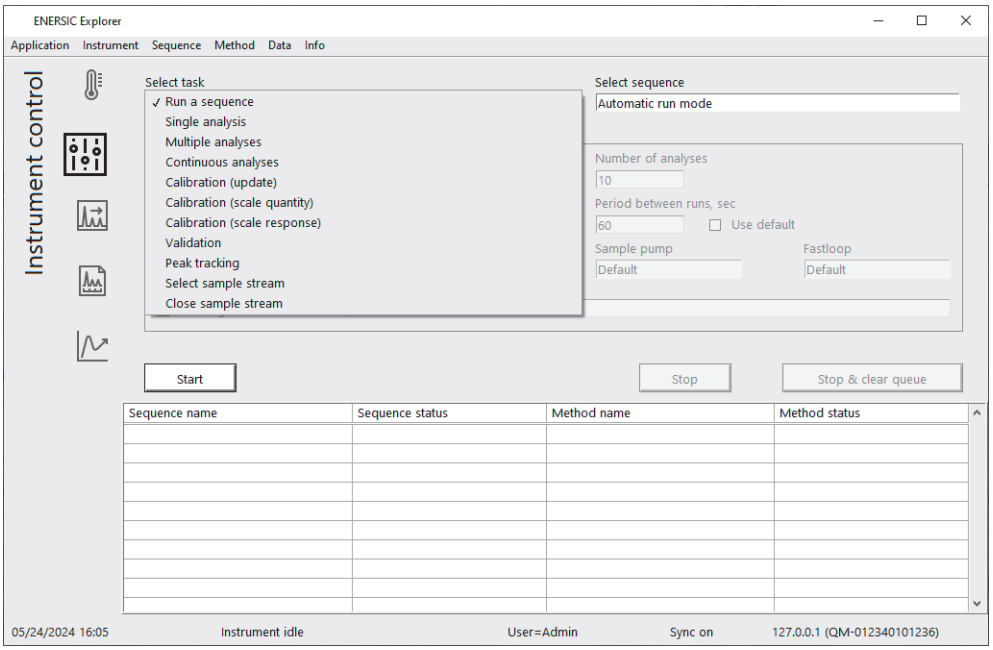


Fig. 24: Instrument control field

Run a sequence starts a sequence already available on the instrument. The sequence must be selected under Select sequence.

Single analysis run runs a single analysis. The method and the sample stream must be selected.

Multiple analysis runs runs multiple analyses. The number of analyses and the period between runs must be selected as well as the method and the sample stream. The period between runs is the time between the start of consecutive runs. This cannot be less than the analysis time which is defined in the selected method. If no delay between runs is needed, the delay can be set to zero by enabling the “Use default” option.

Continuous analysis runs runs the selected method continuously, i.e. until the sequence is stopped.

Calibration (update) runs an analysis with a selected standard to update the response factor. In case of a multi-point calibration, only one point is updated. The method, the standard, the sample stream, the number of analyses and the period between runs must be selected. When the calibration (update) completed, the Calibration viewer and the Notification window appear, when the Post-calibration/validation notice is enabled in the preferences dialog (see Chapter 5.1.2). The calibration procedures are explained in detail in Chapter 4.2.4.

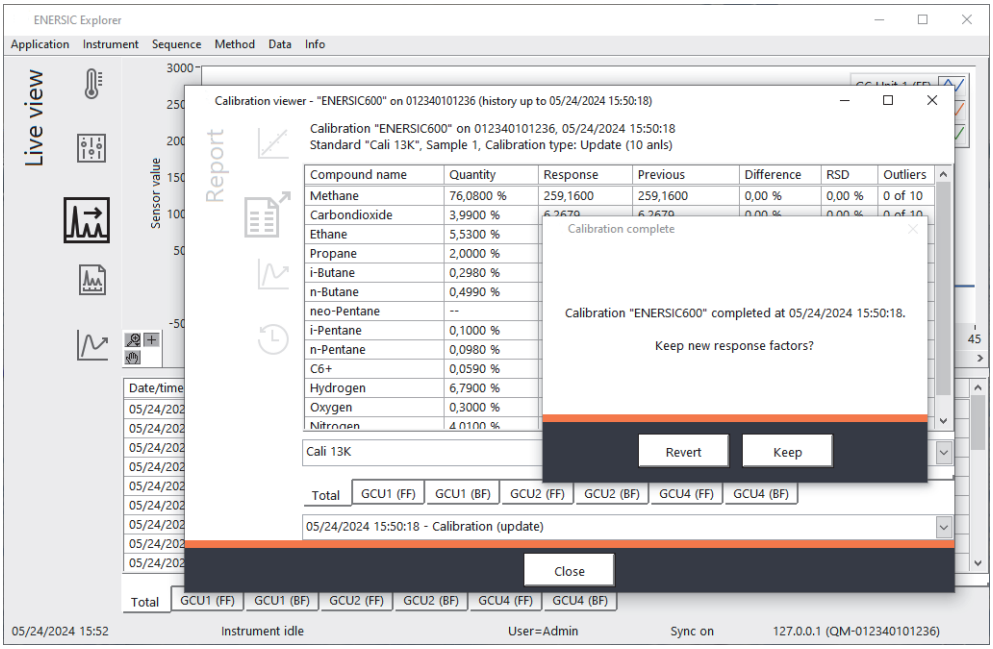


Fig. 25: Calibration update

Calibration (scale multilevel) runs an analysis with a selected standard to update all points in a multi-point calibration by multiplying with a factor. The factor is calculated such that after calibration, the response curve crosses the calibration point again. This method scales the response factors by the ratio between the calculated and certified concentrations and recommended to use when the deviation between the response factors and the calculated regression polynomial is small. The method, standard, sample stream, number of analyses and period between runs must be selected. When the calibration (scale multilevel) has completed, the Calibration viewer and the Notification window appear when the Post-calibration/validation notice is enabled in the preferences dialog (see Chapter 5.1.2). The calibration procedures are explained in detail in Chapter 4.2.4.

Calibration (scale response) runs an analysis with a selected standard to update the calibration curve. The response factors are scaled by the ratio between the measured and stored response factors of the used standard. This reduces the error introduced by the single-point calibration considerably, in case of a linear regression being used, while the response is slightly non-linear. The method, the standard, the sample stream, the number of analyses and the period between runs must be selected. When the calibration (scale response) has completed, the Calibration viewer and the Notification window appear, when the Post-calibration/validation notice is enabled in the preferences dialog (see Chapter 5.1.2). The calibration procedures are explained in detail in Chapter 4.2.4.

Validation runs analyses using calibration standards to calculate difference between known and calculated results. The method, standard, sample stream, number of runs and period between runs must be selected. When the validation has completed, the Calibration viewer and the Notification window appear. If the validation is OK, it can be selected whether to use the response factors to calibrate the method (update or scale).

Peak tracking runs analyses for automatic adjustment of integration and identification timing to compensate for retention time drift. The method, the standard, the sample stream, the number of runs and the period between runs must be selected (see Chapter 4.2.5).

Select sample stream switches the sample stream to the selected sample stream.

Close sample stream switches the sample stream to closed position.

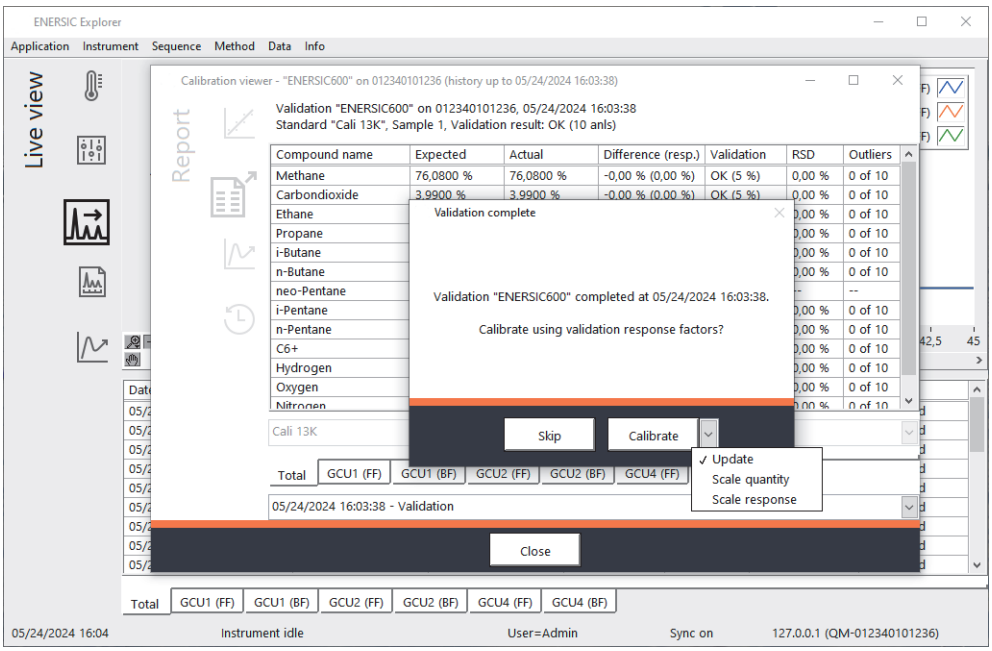


Fig. 26: Validation

4.3.2 Instrument status (online only)

The Instrument status field shows the current sensor values of the instrument (Figure 27). The green color indicates which Stream is active. Keep in mind that the flow rate cannot be set but is controlled by the sample inlet pressure. It is also possible to see the status of each channel by clicking the corresponding channel (Figure 28). The table below the instrument diagram shows error, warning or status messages.

A double click or a right click on instrument diagram area shows a detailed list of sensor readings (admin access only). The right click on the window expands/collapses all items (Figure 29).

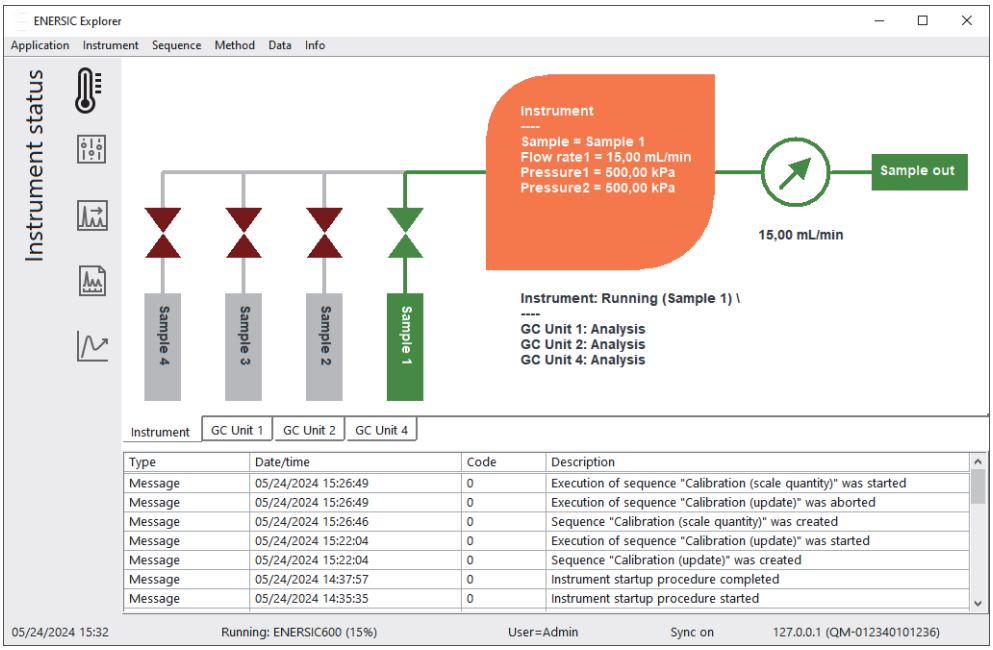


Fig. 27: Instrument status

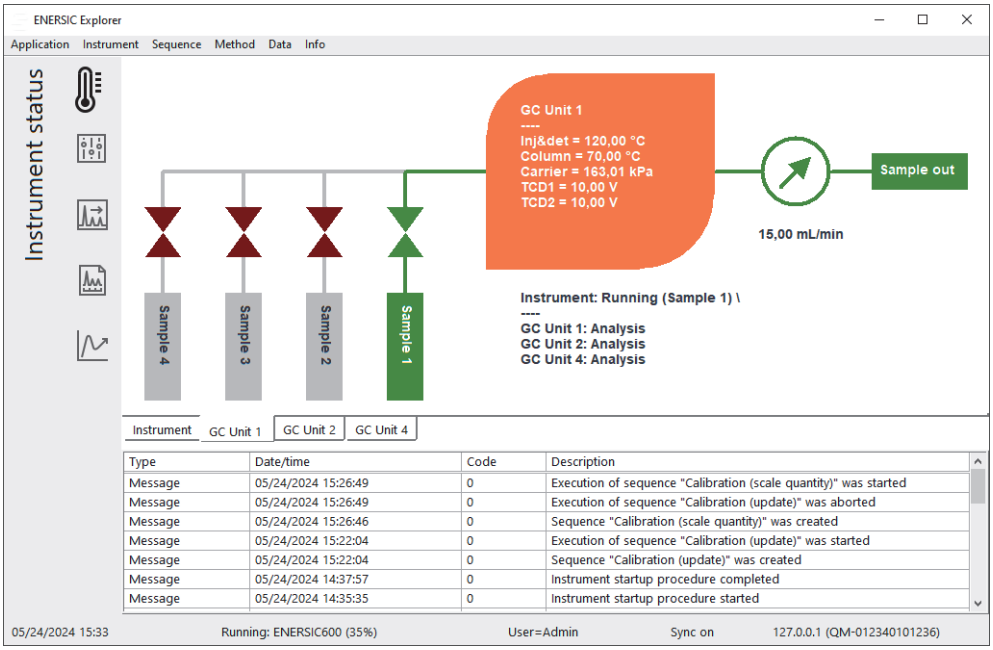


Fig. 28: GC unit status

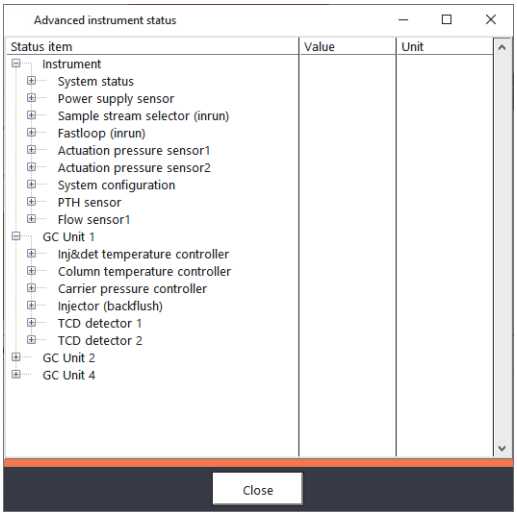


Fig. 29: Advanced instrument status

4.3.3 Live view (online only)

The Live view field shows the currently incoming TCD data and the sequence execution summary Table. It can be chosen to view the total chromatogram or individual chromatograms for each channel via Channel selector which is below the sequence execution summary Table. The appearance of chromatogram can be adjusted via the zoom palette (see Chapter 7.1) or by right clicking to change preferences. The right click on the Sequence execution Table allows to export data to clipboard.

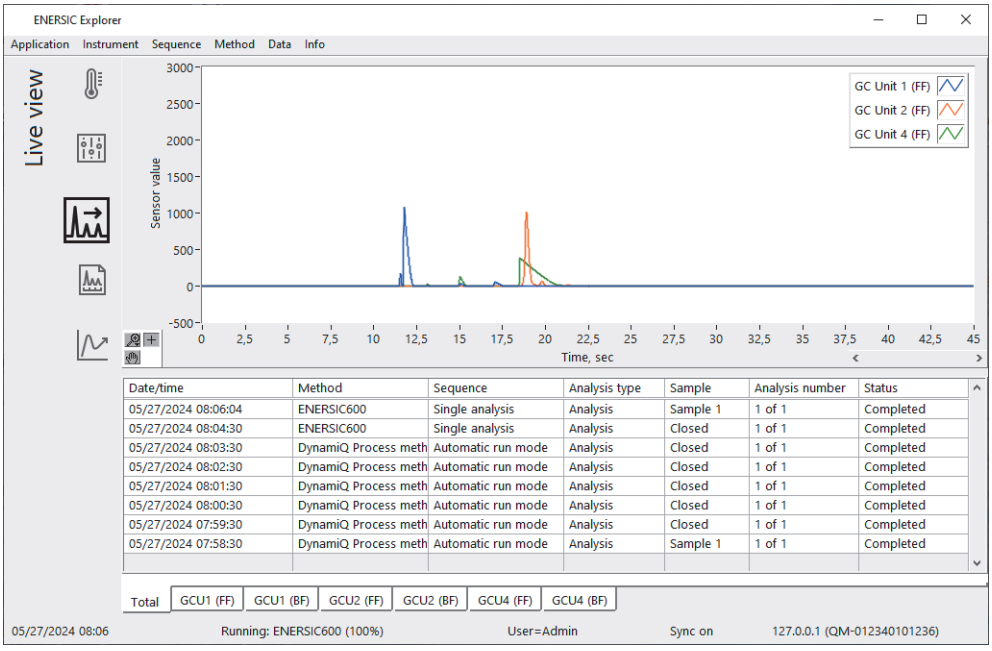


Fig. 30: Live view

4.3.4 Result view

The Result view field shows the previously saved method result data with calculated baseline and the Result Table for each channel. There are two result view modes which can be selected using the selector on the right-hand side of the field or by double-clicking the Result Table (Figure 31). Analysis result shows peak areas, retention times, etc. and instrument status at the moment of injection; Post-calculation result shows overall analysis results and per-channel post-calculation results.

The result to be shown is selected by choosing Instrument ID, Injection date and Injection time via the Result select window which is on the right-hand side of the field. The results are stored locally in the result database. It allows to view the results offline and also from different instruments. The navigation arrows allow the user to steps forward or backward one run. Fast forward or Fast reverse controls multiple simultaneous step forward or back. The number of steps can be adjusted in the Application preferences dialog (see Chapter 5.1.2). It is also possible to use the keyboard short-cuts- Arrow Up or Arrow Down to go to the next or previous run; Home or End to go to the first or the last run for the selected injection date. Another option is the fast navigation (see Chapter 4.3.4.1).

Key information on the selected result is displayed at the bottom right. More extensive information can be seen in the Result info viewer which can be opened by pressing Ctrl+Shift+Y, from the menu bar at the top by selecting Data-> Result info viewer or by double clicking on the key information.

The location to save the results can be adjusted in Application preferences dialog (see Chapter 5.1.2). When an instrument is connected to the software, the results are automatically synchronized with the result database. The progress is shown by orange indicator at the status bar at the bottom.

The appearance of the chromatogram can be adjusted via the zoom palette (see Chapter 7.1) or by right clicking to change preferences.

The right click on the Result Table allows to open the Calibration viewer (see Chapter 4.3.6) or to export data to clipboard.

A result report can be created by right clicking on the blank area below the Result select window and selecting “Create report for selected result” from the drop-down list (Figure 32) (see Chapter 7.4).

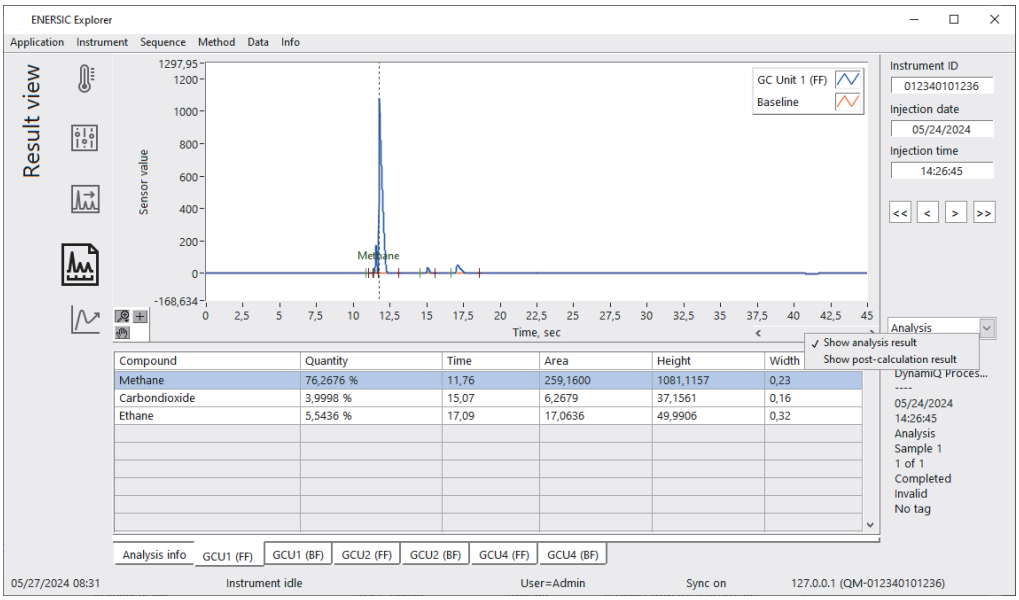


Fig. 31: Result view, selecting the view mode

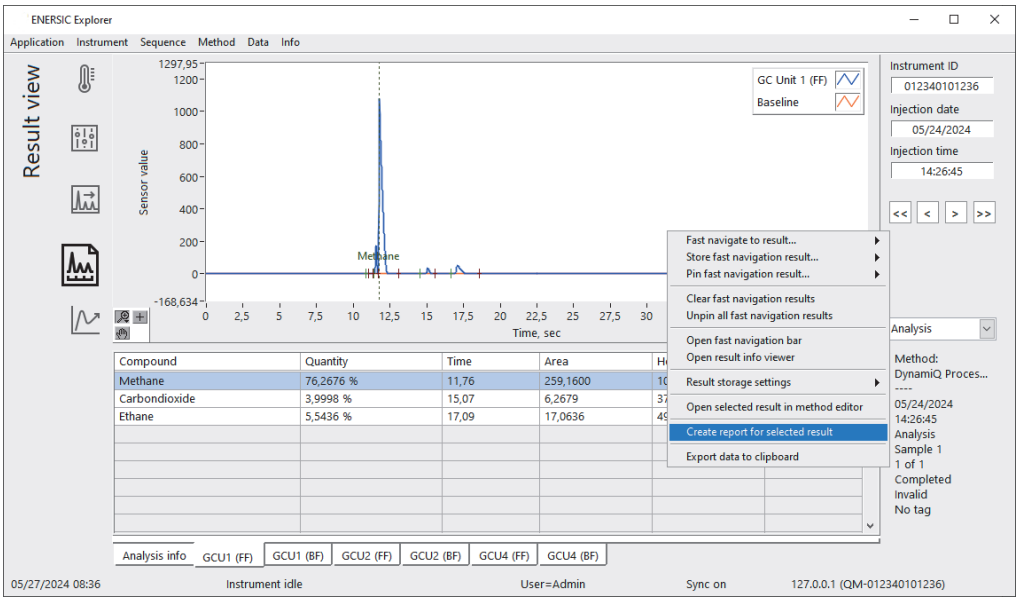


Fig. 32: Result view, creating a result report

4.3.4.1 *Fast navigation*

The Fast navigation tool allows to navigate to selected results quickly. It is achieved by right clicking on the blank area below the Result select window (Figure 33). It is possible to assign up to 10 results to the fast navigation. The assigned results can be viewed also on a bar for easier use (Figure 34). Results no longer accessible are shown in red. The fast navigation bar can be opened from the Data menu, by pressing Ctrl+Shift+M or by double-clicking the Result navigation window in the Result view and Trend view windows.

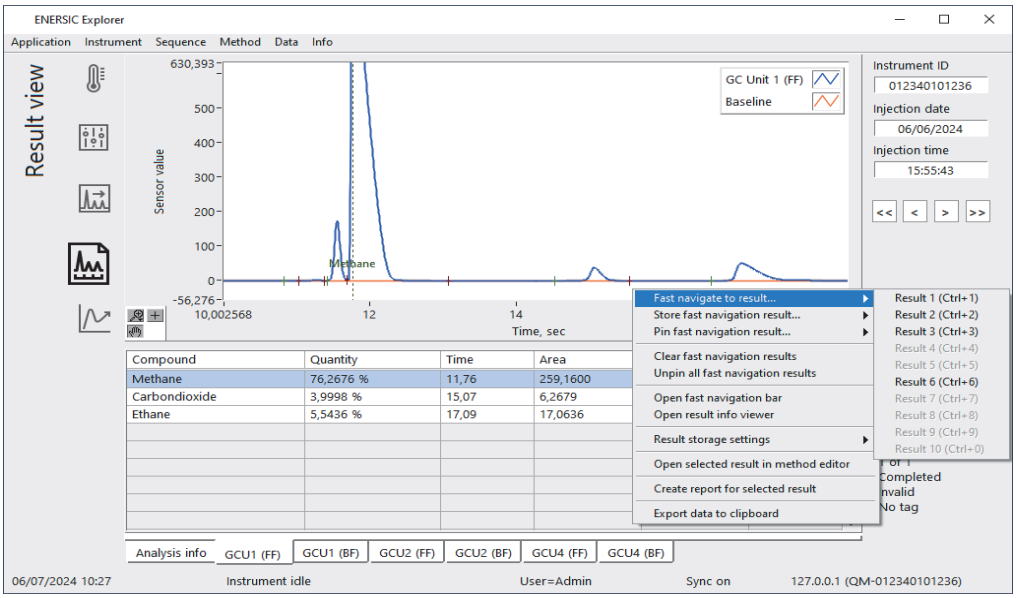


Fig. 33: Fast navigation

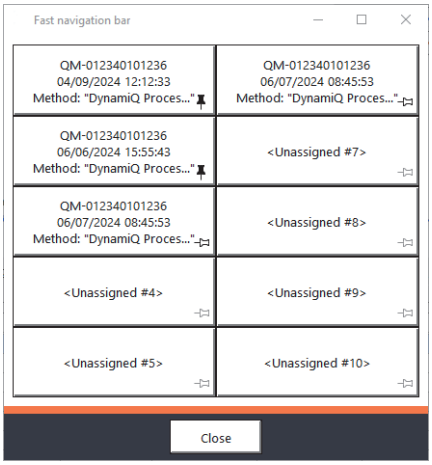


Fig. 34: Fast navigation bar

4.3.4.2 *Overlaying chromatograms*

The Fast navigation tool allows to compare a selected chromatogram with other chromatograms. It is possible to show selected reference chromatograms as overlays in the Result view and in the Method preview tool.

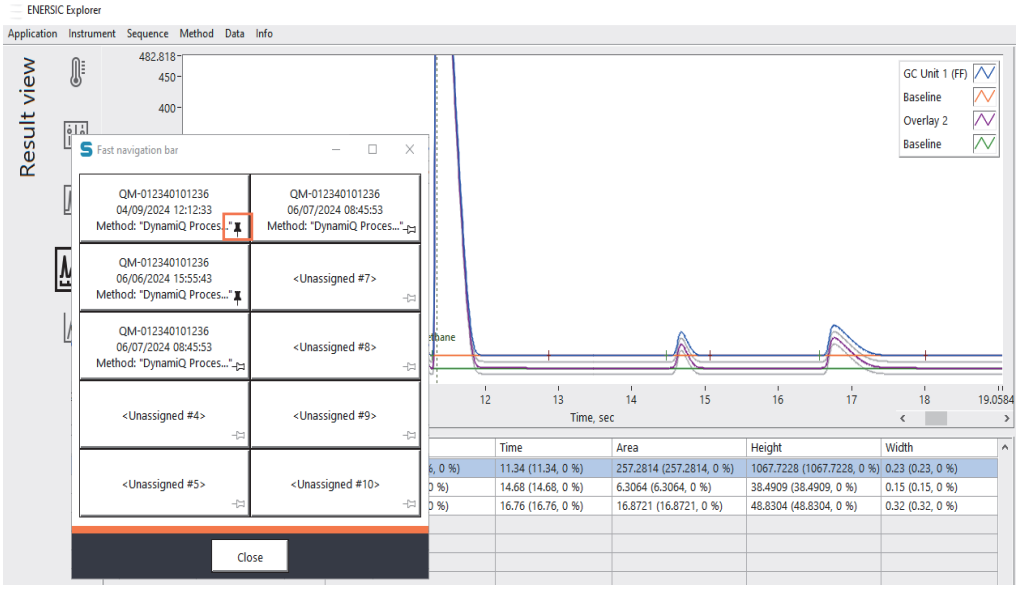


Fig. 35: Chromatogram overlay functionality

The results assigned to the fast navigation bar can be selected to be shown as overlay using the pin buttons (Figure 35). When selected, results are shown in light grey in the chromatogram view (Figure 35). The overlays are offset with respect to the original selected chromatogram to allow easy comparison. The used offset can be customized via the Application preferences (Ctrl+O), or via the chromatogram context menu. Note that in the Result view, overlays are only shown in single-channel view.

Using (Shift+)Tab, overlays can be highlighted. When an overlay is highlighted, the overlay chromatogram and baseline are shown in more contrasting colors (Figure 36). Also, additional information on the selected overlay is shown.

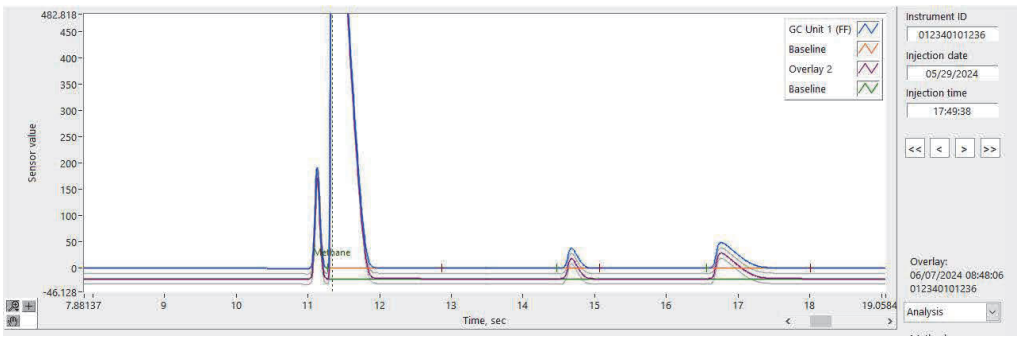


Fig. 36: Chromatogram result view showing a highlighted overlay

In analysis view, when an overlay is highlighted, the Result Table shows a comparison between peak metrics of the selected result and the overlay (Figure 37). Between brackets, the corresponding result of the overlay is shown, as well as the percentage difference with regard to the selected result.

Compound	Quantity	Time	Area	Height	Width
Methane	87.3863 % (87.3863 %, 0 %)	11.34 (11.34, 0 %)	257.2814 (257.2814, 0 %)	1067.7228 (1067.7228, 0 %)	0.23 (0.23, 0 %)
Carbondioxide	1.4993 % (1.4993 %, 0 %)	14.68 (14.68, 0 %)	6.3064 (6.3064, 0 %)	38.4909 (38.4909, 0 %)	0.15 (0.15, 0 %)
Ethane	3.9980 % (3.9980 %, 0 %)	16.76 (16.76, 0 %)	16.8721 (16.8721, 0 %)	48.8304 (48.8304, 0 %)	0.32 (0.32, 0 %)

Fig. 37: Analysis result Table showing a comparison of the selected result with a highlighted overlay result

The maximum number of overlays is 10 (as limited by the Fast navigation bar).

Overlays do not necessarily have to originate from the same instrument or from the same method. However, the overlay shown is selected to originate from the same detector (e.g. channel 3 foreflush). If no matching detector signal is available, no overlay is shown. The peak metrics comparison shown in the Analysis result Table selects matching compounds based on compound name. If no matching compound is found, no comparison result is shown.

4.3.5 Trend view

The Trend view field shows a trend plot for the results of a series of analyses for a selected parameter e.g. quantity, time, area, height, width or a status parameter of the instrument at run start (Figure 38). The parameter can be selected from the Result Table of the selected channel or Run info Table which are shown below the trend plot and can be selected via the Channel selector.

The navigation through the results is achieved via the Result select window (See Chapter 4.3.4). The range of data of points can be selected by right click on the plot and can be modified by selecting the cursor tool (see Chapter 7.1) and dragging the cursors.

Right clicking on the plot area shows the available options for the view.

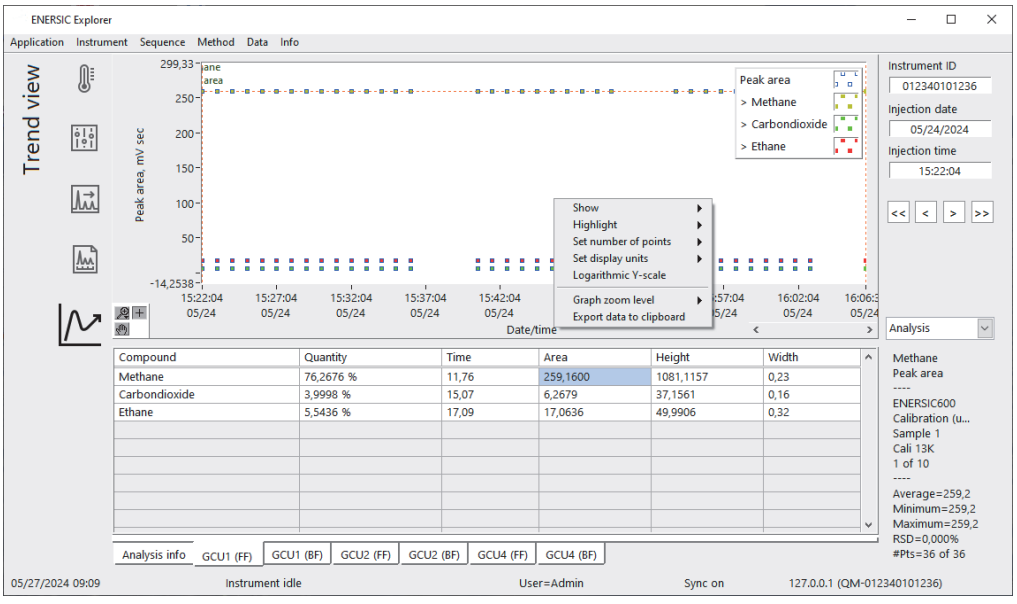


Fig. 38: Trend view

4.3.6 Calibration viewer

The Calibration viewer allows to see calibration details for each compound. It consists of 4 fields.

The *Regression window* shows the calibration curve with the calibration points and its properties (regression model and equation, number of points, R2 coefficient) (Figure 39). The plot shows the calibration curve for the selected compound by left click on the table. The zoom mode can be selected via context menu by right clicking on the plot or be set in the application preferences (See Chapter 5.1.2).

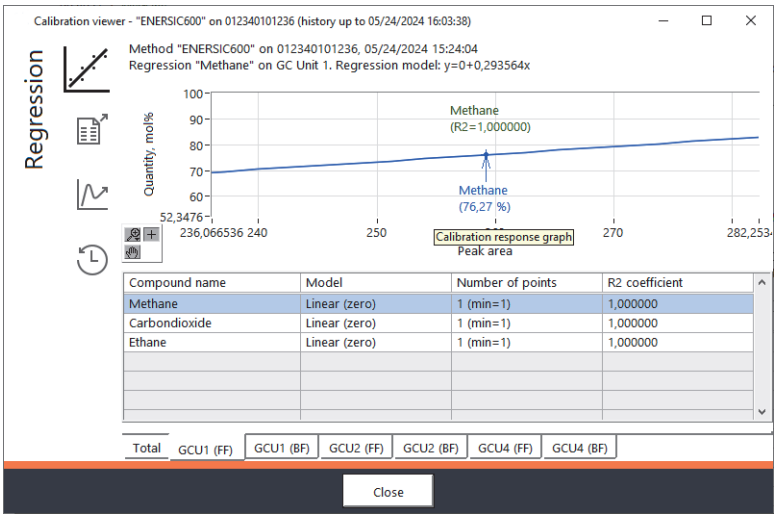


Fig. 39: Calibration viewer, Regression window

The *Report window* shows the calibration and validation results (Figure 40). The undermost drop-down list allows to select the results to be shown. When the calibration results are selected to view, the calibration standard may be selected from the upper drop-down list.

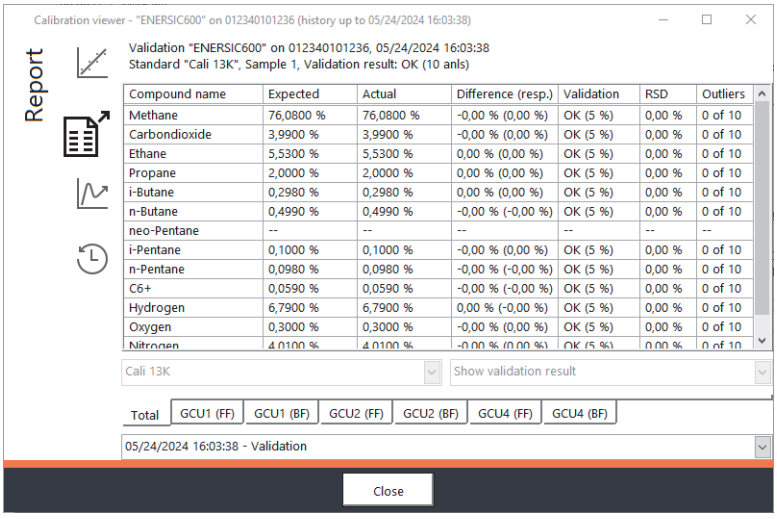


Fig. 40: Calibration viewer, Report window

The *Trend window* shows the trend in calibration/validation response (Figure 41). The undermost drop-down list allows to select the results to be shown. The plot shows the trend for the selected compound by left click on the table. Note that the response factors are only changed after all calibration runs are completed.

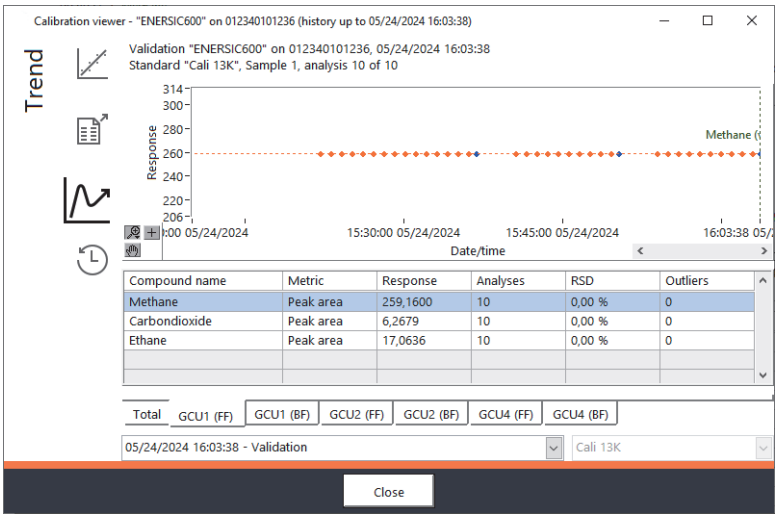


Fig. 41: Calibration viewer, Trend window

The *History window* shows the overview of method calibrations, updates and validations (Figure 42). A double click on an item shows the report.

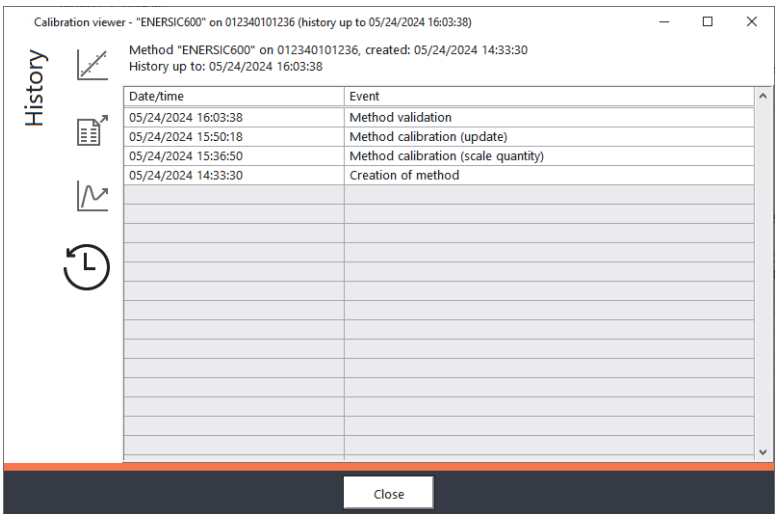


Fig. 42: Calibration viewer, History window

5 User interface reference

5.1 Application menu

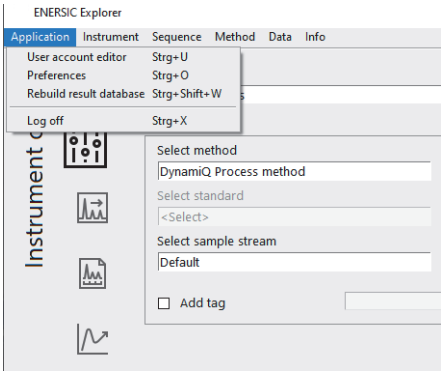


Fig. 43: Application menu

5.1.1 User account editor (admin access only)

The user accounts can be managed by admin level users via the “User account manager” window which is in the Application tab.

Application-> User account editor (Ctrl+U)

The right click on the rows opens the context menu to add/remove users.

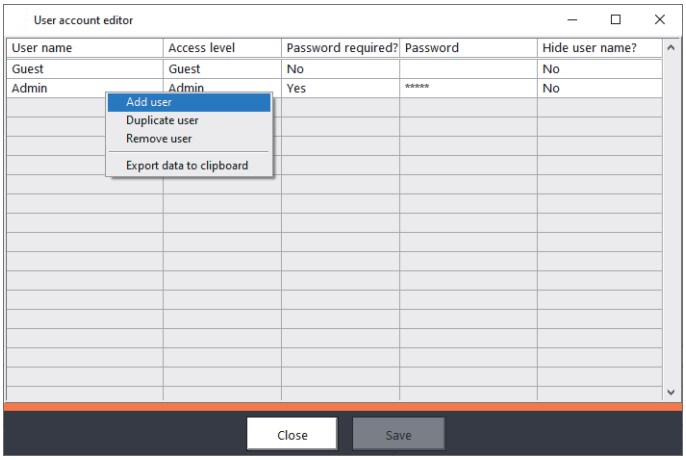


Fig. 44: User account manager

It is possible for users to have different levels of access: Guest, User, Admin.

Guest users are only allowed to view the current status of the instrument and view the stored result data. The Instrument control window is not available for guest users.

The features of the ENERSIC600 software for user and admin level access are described in detail in this Manual.

5.1.2 Application preferences

The users can set their preferences via the “Application preferences” window which is in the Application menu.

Application-> Preferences (Ctrl+O)

A left click on the options listed under the Value column shows the other available options to change the listed application preferences.

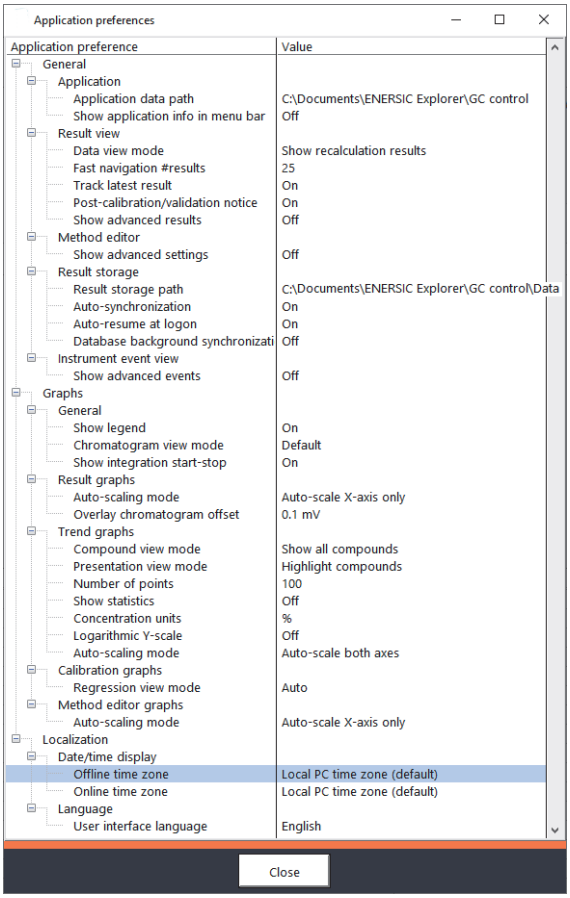


Fig. 45: Application preferences (admin access)

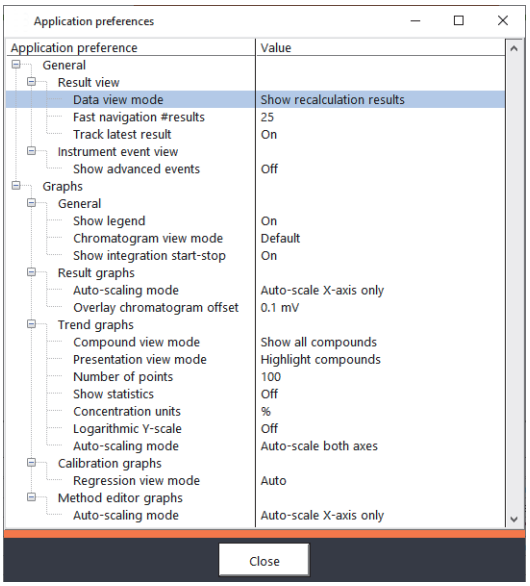


Fig. 46: Application preferences (user access)

5.1.3 Rebuild result database (admin access only)

The admin level users can rebuild the result database via the Application menu. Rebuilding the result database allows to refresh the local database by loading available results from the network to the local database.

Application-> Rebuild result database (Ctrl+Shift+W)

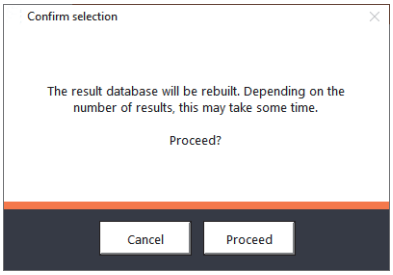


Fig. 47: Rebuild result database

5.1.4 Log off

Log off in the Application menu, then the login screen appears.

Application-> Log off (Ctrl+X)

5.2 Instrument menu (online only)

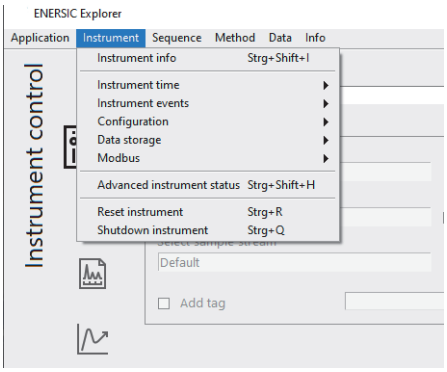


Fig. 48: Instrument menu

5.2.1 Instrument info

Instrument info shows the serial number, manufacture date and firmware version of the instrument and the serial number of the installed cartridge.

Instrument-> Instrument info (Ctrl+Shift+I)

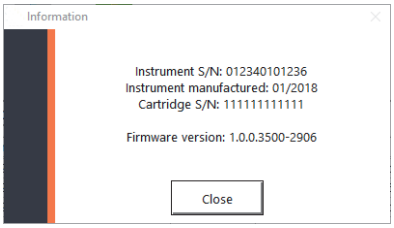


Fig. 49: Instrument info

5.2.2 Instrument event history (admin access only)

Instrument event history allows access to the Instrument logbook. The logs are listed by date. The log type can be filtered using the Context menu.

Instrument-> Instrument event history (Ctrl+Shift+L)

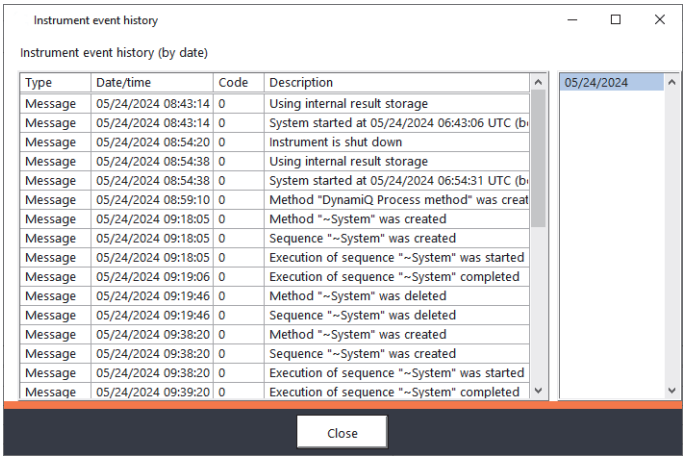


Fig. 50: Instrument event history

5.2.3 Instrument time

The instrument time can be synchronized with the local time.

Instrument-> Synchronize time (Ctrl+T)

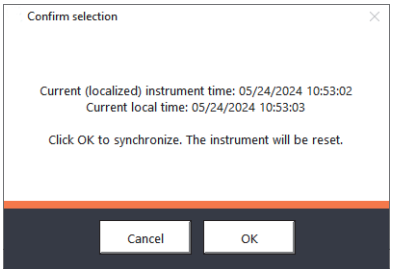


Fig. 51: Synchronize time

The instrument time zone can be selected from the drop-down list (admin access only).

Instrument-> Instrument time zone (Ctrl+Shift+T)

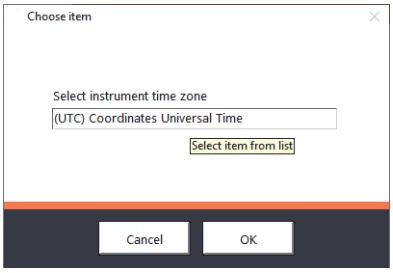


Fig. 52: Select time zone

A successful time settings adjustment requires resetting the instrument.

5.2.4 Configuration

5.2.4.1 *Ethernet configuration (admin access only)*

The Ethernet configuration allows to configure the instrument Ethernet port, e.g. setting a fixed IP address.

Instrument-> Ethernet configuration (Ctrl+L)

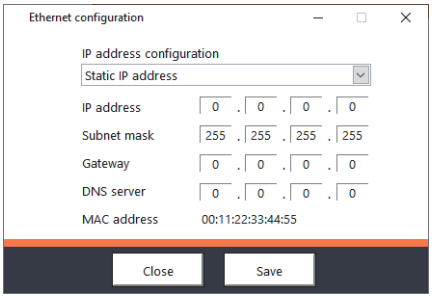


Fig. 53: Ethernet configuration

5.2.4.2 *Serial port configuration editor (admin access only)*

The Serial port configuration editor allows to configure the selected serial port, e.g. setting Baud rate. This is done by clicking on the parameter and selection from a list of available options. Click Save to store the changes.

Instrument-> Serial port configuration (Ctrl+#)

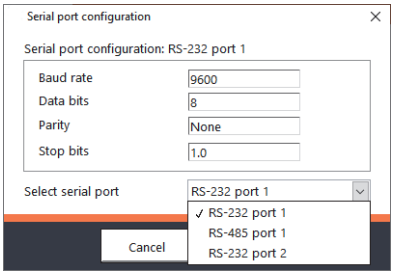


Fig. 54: Serial port configuration editor

5.2.4.3 *Export/Import instrument configuration (admin access only)*

The instrument configuration can be exported to a selected file.

Instrument-> Export instrument configuration (Ctrl+F12)

The instrument configuration can be imported from a file. The loaded instrument configuration must match the instrument.

Instrument-> Import instrument configuration (Ctrl+Shift+F12)

5.2.5 Data storage (admin access only)

The internal storage medium, file system, its size, free space on the disk and number of the stored results can be seen.

Instrument-> Storage space info (Ctrl+Shift+S)

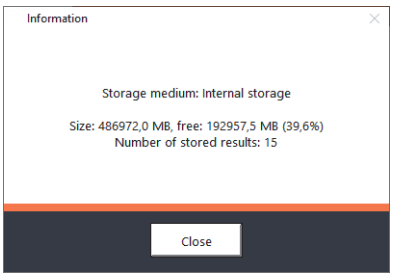


Fig. 55: Storage space info

All the result data stored on the instrument can be deleted.

Instrument-> Clear stored results (Ctrl+Shift+C)

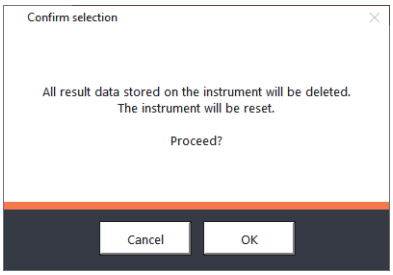


Fig. 56: Clear stored results

5.2.6 Modbus (admin access only)

The Modbus settings allow to set an offset between Modbus internal and external address, data format, device ID and wait time before connection time-out.

Instrument-> Modbus settings (Ctrl+M)

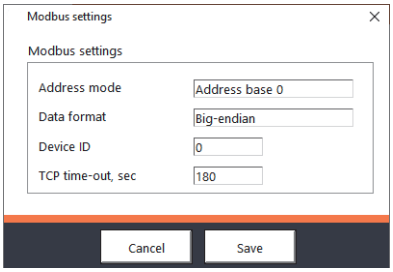


Fig. 57: Modbus settings

The available data formats can be found in Table 1.

Formatting option	Word (register) order	Byte order within each register
Big endian (default)	Most significant at lowest address	Most significant transferred first
Little endian	Least significant at lowest address	Most significant transferred first
Big endian, byte swap	Most significant at lowest address	Least significant transferred first
Little endian, byte swap	Least significant at lowest address	Least significant transferred first

Table 1: Modbus formatting options

The Modbus configuration allows to re-map Modbus registers from one address to another. It is mainly useful to interface with existing Modbus software/hardware.

Instrument-> Modbus address mapping (Ctrl+Shift+G)

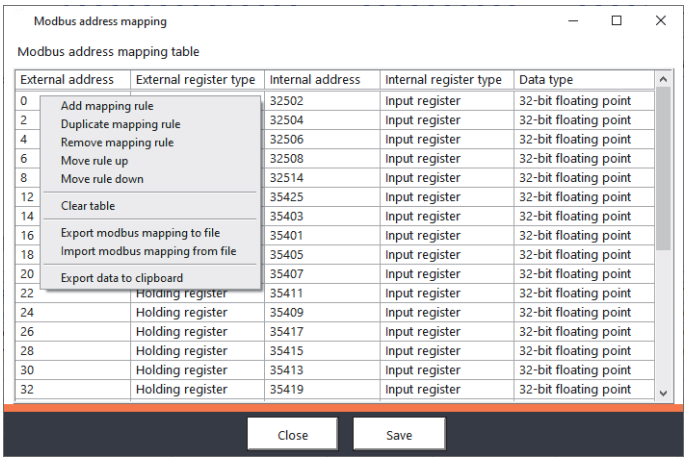


Fig. 58: Modbus configuration

The Modbus register viewer tool is available to view Modbus registers and test Modbus communication.

Instrument-> Modbus register viewer (Ctrl+Shift+Z)

After starting the Modbus register viewer, a connection dialog is opened which allows to make a Modbus connection using LAN or RS-232/485 (Figure 59). The connection settings (e.g. baud rate, address mode, device ID) are automatically set in accordance with the configuration of the connected instrument.

After a connection is established, a list of registers is shown, as shown in Figure 60. For each register, the address, register type, data type, (interpreted) value and description are shown. Read/write values can be changed by clicking the value and selecting one of the available options. Using the context menu, the register view can be changed to show a) raw/hexadecimal or interpreted data and b) the internal or external (i.e. offset in accordance with the address mode) register address.

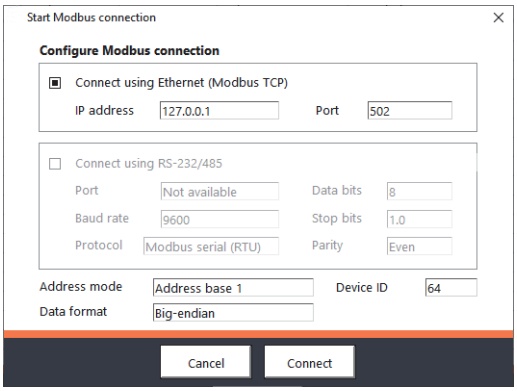


Fig. 59: Modbus register viewer connection

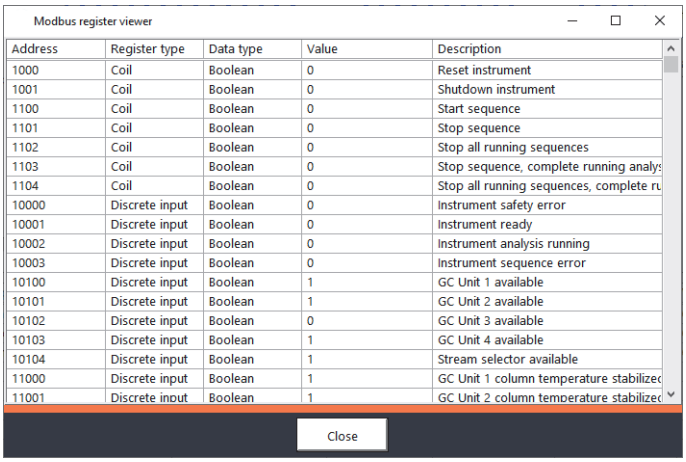


Fig. 60: Modbus register viewer register display

5.2.7 Advanced instrument status (admin access only)

See Chapter 4.3.2 for the details.

Instrument-> Advanced instrument status (Ctrl+Shift+H)

5.2.8 Reset/shutdown instrument

The instrument can be reset/shutdown from the Instrument menu.

Instrument-> Reset instrument (Ctrl+R)

Instrument-> Shutdown instrument (Ctrl+Q)

5.3 Sequence menu

The sequence is a measurement script, which can be programmed by the user to control which methods are run, which streams are used, etc. Sequences can be programmed using the sequence task editor, the sequence editor (advanced) or created automatically using the Instrument control window.

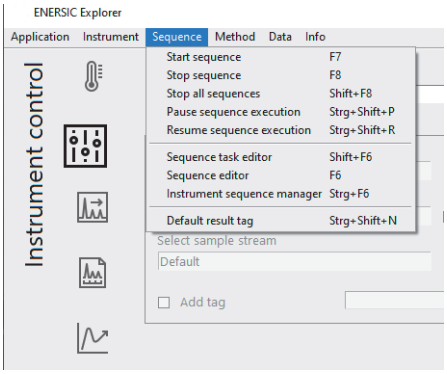


Fig. 61: Sequence menu

5.3.1 Sequence execution

Start sequence (F7): Opens a window to select a sequence to start. The sequence to start then can be selected from the drop-down list.

Stop selected sequence (F8): Opens a window to select a sequence to abort. The sequence to stop then can be selected from the drop-down list which shows all currently running and waiting sequences.

Stop all sequences (Shift+F8): Aborts all currently running and waiting sequences.

Pause sequence execution (Ctrl+Shift+P): Pauses the currently running sequence when the current run is completed.

Resume sequence execution (Ctrl+Shift+R): Resumes the currently paused sequence.

5.3.2 Sequence task editor

The Sequence task editor allows users to create sequences based on a set of standardized tasks. The Sequence task editor aims to bridge the gap between creating sequences from the Instrument control window and the more advanced Sequence editor (see Chapter 5.3.3). Sequence task editor is started from the Sequence menu or by pressing Shift+F6.

Sequence-> Sequence task editor (Shift+F6)

5.3.2.1 *Select sequence*

The sequence to be edited should be chosen via the Sequence selection window (Figure 62). The following options are available:

New sequence creates a new sequence (blank or from a template).

Existing sequence (online) loads an existing sequence residing on the connected instrument.

Saved sequence (offline) loads an offline sequence saved locally on the PC.

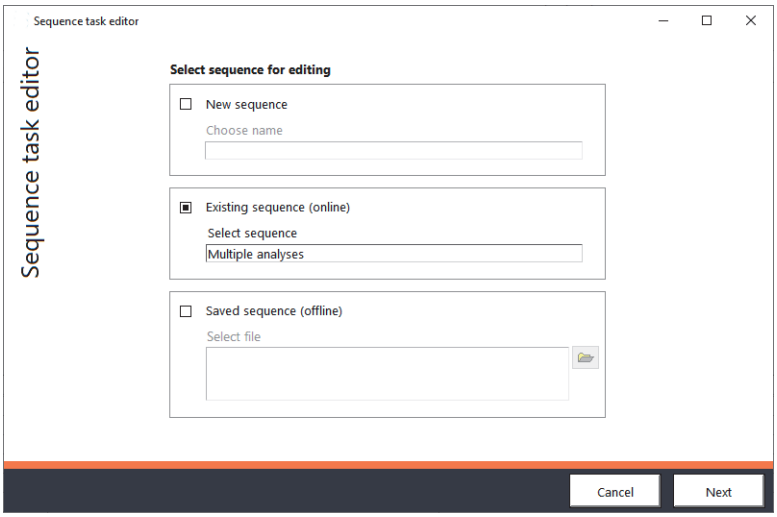


Fig. 62: Sequence task editor, Sequence selection window

Note that a Sequence task is essentially a normal sequence, which contains additional information to be able to convert it into a Sequence task. Before editing, the sequence is converted into a Sequence task. After completing editing, the Sequence task is converted back into a sequence again. If conversion fails, a notification is shown.

5.3.2.2 *Edit sequence task*

A Sequence task consists of a series of standardized tasks executed in sequence. The following tasks are currently implemented:

Task name	Description
Single analysis	Run one analysis
Multiple analyses	Run multiple analyses
Continuous analyses	Run analyses continuously until the task is stopped
Calibration (update)	Run a calibration (update type)
Calibration (scale multilevel)	Run a calibration (scale multilevel type)
Calibration (scale response)	Run a calibration (scale response type)
Validation	Run a validation
Peak tracking	Run peak tracking
Conditioning	Condition one or more columns
Wait	Wait for a specified amount of time
Wait (idle mode)	Wait for a specified amount of time, using Idle mode conditions
Select sample stream	Switch the stream selector to a specified stream
Close sample stream	Close the stream selector
Method optimization	Vary one or more parameters to optimize a method

Table 2: Sequence tasks

For each task, a start and stop condition can be specified:

- When a task is ready to be executed, the start condition is evaluated. The task is executed only if the start condition is true. If not, it is skipped. If no start condition is specified, the task is always executed.
- During task execution, the stop condition is evaluated after each analysis run. If the condition is true, the task is stopped. If the stop condition is false, or if no stop condition is specified, the task continues running until it is complete.

The complete task list can be specified to run once, or continuously in a loop.

The Sequence task editor window consists of three parts: the task list (top part of the window), the Run continuously option (middle part of the window) and the Task setting Table (bottom part of the window) (Figure 63).

Task list shows a list of tasks which will be executed in sequence. Tasks can be added and removed, and the order can be changed using the context menu. Subsequent tasks often have several settings values in common, such as the used method or sample stream. These settings can be copied from another task via the context menu option.

The *Task setting Table* shows the task, start condition or stop condition settings depending on the selected tab.

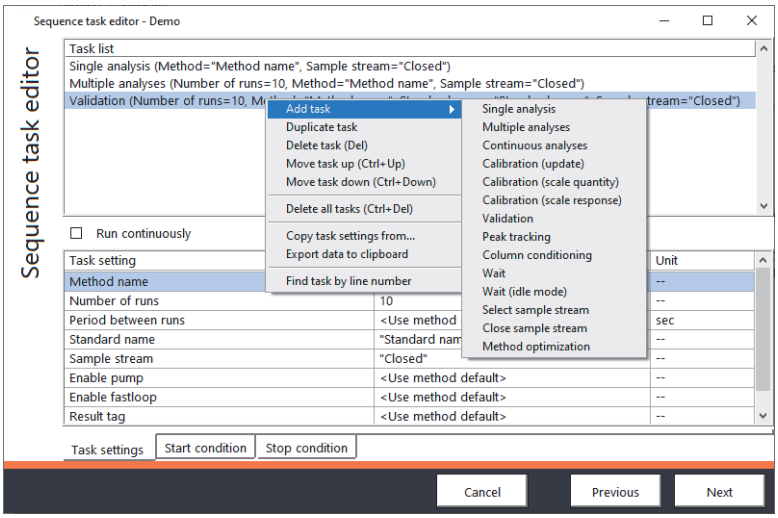


Fig. 63: Sequence task editor, edit sequence task

The *Task setting* tab shows the (task-specific) list of available settings. To edit a setting, left-click the value in the table. An edit box is shown (Figure 64), which allows the setting value to be changed. A drop-down menu provides a list of suggestions for values (e.g. method names or available sample streams).

After editing, click outside the edit box, to apply the change. After changing a setting value, it is checked for correctness. If the input is invalid, this is indicated by coloring the edit box red.

For some settings, the option “Use method default” is available. By selecting this option, instead of specifying a value, the setting specified in the method is used.

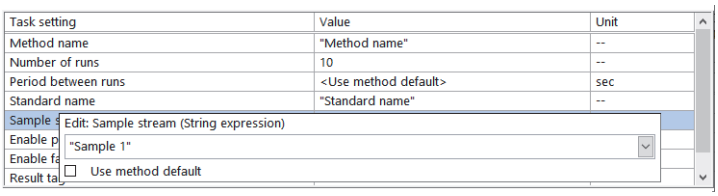


Fig. 64: Sequence task editor, Task setting edit box

The Stop condition edit section is shown in Figure 65 (the Start condition edit section looks very similar). The condition is specified as “If <condition type> is <criterion>”. Condition options are: None, Clock time, Task duration (only for stop condition) and Numeric expression. Available criterion options are: None, Equal, Unequal, In range, Out of Range, Greater, Greater or equal, Smaller, Smaller or equal.

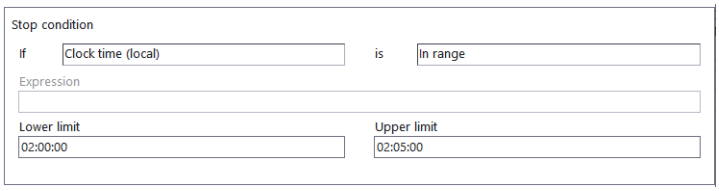


Fig. 65: Sequence task editor, Stop condition edit section

5.3.2.3 *Save sequence*

The last step is saving the sequence. The following options are available (Figure 66):

Create new sequence (online) saves the sequence as a new sequence on the instrument.

Update existing sequence (online) replaces an existing sequence residing on the connected instrument.

Save locally (offline) saves the sequence in a directory on the local computer.

Run sequence task after save starts the sequence immediately if an online save option is chosen.

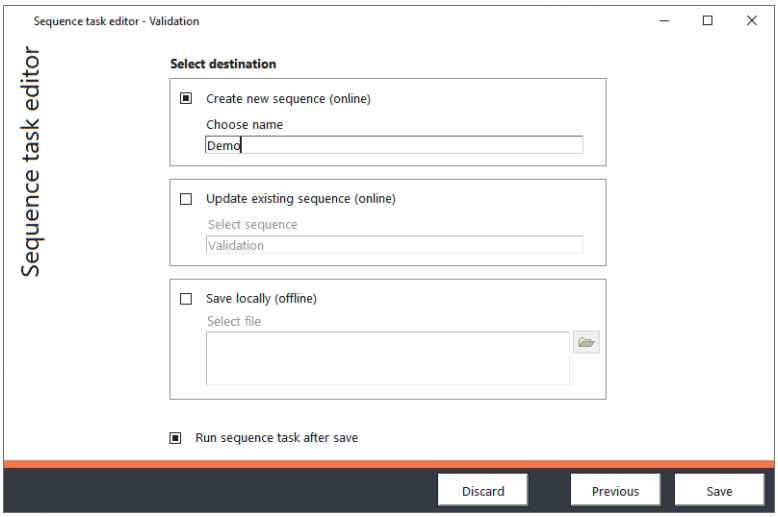


Fig. 66: Sequence task editor, save sequence

5.3.3 Sequence editor

Sequences can be automatically generated on the Instrument control window for common tasks (see Chapter 4.3.1). For advanced purposes, a sequence can be defined via Sequence editor which is started from Sequence menu or by pressing F6.

Sequence-> Sequence editor (F6)

The sequence is an analysis program, written in “C-like” pseudo code, which contains one or more “run” commands and scheduling logic. It includes if...else, while, for and switch constructs. It requires some programming knowledge to write a correct sequence.

The sequence to be edited should be chosen via the Sequence selection window. It is similar to the Select sequence window from the Sequence task editor. See Chapter 5.3.2.1for details.

5.3.3.1 *Edit sequence*

The Sequence edit window consists of two parts: Sequence tree (left part of the window) and Sequence element editor (right part of the window) (Figure 67).

Sequence tree shows the layout of the sequence in a hierarchical form and allows to add/ remove elements from the context menu by right click. The hierarchy can be modified using drag drop. The available logical elements can be seen on Figure 67.

Sequence element editor allows to edit of a selected structure element.

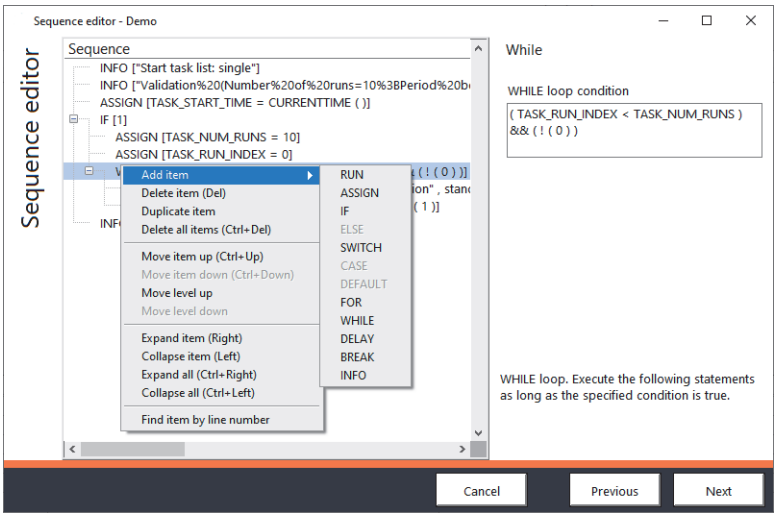


Fig. 67: Sequence editor, Edit window

The sequence editor allows users without programming experience to create or edit a sequence. Sequence correctness is ensured by the following features:

- Context menu options resulting in an invalid sequence are disabled, e.g. ELSE can only be added after an IF, CASE can only be added inside a SWITCH.
- Context menu options are available for specific input fields, allowing e.g. to select a method name or stream from a list of available options.
- Drag/drop is only executed if the result is valid.
- Edited items are checked after each edit and need to be correct before selecting another item.
- The complete sequence is checked when the Next button is clicked. Errors are highlighted.

5.3.3.2 *Save sequence*

The last step is saving the sequence. It is similar to the Select save window from the Sequence task editor. See Chapter 5.3.2.3 for details.

5.3.4 Instrument sequence manager (admin access only)

The sequences can be managed by admin level users via the “Instrument sequence manager” window. The right click on the sequence name shows the available options.

Sequence-> Instrument sequence manager (Ctrl+F6)

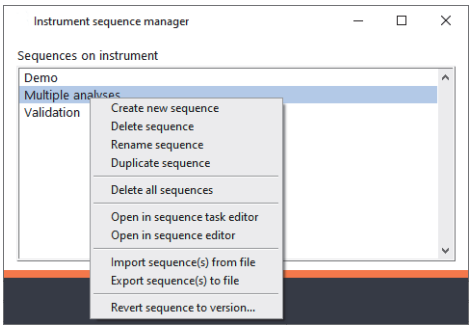


Fig. 68: Instrument sequence manager

5.3.5 Set result tag

It allows to define a tag, which is added to the results and can be used to identify groups of results. For example: “Calibration Mix L”. When the tag is changed, all subsequent results will show the new tag. The tag can also be changed from the sequence.

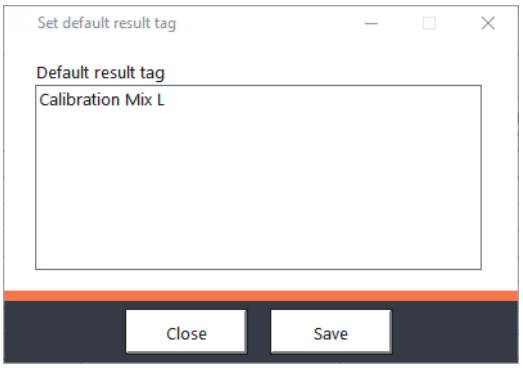


Fig. 69: Set result tag

Sequence-> Set result tag (Ctrl+Shift+N)

5.4 Method menu

The method is a set of analysis parameters (e.g. column temperature, cycle time, injection time, etc.) and data processing (e.g. integration, identification, etc.)

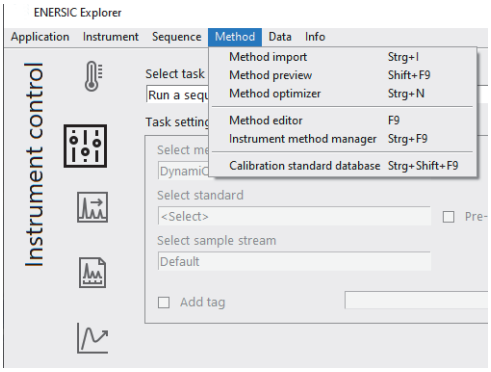


Fig. 70: Method menu

5.4.1 Method import

The previously saved methods can be imported to the instrument. The method path can be chosen by clicking on the file icon.

Method-> Method import (Ctrl+I)

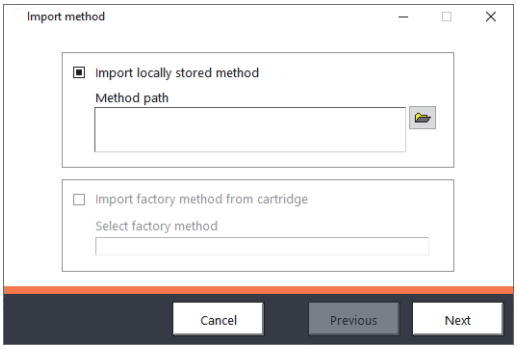


Fig. 71: Import method

5.4.2 Method preview

The Method preview tool allows to view the effect of changes in the method on a specific result. Typically, both the Method editor (see Chapter 4.2) and the Method preview are open at the same time. By selecting an existing result, the viewer shows how the analysis results would be when the method was applied to this result. If a parameter in the method editor is changed, the result is updated automatically. The arrows on right-side bottom navigate between the runs (Figure 72). This tool is very helpful when changing integration settings, to quickly view the calculated baseline for different sample concentrations, and is used in combination with the fast navigation bar (see Chapter 4.3.4.1) to toggle between different results.

The appearance of the chromatogram can be adjusted via the zoom palette (see Chapter 7.1) or by right clicking to change preferences. The position of the compound can be visualized by selecting the compound in the Result Table.

Method-> Method preview (Shift+F9)

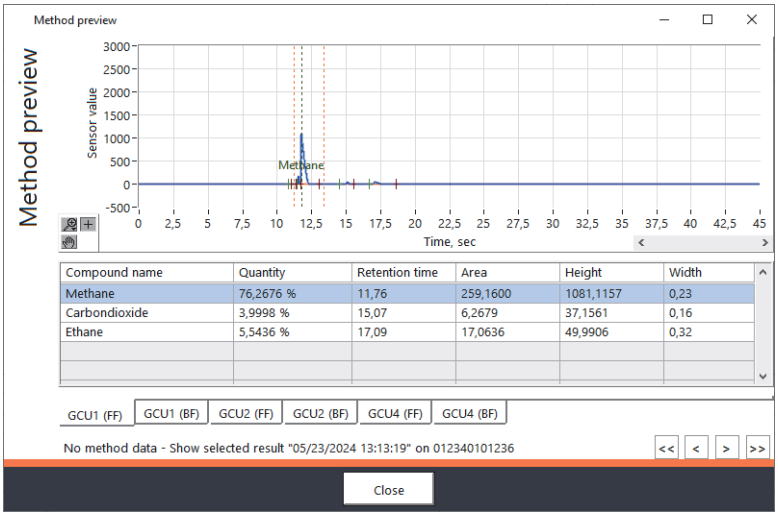


Fig. 72: Method preview

5.4.3 Method optimizer

It is a tool to optimize the existing method for selected parameter(s). The right click on the parameter column allows adding and removing the parameters to vary (Figure 73) and the left click on the parameter allows to select and configure the parameter (Figure 71). After setting start and end value of the parameter and number of steps, the step size can be seen.

Method-> Method optimizer (Ctrl+N)

As an example, this tool might be used to vary the column temperature to find an optimum compromise between separation and analysis speed. Multiple parameters can be varied simultaneously, so optimizations can be done on multiple channels in parallel. Note that, like the Instrument control window, this tool automatically creates and runs an optimization sequence.

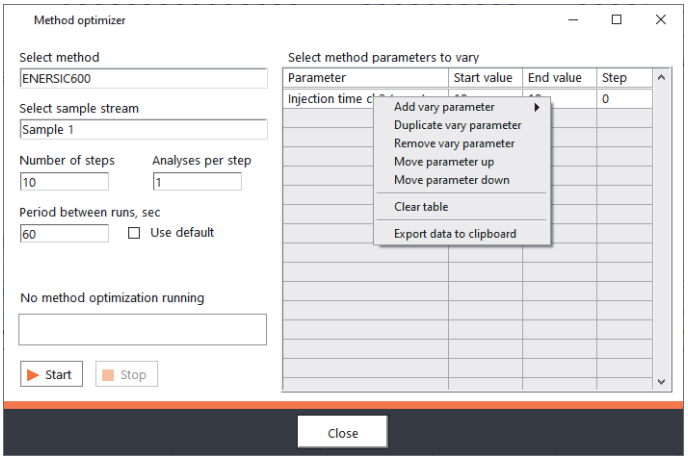


Fig. 73: Adding vary parameter to method optimizer

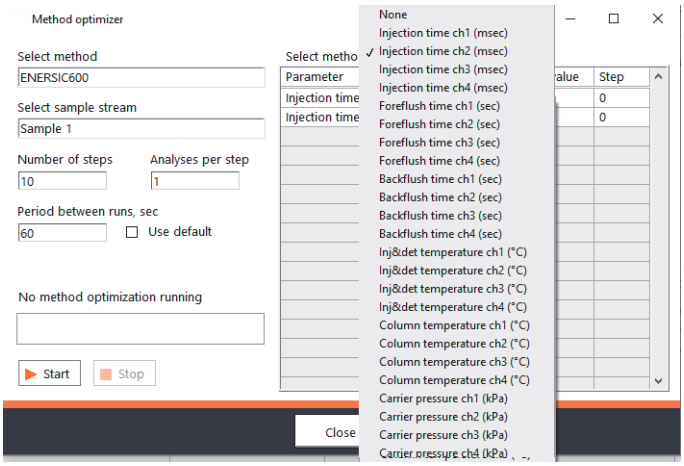


Fig. 74: Selecting the vary parameter

5.4.4 Method editor

The new and/or existing methods can be edited and saved by Method editor. Method edit is explained in detail in Chapter 4.2.

Method-> Method editor (F9)

5.4.5 Instrument method manager (admin access only)

The methods can be managed by admin level users via the “Instrument method manager” window. The right click on the method name shows the available options.

Method-> Instrument method manager (Ctrl+F9)

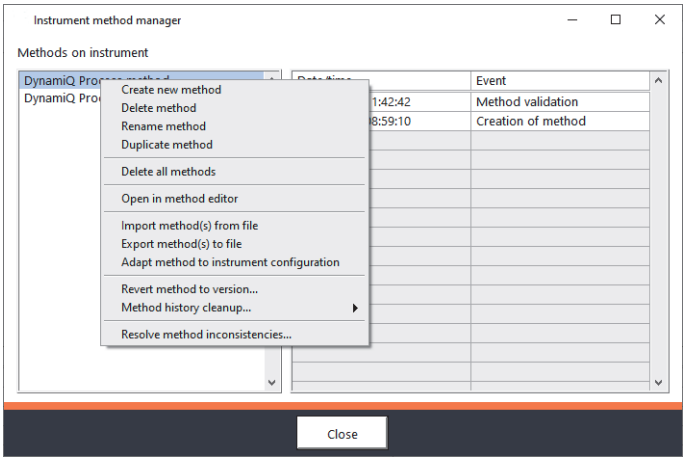


Fig. 75: Instrument method manager

5.4.6 Calibration standard database (admin access only)

The calibration standard database allows to store gas standard data and easy exchange of standard data between the methods.

Method-> Calibration standard database (Ctrl+Shift+F9)

The user interface consists of three parts (Figure 76): List of available standards (red box) allows to add/remove and/or export/import standards; list of specifications of the standard i.e. standard name, cylinder number, etc. (green box) allows to specify the selected standard, composition of the standard (blue box) allows to specify the composition of the selected standard.

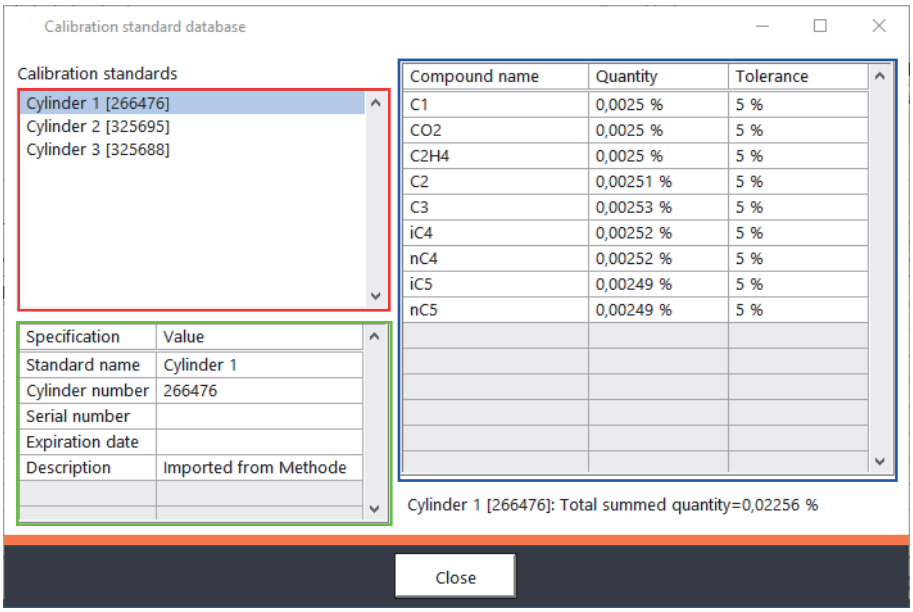


Fig. 76: Calibration standard database

5.5 Data menu

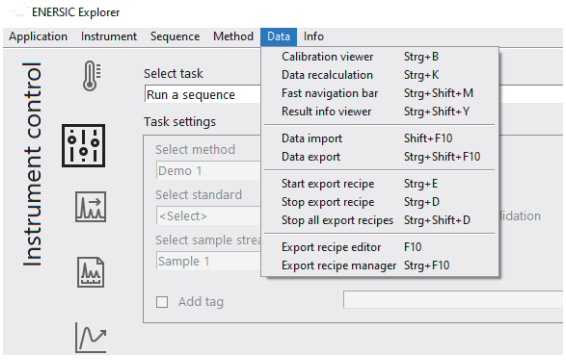


Fig. 77: Data menu

5.5.1 Calibration viewer

The Calibration viewer allows to see calibration details for each identified compound in the application. See Chapter 4.3.6 for the details.

Data-> Calibration viewer (Ctrl+B)

5.5.2 Recalculation tool

The Recalculation tool allows post-processing the same analysis data using different settings, e.g. integration, identification, calibration etc. The post-processing results are adjusted without needing to re-run the analyses. The right click on Previous or Next on the Recalculation tool windows allows to open the desired Method editor window directly.

When a recalculation is complete, the result and trend views (see Chapter 4.3.4 and Chapter 4.3.5) are automatically updated and the recalculation results can be viewed immediately. The result viewer shows recalculation data, if available. The recalculated data can be reverted to the original data via the Recalculation tool.

Data-> Recalculation (Ctrl+K)

5.5.2.1 *Select data and action*

The first step of the recalculation is selecting data to recalculate (Figure 78). The consecutive series of results are selected by Instrument ID, Start date/time and End date/time. The recalculation dataset may contain only compatible results, i.e. the same method name, the same instrument settings and the same configuration. The incompatible results are automatically excluded from the dataset. The action (recalculate or revert) must be chosen.

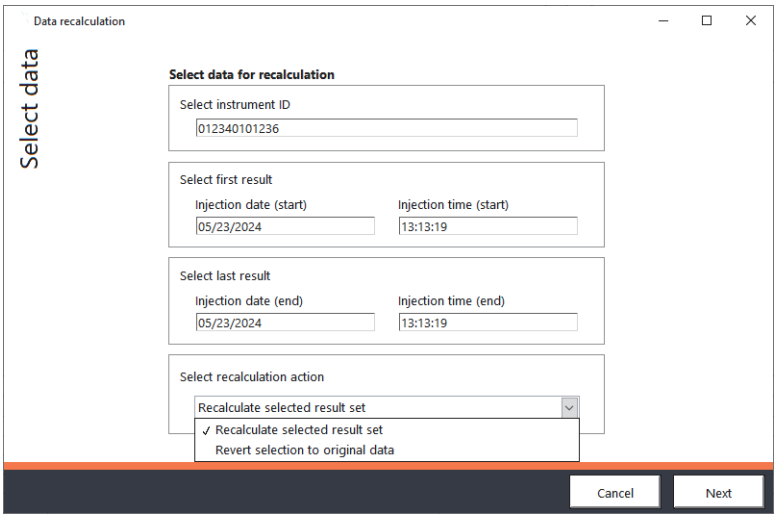


Fig. 78: Data recalculation, select data

5.5.2.2 *Select recalculation method*

The selected data set is recalculated using the method settings in the recalculation method (Figure 79). The method can be a method of one of the results from the selected dataset, an instrument method (online only) or a saved method (offline). The method must be compatible, i.e. the same instrument settings and the same configuration.

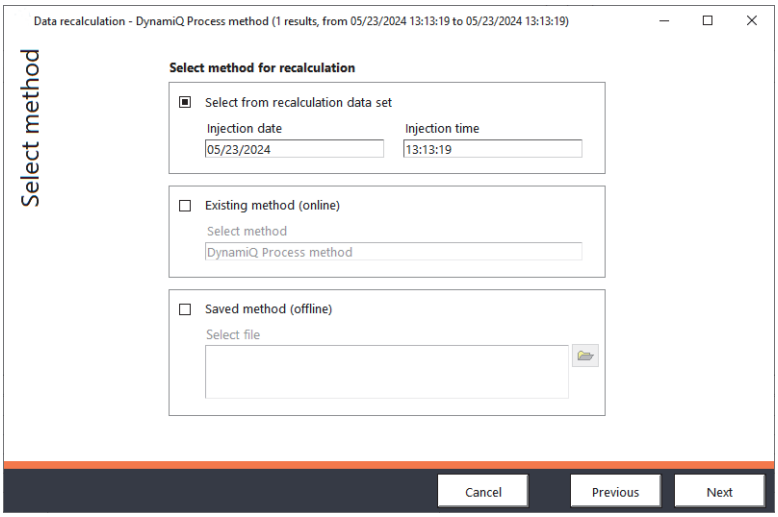


Fig. 79: Data recalculation, select method

5.5.2.3 *Edit recalculation method*

After selecting the recalculation method, the Method editor windows allow to edit integration, identification, calibration and post-processing settings. See Chapter 4.2 for further detail.

Fig. 80: Data recalculation, Edit method

5.5.2.4 *Recalculate*

When the method parameters are set, recalculation can be started (Figure 81).

The recalculated data are saved automatically. To do this, a backup of the original data is made and the original data can be recovered via the Recalculation tool. This keeps the original data secure. In case of a multiple recalculations of the same result, only the last recalculated version of the result is stored. There is no copy of the data made for each recalculation, therefore there is no excessive data generation.

The recalculated data are marked, e.g. Analysis-> Analysis (recalc); Calibration (update)-> Calibration (update, recalc)

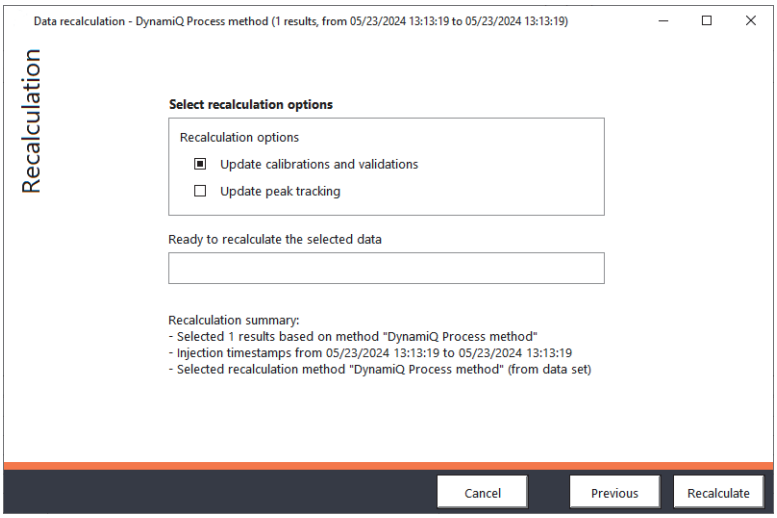


Fig. 81: Data recalculation, Recalculation

5.5.2.5 *Save recalculation method*

The last step is saving the recalculation method. The following options are available (Figure 82):

Create new method (online) saves the method as a new method on the instrument.

Update existing method (online) replaces an existing method residing on the connected instrument.

Save locally (offline) saves the method in a directory on the local computer.

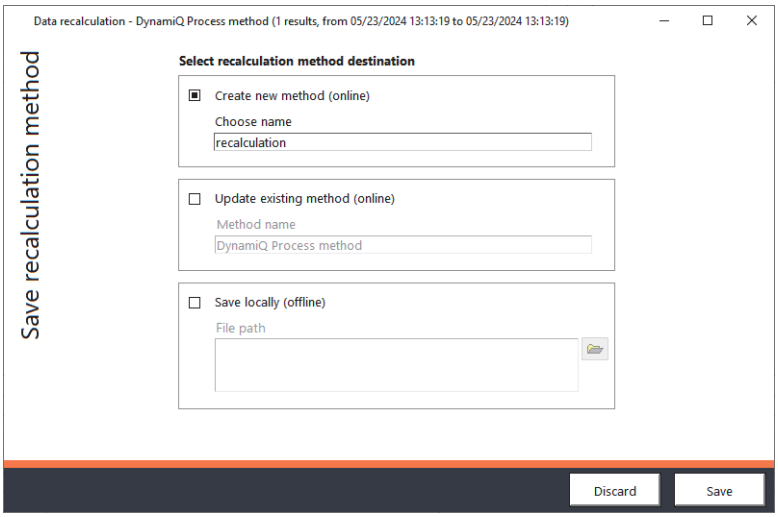


Fig. 82: Data recalculation, Save method

5.5.3 Fast navigation bar

The Fast navigation tool allows to navigate to selected results quickly. See Chapter 4.3.4.1 for the details.

Data-> Fast navigation bar (Ctrl+Shift+M) or by double-clicking the result navigation pane in the Result view and Trend view windows.

5.5.4 Data import (admin access only)

The Data import tool allows to import data from a selected instrument. This can be done online or offline. In combination with ENERSIC600 firmware version 1.0.0.3360 or newer, fast download rates of up to 25 results per second are feasible. With older firmware, the download rate is similar to the normal data synchronization rate.

The tool can be accessed via the main menu bar (Data-> Data import, Shift+F10) and is available at Admin access level.

When starting the Data import tool in online mode, a selection dialog is shown, as shown in Figure 83. When selecting Offline import, the Offline import tool is opened. In Offline mode, the Offline tool is automatically opened.

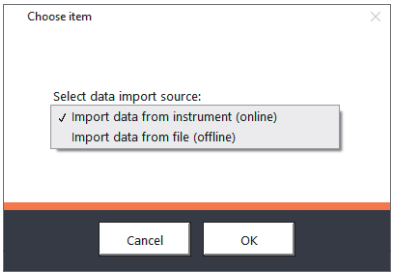


Fig. 83: Data import tool: Select import source dialog

When selecting “Online” as data import source, the Data import tool is opened (Figure 84). The tool consists of start and end of range selectors, which allow to define a date/time range of results to be imported. After clicking Import, a list of results with injection timestamps in the defined date/time range is collected from the instrument. A dialog shows the number of results found (Figure 84). After clicking OK, the results are downloaded from the instrument.

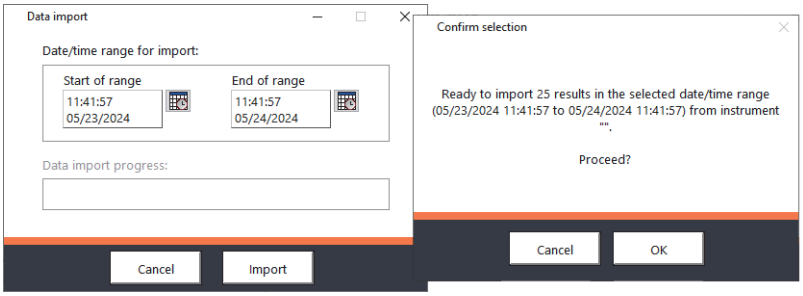


Fig. 84: Online data import tool

When selecting “Offline” as data import source the Data import tool is opened (Figure 80) is opened. The instrument ID can be selected and file(s) and folder(s) can be added.

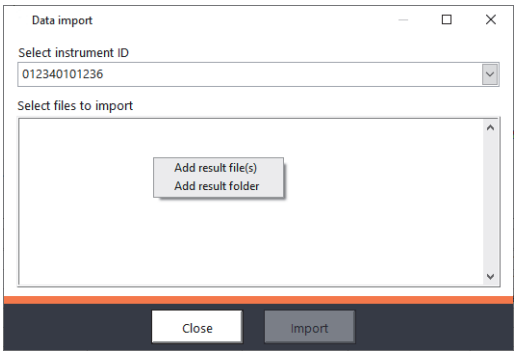


Fig. 85: Data import

5.5.5 Data Export (admin access only)

The Data export tool allows to export a selected range of data from a selected instrument. There are three options available:

Create ZIP archive stores the data in a zip archive, when it is deselected, data are stored in a selected folder.

Export original data exports only the original data, when it is deselected, recalculated data (if available) are also exported with the original data.

Export ASCII chromatograms exports the data in tab-separated ASCII files containing chromatogram and calculated baseline data for each result, when it is deselected, data are exported in .mtd files.

Data-> Data export (Ctrl+Shift+F10)

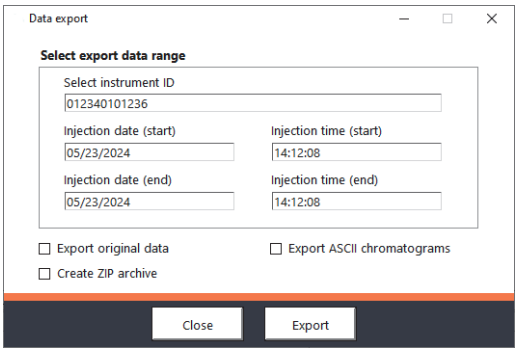


Fig. 86: Data export

5.5.6 Export tool

The Export tool can be used to export result data to a delimited ASCII spreadsheet, which can be imported to other formats, e.g. Microsoft Excel. The export process does not require a connection to the instrument (can be offline).

The Export tools are available from the Data menu.

5.5.6.1 *Export recipe execution*

An export recipe is an ASCII-based export method description, which can be reused. It contains general settings, list of items to export and export filters.

The execution of the export recipes is a background process in the ENERSIC600 software. When an export recipe is started, it keeps running while the ENERSIC600 software runs, until complete. It goes to sleep when the software is closed and resumes when the software is started again. The export process is indicated by the blue progress indicator on the status bar (Figure 3 and Figure 87).

Fig. 87: Export progress indicator

Start export recipe (Ctrl+E): It opens a window to select an export recipe to start. The export recipe to start can then be selected from a file. The data range to be exported and export file destination must be selected in the next windows.

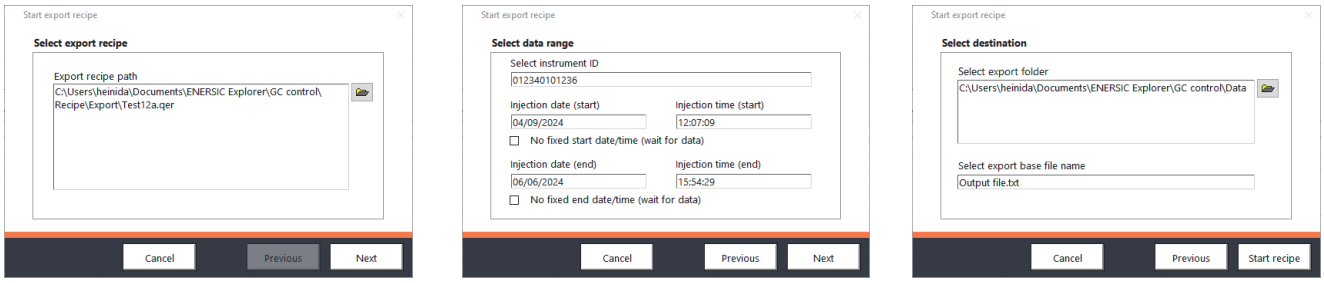


Fig. 88: Start export recipe

Stop selected export recipe (Ctrl+D): It opens a window to select an export recipe to abort. The export recipe to stop can then be selected from the drop-down list which shows all currently running export recipes.

Stop all export recipes (Ctrl+Shift+D): It aborts all currently running export recipes.

5.5.6.2 *Export recipe editor (admin access only)*

The export recipe editor allows to create and to edit the export recipes for a selected range of data. (Figure 84 and Figure 85). The right click on Previous or Next on the Export recipe editor windows allows to open the desired Export recipe editor window directly.

Data-> Export recipe editor (Shift+F10)

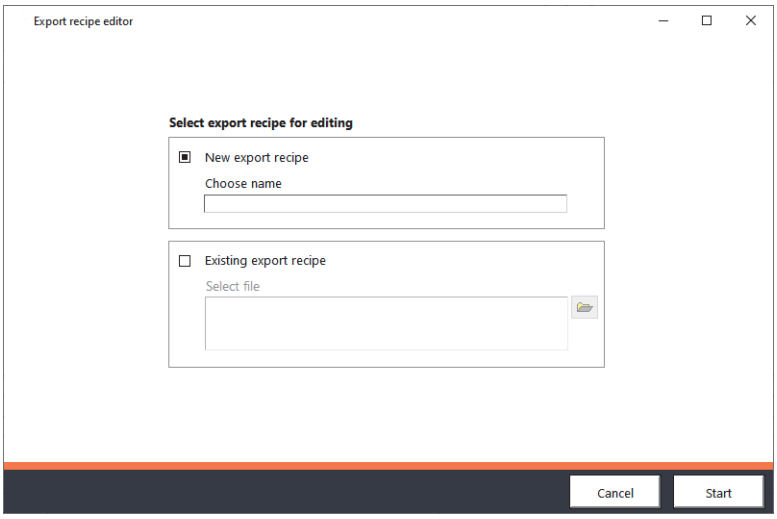


Fig. 89: Export recipe editor

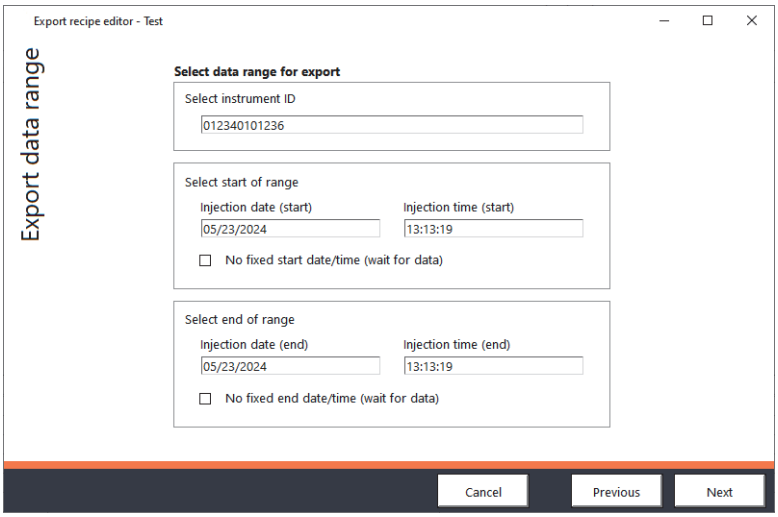


Fig. 90: Export recipe editor, Export data range

After the data range to be exported has been selected, the next step is selecting the export items. The items can be selected from available items list by Drag & Drop. The formatting of the output and the used output units can be specified for each item in the Item properties section (Figure 91).

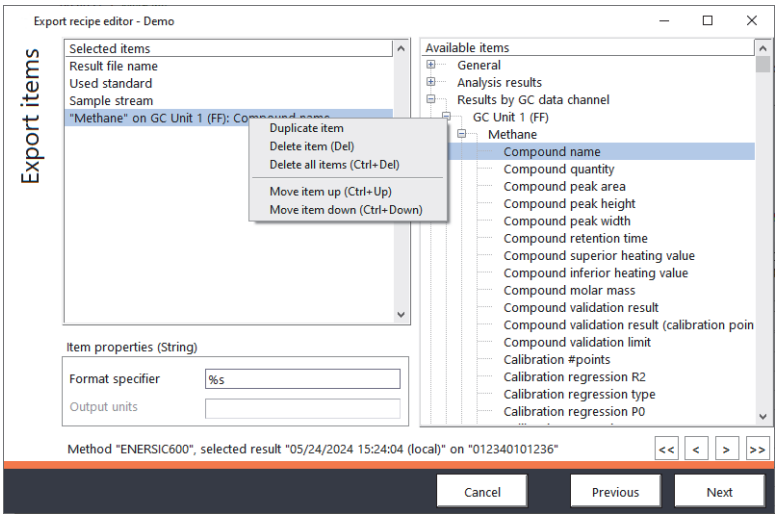


Fig. 91: Export recipe editor, Export items

The next step is to specify the data filter(s). The items can be selected from available items list by Drag & Drop. The type of filter can be defined in the Filter specification section, e.g. only include results with a concentration value in the range 30-40% in the export (Figure 92).

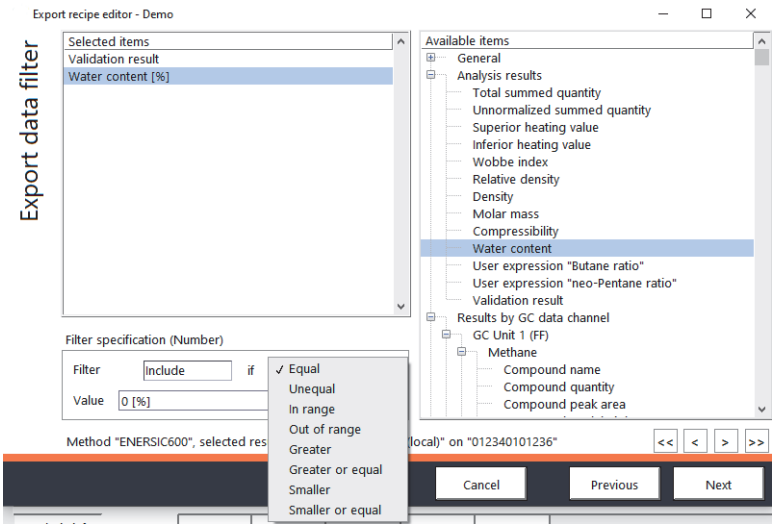


Fig. 92: Export recipe editor, Export data filter

After specifying the export options which are used (delimiter, decimal symbol and time zone, and inclusion recalculated data) (Figure 93), the export destination must be chosen (Figure 94).

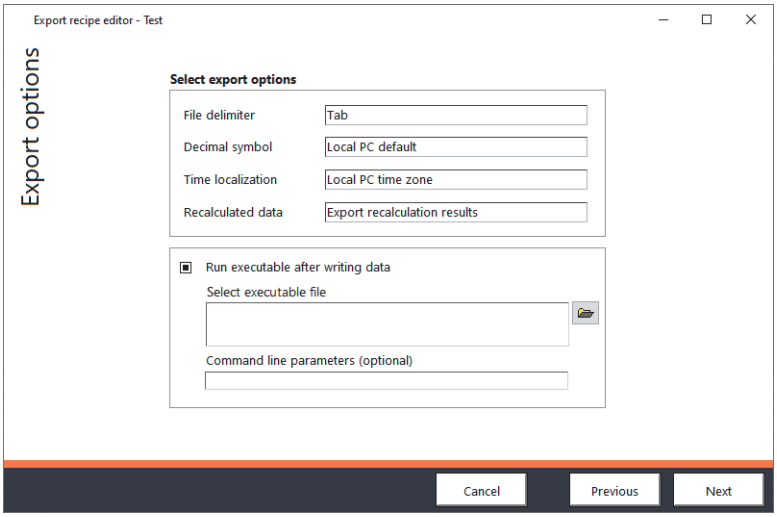


Fig. 93: Export recipe editor, Export options

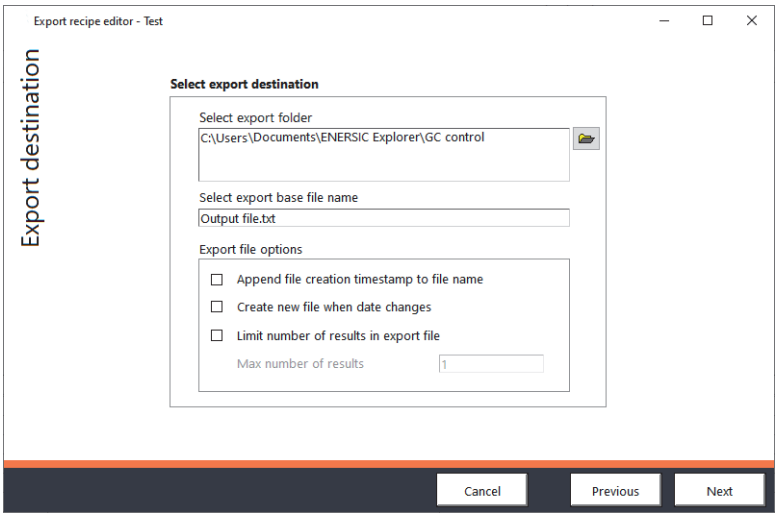


Fig. 94: Export recipe editor, Export destination

The last step is saving the export recipe to a selected file. The export recipe may also be run in this step (Figure 95).

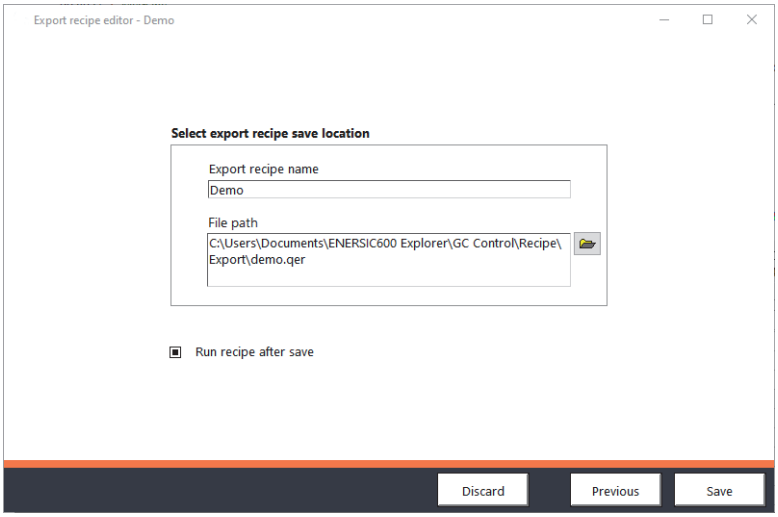


Fig. 95: Export recipe editor, Save export recipe

5.5.6.3 *Export recipe manager*

The export recipe manager shows running export recipes and allows to start/stop them. It also shows an event log for the export jobs.

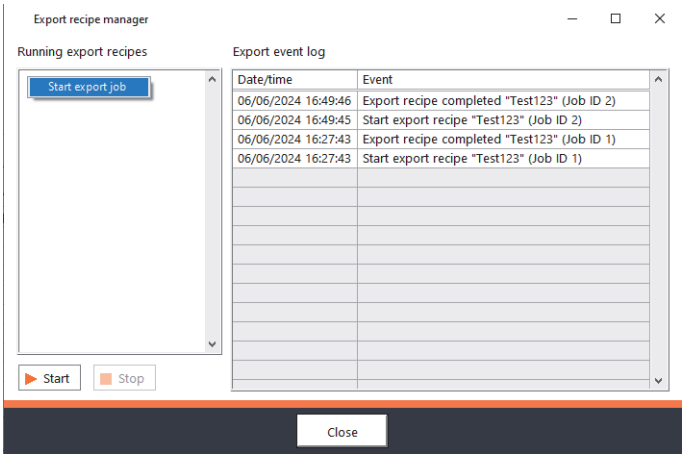


Fig. 96: Export recipe manager

5.5.7 Info

Shows the installed version of the ENERSIC600 software.

Info-> About (Ctrl+A)

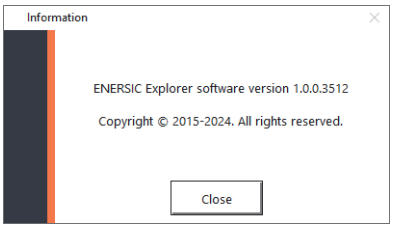


Fig. 97: Info

6 Troubleshooting

For troubleshooting and support, reference is made to the support section of the website:

http://www.endress.com

For field support contact local Endress+Hauser support.

7 Appendices

7.1 Zoom palette

The zoom palette is available for all graphical displays in the ENERSIC600 software. It allows to control the appearance of a graph and combines the following tools:

The Zoom tool (top left) zooms in and out of the display.

The Cursor tool (top right) drags horizontal or vertical cursor lines, for instance to adjust a Retention time window.

The Pan tool (bottom left) picks up the plot and moves it around on the display.

Fig. 98: Zoom palette

The Zoom tool has several options. From top left to bottom right:

Zoom to rectangle, clicking on a point on the corner of the desired zoom area allows to drag the tool until the rectangle covers the zoom area.

X-zoom zooms in on an area of the graph along the x-axis.

Y-zoom zooms in on an area of the graph along the y-axis.

Zoom to Fit zooms out completely.

Zoom in about point allows to choose a point to zoom in on. Clicking and holding the SHIFT key allows to switch between Zoom in and Zoom out.

Zoom out around point allows to choose a point you want to zoom out from. Clicking and holding the SHIFT key allows to switch between Zoom out around point and Zoom in around point.

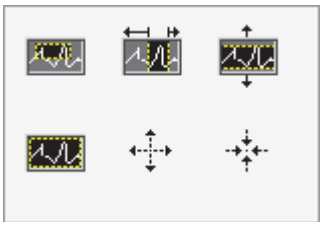


Fig. 99: Zoom tool

7.2 Tips and tricks for the integration of the peaks

Work from left to right (chromatogram) and top to bottom (Integration Table).

Check if all peaks of interest are identified. If not, reduce Threshold or adjust Peak width.

Check if any false peaks are present. If present, increase Threshold or add filtering events.

Check the baseline whether the peak areas are representative. If not, add baseline selection or baseline skimming events.

Use preferably only Peak width and Threshold.

Place events well separated from peaks.

Use Stop=End if possible, avoid intervals.

Start with (Start-End) Peak width and Threshold events with values optimized for the early eluting peaks as a starting point, use subsequent events to fine-tune the result for later-eluting peaks.

Make sure peaks are integrated as much as possible as isolated peaks, no valley in between.

Check result for a range of concentrations (use method preview + fast navigation bar).

Check sensitivity to parameter values, in particular Threshold.

On defective or unused (BF) channels, set a high Peak width, e.g. 1000, to minimize CPU usage.

Use Integration off at the end and sparingly to mask sections of baseline.

Keep it as simple as possible.

7.3 Calibration

Method Set-Up

The Calibration window of the Method editor (see Figure 18) allows to specify calibration parameters for each identified compound. It also allows the user to define the standards to be used for the calibration.

Calibration runs

The Instrument control field allows to run calibration samples (see Chapter 4.3.1). It is recommended to have multiple runs (5-10) to have more accurate results. Note that zeroes and outliers are automatically removed, and average of the remaining data points are used for the response calculation.

Calibration viewer

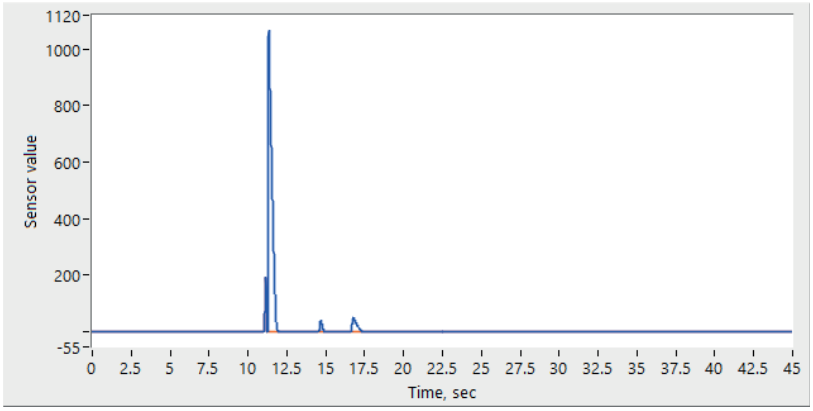
Calibration viewer (see Chapter 4.3.6) allows to view the calibration results.

7.4 ENERSIC600 analysis report (an example)

ENERSIC Explorer analysis report

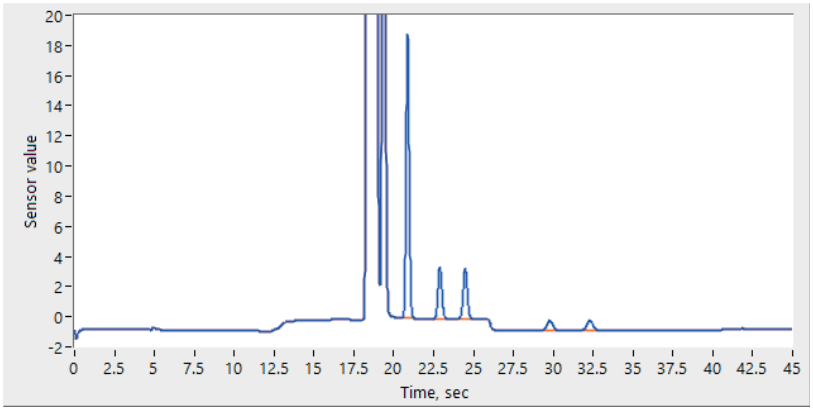
Instrument: 012340101236
Cartridge: 111111111111
Date/time: 05/29/2024 17:52:38 (local)
Method: Idle method
Sample: Sample 1
Analysis type: Analysis

GC Unit 1, TCD1



Compound name	Quantity	Retention time	Peak area	Peak height	Peak width
Methane	87.3863 %	11.34 sec	257.2814	1067.7228	0.23 sec
Carbondioxide	1.4993 %	14.68 sec	6.3064	38.4909	0.15 sec
Ethane	3.9980 %	16.76 sec	16.8721	48.8304	0.32 sec

GC Unit 2, TCD1

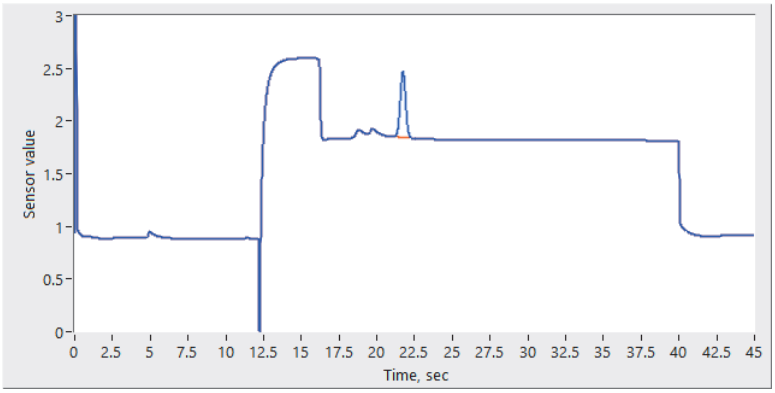


Compound name	Quantity	Retention time	Peak area	Peak height	Peak width
Propane	0.9995 %	20.86 sec	4.2305	18.8116	0.21 sec
i-Butane	0.2009 %	22.89 sec	0.9660	3.4127	0.27 sec
n-Butane	0.1989 %	24.48 sec	0.9799	3.3035	0.28 sec
neo-Pentane	499.8 ppm	27.62 sec	0.0028	0.0105	0.27 sec

Page 1 of 2

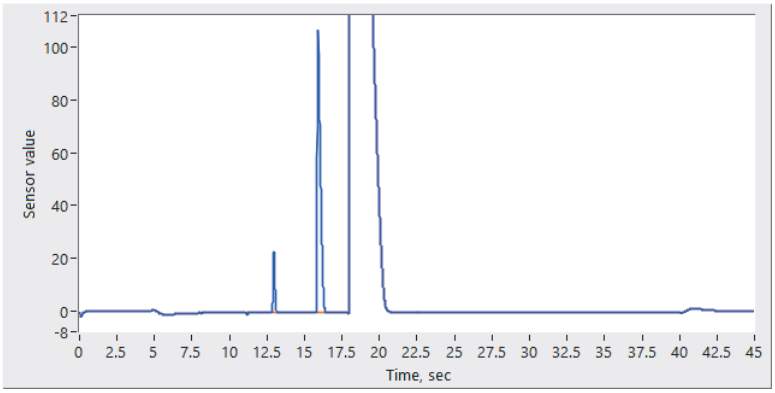
Compound name	Quantity	Retention time	Peak area	Peak height	Peak width
i-Pentane	499.8 ppm	29.77 sec	0.2692	0.6308	0.40 sec
n-Pentane	499.8 ppm	32.29 sec	0.2796	0.6472	0.41 sec

GC Unit 2, TCD2



Compound name	Quantity	Retention time	Peak area	Peak height	Peak width
C6+	499.8 ppm	21.72 sec	0.2585	0.6229	0.39 sec

GC Unit 4, TCD1



Compound name	Quantity	Retention time	Peak area	Peak height	Peak width
Hydrogen	0.9995 %	11.15 sec	0.1055	1.0159	0.10 sec
Oxygen	0.4998 %	12.95 sec	2.9661	23.2522	0.12 sec
Nitrogen	4.0080 %	15.88 sec	25.4692	107.2530	0.22 sec
Carbonmonoxide	100.0 ppm	30.79 sec	0.0627	0.1262	0.47 sec

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