



EagerSmart

Data Handling Software for FLASH Elemental Analyzers

Software Manual

Software Version 1.0

31707004 Revision B December 2016

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Revision B, December 2016

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Preface

Overview

This manual is organized as follows:

- [Chapter 1, “Software Installation,”](#) provides a description and the instructions for installing the Thermo Scientific™ *EagerSmart*™ Data Handling Software in the versions for *FlashSmart*, Flash 2000, Flash 4000, EA 1110 USB and A/D.
- [Chapter 2, “Getting Started,”](#) provides a general overview of *EagerSmart*.
- [Chapter 3, “Method Editor,”](#) provides instructions to modify the method parameters.
- [Chapter 4, “Component Table,”](#) provides the instructions for editing the Component Table.
- [Chapter 5, “Sample Table,”](#) , provides information about the sequence of samples to be acquired and processed.
- [Chapter 6, “Wizard Method Development,”](#) provides the instructions for developing the various methods.
- [Chapter 7, “Edit Elemental Analyzer Method,”](#) provides the instructions for setting Elemental Analyzer parameters in *EagerSmart* for *FlashSmart*, Flash 2000, Flash 4000, and EA 1110 USB or A/D versions.
- [Chapter 8, “Edit Sampler Parameters,”](#) provides the instructions for setting the parameters for the AI 1310/AS 1310 and AI 3000/AS 3000 II autosamplers for liquid samples.
- [Chapter 9, “View Sample Being Acquired,”](#) provides the instructions for monitoring the sample currently being acquired.
- [Chapter 10, “View Calibration Curves,”](#) provides the instructions to see the calibration curve of the method in memory.
- [Chapter 11, “View Chromatograms,”](#) provides the instructions to view or modify the peak integration.
- [Chapter 12, “Overlay Chromatograms,”](#) provides the instructions to view and compare different chromatograms.
- [Chapter 13, “Operate on Chromatograms,”](#) provides the instructions to operate on the chromatograms.
- [Chapter 14, “Compare Chromatograms,”](#) provides the instructions to compare chromatograms.

- [Chapter 15, “Elemental Analyzer Status,”](#) provides the instruction to visualize the status of the Elemental Analyzer in EagerSmart for FlashSmart, Flash 2000, Flash 4000, EA 1110 USB or A/D versions.
- [Chapter 16, “View Maintenance,”](#) provides the instructions to view and set-up the instrument maintenance program.
- [Chapter 17, “Recalculation,”](#) provides the instructions to recalculate sample batches.
- [Chapter 18, “Summarize Results,”](#) provides the instructions to view the results of a batch of sample.
- [Chapter 19, “Report Publisher,”](#) provides the instructions to create or modify the file report layout.
- [Chapter 20, “Custom Report Editor,”](#) provides the instructions to generate a report designed by you.
- [Chapter 21, “Peaks Detection,”](#) provides the instructions to test the entered parameters of a stored chromatogram.
- [Chapter 22, “Time Events,”](#) provides the instructions to improve the integration of different peak shape.
- [Chapter 23, “Use of Eager Simplified User Interface,”](#) provides the instructions for the use of the simplified user interface of EagerSmart for FlashSmart, Flash 2000 and Flash 4000 versions.
- [Chapter 24, “Electronic File Signature,”](#) provides the instructions to authenticate an analytical method in compliance with the directive CFR 21 parts 11.

Types of Alerts and Signal Word

Make sure you follow the precautionary notices presented in this guide. Safety and other special notices appear in boxes and include the following:

WARNING Highlights hazards to humans or the environment. This is the general warning safety symbol and safety alert word to prevent actions that could cause personal injury. Each **WARNING** safety alert is preceded with this safety symbol and another appropriate safety symbol. Then it is followed with an appropriate safety precautionary message. When you see a safety alert on your instrument or in the publications, please carefully follow the safety instructions before proceeding.

CAUTION Highlights actions that might cause personal injury or instrument damage. We use it to highlight information necessary to prevent personal injury or damage to software, loss of data, invalid test results, or to information that is critical for optimal system performance. A **CAUTION** safety alert is always preceded with an appropriate safety symbol. It is followed with an appropriate safety precautionary message. When you see a safety alert on your instrument or in the publications, please carefully follow the safety instructions before proceeding.

IMPORTANT Highlights information necessary to prevent damage to software, loss of data, or invalid test results, or it might contain information that is critical for optimal performance of the system.

Note Emphasizes important information about a task.

Tip Provides information that can make a task easier.

Terminology

Table 1 lists terms as acronyms, metric prefixes, symbols and abbreviations used in this manual.

Table 1. Terminology (Sheet 1 of 2)

Term	Description
A/D	Analog to digital conversion
ASCII	American Standard Code per Information Interchange
BMP	Bitmap
C	Carbon
CD	Compact Disk
CO ₂	Carbon Dioxide
CR	Carriage Return
DIF	Directory Interchange Format
EXE	Executable File
FDA	U.S. Food and Drugs Administration
GB	Giga Byte
GHV	Gross Heating Value
GLP	Good Laboratory Practice
H	Hydrogen
HPGL	Hewlett Packard Graphic Language
HTML	Hyper Text Mark-up Language
Hz	Hertz
IP	Internet Protocol (Network address)
IRMS	Isotope Ratio Mass Spectrometer
LAN	Local Area Network
LIMS	Laboratory Management System
LPT	Parallel port
M	Mega(10 ⁶)
m	milli (10 ⁻³)
μ	micro (10 ⁻⁶)
min	minute
mL or ml	milliliter
mm	millimeter
N	Nitrogen
NHV	Net Heating Value
O	Oxygen

Table 1. Terminology (Sheet 2 of 2)

Term	Description
PC	Personal Computer
S	Sulfur
s	second
t	Tonne
TCD	Thermal Conductivity Detector
TCP/IP	Transmission Control Protocol/Internet Protocol
TMW	Total Molecular Weight
TJ	Tera Joule
V	Volt
USB	Universal Serial Bus

Software Installation

This chapter provides a description and the instructions for installing the Thermo Scientific™ *EagerSmart*™ Data Handling Software in the versions for Flash*Smart*, Flash 2000, Flash 4000, EA 1110 USB and A/D.

Contents

- Overview
- Installing *EagerSmart*
- Starting *EagerSmart*

Overview

EagerSmart is the dedicated software that fully controls all the operations of the Flash*Smart*, Flash 2000, Flash 4000, and EA 1110 elemental analyzers. It is designed to be compatible with commercially available computers, and requiring the use of Windows™ 2000 / XP / Vista / 7 / 8 operating system.

Hardware Minimum Requirements

Table 1 lists the hardware minimum requirements:

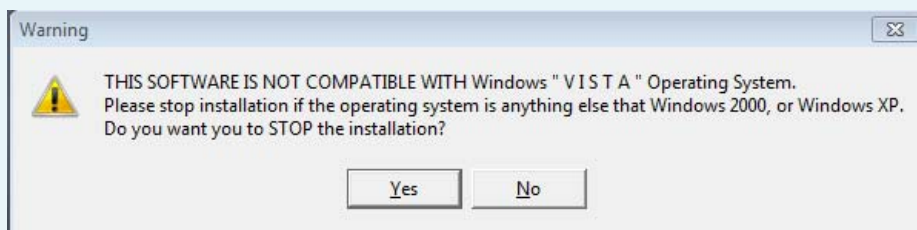
Table 1. Hardware minimum requirements

Component	Description
Computer	Any PC can be used, including laptop computer Operating System: Windows™ 2000 / XP / Vista / 7 / 8 Pentium Processor minimum 256 MHz Hard drive with at least 2 GB free One free COM port for instrument control LAN device alternatively to COM port (for Flash 4000 only) One free COM port for balance, if required One free USB port
Monitor	Color 1024 x 768 or better
Printer	Any printer accepted by the operating system

Installing EagerSmart

IMPORTANT Prior installation of *EagerSmart* please make sure any precedent version of Eager is removed from the disk.

ATTENTION *EagerSmart* A/D version is NOT compatible with Windows™ Vista operating system. Please stop installation if the operating system is anything else that Windows™ 2000 or XP.



Removing the Precedent Eager Software Version

❖ **To remove the precedent Eager software version**

1. Select **Control Panel | Add/Remove Programs**.
2. In the dialog window visualized, select the precedent **Eager** version to remove.
3. Click **Add/Remove**.
4. In C:\ remove the folder **Eager for Flash**.

Installing the New EagerSmart Software Version

The software can be installed by using the USB stick provided in the standard outfit.

❖ **To install new EagerSmart software version**

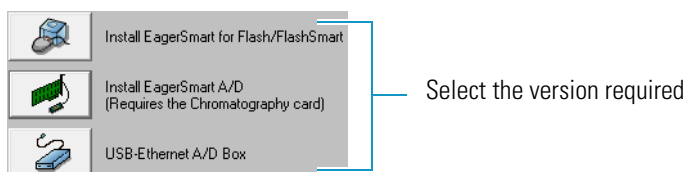
1. When the USB stick is introduced in a free USB port of the computer, the following installation window is visualized. See [Figure 1](#).

Figure 1. *EagerSmart* Installation Package



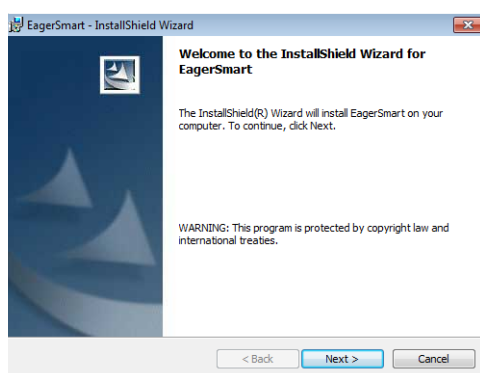
If when the USB stick is introduced in a free USB port of the computer, the installation menu does not automatically appear, through the Windows command **Start-Run**, start the program **Autorun** on the USB stick.

1. Click the icon corresponding to the **Eager** version to install.

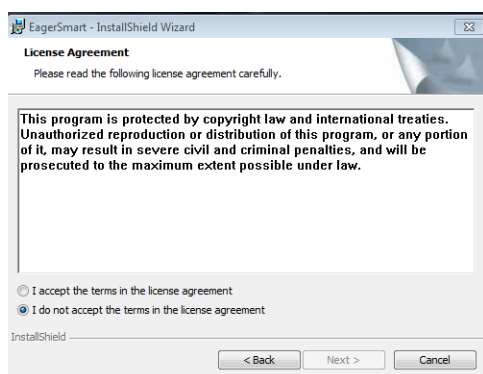


ATTENTION The procedure of installation is common for all the Eager Smart for Flash/Flash Smart, Eager Smart A/D, and USB-Ethernet A/D Box versions. Each window visualized shows the indication of the version selected. For writing convenience the installation of the Eager Smart for Flash/Flash Smart is considered in this procedure.

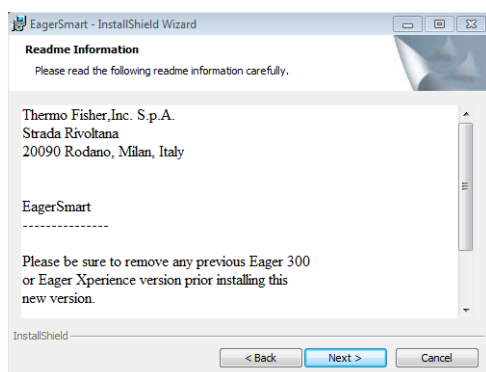
2. Wait for the installation initialization. According to the version selected, the relevant **Welcome to the InstallShield Wizard for Eager** window is visualized. See the following example.



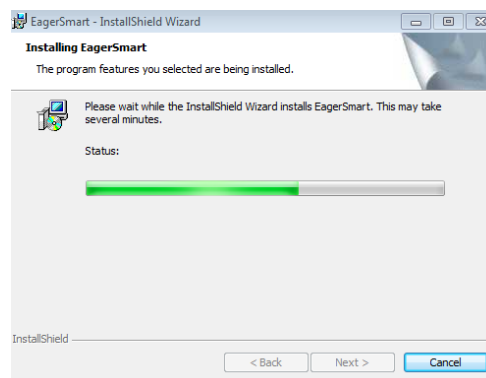
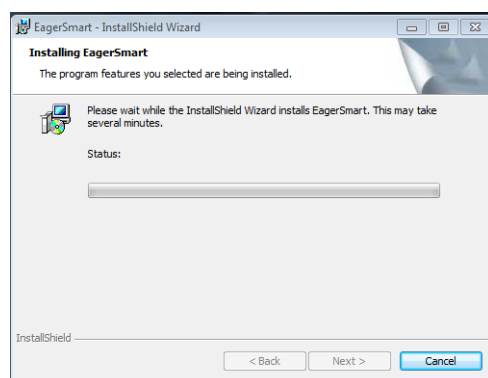
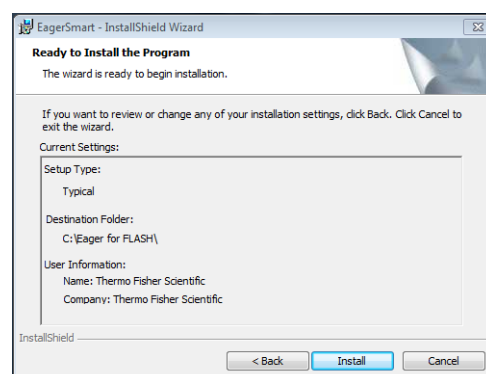
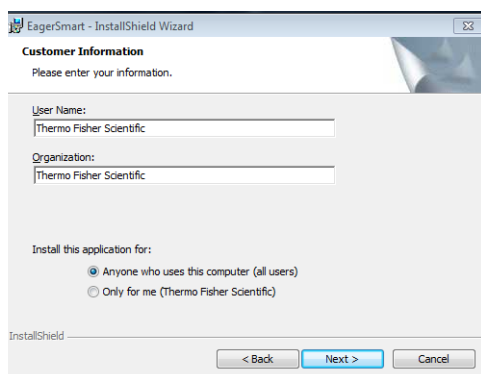
3. Click **Next** to continue. The installation can continue only if the **License Agreement Terms** are accepted.



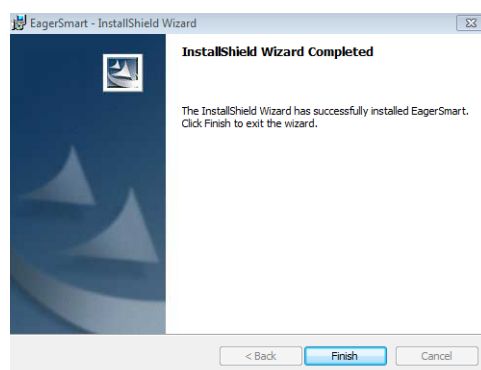
4. Click **Next** to continue. The system ask you to be sure to remove the precedent **Eager** version prior installing the new version. See the following example.



5. Continue the installation following the instructions visualized pressing **Next** at each step.



6. At the end of the installation, the relevant **InstallShield Wizard Completed** window is visualized. See the following example.
7. Click **Finish** to continue.



8. Start the [EagerSmart](#) version installed selecting it in the page **Start | Program** of the desktop.
9. Continue referring to the relevant section contained in the paragraph [Starting EagerSmart](#) on [page 5](#).

Starting EagerSmart

The **EagerSmart Start Form** configures three elemental analyzers plus the OFF-Line one:

- “To start EagerSmart for Flash/Flash Smart version” on page 5
- “To start EagerSmart for USB-Ethernet A/D Box version” on page 7
- “To start EagerSmart for A/D version” on page 10

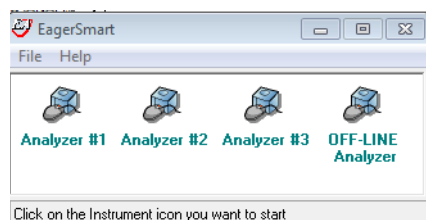
Starting EagerSmart for Flash/Flash Smart Version

❖ To start EagerSmart for Flash/Flash Smart version

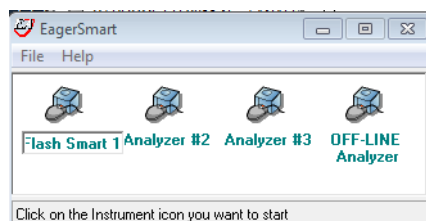
1. Start **EagerSmart** again selecting **Start | Programs | EagerSmart**.

Click on the icon of the instrument selected. The following windows is visualized. See [Figure 2](#).

Figure 2. Instrument Name (Flash- Flash Smart Version)

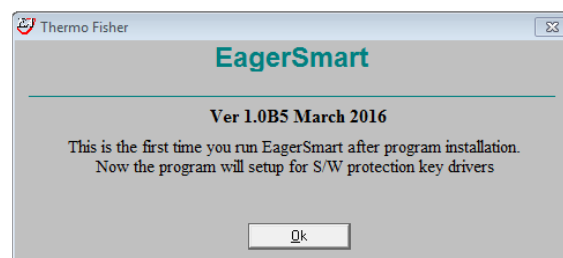
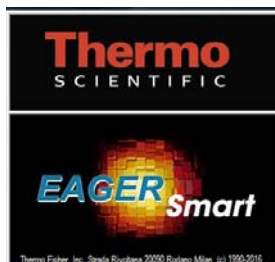


The program is designed to work with three analyzers and one analyzer connected on-line. Each icon corresponds to one instrument. The instrument name icon can be changed. To do this, click on the existing name and overwrite it with the new one.

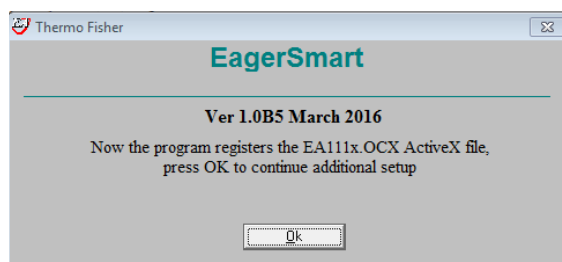


Assign to the icon an instrument connected to the computer by a selected **Serial Port**; for example **Flash Smart 1**. The entered name will be reported in the header of the window of **EagerSmart** Main Menu.

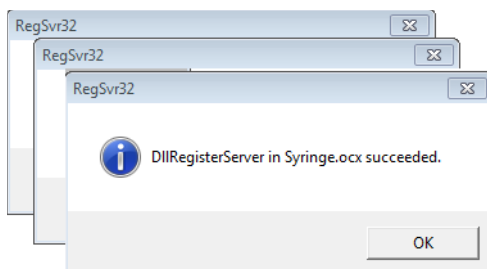
2. Click the icon of the instrument of interest; for example **Flash Smart 1**.



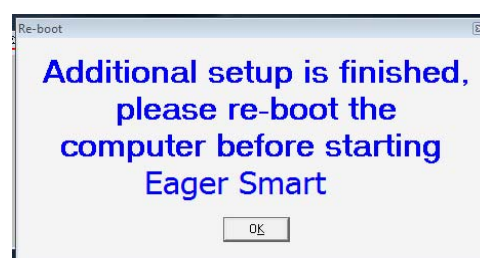
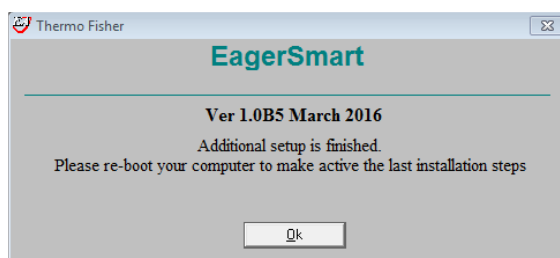
3. Click **OK**. **EagerSmart** proceeds with the registration and the activation of some drivers needed for the correct software functioning. Click **OK**.



4. Click **OK** to the answers prompted step by step.

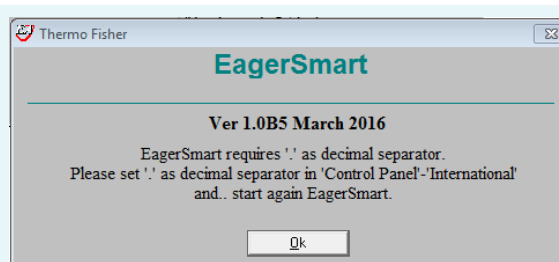


5. At the end click OK. The system ask you to reboot the computer, then click **OK** at each window.

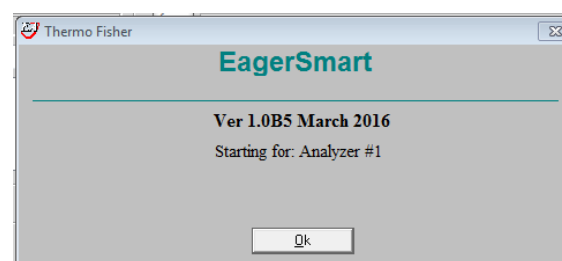
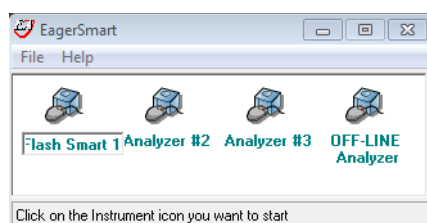


6. Reboot the computer. Start *EagerSmart* again selecting **Start | Programs | EagerSmart | EagerSmart for Flash**.

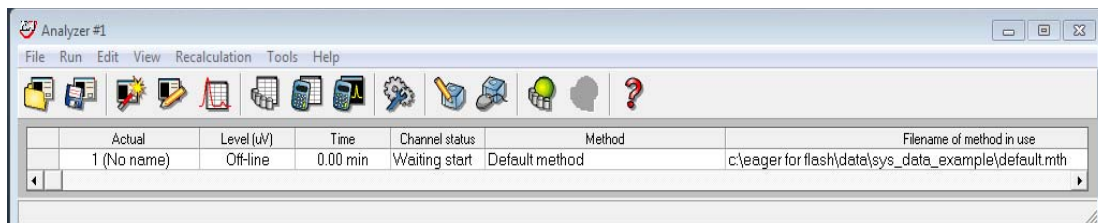
Note If the decimal separator is a comma, the system ask you to change it in the Control Panel. At the end of the operation click OK and start *EagerSmart* again.



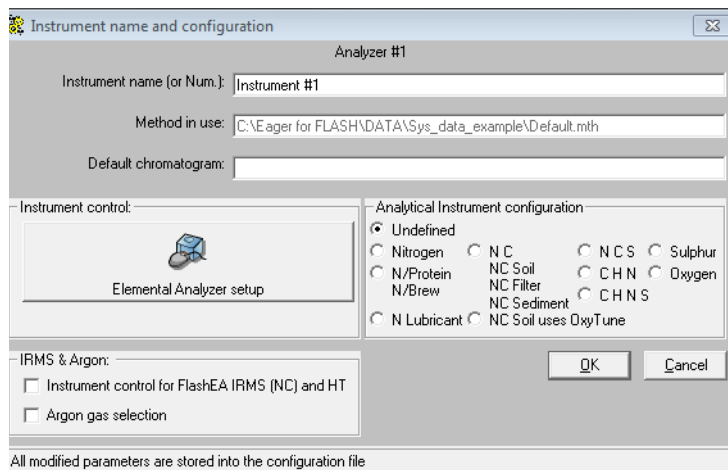
7. Start *EagerSmart* again selecting **Start | Programs | EagerSmart**. Select the instrument of interest.



8. The Main Menu of *EagerSmart* is visualized.



9. Configure the instrument selecting **File | Instrument Name and Config.**



10. Proceed the configuration as described in the section “[Instrument Name and Configuration](#)” on [page 16](#).

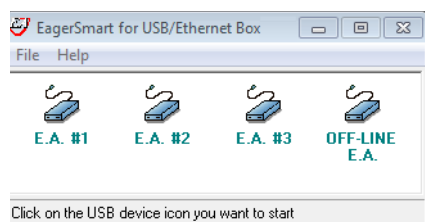
Starting EagerSmart for USB - Ethernet A/D Box Version

❖ To start EagerSmart for USB-Ethernet A/D Box version

1. Start [EagerSmart](#) again selecting **Start | Programs | EagerSmart for USB.**

Click on the icon of the instrument selected. The following windows is visualized. See [Figure 3](#).

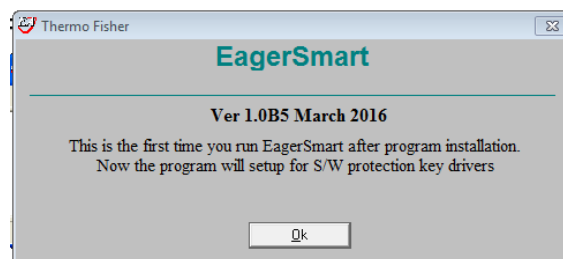
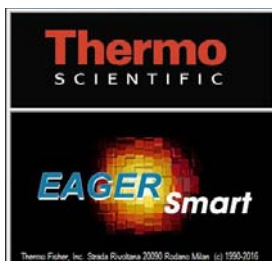
Figure 3. Instrument Name (USB- Ethernet A/D Version)



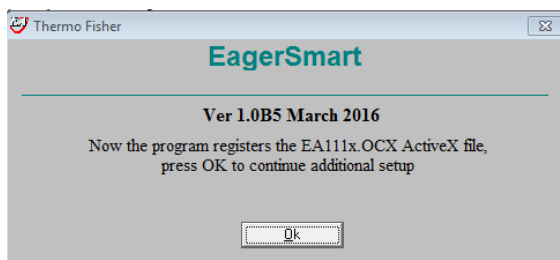
The program is designed to work with three analyzers and one analyzer connected on-line. Each icon corresponds to one instrument. The instrument name icon can be changed. To do this, click on the existing name and overwrite it with the new one.

Assign to the icon an instrument connected to the computer by a selected **Serial Port**. The entered name will be reported in the header of the window of [EagerSmart](#) Main Menu.

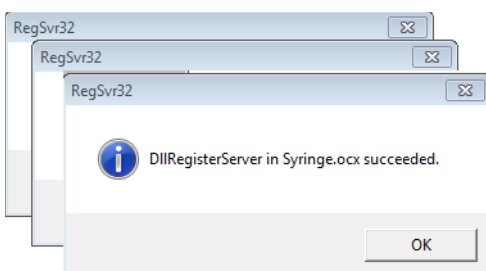
2. Click the icon of the instrument of interest; for example **Flash Smart 1**.



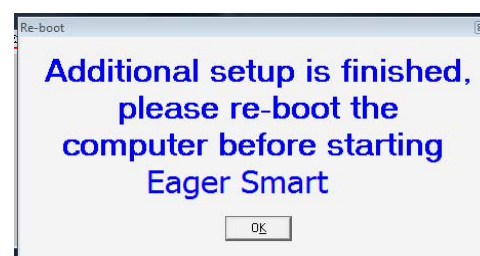
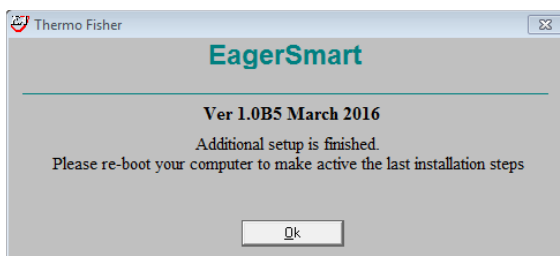
3. Click **OK**. *EagerSmart* proceeds with the registration and the activation of some drivers needed for the correct software functioning. Click **OK**.



4. Click **OK** to the answers prompted step by step.

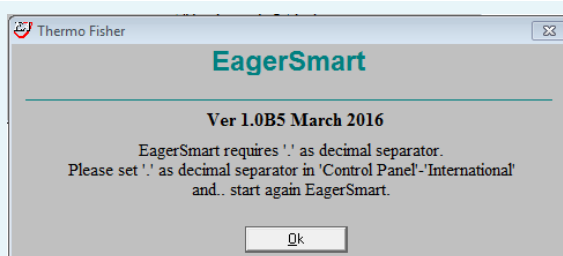


5. At the end click **OK**. The system ask you to reboot the computer, then click **OK** at each window.

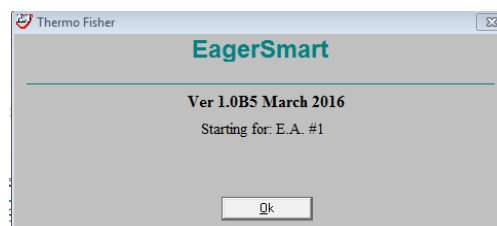
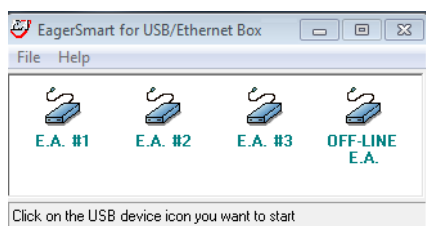


6. Reboot the computer. Start *EagerSmart* again selecting **Start | Programs | EagerSmart for USB**.

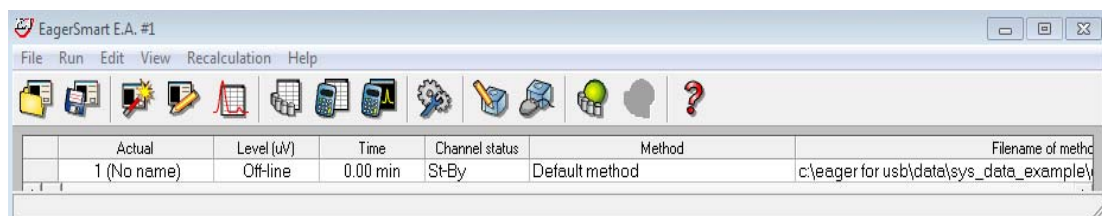
Note If the decimal separator is a comma, the system ask you to change it in the Control Panel. At the end of the operation click **OK** and start *EagerSmart* again.



7. Start *EagerSmart* again selecting **Start | Programs | EagerSmart for USB**. Select the instrument of interest.

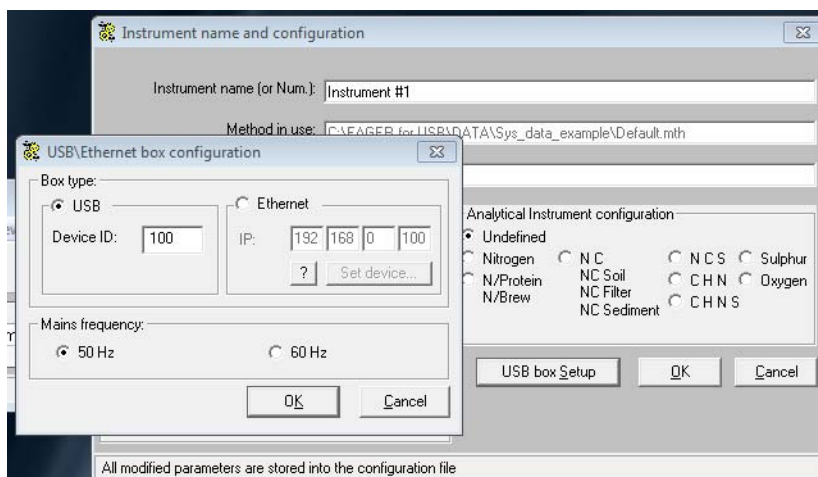


8. The Main Menu of **EagerSmart** for USB is visualized.



9. Configure the USB Box. From Main Menu, select **File | Instrument Name and Config**, then click **USB box Setup**. The following window is visualized. See [Figure 4](#).

Figure 4. USB \ Ethernet Box Configuration Page



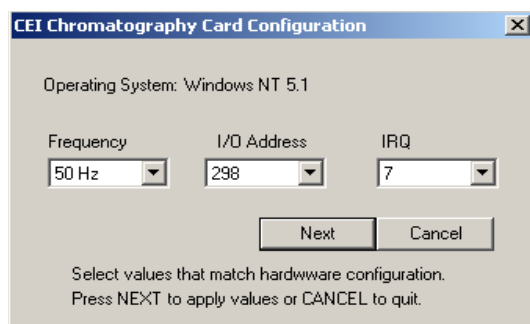
10. This configuration supports both the **USB box** and the **Ethernet box**. Select the option button of interest. According to the box type checked, select the device identification with **Device ID** in case of USB, or **IP** (network address) in case of **Ethernet**.
- In **Device ID** box, type the number reported on the bottom side of the **USB Box**.
 - In **IP** box, enter the address to allow the LAN control of the **Ethernet box** through the Thermo Fisher Scientific data systems. The Ethernet box is shipped with a default IP address, that may not match the needs of the LAN where the box must be installed. To change the default values, contact your network administrator, ask for the IP address to be assigned, and the netmask.
 - The IP address is a 3 digits x 4 fields given by the network administrator e.g. 192.168.127.10
 - The netmask is a 3 digits x 4 fields given by the network administrator e.g. 255.255.255.0
 - The default IP address of the Ethernet box is 10.1.1.2.
 - In **Mains frequency** field, select the mains frequency 50 Hz or 60 Hz.
 - Click **OK**.

Starting EagerSmart for A/D Version

❖ To start EagerSmart for A/D version

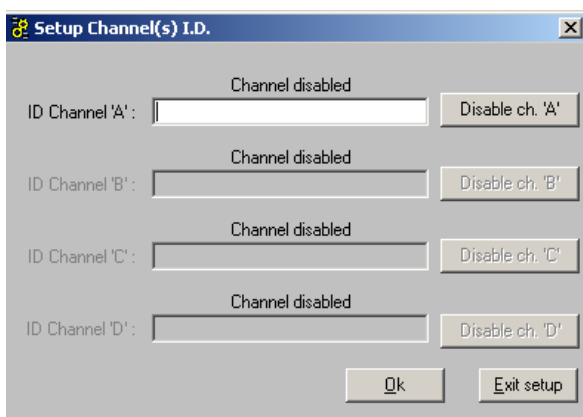
1. Being EagerSmart first time start, some drivers, required for the correct functioning of the software, is activated and registered. Answer by clicking **OK** at each message visualized.
2. Configure the Chromatography Card, then click **Next**. See [Figure 5](#).

Figure 5. Configure Chromatography Card



3. When the following window is visualized, type in **ID Channel "A"** box the identification number reported on the channel module connected. See [Figure 6](#).

Figure 6. Channel Module Configuration



Getting Started

This chapter provides a general overview of *EagerSmart*.

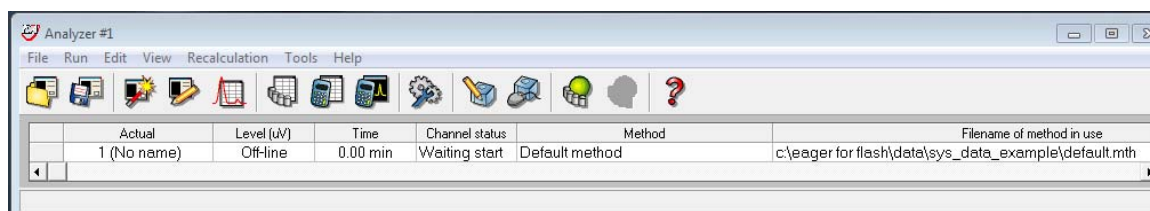
Contents

- [Main Menu Overview](#)
- [File Menu](#)
- [System Administration In Compliance with CFR 21 Part 11 Regulation](#)
- [Run Menu](#)
- [Edit Menu](#)
- [View Menu](#)
- [Recalculation Menu](#)
- [Tools Menu](#)
- [MVC Management](#)
- [Help Menu](#)
- [Instrument Control for IRMS](#)

Main Menu Overview

EagerSmart Main Menu is the starting point to enter all the menus and the relevant functions. See [Figure 7](#).

Figure 7. *EagerSmart* Main Menu



Menus and icons of *EagerSmart* Main Menu are described in [Table 2](#) and [Table 3](#) respectively.

Table 2. Main Menu: Description of Menus (Sheet 1 of 2)

Menu	Description	Sub-menus and Options
“File Menu” on page 14	Contains functions concerning the instrument operation. Used during the analyzer installation procedure.	• Set language • Color setup • Instrument name and configuration • System administration • Installation qualification • Load method • Load system defined method • Save method • Copy method from... • Printer setup • Print method • Exit <i>EagerSmart</i>
“Run Menu” on page 31	Chooses the type of start command to be sent to the analyzer, to stop the analytical cycle, or abort the current analysis.	• Start sequence of samples • Stop sequence in progress • Start single sample data acquisition • Stop data acquisition • Abort data acquisition • Run macro
“Edit Menu” on page 36	Provides functions related to the instrument setup and analytical parameters.	• Edith Method • Component table • Sample table • Wizard method development • Edit Elemental Analyzer parameters • Edit Sampler Parameters¹ • Evaluate Injection Delay² ¹⁻² These sub-menus are visualized only if an autosampler for liquids has been configured in Instrument Configuration
“View Menu” on page 37	Monitors the analysis in real time. Reads the result of the last sample run; checks the calibration curve; compares and overlays chromatograms; checks the instrument status and maintenance.	• View sample being acquired • Last sample calculated results • View Calibration curve • View Chromatograms • Overlay Chromatograms • Operate on Chromatograms • Compare Chromatograms • View Elemental Analyzer Status • View Maintenance
“Recalculation Menu” on page 37	Cancels the calibration curve and the results of previous analyses. You can recalculate previous results individually or sequentially. Provides also the summary of results.	• Reset calibration factor • Recalculation • Summarize results

Table 2. Main Menu: Description of Menus (Sheet 2 of 2)

Menu	Description	Sub-menus and Options
“Tools Menu” on page 37	Used when ashes removal, reactor replacement, or both, are required as maintenance. The command MVC management is enabled when the Multi Valve Control module is connected to your FlashSmart or Flash 2000 for CHN, CHN/O, CHNS, and CHNS/O determinations.	• Ashes removal • Reactor replacement • Cleaning the MAS Piston • MVC management (enabled when selected in “Configuration Dialog Window” on page 18).
“Help Menu” on page 40	Enters <i>EagerSmart</i> help program. Subdivided into different modules, each one designed to cover specific issues of the module currently in use.	• Help • About <i>EagerSmart</i>

Table 3. Main Menu: Description of Icons (Graphic Buttons) (Sheet 1 of 2)

Icon	Function	Description
	Load method	Loads a previously saved analytical method.
	Save method	Stores new operating methods.
	Wizard method development	Develops new operating methods
	Edit Method	Gives access to the functions for changing the aspect of the chromatogram display to the integration and calculation parameters, and to the parameters for printing analytical reports.
	Components Table	Contains the stored retention times, which allow to identify N, C, H, S, and O.
	Sample Table	Contains all functions related to sample records, and the function allowing communication with the balance.
	Summarize Results	Contains analytical results, print options and chromatograms.
	Recalculation	Recalculates previous results.
	View Maintenance	Programs current maintenance by recording the number of analyses run by each reactor of the analytical circuit.
	Edit Elemental Analyzer Parameters	Opens the pages containing the commands for the setting of temperatures, flows, times, detector, and the analyzer control functions.

Table 3. Main Menu: Description of Icons (Graphic Buttons) (Sheet 2 of 2)

Icon	Function	Description
	View Elemental Analyzer Status	Comprises four pages displaying the analyzer conditions. Contains special functions to check the system pneumatic tightness (Leak Test), to check the baseline level, and to program automatically the “Autoready” function.
	Edit Sampler Parameters	Visualized in Main Menu when an autosampler for liquids has been configured in “ Configuration Dialog Window ” on page 18 .
	Start Sequence	Starts a series of analyses having different current and timed requirements. At the end of the analytical cycle, the instrument can either be put in Stand-by Mode, or the furnace and detectors be switched off, or the gas flows turned off.
	Stop Sequence	Stops in any moment the sequence of analyses only completing the current run.
	Access the Help System	Displays the list of chemical products and parts relating to the analytical circuits with relevant part numbers.

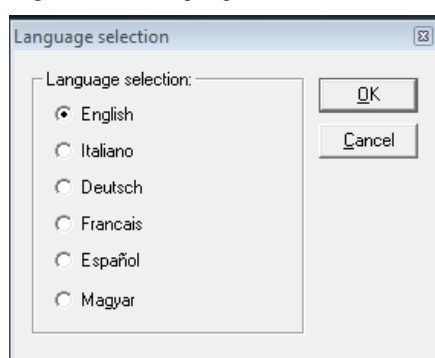
File Menu

This menu gives access to the following functions:

Set Language

Selects the language to be used for [EagerSmart](#). When this function is selected, a specific page is visualized where you can choose the language among those available.

Figure 8. Language selection



Once any of the available language is selected, the Main Menu and all other [EagerSmart](#) windows, functions and messages, is in the selected language. The local language support is limited to menus and messages of [EagerSmart](#) system, the help files are all in English language, as well as the instrument control that shares common code of other applications that cannot support multiple languages.

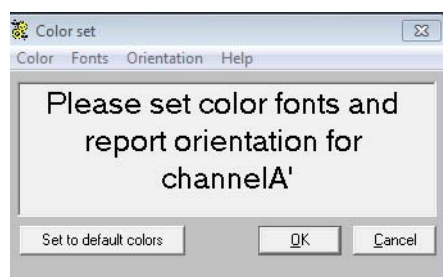
The supported languages at this moment are here above listed, however [EagerSmart](#) directory contains a program named **EATranslator.exe** that changes any message, or menu item shown by [EagerSmart](#) into a new local language not yet present.

Step by step all messages are presented on the screen for an easy translation. Once the new set of message translated into a new language are ready, in [Figure 8](#) appears also the selection of the inserted language, and it is available as one of the possible selections.

Color Set

Changes the colors used by different instruments. Moreover, it changes the fonts for the report printout, the printer type, the orientation of the report, and the stripchart.

Figure 9. Color and Fonts Selection (1)

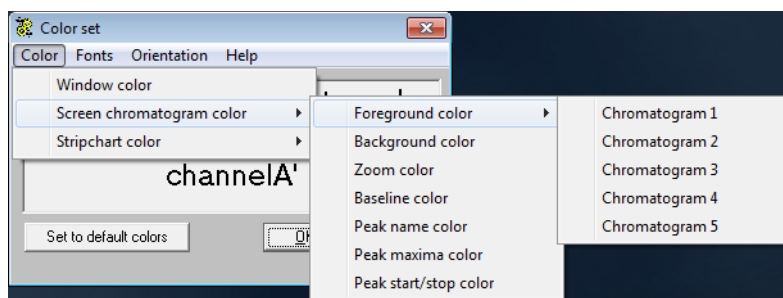


Each instrument can be assigned to a unique set of colors so you can recognize the channel currently being edited by the color used.

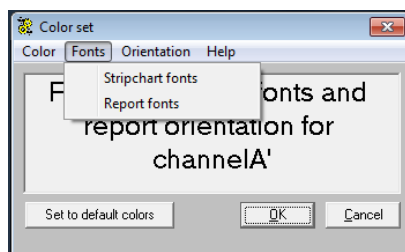
Note All editing pages use the system default colors, only the main page is using the channel color assigned.

This module provides the following functions:

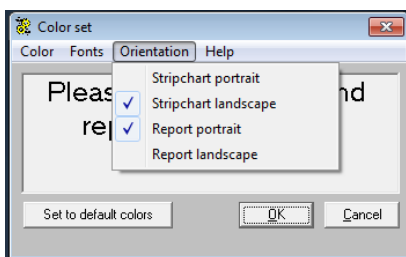
- **Color** — Each instrument can be assigned to a unique set of colors. **Window color**, **Screen chromatogram color**, and **Stripchart colors** options are easily entered through this dialog box



- **Fonts** — Selects the type and the size of the fonts to be used for the report, and the stripchart label



- **Orientation** — Selects the landscape or portrait orientation of the peaks report, and the stripchart. The orientation is a non-standard function for Windows™. With some printers it may not work within [EagerSmart](#). In this case, you should select the orientation from the specific printer setup page.



- **Set the default colors** — Sets the default colors. The system requires to confirm the selection.
- **Cancel** — Clears all the modifications done in the current section. The program returns to Main Menu.
- **Ok** — Confirms all modifications done in the current section. The program returns to Main Menu. All modifications are stored in *EagerSmart* configuration file. At the start-up, *EagerSmart* always loads and uses the entered colors and system setting.

Instrument Name and Configuration

According to the instrument to configure, the relevant dialog box is visualized. See [Figure 10](#) and [Figure 11](#).

Figure 10. Instrument Name and Configuration Dialog Box for Flash*Smart* and Flash 2000

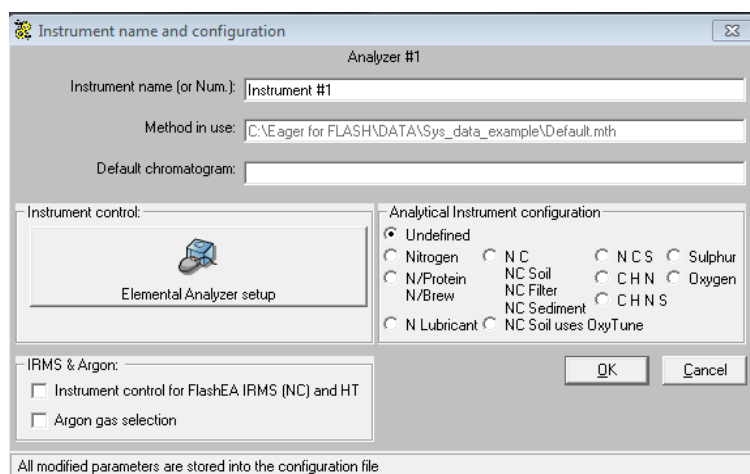
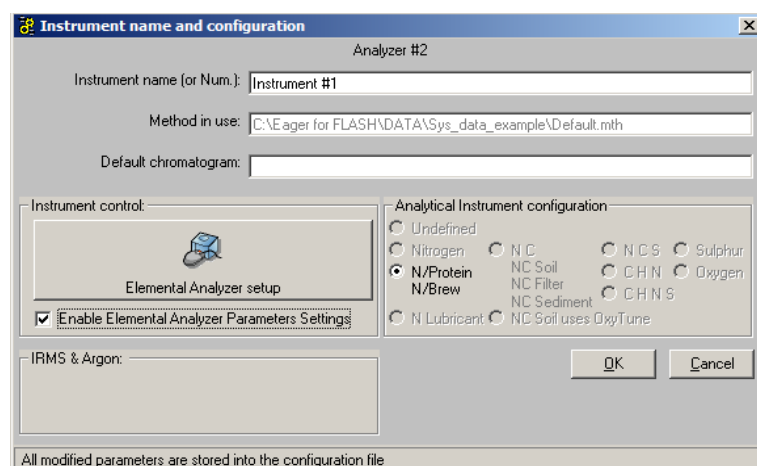


Figure 11. Instrument Name and Configuration Dialog Box for Flash 4000



Note In the USB and A/D configurations, an appropriate button (**USB BOX SETUP** and **CHANNEL ID** respectively), appears on the left of **OK** button.

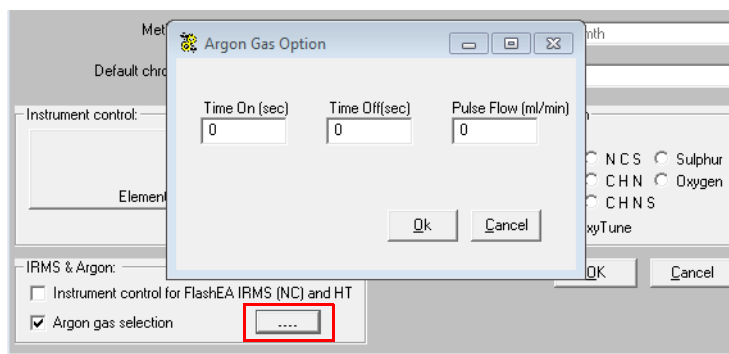
Each button allows to enter the identification number of the channel module if **A/D** is a **Chromatography Card**, or the **Device ID** if **A/D** is a **USB Box**.

This module provides the following functions:

- **Instrument Name** — Enters the **name** or the **serial number** of the instrument.
- **Method in Use** — Contains the path and filename of the method currently in memory.
- **Default Chromatogram** — The chromatogram entered (path and filename) in this box is loaded at the start-up for chromatogram views.
- **Analytical Instrument Configuration Box** — Selects the configuration of your instrument.

Note The option **Undefined** can be used in case the desired operating conditions are different from those defined for all the instrument configurations.

- **Instrument Control for FLASHEA IRMS(NC) and HT** — Select this box when a **FlashSmart** or a **Flash 2000** is coupled with a **IRMS** detector. At the reboot of **EagerSmart**, the simplified **Main Menu for IRMS** is visualized. For details, see the section “**Instrument Control for IRMS**” on page 40.
- **Argon Gas Selection** — **For FlashSmart and Flash 2000 for N/Protein determinations only.** Select this box if the instrument is equipped with the optional kit for Argon. The gas control page is visualized for setting the **Argon Gas Option** parameters. Click ... button.



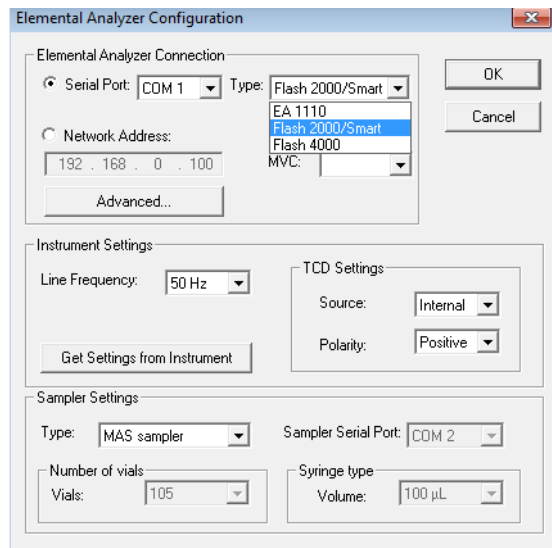
Argon Gas Option parameters injects a supplementary flow of Argon in the first part of the analysis to obtain a smoothly baseline allowing an excellent integration of the Nitrogen peak.

- In **Time On** field set the time at which the injection must begin.
- In **Time Off** field set the time at which the injection must end.
- In **Purge Flow** field set the desired flow.
- **Enable Elemental Analyzer Parameters Setting** — **For Flash 4000 only.** Select this box to enable the setting of the method parameters.
- **Instrument Control Box** — Select **Elemental Analyzer setup** to access the Configuration dialog window of Figure 12, where the configuration parameters must be set. See the section “**Configuration Dialog Window**” on page 18.

Configuration Dialog Window

In this window you set the parameters for configuring your instrument. See [Figure 12](#).

Figure 12. Elemental Analyzer Configuration Dialog Window



The windows includes the following fields:

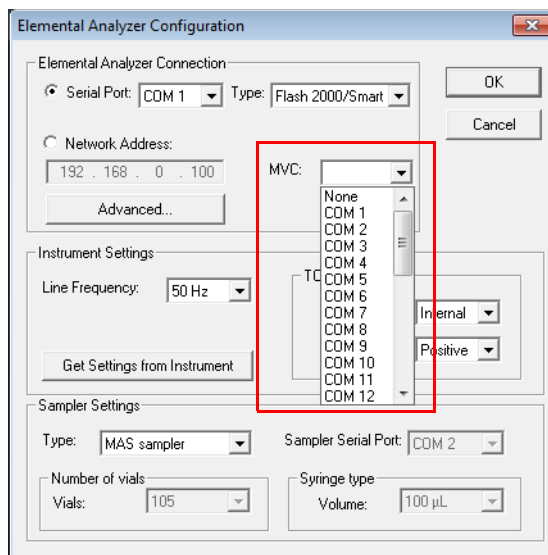
- “[Elemental Analyzers Connection](#)” on [page 18](#)
- “[Instrument Setting](#)” on [page 19](#)
- “[Sampler Setting](#)” on [page 19](#)
- “[Function Buttons](#)” on [page 20](#)

Elemental Analyzers Connection

This field includes the following options:

- **Serial Port** — Selects the computer **serial port** to which the Elemental Analyzer is connected. The range is from None to 32. For example select COM1.
- **Type** — Selects the which type of Elemental Analyzer is connected.
- **Network Address** — Enters the **IP address** for the LAN control of the **Flash 4000** through the Thermo Fisher Scientific data systems. The instrument with the LAN option is shipped with a default IP address, that may not match the needs of the LAN where the instrument must be installed. To change the default values, contact your network administrator, ask for the IP address to be assigned, the netmask, and eventually the communication port.
 - The IP address is a 3 digits x 4 fields given by the network administrator e.g. 192.168.127.10
 - The netmask is a 3 digits x 4 fields given by the network administrator e.g. 255.255.255.0
 - The port is a 4 digits number given by the network administrator e.g. 4001 (4001 is usually the CPU/LAN default).
 - The default IP address of the Flash 4000 CPU is 192.168.127.254.

- **MVC** — Selects the COM port to which the **Multi Valve Control** module is connected. The range is from None to 32. The serial port selected for the Multi Valve Control module must be different respect the serial port selected for the instrument in **Elemental Analyzer Connection**. For example select COM 2.



Instrument Setting

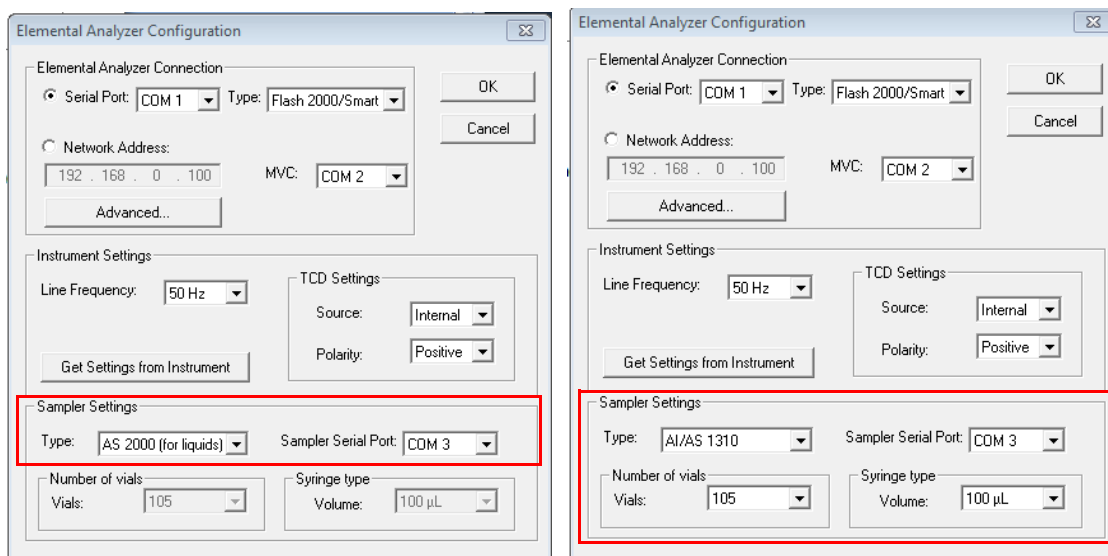
This field includes the following options:

- **Line Frequency** — Sets the value of the mains frequency in use in your country. This data allows the instrument to optimize the chromatogram points acquisition.
- **TCD Settings Source** — Normally selected to **Internal**. Select **External** when a different detector is used instead of the TCD mounted in the analyzer.
- **TCD Settings Polarity** — Normally selected to **Positive**. Select **Negative** for the Oxygen determination in CHN/O and CHNS/O configurations.

Sampler Setting

This field includes the following options:

- **Type** — Selects the type of autosampler installed on the instrument: MAS Sampler, AI/AS 1310, and AS 2000 (**for Liquids**). If an autosampler for liquids is selected, also specify the computer serial port to which the autosampler is connected.
- **Sampler Serial Port** — Selects the COM port to which the AI/AS autosampler for liquid is connected. The range is from None to 32. The serial port selected for the autosampler for liquid must be different respect the serial ports selected for the instrument in **Elemental Analyzer Connection** and MVC. For example select COM 3.
- **Number of Vial** — Enabled when the AI/AS 1310 autosampler for liquids is selected. Selects the number of vials of the sample tray. Select 8 for the AI 1310 or 105 for the AS 1310.
- **Syringe type** — Enabled when the AI/AS 1310 autosampler for liquids is selected. Selects the volume of the syringe installed in the AI/AS 1310: 10 µL, 50 µL, 100 µL or 250 µL.



Function Buttons

The window includes the following function buttons:

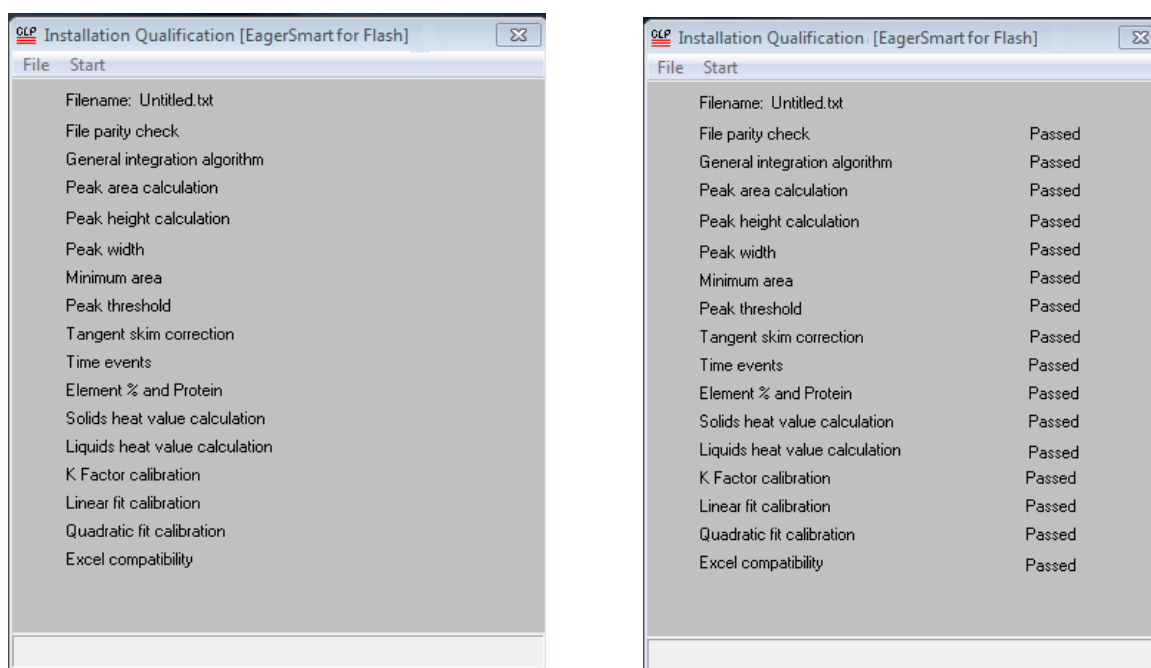
- **Advanced** — Sets the LAN communication port used by the TCP-IP protocol and timeout.
- **Get setting from Instrument** — Transfers the instrument data to [EagerSmart](#).
- **Ok** — Confirms all modifications done in the current section. **Line Frequency** and **TCD parameters** are send to the Elemental Analyzer. The program returns to the [Instrument Name and Configuration](#) dialog window.
- **Cancel** — Clears all modifications done in the current section. The program returns to Main Menu.

System Administration

This option allows the authentication of an analytical method in compliance with the CFR 21 Part 11 regulation. For details see the section “[System Administration In Compliance with CFR 21 Part 11 Regulation](#)” on [page 24](#).

Installation Qualification

The **Installation Qualification** is the tool to verify the performances of [EagerSmart](#). Qualification window is visualized. See [Figure 13](#).

Figure 13. Installation Qualification Window

In line to the Quality Manual of each laboratory, this tool verifies the correct functionality of all *EagerSmart* modules. Integration and quantization algorithms are fully tested and documented with a report automatically generated.

The **Qualification** is based on the calculation of several known chromatograms. The known results of areas, heights, and concentrations, calculated independently from *EagerSmart*, are compared with the results obtained by *EagerSmart* calculation. The report of the comparison is stored, printed, or both.

The main page provides the following menu:

- **File** — Gives access to the **Load** and **Quit** functions.
- **Start** — Contains the functions to **Start** or **Stop** the **Qualification** sequence.

Load Method

Loads any method previously stored on disk. The system shows the **Open dialog box**. You specify a file to be opened loading all analytical conditions in use when the method has been generated and saved.

Note The method currently in memory is not automatically saved. Therefore, if you have done some modifications to the method in use, and you want the modifications to be stored for later use, you must save the method before using this function.
To save in memory a method really changed, a specific save window is shown for the task.

Load System Defined Method

Loads a predefined method that is suitable for your instrument configuration. *EagerSmart* loads a method with the extension ***.mth** to which a method with extension ***.eam** is also assigned for the instrument setting.

The method is chosen according to the setting done in the **Analytical instrument configuration** box of **Instrument name and configuration** window from **File** menu of Main Menu.

The predefined methods are saved in the subdirectory **\System defined methods** located in the directory where *EagerSmart* has been installed. To avoid overwriting and modification, the predefined method currently loaded must be saved in another directory.

Save Method

Saves the method currently in use. The system asks the filename and the directory. All the analytical conditions are immediately saved in the desired file with the extension ***.mth**.

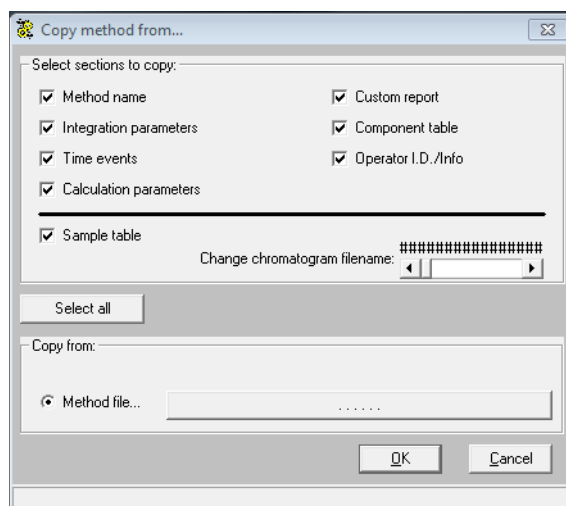
The method includes all parameters of all sections of the analytical method of all channels and with a single keystroke you can reload in a later exactly the same conditions you have at the save command.

Copy Method From...

Copies a method or partial sections of a method currently in use on other channels, or from any other method stored on disk. The system shows a dialog window with the sections to be copied.

See [Figure 14](#).

Figure 14. Copy Method Dialog Window



You can select the following options:

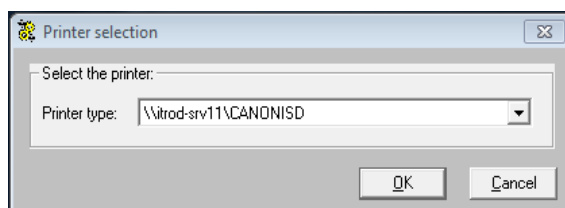
- **Section to Copy** — Selects the method sections to be copied. Tick the box of the sections you would like to copy into the current method. The available sections you may copy are:
 - Method name
 - Integration parameters
 - Time events
 - Calculation parameters
 - Custom report
 - Component table
 - Sample table
 - Analytical conditions

- **Change chromatogram name** — When you decide to copy the **Sample table**, you may decide to change one of the character of the chromatogram filename you copy from a stored method, or from another channel. This function changes automatically one character of the chromatogram filename with the letter corresponding to the channel in use, for example **Channel A**, places a letter “A” at the position you want. Move the scroll bar to change the letter position you want to be replaced during the copying of the sample table.
- **Select all** — Enables or disables all the method sections to be copied. When you want to copy one single section, it is easier to disable **Select all** option first, then to enable only the desired section.
- **Copy from** — Copies entirely or partially the different analytical sections from any stored method. With **Copy from** you specify the source method filename of the method to be copied.
- **Method file** — Click on the bar to supply the method filename from the disk.

Printer Setup

Visualizes a dialog box where the type of printer to use for printing a job can be set. See [Figure 15](#).

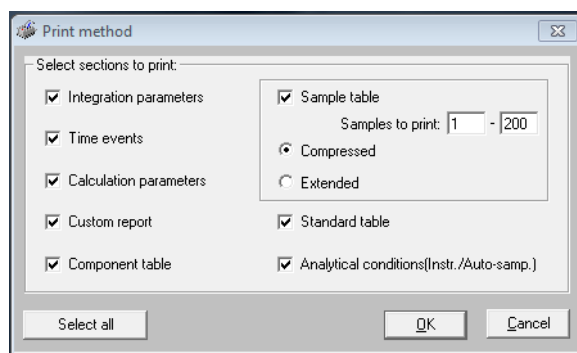
Figure 15. Print Selection



Print Method

Prints the analytical method being used. A dialog box is visualized for the selection of the method sections to be printed. See [Figure 16](#).

Figure 16. Print Method



If all the method is required for printing, click **Select all**, or only click the check box of the required sections.

Exit EagerSmart

- Exits [EagerSmart](#). When [EagerSmart](#) is closed, the data of all sections and of all channels in memory are saved on a temporary file, **Tmp-a.mth** or **Tmp-b.mth**, in the directory ***.tmp**.

- When *EagerSmart* is started again, the data are relocated in memory.

Note This function is not available if any of the Status is acquiring data. The file method from which data are drawn is not updated. To save permanently the data on disk, click **Save** in **File** menu.

System Administration In Compliance with CFR 21 Part 11 Regulation

The CFR 21 Part 11 (Code of Federal Regulation Electronic Records; Electronic Signatures) has been published by FDA (Food and Drug Administration) in 1997. It consists of a series of guidelines for completion of procedures in a productive process.

These rules, (validation) are required especially for pharmaceutical, cosmetic and food safety industries, where the access, storage and treatment of the data cover an important role. *EagerSmart* is built taking in account the use of this regulation.

Important features of the regulation are:

- Access to the data through login with username and password.
EagerSmart has two levels of authorization:
 - The first is an intrinsic part of the operating system.
 - The second is supported by *EagerSmart* according to following path: **Main Menu | File | System administration**.
- The use of passwords differentiates the roles. This means that only the person responsible of the laboratory or a delegated person [**laboratory head (System Manager)**] has all the rights and full functionality of the software and data base, while the analyst or a simple user [**User (Limited rights)**] has reduced functionality and rights.

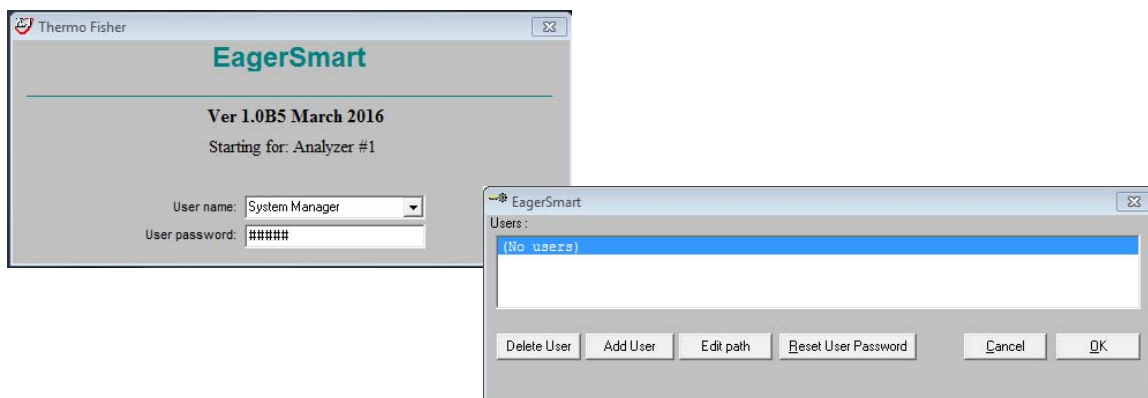


IMPORTANT For creating new users and passwords and using the password the first time see the section “[Making New Users and Passwords](#)” on [page 26](#).

Password Dialog Windows Options

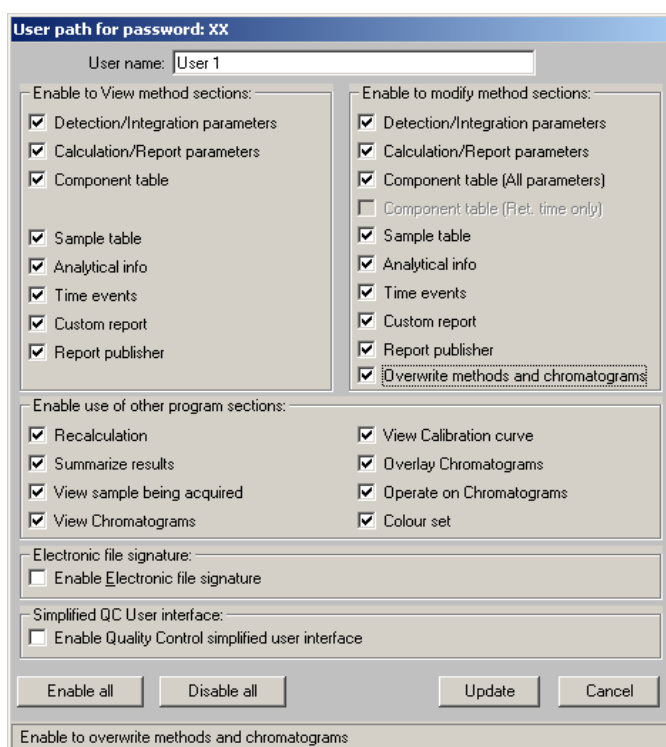
System Administration option runs the program for setting up the password accessible path for all users. See [Figure 17](#).

Figure 17. Password Dialog Window



- **Delete User** — Erases the addressed Password from your list.
- **Add User** — Shows the box to enter a new user password.
Enter name or any string expression that is used to enable one of you to enter only some parts of the program indicated in the **Edit Path** dialog window.
- **Reset User Password** — Resets the user password.
- **Edit Path** — Edith path dialog window features five group boxes. See [Figure 18](#).
 - Enable to view method sections.
 - Enable to modify method sections.
 - Enable use of other program sections.
 - Electronic file signature. See [“Electronic File Signature”](#) on page 26.
 - Simplified QC User Interface. See [“Simplified QC User Interface”](#) on page 26.

Figure 18. Edith Path Dialog Window



- **Enable to view method sections** selects the access to the particular section of the program without making modifications.
- **Enable to modify method sections** gives access to particular sections of the program, and modifications to the section may be also performed. The access to any of the listed options, i.e. **Detection/Integration Parameters**, **Calculation/Report Parameters**, **Component Table** and so on, is carried out by ticking the corresponding box.
If the check box is not ticked, it means that you are not able to view the relevant method section, to perform any type of modifications in the specified section of the program, or both.
- **Enable use of other program sections** gives access to the other sections of the program, and modifications to the section may be also performed. The access to any of the listed options, i.e. **Recalculation**, **Summarize Results** and so on, is carried out by ticking the corresponding box.

2 Getting Started

System Administration In Compliance with CFR 21 Part 11 Regulation

- **Enable all** — Enables all the sections.
- **Disable all** — Disables all the sections.
- **Update** — Quits the Access path configuration program. The system saves on disk all the modifications you have made on the accessible paths.

Electronic File Signature

Select **Enable Electronic File Signature** check box to allow the electronic file signature in compliance with the directive *FDA CFR21 Part 11*. For details, see [Chapter 24, “Electronic File Signature.”](#)

Simplified QC User Interface

This function is only available for FlashSmart and Flash 2000.

Select **Enable Simplified Quality Control User Interface** check box to allow the partial use of *EagerSmart*. At the reboot of *EagerSmart*, the simplified Main Menu is visualized. For details, see [Chapter 23, “Use of Eager Simplified User Interface.”](#)

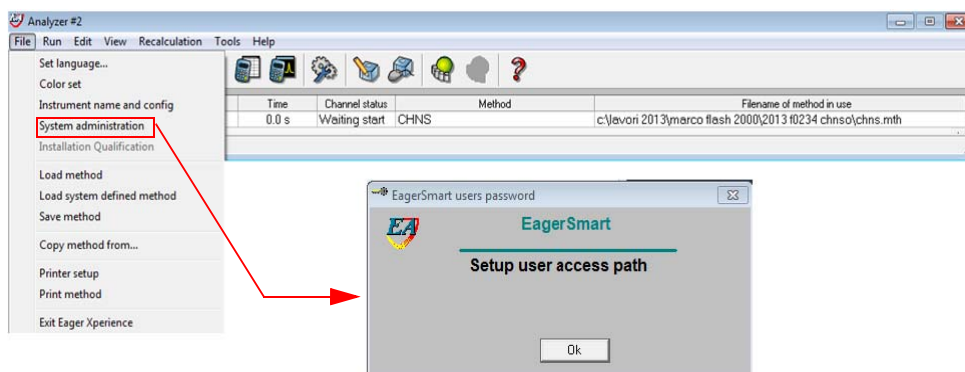
Making New Users and Passwords

This section provides the instructions for creating new users and passwords respecting some rules.

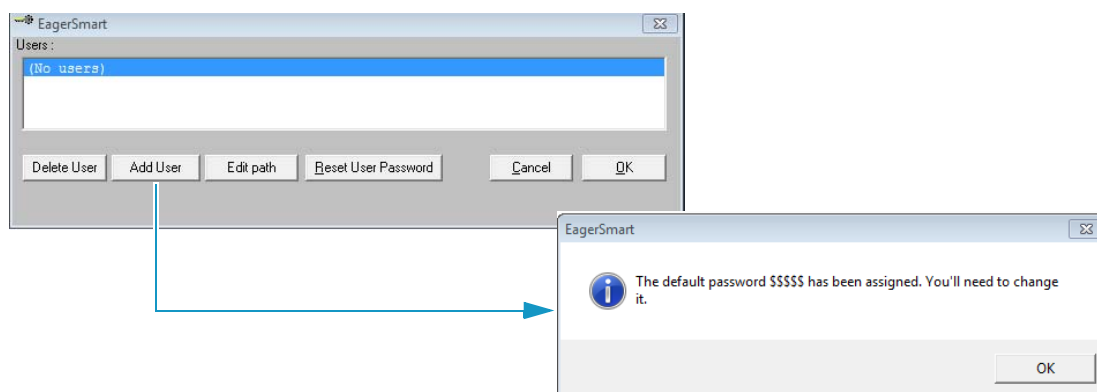
❖ To make new users the passwords

Note The procedure is the same also for higher *EagerSmart* software versions than 1.o.

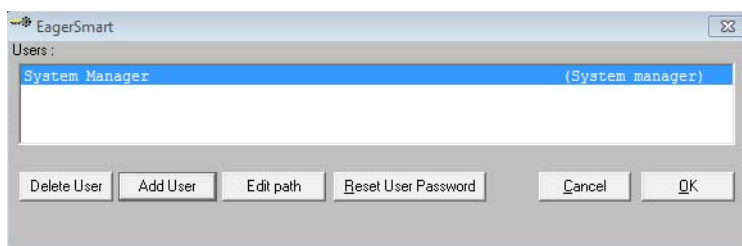
1. From Main menu select **File | System Administration**. The System Manager page is visualized.



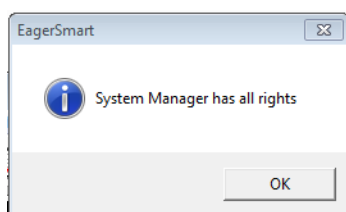
2. Click OK. The following page is visualized.



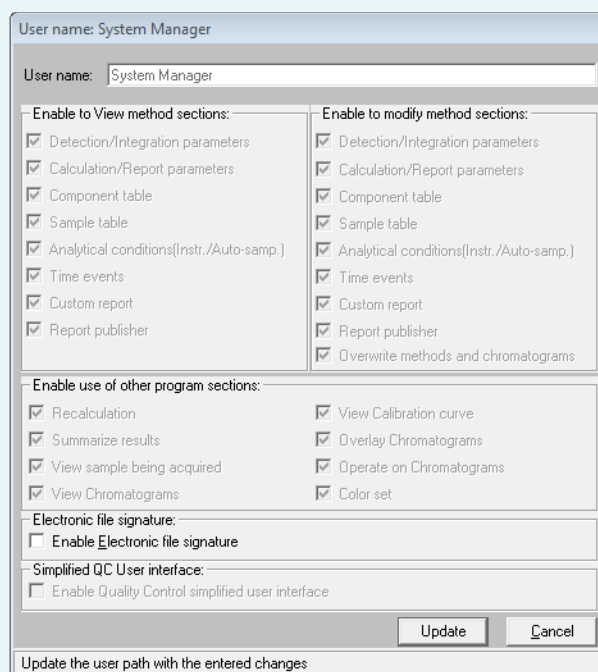
3. Click **Add User**. The first user created is **System Manager** that has all rights. The default password assigned for the first access is \$\$\$\$\$. You need to change it. Next click **OK**, System Manager user is created.



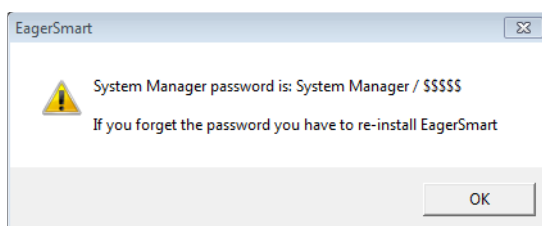
4. Click **Edit path**. A message indicating that **System Manager** has all rights is visualized.



Note System Manager has the control of all the system. Click **OK**, the property window is visualized. Click **Update** to return **System Manager** page.



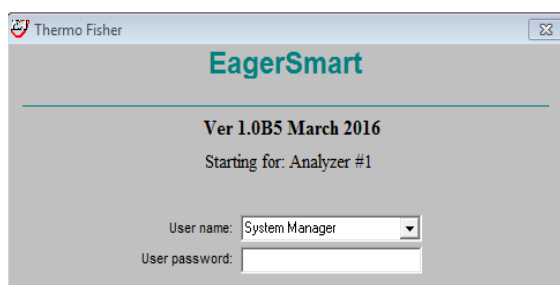
5. Change the password for the System Manager.
 - a. From System Manager page click **OK**. The following message is visualized. Then click **OK**.



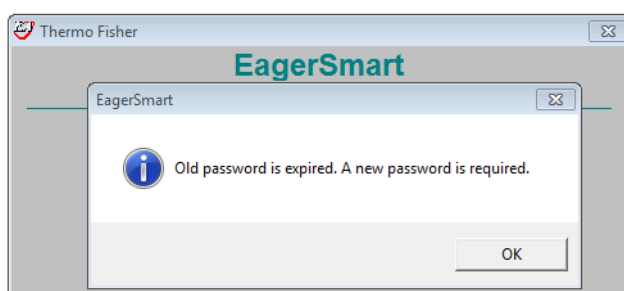
2 Getting Started

System Administration In Compliance with CFR 21 Part 11 Regulation

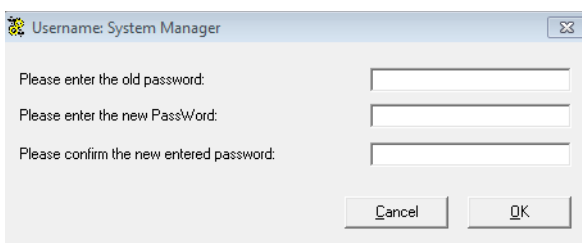
- b. From Main menu select **File | Exit Eager Smart** to exit the program.
- c. Start *EagerSmart* again selecting **Start | Programs | EagerSmart**.
- d. Click on the instrument icon you want to start. The system ask for the password.



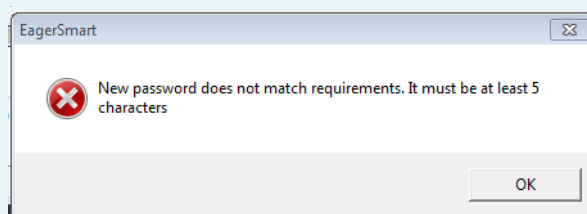
- e. In the **User password** field, digit the default password \$\$\$\$ and press **Enter**. The following message is visualized.



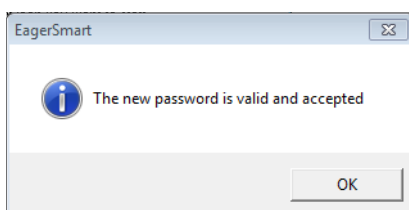
- f. Click **OK**, the following page is visualized where you must change the password. Enter the old password \$\$\$\$\$, then enter and confirm the new password.



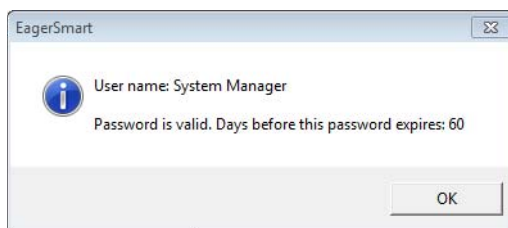
Note The new password should have at least **five** characters. If not, an error message is visualized:



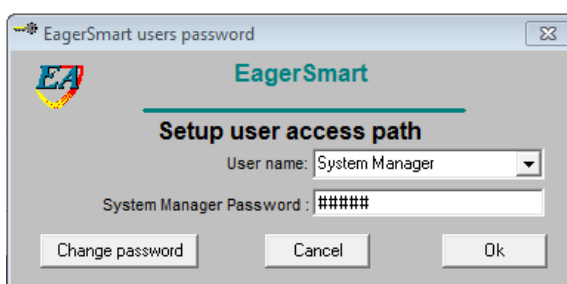
- g. When finish to compile the fields, click **OK**. The following message is visualized to confirm the validity of the password.



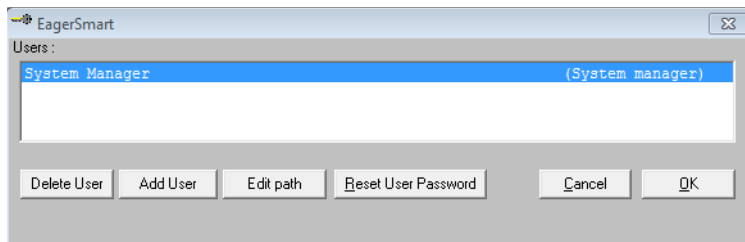
- h. Click **OK**. The following message is visualized indicating the new valid password expires in 60 days.



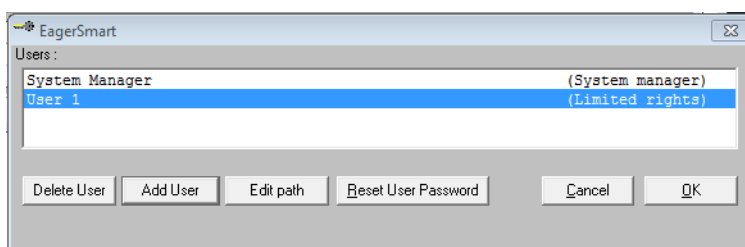
- i. Click **OK** to return to Main Menu.
6. Add a new **User**, if desired. *EagerSmart* allows creating up to 32 users.
- a. From Main menu select **File | System Administration**. The system asks for the System Manager password.



- b. Digit the new password for System Manager assigned at the previous step 6 f. The System Manager page is visualized.



- c. Click **Add User** for introducing new users, the default password is assigned. The following page is visualized indicating that **User1** with **Limited rights** is created. The name of User 1 can be changed clicking **Edit Path**.



- d. Click **Edit Path**. Tick the check box of the desired functions. In the following example User 1 has limited right; only **Sample table** function is active.

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User name: User 1

User name: User 1

Enable to View method sections:

- ☐ Detection/Integration parameters
- ☐ Calculation/Report parameters
- ☐ Component table
- ☒ Sample table
- ☐ Analytical conditions(Instr./Auto-samp.)
- ☐ Time events
- ☐ Custom report
- ☐ Report publisher

Enable to modify method sections:

- ☐ Detection/Integration parameters
- ☐ Calculation/Report parameters
- ☐ Component table
- ☐ Sample table
- ☐ Analytical conditions(Instr./Auto-samp.)
- ☐ Time events
- ☐ Custom report
- ☐ Report publisher
- ☒ Overwrite methods and chromatograms

Enable use of other program sections:

- ☐ Recalculation
- ☐ Summarize results
- ☐ View sample being acquired
- ☐ View Chromatograms
- ☐ View Calibration curve
- ☐ Overlay Chromatograms
- ☐ Operate on Chromatograms
- ☐ Color set

Electronic file signature:

- ☐ Enable Electronic file signature

Simplified QC User interface:

- ☐ Enable Quality Control simplified user interface

Enable all Disable all Update Cancel

Enable to view the Sample table

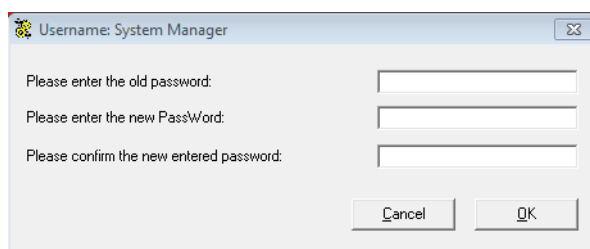
- e. Click **Update** to return System Manager page. For all the added users the default password \$\$\$\$ is given; you must change it to the first access.

Note If you want working as **User 1**, exit *EagerSmart*, then follows the instructions at the next step 8.

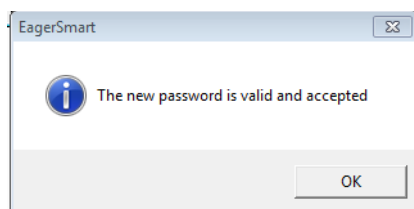
7. For working as **User 1**.
- Exit and start *EagerSmart* again selecting **Start | Programs | EagerSmart**.
 - Click on the instrument icon you want to start.
 - In Main Menu select **System Administration**. The following page is visualized.

- d. Select User name **User 1**, then in the User password field type the default password \$\$\$\$\$. The following message is visualized.

- e. Click **OK**, the following page is visualized where you must change the password.

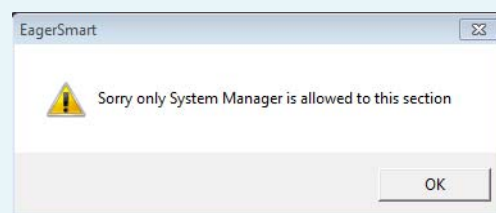


- f. The new password should have at least **five** characters; if not, an error message is visualized. When finish to compile the fields, click **OK**. The following message is visualized.



- g. Click **OK**. The following message is visualized indicating the new valid password expires in 60 days.
- h. Click **OK** to return to Main Menu. Only the functions selected in **Edit Path** page is active.

Note If an user tries to accede to a function for which he has been enabled to use, a denial message is visualized.



Run Menu

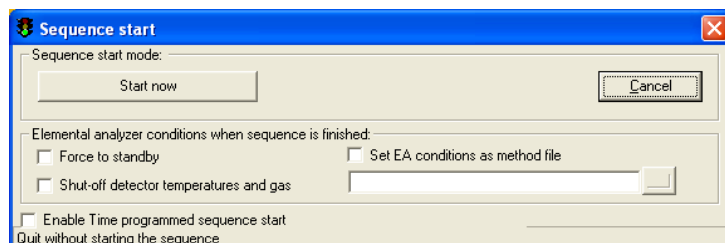
Gives the access to the following functions:

- [Start Sequence of Samples](#)
- [Stop Running in Progress](#)
- [Start Single Sample Data Acquisition](#)
- [Stop Data Acquisition](#)
- [Abort Data Acquisition](#)
- [Run Macro](#)

Start Sequence of Samples

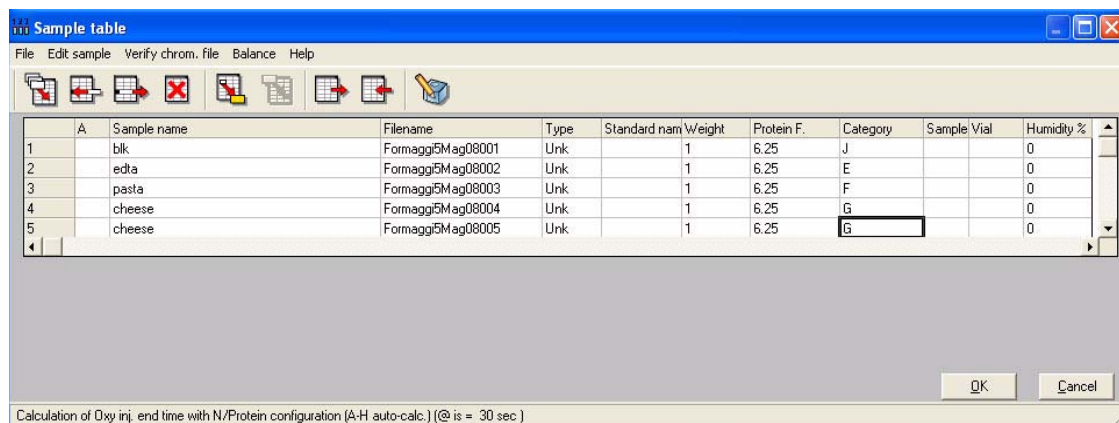
This function can also be selected clicking the  icon. **Start sequence** dialog box is visualized. The sequence starts clicking **Start now**. See [Figure 19](#).

Figure 19. Start Sequence



All parameters set in **Detection Parameters** and **Integration Parameters** is used for starting the acquisition. The sequence begins from **Actual** and finishes when a sample line in the **Sample Table** is empty. See the example of [Figure 20](#).

Figure 20. Example of Sample Table



In the example the sequence begins from Sample **n.4** and finishes at Sample **n.6**.

Elemental Analyzer Condition While Start Sequence Is Finished

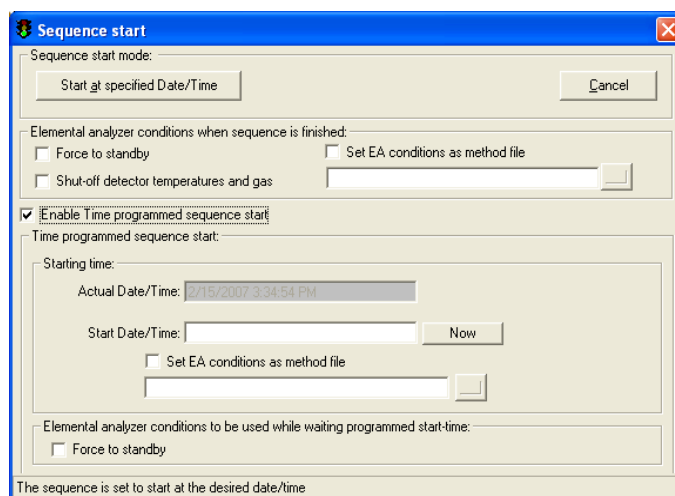
Provides options for selecting the instrument condition at the end of an analytical sequence.

- **Force to Stand-by** — Decreases the temperature of the furnaces at the stand-by condition and decreases the flow of gases to reduce consumption.
- **Shut-off temperatures, detector and gas** — The furnaces and oven temperatures are shut off; the flows of carrier and reference gases are cut off.
- **Force to EA conditions as method file** — The instrument is put in the conditions set in a file with *.eam extension. Create this file by using the window [Edit Elemental Analyzer Method](#) in [Chapter 7](#) and save it. In the input-box below, enter the path/filename, or look for the file using the icon .

Enable Time Programmed Sequence Start

Select this box when you want **Start sequence** to be programmed in time. See [Figure 21](#).

Figure 21. Start Sequence (1)



Time Programmed Sequence Start

Enter the desired date and time (hours/minutes) in **Start Date/Time** input-box in the same format as visible in **Actual Date/Time** box, then click **Now** visualized when the function **Start at specified Date/Time** is enabled.

If while waiting **Start sequence** you want the instrument be put in Stand-by condition, select the **Force to Stand-by** box.

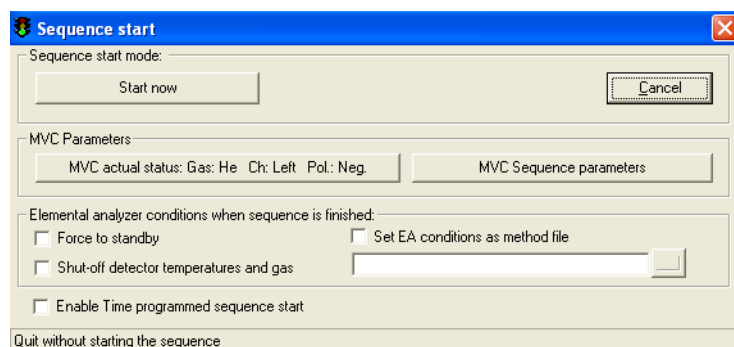
On the specified date, **Start sequence** is activated. If the instrument was forced in Stand-by condition, this condition is removed. The system waits for the instrument to be ready, and then it sends the start sequence command.

When you want setting the instrument conditions as method file before to start the sequence, select the box **Set to EA conditions as method file** and look for the file using the  icon. On the specified date, the system downloads the EA method file, waits for the instrument to be ready, then sends the start sequence command.

MVC Parameters

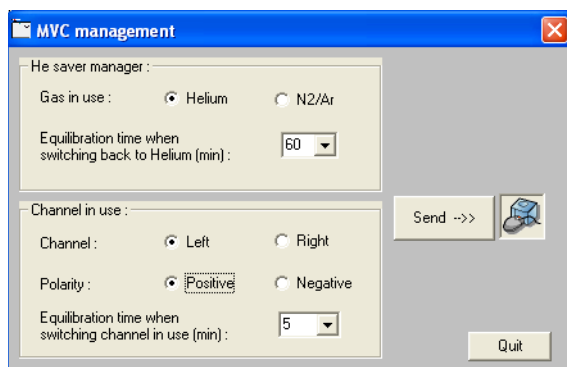
When the **Multi Valve Control** module is connected to your FlashSmart Elemental Analyzer, the **MVC Parameters** field is visualized. See [Figure 22](#)

Figure 22. Start Sequence Page with MVC Parameters

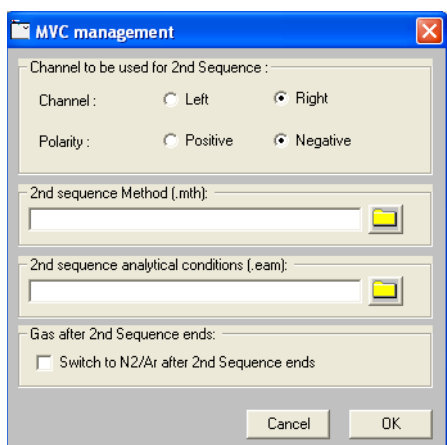


The MVC Parameters field includes the following buttons:

- **MVC actual status** — Reports on its bar the actual parameters for gas, channel, and polarity, set in the **MVC management** page.
Click **MVC actual status** to visualize the MVC management page with the actual parameters set. If needed, the gas and channel setting can be modified.



- **MVC sequence parameters** — Allows choosing the method (*.mth) of the sequence and the analytical conditions (*.aem) to use for the sequence. Select the file of the method to use selecting it from the relevant list box using  button. The channel set is visualized. If needed, the channel setting can be modified. If Argon is required after the end of the sequence, select the relevant check box.



When all the parameters have being set, start the sequence by clicking **Start now**.

Stop Running in Progress

This function can also be selected by clicking the  icon. Interrupts the analytical sequence at the end of the analysis currently being acquired.

Start Single Sample Data Acquisition

Starts the acquisition of single sample of the instrument currently in use.

All parameters set in **Detection parameters** and **Integration parameters** are used for starting the acquisition. The function **View Sample Being Acquired** permits to view the chromatogram being acquired.

Stop Data Acquisition

Stops the acquisition of the instrument currently in use. After a confirmation, the system stops the acquisition saving the chromatogram data up to the moment of the stop command, and a report is generated if required.

Abort Data Acquisition

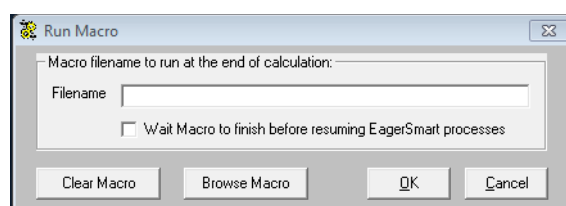
Stops the acquisition of the instrument currently in use. After a confirmation, the system aborts the acquisition without saving the chromatogram data, and without generating the report.

Run Macro

EagerSmart features Macro programming capabilities that help solving specific problems in instrument control. *EagerSmart* produces a file in the \Tmp0, \Tmp1, \Tmp2, \Tmp3 directory containing the analysis result, then calls the executable Macro if required.

The Macro can process the generated results, can take decisions, or simply generate additional report. To activate a Macro, just enter **Run** pull-down menu, then **Run Macro**. The following dialog box is visualized. See Figure 23.

Figure 23. Run Visual Macro



At the end of the analysis acquisition, the system calls and runs the customer's Visual Basic program. Click **Browse Macro** to select or insert the Macro filename in the input box.

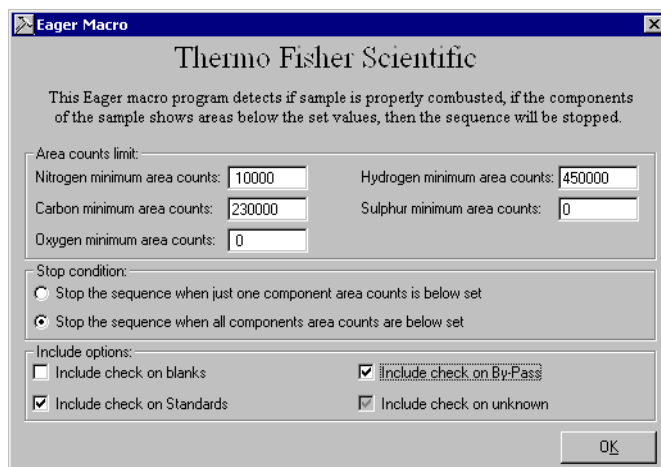
Note The filename entered is part of the method. Therefore, the Macro is always automatically enabled when the method is loaded.

EagerSmart is delivered with a practical Macro that stops a sequence of samples being acquired when a sample is not properly burned or missing. Locate the folder named **User macro example** inside *EagerSmart* folder, then enter the folder **Stop if no sample**. This folder contains an executable program to stop the sequence if the components of interest shown area counts below a minimum value.

The following Macro is an *.exe program having two working modes:

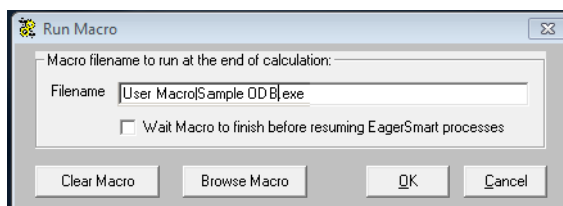
- when called by *EagerSmart*
- when lunched as stand-alone program to set the conditional parameters

Just clicking the program **Stop_if_no_sample.exe**, the program shows the conditional parameter.



The stand-alone program enters area counts threshold for all the components: **nitrogen, carbon, hydrogen, sulfur, and oxygen**. Next, a couple of other options allow to enable the check on different samples, and the condition when stopping the sequence.

Once clicking **OK**, the entered parameters are saved and used afterward by the program when called by *EagerSmart*. Remember to set your *EagerSmart* method to call the Macro program by entering the name in the relevant window. Also remember to click **Wait Macro to finish**.



Once you set your method, the system calls the Macro at the end of each real time analysis. If the condition test are true, the Macro stops the sample sequence by displaying a relevant message. This Macro program can be freely used and copied anywhere in the hard disk, or on accessible path of the network, and can also be modified and recompiled with just a bit of VB6 knowledge.

Edit Menu

This menu gives access to the following functions:

- Method Editor, see [Chapter 3](#) on [page 45](#)
- Component Table, see [Chapter 4](#) on [page 65](#)
- Sample Table, see [Chapter 5](#) on [page 73](#)
- Wizard Method Development, see [Chapter 6](#) on [page 95](#)
- Edit Elemental Analyzer Parameters, see [Chapter 7](#) on [page 97](#)

If and autosampler for liquids has been configure, the following function are added to the list.

- Edit Sampler Parameters, see [Chapter 8](#) on [page 111](#)
- Evaluate Injection Delay, see [Chapter 8](#) on [page 115](#)

View Menu

This menu gives access to the following functions:

- View Sample Being Acquired, see [Chapter 9](#) on [page 119](#)
- Last Sample Calculated Results, see [Chapter 9](#) on [page 121](#)
- View Calibration Curve, see [Chapter 10](#) on [page 123](#)
- View Chromatograms, see [Chapter 11](#) on [page 129](#)
- Overlay Chromatograms, see [Chapter 12](#) on [page 137](#)
- Operate on Chromatograms, see [Chapter 13](#) on [page 143](#)
- Compare Chromatograms, see [Chapter 14](#) on [page 147](#)
- View Elemental Analyzer Status, see [Chapter 15](#) on [page 151](#)
- View Maintenance, see [Chapter 16](#) on [page 167](#)

Recalculation Menu

This menu gives access to the following functions:

- Reset Calibration Factors, see [“Reset Calibration Factors”](#) on [page 37](#)
- Recalculation, see [Chapter 17](#) on [page 173](#)
- Summarize Results, see [Chapter 18](#) on [page 177](#)

Reset Calibration Factors

Resets the calibration factors when a re-calibration is going to be performed. When processing an **STD** (Standard) sample, *EagerSmart* performs the calculation of new calibration curves by using the standard results previously found in the sequence.

When a new calibration is required, starting from scratch, the reset calibration factor and blank area must be manually performed by selecting the mentioned function. *EagerSmart* automatically performs this operation when in a sequence of samples a STD is processed after one or more **UNK** (Unknown) samples.

Example of sample sequence:

#1 STD	#2 STD	#3 STD	#4 UNK
#5 STD	#6 STD	#7 STD	#8 UNK

The UNK #4 is calculated with factors KF, Linear or Quadratic from standards #1, #2, and #3.

The UNK #8 is calculated with factors KF, Linear or Quadratic from standards #5, #6, and #7.

Tools Menu

Used for maintenance purpose when the ashes removal, the reactor replacement, a MAS autosampler piston cleaning is needed, and for the setting of the **Multi Valve Control module** when connected to your *FlashSmart* or Flash 2000 Elemental Analyzer for CHN, CHN/O, CHNS, and CHNS/O determinations. The CHN/CHN, CHNS/CHNS, CHN/O and CHNS/O dual configurations are equipped with the **Multi Valve Control module** as standard component.

This menu includes the following commands:

- “Ashes Removal” on page 38
- “Reactor Replacement” on page 38
- “Cleaning the MAS Piston” on page 38
- “MVC Manager” on page 38

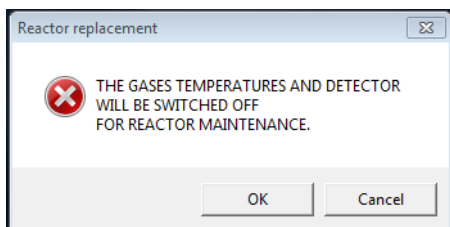
Ashes Removal

Use this command when the ashes removal is needed.

Turns **Off** the gases and the detector filaments. Wait few minutes to discharge the pressure, then proceed to the ashes removal. At the end of the operation, click **OK** to turn **On** gases and filaments.

Reactor Replacement

Use this command when the maintenance of the reactor is required. The following message is visualized.



Clicking **OK**, gases and detector filaments are turned **Off**, and the temperature decreases up to room temperature. Proceed to replace the reactor. At the end of the operation, turn **On** gases, detector filaments, and working temperature set-point.

Cleaning the MAS Piston

Use this command when the cleaning of the MAS autosampler piston is required.

This options turns **Off** the gases and the detector filament. Wait few minutes to discharge the pressure, then proceed to clean the MAS piston. For details, refer to the relevant EA operating manual.

- In the case of a **MAS Plus** or **MAS 200R**, by using the function **Step sampler tray position**, the autosampler mechanism pushes the piston forward and then ejects it. At the end of the operation, click **OK** to turn **On** gases and filaments.
- In the case of a **MAS 4000**, the operation previously described is performed choosing **Tool | Cleaning the piston**.

MVC Manager

This command is enabled when the **Multi Valve Control module** is connected to your *FlashSmart* or Flash 2000 Elemental Analyzer.

Selecting **MVC manager**, the **MVC management** page is visualized, where you choose the gas and the channel to use for your applications. See the section “[MVC Management](#)” on page 39 for details.

MVC Management

This module sets the connection parameters of the Multi Valve Control module connected to the Flash*Smart* or Flash 2000 Elemental Analyzer.

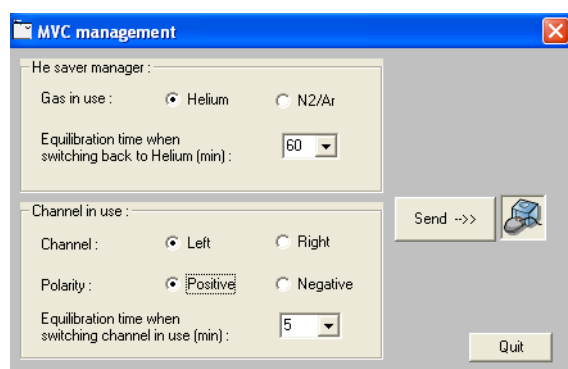
The Multi Valve Control module performs the following functions:

- Switches automatically from the **left** channel to the **right** channel and vice-versa.
- Saves helium or argon by switching from helium or argon, used as carrier gas for the analysis, to nitrogen when the instrument is not used overnight, or on weekends, or for a prolonged period of time.
- Possibility to insert by software an external command, for example the actuation of a gas valve.

The MVC management page is visualized selecting from Eager*Smart* Main Menu the commands **Tools | MVC manager**. See “[Tools Menu](#)” on [page 37](#).

The MVC management page includes the following fields and buttons. See “[MVC Management Page](#)” on [page 39](#).

Figure 24. MVC Management Page



- **He Saver Manager** — This field includes the following options:
 - **Gas in use:** — Choose **Helium** or **N2/Ar**. Helium is the carrier gas used for the analysis while nitrogen or argon can be used for saving helium when the instrument is not being used for a prolonged period of time, for example, overnight or on weekends.
 - **Equilibrium time when switching back to Helium (min):** — In the adjacent combo box select the time required for equilibrating the system when the gas supply switches back from argon to helium. Choose a time from 15 minutes to 75 minutes in steps of 15 minutes.
- **Channel In Use** — This field includes the following options:
 - **Channel:** — Choose **Left** or **Right**. Select the function according to your determination to be done.
 - **Polarity:** — Choose **Positive** or **Negative**.
The polarity of the TCD signal is automatically set according to the channel selected: positive for CHNS determination, and negative for Oxygen determination.
 - **Equilibrium time when switching channel in use (min):** — In the adjacent combo box select time required for equilibrating the system when the channel switches back from CHNS to O or vice-versa. Choose a time from 5 minutes to 75 minutes with step of 5 minutes.

- **Send:** — Transfers the information set in MVC management page to the instrument.
- **Quit:** — Exits the MVC management page.

Note The MVC management page can be visualized and modified before starting the sequence of the analysis. See “Start Sequence of Samples” on page 32 for details.

Help Menu

Help

Gives the access to [EagerSmart](#) help system. The help is divided into modules; each of them has been designed to cover specific arguments of the module currently in use.

About EagerSmart

Displays the version and the copyright of the program.

Instrument Control for IRMS

Available only if the **Instrument Control for Flash EA IRMS (NC) and HT** check box has been selected in [Instrument Name and Configuration](#) dialog box. At the reboot of [EagerSmart](#), the simplified **Main Menu for IRMS** is visualized. See [Figure 25](#).

Figure 25. Example of Main Menu for FLASH IRMS



Menus and buttons of the Main Menu for IRMS are described in the following [Table 4](#) and [Table 5](#) respectively.

Table 4. Main Menu for IRMS: Description of Menus

Menu	Description	Sub-menus and Options
File	Monitors the analysis in real time.	• Instrument name and configuration • View sample being acquired • Exit EagerSmart
Tools	Used when the ashes removal, the reactor replacement, or both, are required as maintenance.	• Ashes removal • Reactor replacement
Help	Gives the access to the help system of EagerSmart .	• About EagerSmart

Table 5. Main Menu for IRMS: Description of Icons (Graphic Buttons)

Icon	Function	Description
	Edit elemental analyzer parameters	Gives the access to the three pages containing the commands for setting temperatures, flows, times, detector, and the analyzer control functions.
	Elemental analyzer status	Comprises four pages displaying the analyzer conditions.

File Menu

This menu gives the access to the following functions:

- **Instrument name and configuration**, see [“Instrument Name and Configuration” on page 16](#)
- **View Sample Being Acquired**, see [Chapter 9, “View Sample Being Acquired,” on page 119](#)
- **Exit EagerSmart**, see the command [“Exit EagerSmart” on page 23](#)

Tools Menu

This menu gives the access to the following functions:

- **Ashes Removal**, see [“Ashes Removal” on page 38](#)
- **Reactor Replacement**, see [“Reactor Replacement” on page 38](#)

Help Menu

This menu gives the access to the following function:

- **About Eager Smart**, see [“Help Menu” on page 40](#)
- **Edit Elemental Analyzer Method**, see [Chapter 7, “Edit Elemental Analyzer Method,” on page 97](#)
- **Elemental Analyzer Status**, see [Chapter 15, “Elemental Analyzer Status,” on page 151](#)

Method Editor

This chapter provides instruction to modify the method parameters.

Contents

- [Introduction](#)
- [Method Title](#)
- [Detection Parameters](#)
- [Integration Parameters](#)
- [Calculation Parameters](#)
- [Report Parameters](#)
- [Report Stripchart](#)
- [Operator ID/Info](#)

Introduction

Method editor tabs modifies the method parameters and gives the access to the following sections:

- [“Method Title” on page 46](#)
- [“Detection Parameters” on page 47](#)
- [“Integration Parameters” on page 49](#)
- [“Calculation Parameters” on page 51](#)
- [“Report Parameters” on page 55](#)
- [“Report Stripchart” on page 61](#)
- [“Operator ID/Info” on page 63](#)

All the sections have the following buttons:

- **Cancel** — Clears all modifications done in the current section. The program returns to the previous tab.
- **OK** — Confirms all modifications done in the current tab. The program returns to the previous tab.
- **Help** — Opens help instruction.

Any tabs may have the following icons:

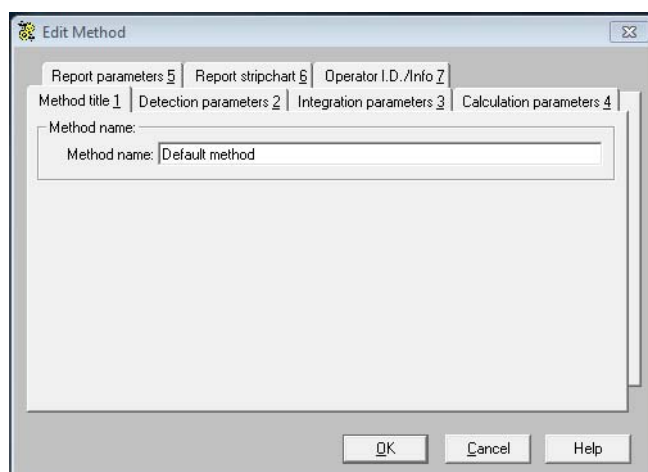
Icon	See:	Icon	See:
	Heat Value box on page 53 .		Protein Calculation on page 54
	Customer Report Editor on page 56 .		Signal To Noise Report on page 58
	Append To Summarize on page 59 .		Report Parameters on page 55 .

Note All modifications are stored in the method currently in memory, but you must use the **Save Method** command for saving the modifications permanently.

Method Title

Method title is the section of the analytical method used to add a comment to the method. This comment is visualized in Main Menu, saved with the parameters of the analysis, and retrieved any time the analysis is loaded. See [Figure 26](#).

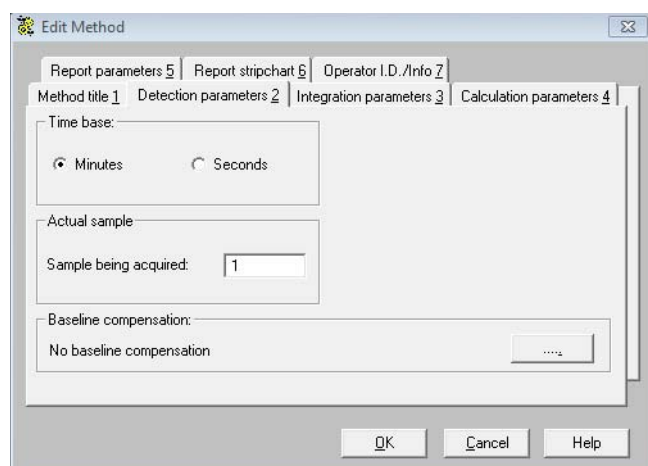
Figure 26. Method Title Tab



Detection Parameters

Detection parameters is the section of the analytical method that contains all the parameters for the data acquisition. See [Figure 27](#).

Figure 27. Detection Parameters Tab



ATTENTION For Eager USB and A/D versions, the *Analysis Duration Box* is also visualized in the window of [Figure 28](#). For details refer to “[Analysis Duration Box.](#)” on [page 48](#).

This tab provides the following functions:

- Time Base
- Actual Sample
- Baseline Compensation
- Analysis Duration (only for Eager USB and A/D versions)

Time Base Box

EagerSmart can work with two time bases. Choose to work in **Seconds** or in **Minutes**. Changing from minutes to seconds, the system updates the parameters **Analysis Time** and **Pre-acquisition delay**.

- **Minutes** — Specifies you want to work in minutes.
- **Seconds** — Specifies you want to work in seconds.

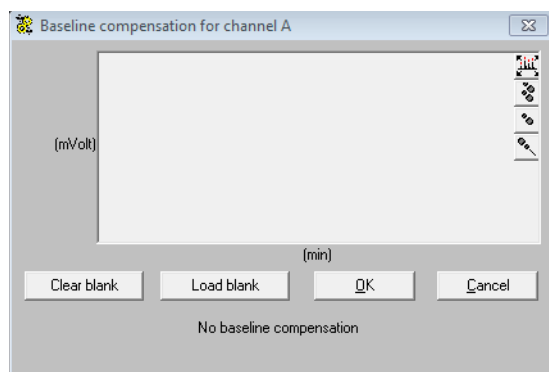
Actual Sample Box

This dialog box contains the pointer to the **Sample Table** that indicates the **Sample being acquired**. Contains also the box **Enable external start/stop**.

- **Sample Being Acquired** — Contains the number of the sample being acquired.
To store the chromatogram data, the system uses the filename found in the corresponding line in the **Sample Table**. If the filename field is not edited, the system provides a default filename where the report for the analyzed sample and the chromatogram are saved on the hard disk.

Baseline Compensation Box

EagerSmart compensates in real time the acquired chromatogram with the baseline background.



You can select the **blank chromatogram** to be subtracted to all chromatogram analyses. **Sample being acquired window** shows the result of the sample acquired already compensated. The system creates the compensated sample raw data chromatogram directly on disk. Moreover, in compliance with *Good Laboratory Practice (GLP)*, *EagerSmart* also creates the original sample raw data chromatogram with the name specified in the **sample table** having an **underscore** at the beginning of the name, for example **_Filename.raw**.

By requesting this function, you can load any chromatogram to be used as baseline background compensation. Besides, the window contains the function to switch off the baseline background compensation.

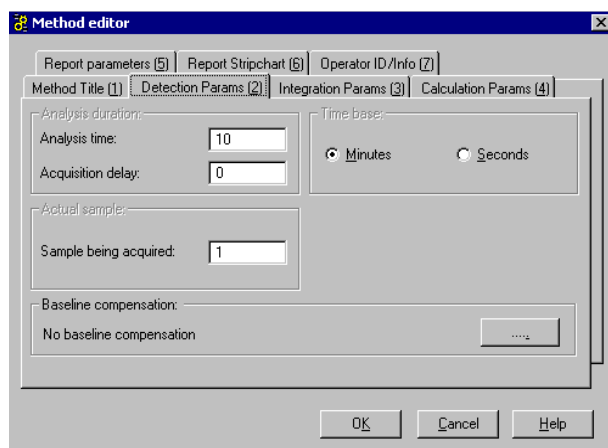
Note The samples to be compensated and the blank chromatogram must have the same acquisition speed.

Analysis Duration Box



CAUTION This box is visualized in the window of [Figure 27](#) only when *EagerSmart* USB or A/D version is used.

Figure 28. Detector Parameters for *EagerSmart* USB and A/D versions



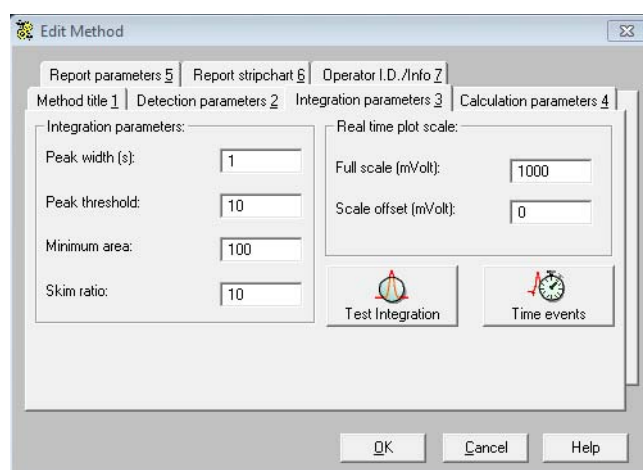
This tab contains the parameters for the detection. The data acquisition is controlled by the parameters **Analysis time** and **Acquisition delay**. They should be entered according to the chosen time base before starting the acquisition. Any modification to these two parameters during the data acquisition has effect only from the next sample.

- **Analysis time** — Specifies the duration of the analysis according to the chosen time base. If the analysis is an **unknown** sample, and the complete elution is not predictable, you should set a time longer than you expect. When all peaks are eluted, you interrupt the acquisition at the desired moment by using the **Stop analysis** command.
- **Acquisition delay** — Used to inhibit the acquisition during a period of time (in seconds) measured from the beginning of the run. The **Inhibit time** parameter is generally used to exclude from integration unwanted peaks due to small sampling noise. The default value is 0. The acceptable entry value range is 0 to 999 seconds.

Integration Parameters

Integration parameters is the section of the analytical method that contains all the parameters for the integration. See [Figure 29](#).

Figure 29. Integration Parameters Tab



This tab provides the following functions:

- Integration Parameters
- Real Time Plot Scale
- Test Integration; see [Chapter 21, “Peaks Detection.”](#)
- Time Events; see [Chapter 22, “Time Events.”](#)

Integration Parameters Field

Contains all parameters used for the integration algorithm. It is based on four parameters:

- **Peak Width** — Specifies the width of the peaks to be integrated. Sometime the integration may be difficult for analyses having large peaks, but collected with fast sampling rate. The best way to overcome these problems is to enter the width of the peak to be integrated. Peak Width can be changed during the analysis through the **Time events** option.

Peak Width is calculated measuring the width of the peak at the 50% of the high. See also “[Peak Menu](#)” on [page 133](#).

- **Peak Threshold** — Sets the threshold in microvolts for peak recognition. The integration algorithm uses this value to discriminate the peaks from the baseline, or the signal noise. Increasing this value, the system becomes less sensitive, while more peaks is found decreasing the value.
- **Minimum Area** — First the peak integration is performed using the parameters **Peak Width** and **Peak Threshold**, then the peaks having an area below the entered value are rejected.
- **Skim Ratio** — Skim ratio parameter is defined as a ratio of two overlapped peaks as follows:

$$\text{Skim Ratio} = \text{H major peak} / \text{H minor peak}$$

where:

- **H major** is the high from the intervening valley to the peak maximum of the major peak.
- **H minor** is the high from the intervening valley to the peak maximum of the minor peak.

This parameter determines whether overlapping peaks are integrated using **tangential skim** or **perpendicular drop** method.

- The **tangential skim** method is normally used for overlapped peaks that are small relative to the major peak.
- The **perpendicular drop** method is used when the overlapped peaks are about the same size.

A tangent correction on the carrier peak is performed if the ratio between the areas of two or more consecutive peaks is higher than the entered value.

Real Time Plot Scale Field

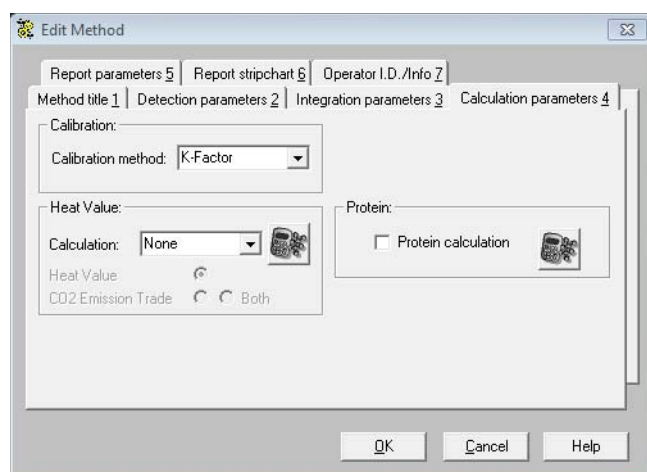
Contains the scale and the offset for the display of the chromatogram being acquired in the module **View sample being acquired**. The **Full scale** and **Scale offset** options are used for the initial chromatogram display. You can change the values at any time for a better view of the acquisition data points.

- **Full Scale** — Contains the value for the full scale in mV. Used for the incoming chromatogram shown on video in real time. Full Scale is used for the initial chromatogram display. You can change the value at any time to improve display of the acquisition data points.
- **Scale Offset** — Contains the value for the scale offset in mV. Used for the incoming chromatogram shown on video in real time, and for the initial chromatogram display. You can change the value at any time to improve display of the acquisition data points.

Calculation Parameters

Calculation parameters is the section of the analytical method that contains all the parameters for the calculation of the peak. See [Figure 30](#).

Figure 30. Calculation Parameters Tab



This tab provides the following functions:

- Calibration
- Heat Value Calculation or/and CO₂ Emission Factor
- Protein Evaluation

Calibration

This field includes the following option:

Calibration Method

Specifies the method of calibration by which the analyzed samples is processed. Three calibration methods are available.

- **K-Factor** method
- **Linear Fit** method
- **Non Linear Fit** method

The selection of any of these methods entirely relies on the operator according to considerations of single-point calibration with blank subtraction (K-Factor), or detector responses between a given weight range of standard and sample.

For selecting the appropriate calibration methods, see the following description.

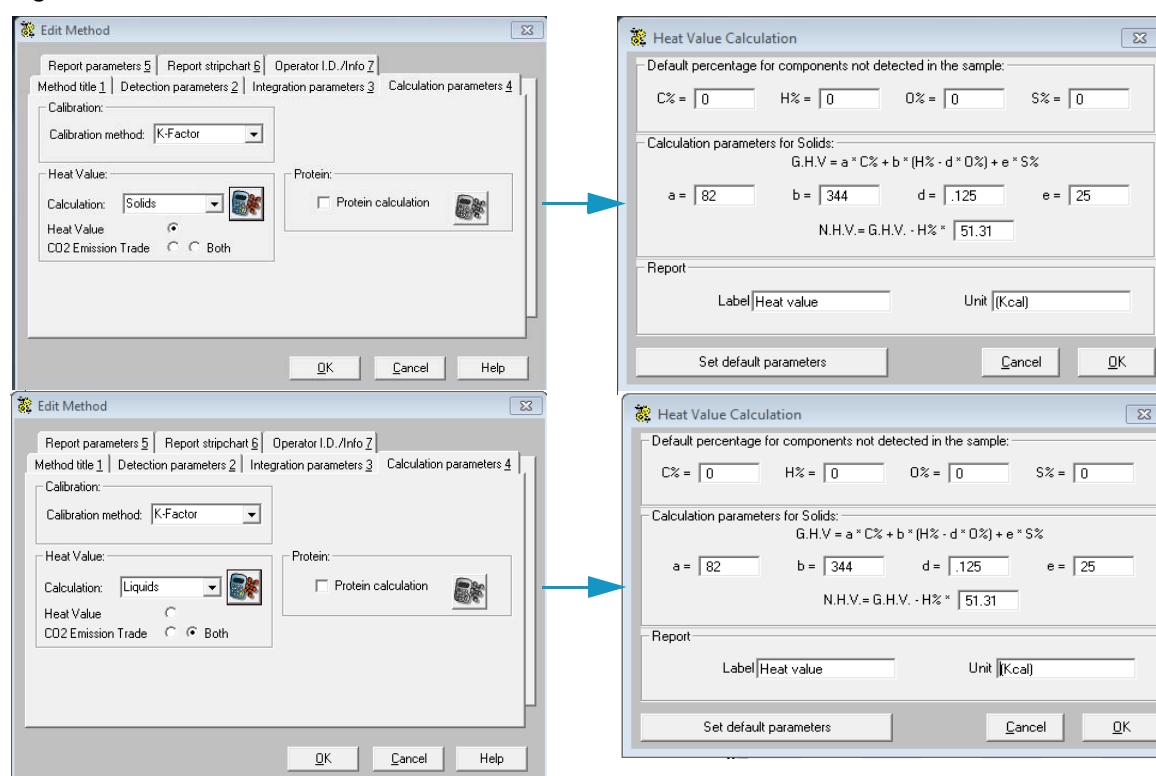
Option	Description
K-Factor	The quantization of the element that has been analyzed, (for example carbon), is determined by comparing the values obtained from the analysis of the sample with the analysis of a suitable standard, and the use of a reference factor known as K-Factor. Such a factor is defined in the following equation: $K = \frac{AreaStd - AreaBlank}{(\%Tstd \times Wstd)/100}$ where: AreaStd = peak area or integral of standard AreaBlank = peak area or integral of blank % Tstd = theoretical percentage of standard Wstd = weight of standard The calculation of the percentage of element (%) is given by the following equation: $Calculated\% = \frac{(AreaUnk - AreaBlk)/K}{Wunk} \times 100$ where: K = Average K-Factor AreaUnk = peak area or integral of the unknown AreaBlk = peak area or integral of the blank Wunk = weight of the unknown
Linear Fit	This method of calculation obeys a calibration function based on the analysis of at least two standards. The results are calculated with the aid of the linear regression method by which one variable is analyzed in relation to another one. This method performs a least-square linear regression between integration data (area counts), and known amount of elemental components of the standard, where a linear equation of calibration is applicable for each element. The percentage composition of an element is defined by the following equation: $\% = \frac{m \times AreaUnk + b}{WheightUnk}$ where: m = angular coefficient calculated with the least-square method b = intercept of straight line calculated with the least-square method The regression is calculated on the standard for calibration, reporting on the X-axis the peak areas obtained, and on the Y-axis the weight multiplied by the theoretical percentage of the single standard.

Option	Description
Non Linear Fit	This method of calculation obeys a calibration function based on the analysis of at least three standards, and the results are calculated with the aid of a quadratic regression method by which one variable is analyzed in relation to another one. This method performs a least-square quadratic regression between integration data (area counts), and known amount of elemental components of the standard, where a quadratic equation of calibration is applicable for each element. The percentage composition of an element is defined by the following equation: $\% = \frac{a \times AreaUnk^2 + b \times AreaUnk + c}{WeightUnk}$ where: a = coefficient calculated with the least-square method b = curvature coefficient calculated with the least-square method c = intercept calculated with the least squares method The regression is calculated on the standards for calibration, reporting on the X-axis the peak areas obtained, and on the Y-axis the weight multiplied by the theoretical percentage of the single standards.

Heat Value Box

These options perform **Heat Value Calculations**, and establish the **calorific content**, the **CO₂ Emission Factor**, or both, either for liquid or solid samples in an automatic manner. See [Figure 31](#).

Figure 31. Heat Value

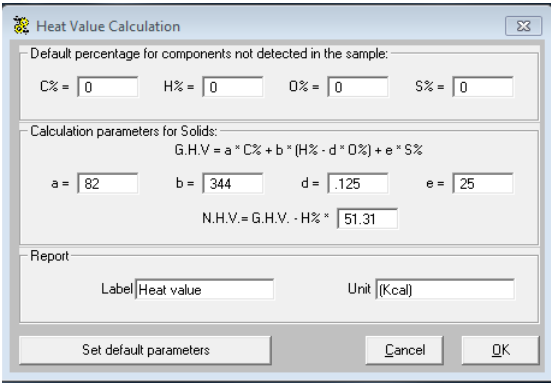


The calculation of the **CO₂ Emission Factor** is based on the percentage composition of the elements, and on the **Gross Heating Value**.

Select in the **Calculation** box the type of sample choosing among **None**, **Liquids**, and **Solids**. Select the relevant option button to choose the desired calculation among **Heat Value**, **CO₂ Emission Trade**, and **Both**. This operation automatically sets the calculation choice on the **Calculation Parameter** and **Report Parameters** tabs.

Clicking the  icon, the **Heat Value** module is visualized. Figure 32 and shows an example of Heat Value module when **Both** is selected.

Figure 32. Heat Value Calculation Module



The module features three parts:

- The **upper** part features the elemental composition boxes where you can enter the composition for the elements not detected in the current sample but determined in a different way.
- The **middle** part specifies the actual calculation of the sample **Gross Heating Value (G.H.V.)** from the known elemental composition of the sample, and some empirical factors found for this type of calculations when samples are solids.

The calculation of the **Net Heating Value (N.H.V.)** is also obtained by subtracting the percentage of hydrogen from the G.H.V. value.

- The **lower** part contains the report label and the report unit you would like to use.

Note If **CO₂ Emission Factor** has been selected, the report contains a column reporting the calculated value expressed in **tCO₂/TJ** (TJ = Terajoule).

Protein

Contains the following option:

Protein Calculation

Calculates the protein content of a bio-organic sample in a fully automatic manner using the equation reported on the module that appears on the screen by clicking the  icon. See Figure 33.

Figure 33. Protein Calculation Module

You may enter the factor used for the calculation, then type in the name or label of the calculation to be reported.

Remember that the first multiplication factor b (Protein Factor) must be typed in the column **Protein Factor** of the **Sample Table**.

Report Parameters

Report parameters is the section of the analytical method that contains all the parameters for the report. See [Figure 34](#).

Figure 34. Report Parameters Tab

This tab provides the following functions:

- Data report format
- Standard report on
- Concentration unit
- Report title
- Report publisher

Data Report Format

Selects various types of report providing some options:

Report Type

Selects the following types of reports:

- **Standard Report** — It can be made consisting of all integrated peak information.

The detailed report consists of:

- component names
- calculated element%
- retention times
- areas
- baseline correction
- area ratio
- K factors

The report column BC identifies the baseline correction of the peak. The available codes are:

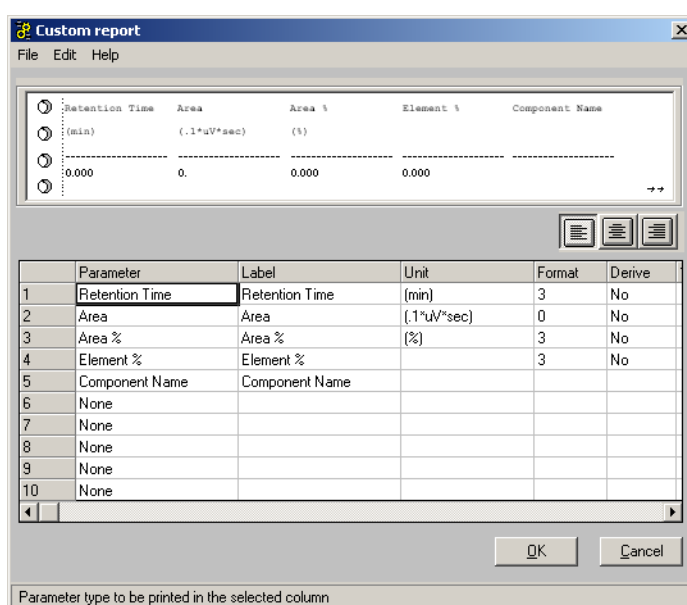
RS = Resolved; FU = Fused; TL = Tailing; CR = Carried; MI = Manually integrated;

^^ = Off-Scale peak

For details see “[Baseline Correction](#)” on [page 57](#).

- **Extended Report** — It can be made by the standard report and a summary report. Both are sent to printer or to disk as required in **Report destination**.
- **Summary Report** — It can be made only for those components that are of interest, for example those in **Component Table**. The summary report consists of the component names and their calculated concentrations.
- **Custom Report** — It is the section of the analytical method that contains the information to generate a report designed by you. Set this option to enable the custom report generation, then click the  icon to open **Custom Report** editor page. The dialog box is visualized. See [Figure 35](#).

Figure 35. Custom Report Editor Dialog Box



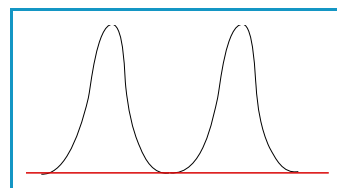
EagerSmart offers you a graphical way to layout in a few seconds the report you desire. All columns of the report are selected through a fast and simple dialog box that offers different columns result. You can customize the title, the format, and eventually to derive the results multiplying and adding constants.

Custom Report editor is printed only if **Custom** is selected in **Report Type** text box of **Report Parameters** tab. For details see [Chapter 20, “Custom Report Editor.”](#)

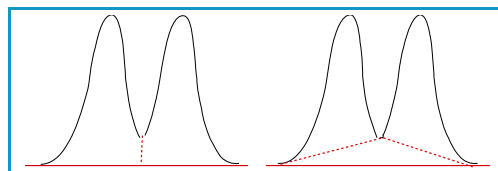
Baseline Correction

This paragraph contains a brief description of the baseline correction identification codes reported in the column BC of the Report. See [“Data Report Format”](#) on [page 55](#).

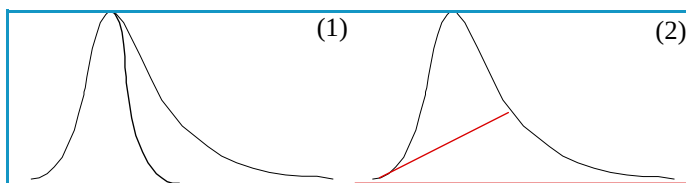
- **Resolved Peak** — The Gaussian form of the peak is symmetrical, then the peak is resolved at the baseline. The **RS** code identifies the resolved peaks.



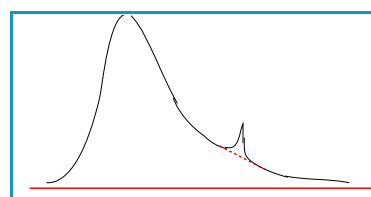
- **Fused Peak** — Two adjacent peaks are not well separated. The **FU** code identifies fused peaks. The separation of fused peaks may be performed by a “cut” perpendicular to the baseline, or valley to valley.



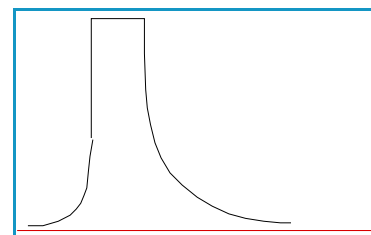
- **Tailing Peak** — The Gaussian form of the peak is not completely symmetrical, the rear being spread out to a greater or lesser extent, forming a tail, hence the expression “**tailing**”. The **TL** code identifies tailing peaks. The baseline correction may be trapezoidal (1) or horizontal (2).



- **Carried Peak** — A peak is found on a tailing peak. The **CR** code identifies carried peaks and thus allow tangential baseline correction.



- **Manually Integrated Peak** — The baseline correction has been manually recalculated by the operator. The **MI** code identifies the manually integrated peaks.
- **Off-Scale Peak** — The signal of the peak (for example the solvent peak) goes off the full scale limit. The **^^** code identifies off-scale peak.



Include Signal to Noise Report

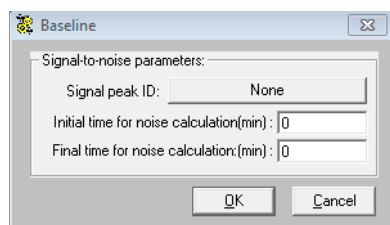
EagerSmart can calculate the **Signal-to-Noise ratio**. This function chooses the peak of interest and the baseline portion on which the noise evaluation should be done.

You should check this option and the report is automatically generated:

```
Signal to noise report
-----
Signal peak name      : Nitrogen
Signal peak RT       (sec): 218.0
Signal value         (uV): 22064.8
Noise eval from/to (sec): 150.0-160.0
Peak to peak noise   (uV): 81.2
Signal to noise ratio : 271.7
```

Set this option by clicking the  icon. The dialog box is visualized. See [Figure 36](#).

Figure 36. Signal to Noise Parameters



The value of the signal is calculated on the selected **Signal peak ID**. The noise is evaluated for the given **Initial time** and **Final time**. According to the found values, the ratio is calculated and reported between the peak signal value and the peak-to-peak noise.

Include Calibration Report

Select this option to have the printout of the samples calibration report for each of the calibration levels. The next image shown an example of report.

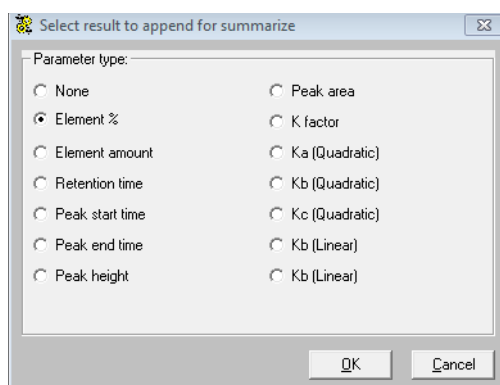
EagerSmart Report						
Method Name: Nitrogen/Protein						
Method File: EagerSmart for FLASH\data\Sys_data_example \N Protein Test.mth						
Chromatogram : FRANKY 2						
Operator ID : Franky Leo Company Name : Thermo Fisher Scientific						
Analysed : 19/02/16 16:32 Printed : 20/02/16 15:15						
Sample ID : ALL-BRAN (# 112) Channel : (Channel 1)						
Analysis Type: UnkNowN (Area) Sample weight : 237.8						
Protein Fact.: 6.25						
Calib. method: using 'K Factors'						
Warning Chromatogram has been subjected to data manipulation.						
Element Name	%	Ret.Time	Area	BC	Area ratio	K factor
Nitrogen	1.6744	218	6868548	FU	1.000000	.172500E+07
2	0.0000	297	198388	FU	0.0000	
Totals	1.6744		7066936			
Protein: 10.46514%						

Append To Summarize

This option enables *EagerSmart* to generate for each sample the internal data base used to summarize the results.

Click the  icon and select the result to append for summarize, normally **Element%** as shown in Figure 37.

Figure 37. Result Type Dialog Window



The internal data base performs the calculation of average standard deviations and other statistical results on a group of samples.

Report On

The report generated by *EagerSmart* can be addressed to the following destinations:

- **None** — Any report at all is not generated. This option is very useful for reprocessing a sequence of samples after changing integration or calibration parameters.
- **Printer** — The report generated is sent directly to the printer.

Note In File menu you have the possibility to select the printer to be used, the fonts and the orientation of stripchart and the report results.

- **ASCII File** — The report generated is sent to an ASCII disk file to be used with third party software word-processors. The generated ASCII file is located in the directory of the method currently in use. The name is the same of the chromatogram of the addressed sample with the extension ***.txt**.
- **DIF File** — The report generated is sent to a DIF file to be used with third party software spread-sheet. The generated DIF file is located in the directory of the method currently in use. The name is the same of the chromatogram of the addressed sample with the extension ***.dif**.
- **Excel File** — The report generated is sent to a XLS file (4.0 format) compatible with Excel. The generated XLS file is located in the directory of the method currently in use. The name is the same of the chromatogram of the addressed sample with the extension ***.xls**.
- **HTLM File** — The report generated is sent to an HTLM format to be used with Intranet/Internet browser. The generated HTLM file is located in the directory of the method currently in use. The name is the same of the chromatogram of the addressed sample with the extension HTM. The generated HTLM file is best viewed with Microsoft Explorer.

- **HTLM + BMP** — The report generated is sent to an HTLM format including the BMP graphic to be used with Intranet/Internet browser. The generated HTLM and BMP file is located in the directory of the method currently in use. The name is the same of the chromatogram of the addressed sample with the extensions ***.htm** and ***.bmp** for the chromatogram graph. The generated HTLM file is best viewed with Microsoft Explorer.

The BMP graph can be adjusted in size by changing the parameters control in **WCC.INI** file in the **WCC** directory.

```
[HTLM]
Graph3D=01(Gives appearance Flat=0 or 3D=1)
GraphWidth=8000(Width in twips)
GraphHeight=4000(Height in Twips)
GraphFontSizeRatio=.6(Reduce / Increase the Fonts used for chromatogram graph.
```

Concentration

This field comprises the following option:

Concentration Unit

Replaces the concentration column heading in the report with a custom heading (up to 8 characters), identifying the concentration units (normally%) for the analysis.

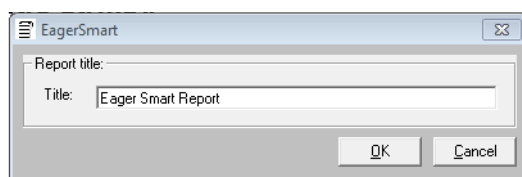
Report Title

This field comprises the following option:

Report Title String

Enters a text to be printed as a title of reports generated by the system. Click the  icon to open **Report Title editor**. See [Figure 38](#).

Figure 38. Report Title String Box



Note This title is different for each channel and independent of the method. It is automatically saved on disk after every change, and automatically loaded at every system start-up.

Report Publisher

Prints the report specified by the file with the extension ***.rep**.

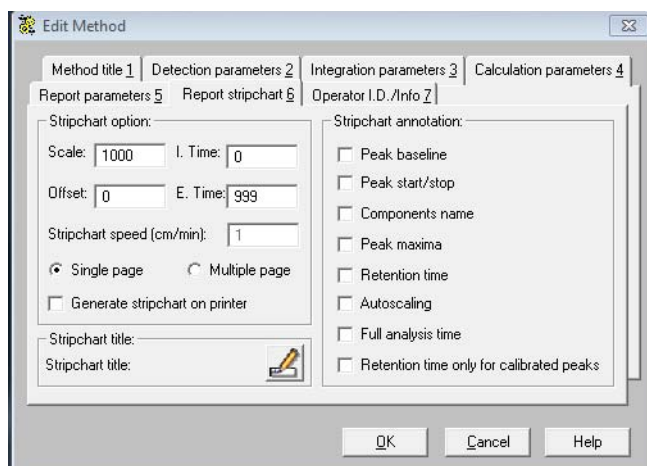
EagerSmart layouts the report with the selected objects placed at the desired position with the desired size.

All report information are saved in a report layout file (**xxx.rep**), by clicking the bottom bar on the right. EagerSmart shows the tool for entering the layout of the report. You can select the objects, their size, and the position. See [Chapter 19, “Report Publisher,”](#).

Report Stripchart

Selects and to set the stripchart options to be included in the report printout.

Figure 39. Report Stripchart Tab



This tab provides the following functions:

- Stripchart options
- Stripchart title
- Stripchart annotation

Stripchart Options

Contains the parameters used for the generation of the stripchart report.

According to the stripchart options selected, you can enter the following parameters:

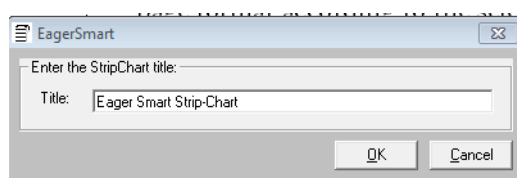
- **Scale** — Contains the full scale value for the stripchart. EagerSmart uses this value as full scale of the strip chart only if the strip chart is required with manual scale. When in [Stripchart Annotation](#) the option **Autoscaling** is checked, this box remains disabled.
- **Offset** — Contains the offset value for the stripchart. EagerSmart uses this scale offset for the stripchart only if the strip chart is required with manual scale. When in [Stripchart Annotation](#) the option **Autoscaling** is checked, this box remains disabled.
- **Initial Time** — Contains the initial time for the stripchart. EagerSmart uses this initial time for a partial strip chart printout only if the stripchart is not required with full time frame. When the stripchart is required with full time, this box remains disabled.
- **Final Time** — Contains the final time for the stripchart. EagerSmart uses this final time for a partial stripchart printout only if the strip chart is not required with full time frame. When the stripchart is required with full time, this box remains disabled.

- **Stripchart Speed** — Contains the chart speed to be used for the chromatogram printout in cm/min (for example: a chromatogram of 40 minutes with Chart Speed of 2 cm/min is 80 cm long).
- **Single Page** — Generates a complete stripchart in the report printout. The stripchart is printed on one single page regardless of the analysis time. The stripchart can be printed in portrait or landscape format according to the selection done in **Color and Fonts** option from Main Menu.
- **Multiple Pages** — Generates a complete stripchart in the report printout. The stripchart is printed on one or more pages according to the analysis time and the stripchart speed. The stripchart can be printed in portrait or landscape format according to the selection done in **Color and Fonts** option from Main Menu.
- **Generate Stripchart On Printer** — Includes the stripchart in the report printout. All calculation is performed, the report if required is generated and the stripchart generates on a single or multiple page format according to the selection.

Stripchart Title

Click the  icon to open **Stripchart title editor**. See [Figure 40](#).

Figure 40. Stripchart Title String Box



This function enters a text to be printed as a title of all stripcharts generated by the system.

Note This title is different for each channel and independent of the method; it is automatically saved on disk after every change and it is automatically loaded at every system start-up.

Stripchart Annotation

EagerSmart sets your selection made with a check mark on the left side of the options:

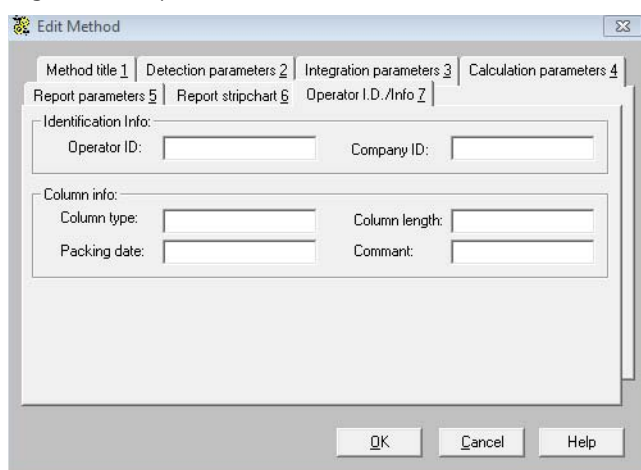
- **Peak Baseline** — Prints the baseline correction of the chromatogram. If a check mark is shown beside the command, the chromatogram is printed with a dashed line of the baseline correction. Otherwise, only the chromatogram data points are printed.
- **Peak Start/Stop** — Displays the start and stop point of each peak. If a check mark is shown beside the command, the chromatogram is visualized with two small dashes indicating the start and end point of the peaks.
- **Component Name** — Displays the name of the components. If a check mark is shown beside the command, the chromatogram is visualized with the name of each component found in the chromatogram. The names of the components are reported only if the chromatogram has been processed, and if the method currently in memory corresponds to the method used for the original sample acquisition.
- **Peak Maxima** — Displays a small tick on the top of each peak. If a check mark is shown beside the command, the chromatogram is visualized with small marks indicating the maximum of the peak, and indicating that the peak is integrated.

- **Retention Time** — Displays the retention time of the peaks. If a check mark is shown beside the command, the chromatogram is visualized with the retention time at the maximum of the peak, and indicating that the peak has been eluted at the reported time.
- **Autoscaling** — Prints the stripchart automatically re-scaling the chromatogram. If a cross mark is shown beside the command, the chromatogram is printed with a scale calculated to keep all integrated peaks in scale.
- **Full Analysis Time** — Prints the stripchart corresponding to the total analysis time. If a cross mark is shown beside the command, the chromatogram is printed with the full analysis time. Otherwise, only the section specified by Strip chart initial time and Strip chart final time is printed.
- **Retention Time Only for Calibrated Peaks** — Prints the retention time on the apex of the peaks. The function enables to print the retention time only for those peaks that have been entered in the component table.

Operator ID/Info

The Operator ID/Info tab is shown in [Figure 41](#).

Figure 41. Operator ID/Info Tab



ID Info Box

- **Operator ID** — Contains the **Operator Identification**, that is printed on each report generated by *EagerSmart*. Operator ID is replaced in the reports by user's name if *EagerSmart* is configured with passwords.
If you have logged in for *EagerSmart* system by entering the given password, all report headers include the assigned user name in place of the Operator ID.
- **Company ID** — Contains the **Company Identification**, and it is printed on each report header generated by *EagerSmart*.

Column Info

Contains all the information on the column in use.

- **Column Type** — Contains the column type and it is used as a comment of your analytical method. This box is not printed in the report, but it is saved with the analytical method. It can be printed with the function **Print Method**.
- **Column Length** — Contains the column length and it is used as a comment of your analytical method. This box is not printed in the reports but it is saved with the analytical method. It can be printed with the function **Print Method**.
- **Packing Date** — Contains the column packing date and it is used as a comment of your analytical method. This box is not printed in the reports but it is saved with the analytical method. It can be printed with the function **Print Method**.
- **Comment** — Contains a general comment for your analytical method. This box is not printed in the reports but it is saved with the analytical method. It can be printed with the function **Print Method**.

Component Table

This chapter provides the instructions for editing the Component Table.

Contents

- [Introduction](#)
- [File Menu](#)
- [Edit Menu](#)
- [View Menu](#)
- [Show Menu](#)
- [Peak Identification](#)
- [Retention Time Icon](#)
- [Chromatogram Icons](#)
- [Component Table Grid](#)

Introduction

EagerSmart features the five components in Elemental Analysis: **Nitrogen**, **Carbon**, **Hydrogen**, **Sulfur**, and **Oxygen**, entered in their elution order.



ATTENTION You must enter the retention times in seconds or minutes, to identify the peaks of the analysis and determine the elemental composition of samples when chromatograms are processed.

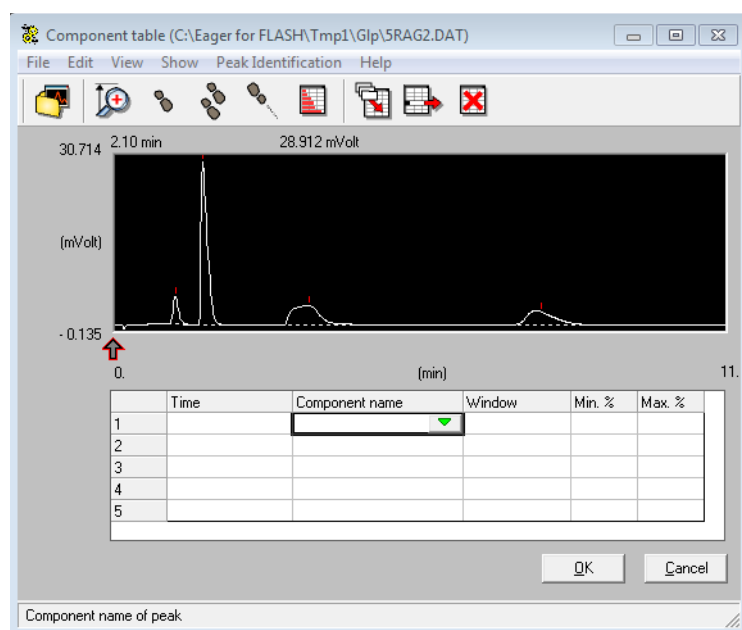
To edit the **Component Table** you must acquire a chromatogram that contains all the components you want to identify. Generally, this is a reference chromatogram achieved from the last **Bypass** sample, which has been analyzed to condition the Elemental Analyzer, and currently present in the computer memory. Another possibility is to use a reference chromatogram from a previous run, and load it in memory by using the **Load Chromatogram** pull-down menu.



ATTENTION When the Component Table has undergone changes, it is absolutely necessary to check in the Sample Table that the element percentages have been correctly assigned.

Component Table is the section of the analytical method that contains all the parameters for the peak identification. See [Figure 42](#).

Figure 42. Component Table



Icon	Description	See on:
	Load Chromatogram	page 67
	Chromatogram Icons	page 70
	Retention Time Icon	page 70
	Fill Component Table	page 67
	Delete Line	page 66
	Clear Component Table	page 66

Button	Description
Cancel	Clears all modifications done in the current section. The program returns to Main Menu.
OK	Confirms all modifications done in the current tab. The program returns to Main Menu.

Note All modifications are stored in the method currently in memory. You should use the **Save Method** command to save them permanently.

The Component Table offers a number of tools to enter the retention times and identification windows through the chromatogram shown on the upper part of the window.

Component Table provides the following menus and functions:

- “File Menu” on page 67
- “Edit Menu” on page 67
- “View Menu” on page 68
- “Show Menu” on page 68
- “Peak Identification” on page 69
- “Retention Time Icon” on page 70
- “Chromatogram Icons” on page 70
- “Component Table Grid” on page 70

File Menu

This menu gives the access to the following functions:

- **Load Chromatogram** — Loads any chromatogram previously acquired and stored on disk. The system shows the Open dialog box where you specifies a file to be opened.
- **Exit** — Confirms all modifications done in the current section and the program returns to Main Menu.

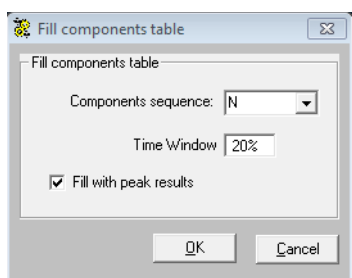
Edit Menu

Note All modifications are stored in the method currently in memory. You should use the **Save Method** command to save them permanently

This menu gives the access to the functions for filling or deleting the Component Table:

- **Fill Component Table** — Fills the Component Table in an automatic way by using the retention times of the peaks calculated from the chromatogram currently visualized. See [Figure 43](#).

Figure 43. Fill Component Table Dialog Window



Once you have selected this function, you must set the elements you want to determine, their elution order, and the **Time Window** width.

In the **Component Sequence** box type the first characters of the elements in the elution order. In the **Time Window** box type the width, in seconds or percentage of retention time, in which a peak is recognized as the given element. When selected, **Fill with peak results** automatically assigns the retention times of the reference chromatogram peaks to the elements entered in the first box by following the sequence reported therein.

- **Delete Line** — Clears the retention time, the name, the window, and the peak type of the currently addressed peak.
- **Clear Component Table** — Clears completely the Component Table currently in memory.
- **Follow Retention Time** — Enables the system to follow the eventual retention time shift from sample to sample. When this function is enabled, and only if all peaks have been found, after each calibration *EagerSmart* updates the Component Table with the average of the original retention time and the retention time of the peaks found.
- **Copy Component Table to Clipboard** — As with most Windows™ applications that use the Clipboard to transfer text, graphics, and other data, you can copy and move text from *EagerSmart* into different applications.

❖ **To copy text between EagerSmart and another application**

1. Select the cells you want to copy.
2. From the **Edit** menu, choose **Copy**.
3. Switch to the other application.
 - a. If the other application is not open, start the other application.
 - b. If the other application is already open, press **CTRL+ESC**, then choose the application from the Task List.
4. Position the insertion point where you want to insert the text.
5. From **Edit** menu, choose **Paste** (ALT, E, P).

View Menu

This menu gives the access to functions for changing the aspect of the chromatogram visualized:

- **Original Scale and Offset** — Restores the original scale and offset after a **Set Manual Scale** has been performed. The chromatogram is generally stored with the original scale and offset calculated to keep in scale all peaks not exceeding 1000 mV full scale.
- **Set Manual Scale** — Enters a manual scale to display the chromatogram in the top window. After any manual modification of the scale, it is always possible to restore the original values with the function **Original scale and offset**. The chromatogram is generally stored with the original scale and offset calculated to keep in scale all peaks not exceeding 1000 mV full scale.
- **Set Manual Zoom** — Enters a manual scale and time to display the chromatogram in the window.
- **Fit to Highest Peak** — Adjusts the scale of the top window in order to keep in scale any peak being part of the chromatogram. Even peaks with height higher than 1000 mV is automatically in scale.
- **Fit to Highest Peak on Scale** — Adjusts the scale of the top window in order to keep in scale any peak being part of the chromatogram, but within 1000 mV of height.

Show Menu

This menu gives the access to the functions for changing the aspect of the chromatogram visualized.

- **Baseline** — Displays the baseline correction of the chromatogram. If a check mark is shown beside the command, the chromatogram is visualized with a dashed line of the baseline correction. Otherwise, only the chromatogram data points are shown.
- **Maxima** — Displays a small tick on the top of each peak. If a check mark is shown beside the command, the chromatogram is visualized with small marks indicating the maximum of the peak and indicating that the peak is integrated.
- **Retention Time** — Displays the retention time of the peaks. If a check mark is shown beside the command, the chromatogram is visualized with the retention time at the maximum of the peak, and indicating that the peak has been eluted at the reported time.
- **Peak Name** — Displays the name of the components. If a check mark is shown beside the command, the chromatogram is visualized with the name of each component found in the chromatogram.

Note The names of the components are reported only if the chromatogram has been processed, and if the method currently in memory corresponds to the method used for the original sample acquisition.

- **Start/Stop** — Displays the start and stop point of each peak. If a check mark is shown beside the command, the chromatogram is visualized with two small arrows indicating the start and end point of the peaks.
- **Peak Window** — EagerSmart uses the retention times to determine whether or not the peaks in the chromatogram are the same as those in the Component Table. This is accomplished by logically selecting peaks within a certain range or window of the retention time specified for each peak. The window is determined for each component in the table based on its retention time value and the component window setting.
For example: If a **Component table RT** value is **2** and the Peak Window is **1**, the window for identification of the component is between **1.9** and **2.1**. The window specified by this box can be in absolute time, or in percentage of the retention time of the addressed peak if the number is followed by %. If a check mark is shown beside the command the chromatogram is displayed with two dashed lines indicating the start and end point of the peak window used for the peak identification. Moving the peak table cursor the window will move automatically to the new addressed peak.
- **Peak List** — When this function is enabled, the peaks list of the chromatogram in memory is shown. In the relative windows you can browse the retention time and the area of each peak being part of the chromatogram in memory.
- **None of Above** — Disables all the functions currently selected for the chromatogram display.

Peak Identification

Verifies the entered **Retention Times** in the table are matching the retention times of the chromatogram in memory. The chromatogram is visualized with the identified peaks marked with their names. If all peaks are recognized, the system asks to update the table with the real time found for the peaks.

Retention Time Icon

Changes the order of the entered retention time events. The time may be entered with a wrong sequence. It is possible to sort in ascending way all the retention times.

Chromatogram Icons

Icon Function	Description
	Restores the chromatogram currently in memory with the original scale and offset. After a number of zoom commands, you would like to review the original chromatogram time frame. Through this command the system immediately restores the full chromatogram view.
	Advances the chromatogram view by the same time frame of the actual window or half the actual window.
	Remembers the last 10 chromatogram time-frame views and restores the last 10 zoom steps.

Component Table Grid

Contains all the information to identify the peaks of the samples. This is the box where new peak information can be entered. See [Figure 44](#).

Figure 44. Component Table grid

	Time	Component name	Window	Min %	Max %
1	44	Nitrogen	8		
2	71	Carbon	14		
3	263	Hydrogen	52		
4	525	Sulphur	104		
5					

Address the component of interest by clicking on the components grid in any column of the line. The cursor automatically addresses the input box ready to accept the new value. Once the new value has been entered and confirmed by pressing the **Enter** key, the system updates the Component Table. Alternatively, you can address the box by a double-click. In this case the system edits the previous content of the box.

- **Retention Time** — Type the **Retention Time** of the peak to be recognized. Alternatively, you may use the pointer under the chromatogram.
- **Component Name** — Specifies the component name of the peaks to be recognized. The name entered here is used to mark the identified peaks.
- **Window** — *EagerSmart* uses the retention times to determine whether or not the peaks in the chromatogram are the same as those in the Component Table.

This is accomplished by logically selecting peaks within a certain range or window of the retention time specified for each peak. The window is determined for each component in the table based on its retention time value and the component window setting.

For example: If a **Component Table RT** value is **2** and the **Peak Window** is **1**, the window for identification of the component is between **1.9** and **2.1**. The window specified by this box can be in absolute time or in percentage of the retention time of the addressed peak if the number is followed by %.

- **Min% and Max%** — These columns are used to respectively enter the low and the high limit expected for the limits flag of the specified element concentration percentage. To set the action that you want to perform when the limit value introduced was overcome, move the mouse pointer on the box related to the limit value (Min% or Max%) that has been entered, next right-click; in the visualized window you choose the action to do. See [Figure 45](#).

Figure 45. Action Window

Select among the following options the action that is wanted to perform in case of limit value overcoming.

- **None** — Selecting this option, only the limit overcoming is notified in the **Custom Report** page if the option **Custom Report** has been required, and the parameter **Limits flag** has been selected.
- **Stop Sequence** — Stops the acquisition of the samples.
- **Stop Sequence and Send Instrument to Stand-by** — The acquisition of the samples is stopped and the instrument goes in Stand-by condition.
- **Send Email** — Sends an e-mail to the address specified in the **Address (receiver)** box.
 - In the **Sender's Address** box insert the own address e-mail.
 - In the **Server SMTP** box insert the address of the server used for the dispatch of the mail.

Besides, it is possible to choose whether to send the Report text of the sample that has overcome the limits (**Send Report**), or to send a generic text typed in the area underlying the **Send Text** option.

- **Apply To** — Selecting this option the **Min%** and **Max%** limits are applied only to those samples whose Name contains the characters string **STD-CHECK** (see [Sample Table](#)). This option is useful for verifying that, after a certain number of analyses, the instrument is calculating the percentages within an acceptable tolerance of error.

Operate as follows:

- Introduce a sample of a known substance (standard) as an **Unknown** sample.
- Knowing the percentages that must have found from the instrument, set the opportune Min% limit.

Sample Table

This chapter provides information about the sequence of samples to be acquired and processed.

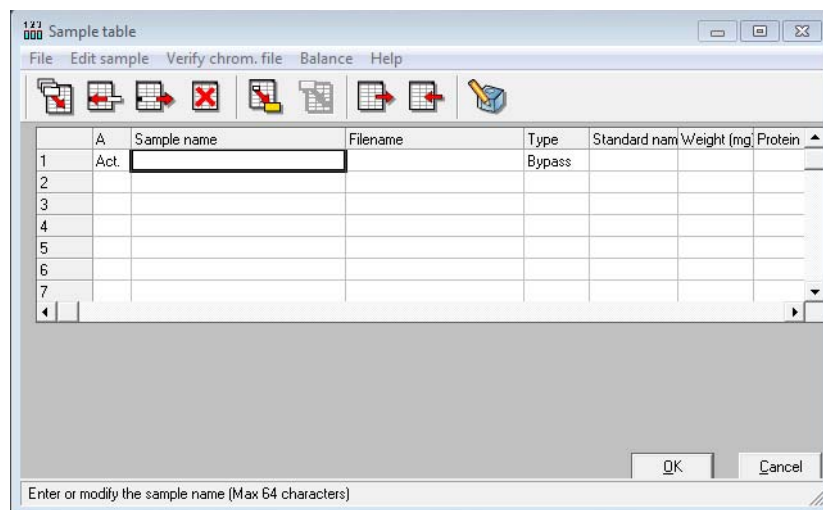
Contents

- [File Menu](#)
- [Edit Sample](#)
- [Verify Chromatogram Files](#)
- [Balance](#)
- [Edit Elemental Analyzer Method Icon](#)
- [Edit Sampler Parameters Icon](#)
- [Sample Table Input Box](#)
- [Sample Table Grid](#)

Introduction

Sample Table is the section of the analytical method that contains all the information about the sequence of samples to be acquired and processed. Select this function to enter the type of sample, name of sample, filename to store the chromatogram, file number, the vial for sampler, and many others parameters. See [Figure 46](#).

Figure 46. Sample Table



Icon	Description	See on:
	Fill Sample Table	page 74
	Insert Line	page 76
	Delete Line	page 76
	Clear Sample Table	page 76
	Copy Line(s)	page 78
	Paste Copied Line(s)	page 78
	Export Sample Sequence	page 78
	Import Sample Sequence	page 79
	Edit Elemental Analyzer Method	page 97 and Chapter 7
	Edit Autosampler Method Parameters (visualized if an autosampler for liquids is configured)	Chapter 8
Button	Description	
Cancel	Clears all modifications done in the current section. The program returns to Main Menu.	
OK	Confirms all modifications done in the current section. The program returns to Main Menu.	

Note All modifications are stored in the method currently in memory. You should use the **Save Method** command to save them permanently.

Sample Table provides the following functions:

File Menu

Includes the functions for selecting the **Print selected area** and for **Exit** from the Sample Table window.

Edit Sample

Gives the access to the functions for filling or deleting the Sample Table. You can select the following functions:

Fill Sample Table

The system automatically fills the following items. See [Figure 47](#).

Figure 47. Fill Samples Table Tab

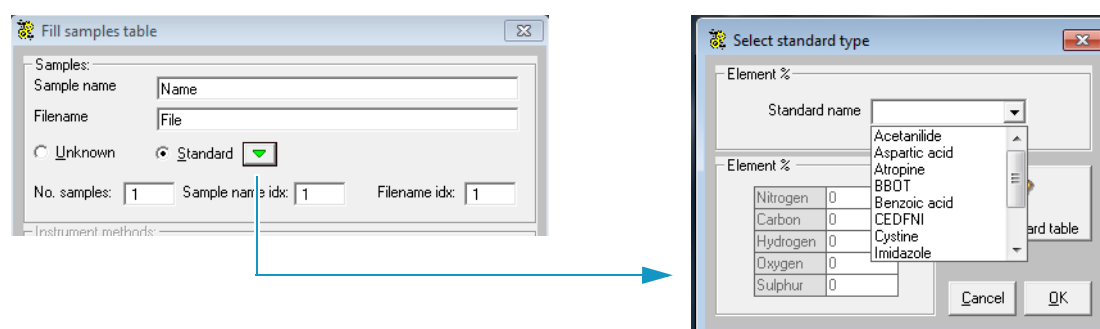
- The same number of lines as the **Number of Samples** which form the batch with a single value of **Weight**
- The **Sample Name**
- The **Filename** made by a root name and an increasing index

Furthermore, either in case you are determining the protein content, or/and you are using the autosampler for liquid samples, it also inserts the relative **Protein Factor**, or/and the relevant information concerning the **Autosampler Method** respectively. If the configuration of the instrument is **N/Protein**, select also **Category**.

Sample Box

In this box edit the following options:

- **Sample Name** — Enter the name of the sample.
- **Filename** — Enter the filename to be used to save the sample.
- **Unknown** — Select it when your sample is unknown.
It is suggested to keep this option button always ticked and to change the sample in the sample list.
- **Standard** — Select it when your sample is a standard. An arrow button appears as shown next:



Select standard type clicking the arrow button to enter the standard type dialog box. See “[Standard Name](#)” on [page 85](#).

- **No sample** — Enter the number of samples, up to 200, to be analyzed.
- **Sample name idx** — Leave it set as 1.
- **Filename idx** — Leave it set as 1.

Sampler box

Enter the parameters if the instrument is equipped with the AI 1310/AS 1310 or AI 3000/AS 3000 II autosampler for liquids.

- **AS Method** — Specifies the sampler method filename to be used for the addressed sample.
- **Repeat** — Sets how many time the AS Method must be repeated.
- **Increase Vial #** — Select it if the option is required.
- **Vial #** — Sets the number of the required vial.

Fill Sample Table Bottom Section

Enter the following parameters. See also [“Edit Elemental Analyzer Method Icon”](#) on [page 82](#).

- **Weight** — The weight is entered time by time. In case of direct injections of constant volumes, the sample volume can be entered directly.
- **Protein Factor** — Select this option only if the instrument configuration is N/Protein or N-Brew. For all other configurations set 0 (zero).
- **Category** — Select the **Category** to which the sample belongs only if the instrument configuration is N/Protein or N-Brew. For all other configurations this parameter is not edited. To enter the sample category, click the arrow. The Category tab is visualized.

For details see [Edit Elemental Analyzer Method Icon](#):

- [“OxyTune™ Function \(for FlashSmart and Flash 2000\)”](#) on [page 86](#) or
- [“OxyTune™ Function for Flash 4000”](#) on [page 87](#)

Buttons

- **Replace** — Replaces from the index line the sample parameters already edited with those from this table and escapes from the routine.
- **Add** — Inserts the edited parameters in this table after the last sample of the sample table.
- **Cancel** — Aborts the editing and escapes from the **Fill Sample Table**.

Insert Empty Line

Creates a room for a new sample. All samples beyond the table pointer are shifted by one position in order to create a new empty sample line.

Delete Line

Eliminates a sample from the table. All samples beyond the table pointer are shifted by one position in order to replace the erased sample line.

Clear Sample Table

Clears completely the sample table currently in memory.

Import Sample Table from LIMS

Imports the sample table generated from an external program or from a LIMS (Laboratory management system). *EagerSmart* can import a specific file format (Comma delimited) with extension *.lms.

The file format is the following:

- LIMS Sample Table for Eager Smart <CR> (*See Note 1*)
- 1,Name1,File1,Std, Acetanilide,1.03,6.28, SamplerMethod,1,-1<CR> (*See Note 2*)
- 2,Name2,File2,Std,Acetanilide,1.22,6.28, SamplerMethod,1,-1<CR>
- 3,Name3,File3,Std,Acetanilide,1.45,6.28, SamplerMethod,1,-1<CR>
- 4,Name4,File4,Unk,1,1.43,6.28, SamplerMethod,1,-1<CR>
- 5,Name5,File5,Unk,1,1.98,6.28, SamplerMethod,4,-1<CR>
- 6,Name6,File6,Std,Cystine,1.33,6.28, SamplerMethod,1,-1<CR>
- 7,Name7,File7,Unk,1,1.02,6.28, SamplerMethod,4,-1<CR>
- Standard table <CR> (*See Note 3*)
- 1,10.36,71.09,6.71,0<CR> (*See Note 4*)
- 2,10.36,71.09,6.71,0<CR>
- 3,10.36,71.09,6.71,0<CR>
- 6,26.69,11.66,29.99,5.03<CR>

Note 1: The file always starts with the message **LIMS Sample Table for Eager Smart <CR>** (CR = Carriage Return).

Note 2: The sample line is made by 10 fields divided by 9 commas and terminated with <CR>

- Field 1: Sample number in the range 1-200, the ascending order is not mandatory.
- Field 2: Sample name (0 to 16 ASCII characters).
- Field 3: Sample Filename for RAW data (0 to 8 ASCII valid Windows file characters).
- Field 4: Sample type (UNK for unknown samples or STD for calibration, BLK for blank, BYP for By-Pass).
- Field 5: Standard name (0 to 16 ASCII characters).
- Field 6: Sample Weight (single-precision floating-point).
- Field 7: Protein factor (single-precision floating-point).
- Field 8: Autosampler filename.
- Field 9: Vial number to be injected in the range 1-90 for AS800 or 1-200 for A200S
- Field 10: Not used, set to -1
- Fields 5,6 and 7 should be set to 1 when no value is entered.
- Fields 8,9 are only used if an autosampler is present otherwise the field is empty.

Note 3: The standard table always starts with the message **Standard table <CR>**.

- The standard table can be omitted even if sample table contains STANDARD samples.

Note 4: The standard line is made by (N+1) fields divided by (N) commas and terminated with <CR>

- (N) is the number of element in the standard mixture in the range 1-5.
- Field 1: This field contains the number of the sample to which the system assigns the standard concentrations. The number of the sample must correspond to an STD sample, otherwise an error importing file is generated.
- Field 2 to N+1: These fields contain the standard concentration of the element (1 to N) (single-precision floating-point). Copy Line(s) Icon.

Copy

EagerSmart copies one or more lines. Use **Paste** command to place the copied information into any place of the Sample Table. Moreover, most Windows™ applications use the Clipboard to transfer text, graphics, and other data. You can copy and move text from EagerSmart into different applications.

❖ To copy text between EagerSmart and another application:

1. Select the cells you want to copy.
2. From the **Edit** menu, choose **Copy**.
3. Switch to the other application.
 - a. If the other application is not open, start the other application.
 - b. If the other application is already open, press **CTRL+ESC**, then choose the application from the Task List.
4. Position the insertion point where you want to insert the text.
5. From **Edit** menu, choose **Paste** (ALT, E, P).

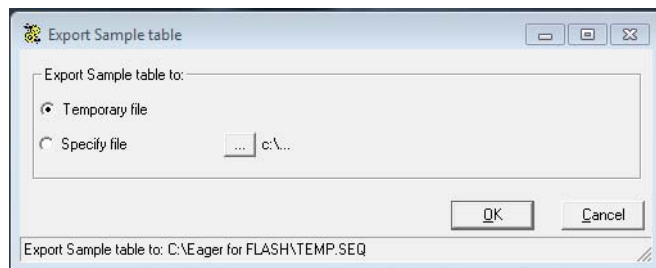
Paste

Use **Paste** command to place the copied information into any place of the Sample Table.

Export Sample Table

Exports into a file the parameters set in the Sample Table (Sample name, Filename, Type, and so on).

Figure 48. Export Sample Sequence



When an analytical sequence is being acquired and you are in Sample Table, the sample acquisition is frozen to be restored when Sample Table is left.

By using **Export Sample table** within *EagerSmart* started for an unused instrument, such as for instance **OFF-LINE Instrument #3** (see “[Starting EagerSmart](#)” on [page 5](#)), you can edit the Sample Table and export it to a file, while *EagerSmart*, started for the connected instrument, (for example **Instrument # 1**), and positioned on Main Menu, can continue sample acquisition without stopping. From time to time you can enter **Sample Table**, quickly update the Sample Table by using **Import Sample Table**, and go on with the acquisition.

The options are:

- **Temporary File** — Saves the sample sequence in the **Temp.seq.** file in the directory where *EagerSmart* is installed.
- **Specify File** — Saves the sample sequence in the file with name and directory to be set by clicking the [...] button.



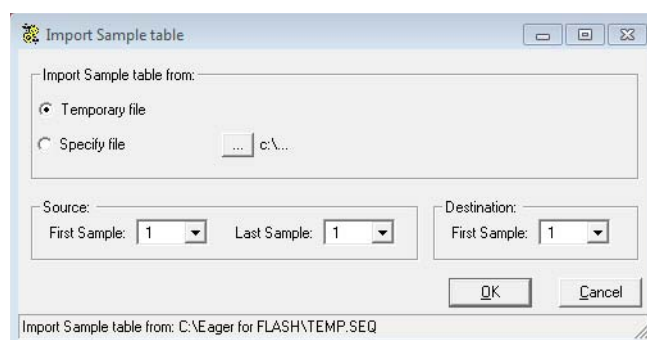
ATTENTION To have compatibility between the exported Sample Table and the imported Sample table, the configuration in **Analytical Instrument Configuration**, (see [Instrument Name and Configuration](#)), must be the same and the components entered in the **Component Table** must be the same.

Note With **Export sample sequence**, all parameters of all the table samples having at least a Sample name and a Filename are saved. Whereas with **Import sample sequence** you can choose which samples to import (First-Last).

Import Sample Table

Imports from a file the data of a sample sequence previously saved. See “[Export Sample Table](#)” on [page 78](#), and enters them into the current Sample Table. See [Figure 49](#).

Figure 49. Import Sample Sequence



The options are:

- **Temporary File** — Imports the sample sequence from the **Temp.seq** file, which is in the directory where *EagerSmart* is installed.
- **Specify File** — Imports the sample sequence from the file with name and directory selected clicking the [...] button.
- **First Sample** — When using **Export Sample Sequence**, all parameters of all the table samples having at least a **Sample Name** and a **Filename** are saved. Whereas, with **First Sample** you can choose from which sample to start importing parameters.

- **Last Sample** — When using **Export sample sequence**, all parameters of all the table samples having at least a **Sample Name** and a **Filename** are saved. Whereas, with **Last Sample** you can choose which should be the last sample for which parameters must be imported.
- **Destination First Sample** — Specifies from which sample of the current Sample Table the system starts entering the parameters of the imported samples.

Verify Chromatogram Files

Gives access to the functions to verify the existing chromatograms and to avoid overwriting. You can select the following functions:

Verify Existing Files

Verifies the entered filenames in the sample table. The system automatically verifies and prompts for a warning message in case any of the specified filename already exists on the hard disk.

View Files On Disk

Views the files existing on the hard disk.

Check Disk Space

Verifies the autonomy of the system before it runs out of disk space. Upon request of this function, the system calculates the available free space on disk. It gives the number of analyses you may run according to the acquisition parameters in memory, and the current sample sequence.

Enable Overwrite Chromatogram

Enables the system to overwrite chromatogram files before saving a new chromatogram automatically. It verifies if a chromatogram already exists, in that case the system adds two characters to the filename until a new unique name is found.

If you want to eliminate this automatic function, select it. *EagerSmart* writes the chromatogram even overwriting an existing one with the name you entered in the Sample Table. The two characters added are \$1 to \$9 added in front to the original name.

Show Disk Space On Exit

Verifies the autonomy of the system before it runs out of disk space. When this function is enabled, the system automatically performs the **Check Disk Space** when you make a modification of the Sample Table.

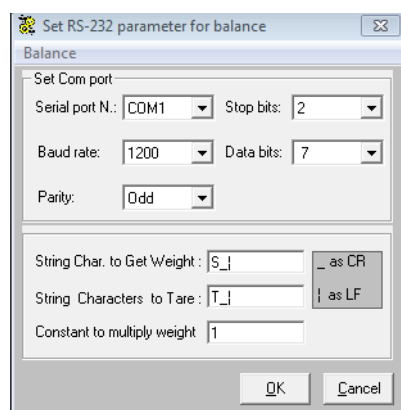
Balance

Allows to set up all the balance parameters according to the balance available in the system. Selecting this section, a pull-down menu with two options is visualized.

Balance Setup

Type in the required value for baudrate, data bits, stop bits, and other parameters relevant to the balance. See [Figure 50](#).

Figure 50. Set RS232 Parameter for Balance Tab

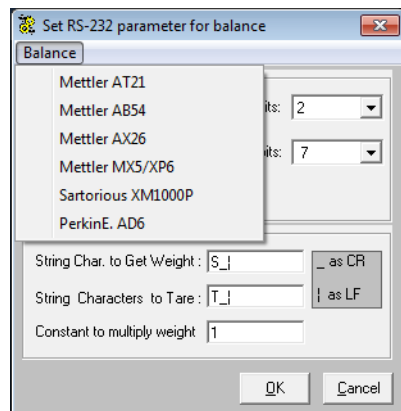


To edit these parameters refer to the instruction manual of the balance used.

Balance Menu

Use this menu to select the balance in use as shown in [Figure 51](#).

Figure 51. Balance Selection



The parameters to be compiled are the following:

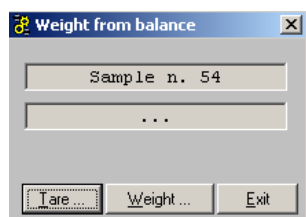
- **Serial Port N.** — Specifies the type of adapter to be used for communication COM1, COM2, COM3, and so on. To select, just move the cursor to the box entry, and left-click. A pop-up window shows the options (from COM1 to COM13). Do your choice by moving the cursor inside the option field, and left-clicking. The choice made is automatically entered.
- **Baudrate** — Selects the data transmission to/from the balance according to the balance used. There several possible baudrate values that suit any balance available in the market. Enters the value, move the cursor to the box entry, and left-click. From the pop-up window select the value compatible with the balance and left-click. The selected baudrate value is automatically entered.
- **Parity** — Enters the parity control according to the balance used. The types of parity are: **None**, **Even**, **Odd**, **Space**, and **Mark**. Refer to the balance instruction manual for further information.

- **Stop Bits** — Enters the number of stop bits according to the balance used. The number may be **1** or **2**.
- **Data Bits** — Enters the number of Data bits according to the balance used. The number may be any value between **4** and **8**.
- **String Characters To Get Weight** — Enters the code of characters recognized by the balance for weight acquisition. Refer to the instruction manual of the balance for code recognition.
- **String Characters To Tare** — Enters the code of characters recognized by the balance for tare acquisition. Refer to the instruction manual of the balance for code recognition.
- **Constant to multiply Weight** — Enters is the factor that multiplies the weight. Type in **1** (one) when no multiplication factor is required.

Receive Weight from Balance

Enables the computer to receive the weight from the balance through the RS232 serial port. When this function is selected, by clicking on a column weight box, the weight received from Balance menu is visualized. See [Figure 52](#).

Figure 52. Weight from Balance Tab



This menu features three commands:

- **Tare** — Sends to the balance the string characters to reset it when there is a capsule on its pan.
- **Weight** — Sends to the balance the string characters to get weight. Alternatively, it is possible to send the weight from the balance to the PC by using a proper balance key, for example **Print** key. The weight the balance has sent to the PC is entered in the Sample Table line corresponding to the sample reported in the first box of the receive weight from Balance menu. The program is now waiting for acquiring the next sample weight. The first box of the weight received from Balance menu shows a sample number increased by 1 unit in respect of the former one.
- **Exit** — Abandons the receive weight from balance section.

Note In case the type of the sample being weighed is not unknown or standard, the software abandons this pull-down menu.

Before starting to acquire the first weight from balance, we suggest to fill the Sample Table entering all required parameters as **Sample name**, **Filename**, **Type**, and so on.

Edit Elemental Analyzer Method Icon

Clicking the  icon, a dialog box is visualized to set temperatures and gas flows for the connected Elemental Analyzer. Once the parameters are set, they can be sent to the instrument. In case the instrument is already correctly set, the parameters can be loaded from the instrument and visualized in the window. See [Chapter 7, “Edit Elemental Analyzer Method,”](#) for details.

Edit Sampler Parameters Icon

The  icon is shown in the Sample Table if the autosampler for liquid samples has been configured in **Instrument Configuration**. See [“Instrument Name and Configuration”](#) on page 16. Clicking this icon, a dialog window is visualized to set the autosampler parameters. See [Chapter 8, “Edit Sampler Parameters,”](#) for details.

Sample Table Input Box

The new sample information can be entered in this box.

First — You should address the sample of interest clicking the mouse on the Sample Table grid in any column of the line.

Second — The cursor automatically addresses the input box ready to accept the new value. Once the new value has been entered and confirmed by pressing **Enter** key, the system updates the sample grid.

Alternatively — You can address the box by double-click. The system edits the previous content of the box.

Sample Table Grid

The grid contains all the information of the sample. Scroll up and down with the arrows located in the corners for showing the part of samples of interest. See [Figure 53](#)

Figure 53. Example of Sample Table Grid

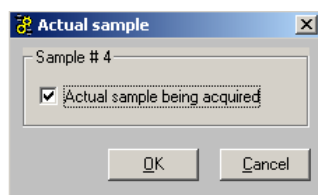
	A	Sample name	Filename	Type	Standard nam	Weight	Protein F.	Category	Sample Vial	Humidity %
1		blk	Formaggi5Mag08001	Unk		1	6.25	J		0
2		edita	Formaggi5Mag08002	Unk		1	6.25	E		0
3		pasta	Formaggi5Mag08003	Unk		1	6.25	F		0
4		cheese	Formaggi5Mag08004	Unk		1	6.25	G		0
5		cheese	Formaggi5Mag08005	Unk		1	6.25	G		0

The grid of the Sample Table includes the following parameters:

ID (Sample Being Acquired)

Contains the pointer to the Sample Table that indicates the sample being acquired. Select **Actual Sample Being Acquired** check box and click **OK**. See [Figure 54](#).

Figure 54. Actual Sample



The system uses the filename found at the corresponding line in the Sample Table to store the chromatogram data. If the filename field is not edited, the system integrates, and the report for the analyzed sample and the chromatogram is saved on hard disk with a default file name.

Sample Name

Contains the name of each sample being part of method. Enter up to 64 characters as a comment for the sample. EagerSmart calculates the variance on a standard sample. You can develop a method with up to 20 calibration levels. The last standard(s) can be used to calculate the deviation to the original standard concentrations. The standard, on which the variance calculation has to be performed, should contain the name **Variance** at any position in the **sample name**. In this case, the standard is not considered for calibration, instead the system calculates and reports the Variance.

$$\text{Variance} = \text{ABS} (C(i) - C_c(i)) / C_c(i) * XF$$

where:

C(i) = Standard concentration of component (i)

Cc(i) = Calculated concentration of component (i)

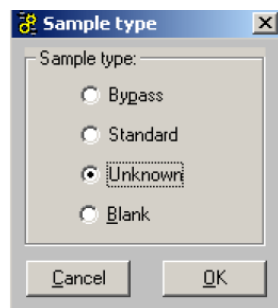
Filename

Contains the **filename** of each sample being part of the method. You can enter up to 8 characters to be used for storing the sample chromatogram on disk. See also [“Enable Overwrite Chromatogram”](#) on [page 80](#).

Type

Selects the type of sample. See [Figure 55](#).

Figure 55. Sample Type Selection



Clicking on this column, an arrow button appears. Clicking the arrow button you can select among the following options:

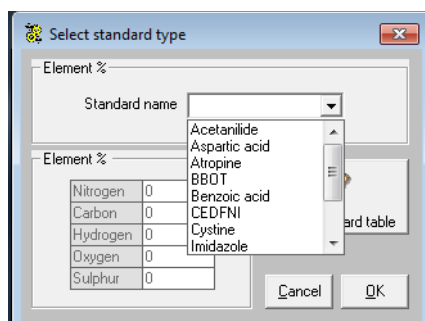
- **Bypass** — The weight of sample is not required when the FlashSmart, Flash 2000 and EA 1110 are used.
The weight of the sample is required when the Flash 4000 is used.
- **Standard** — Used for the calibration samples.
- **Unknown** — Used for all the unknown samples.
- **Blank** — Used for the analyses of samples considered as blank.
 - In case of FlashSmart and Flash 2000 in CHNS, NCS, and S configurations, the blank sample consists of a tin cup filled with **vanadium pentoxide**.
 - In case of Flash 4000, the blank sample consists of a tin cup filled with **glucose**.

EagerSmart processes the results according to the information provided from the sample type.

Standard Name

Selecting **Standard Name** box, then **Type** column box where a **Standard** has been entered, the **Select Standard Type Window** is visualized. See [Figure 56](#).

Figure 56. Select Standard Type



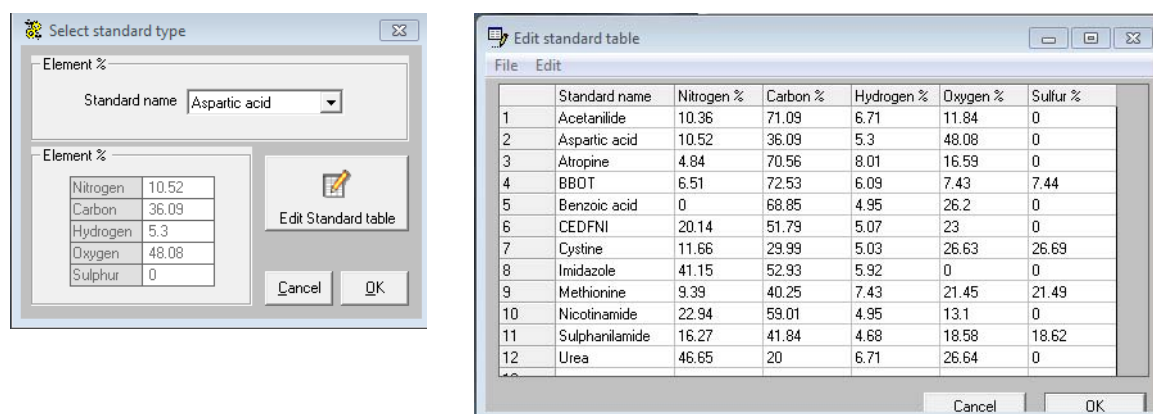
Standard Name

Choose in the **Standard name** list the **Standard** you are using and confirm clicking **OK**.

Edit Standard Table

In case the list does not feature the name of your standard, select **Edit Standard Table**. The **Edit Standard Table** is visualized. See [Figure 57](#).

Figure 57. Edit Standard Table



Add the new chemical and its composition to the standard list, and save the modifications. Now your standard is among those reported in the **Standard name** list, and you can select it to run your analysis.

Weight (mg)

Contains the sample weights. Selecting one of these boxes, you may type in the **Sample weight**. In case the [Receive Weight from Balance](#) option is selected (see [page 82](#)), the weight received from **Balance menu** is visualized.

Elemental%

Enters the elemental percentage information of the new standard.

First — You select the standard name in the proper list, so that the standard elemental composition is automatically loaded in the elemental% table.

Alternatively — Enter directly the elemental composition in the relative box by moving the pointer on it, and typing the proper elemental percentage.

The elemental percentage composition can be set to **zero** when the standard does not contain that element. Instead of “0”, the table shows the message **Not Used**.

Protein Factor

Contains the factor to perform the protein content in the sample. Type in the proper value just in case you have already set the Protein calculation in the [Calculation Parameters](#) menu on [page 51](#), otherwise this box is disabled.

OxyTune™ Function (for FlashSmart and Flash 2000)

This window, **available ONLY in Eager Smart for FlashSmart and Flash 2000 version**, allows to exactly dose the quantity of oxygen required for the best sample combustion, considering the category to which the product belongs (for example: Cheese/*Category A*, Cereals/*Category B*, Soil/*Category C*, and so on), and the weight of the sample to be analyze. See [Figure 58](#).

Figure 58. Window to Select the Sample Category for FlashSmart and Flash 2000)

	A	B	C	D	E
1	Forage	Cereals	Soil	Beer	Juice
2	Fodder	Pasta	Fertilizer	Milk	Ice Cream
3	Leaves	Flour	Milk	Ice Cream	
4	Tobacco	Meat	Ice Cream		
5	Cocoa	Cheese			
6	MilkPowder	Beans			
7		Starch			
8		Yeast			
9					
10					

This automatic dosing system is only used in **N/Protein** and **N Brew** configurations. See [“Instrument Name and Configuration”](#) on [page 16](#).

When the Sample Type is Unknown:

Clear the box **Use fixed oxygen quantity set for all samples marked @**.

According to the sample nature, select in the table the column of the category to which the sample belongs; columns A-B-C-D.

The column selection implies the selection of a multiplying factor which, together with the sample weight, determines the number of seconds of oxygen introduction into the **Carrier circuit**, and which corresponds to the injected oxygen quantity.

The seconds of oxygen injection are visualized on top of the table.

- if **Oxygen time** is zero, it means that the sample weight is too low.
- If the sample nature does not fit one of the four columns **A**, **B**, **C**, or **D**, the sample must be assigned to one of the columns **E**, **F**, **G**, or **H**, entering in the box a multiplying factor to be experimentally found.

When the Sample is Standard, Bypass, or Blank

Select the box **Use fixed oxygen quantity set for all samples marked @**.

The system injects oxygen for a fixed number of seconds written in the box below appearing when selecting this option. 30 seconds are generally set.

The table can be updated by entering in the boxes the names of unlisted substances.

The **Category** column of the Sample Table shows the letter of the column selected for the sample.

The symbol @ is assigned to all those samples not belonging to any category, and they are analyzed introducing the preset oxygen quantity.

OxyTune™ Function for Flash 4000

This window, **available ONLY in Eager Smart for Flash 4000** allows to exactly dose the quantity of oxygen required for the best sample combustion, considering sample matrix and sample weight. See Figure 59.

Figure 59. Window to Select the Sample Category for Flash 4000

The initial and final flows and the sampling delay can be modified. Selecting a specific category the Oxygen quantity is calculated according to the sample weight.



IMPORTANT Select the correct sample category to avoid an incomplete combustion (not enough oxygen) and the premature exhaustion of the copper.

- **Eight categories** can be choose in order to have a correct oxygen dosage for different sample matrices.
- **Three categories** are fixed while **five suggested categories** can be modified by the operator.

Fixed Categories	Suggested Categories
• Glucose	• Starch
• EDTA	• Cocoa
• Pasta, flours, beans, gluten, cereals	• Ham
	• Salame
	• Cheese

The selection is performed by clicking the category of interest, or by typing in the Sample Table the letter of the categories chosen. It is possible to develop a specific category for special samples not included in the previous categories.

❖ To develop a specific Category

Note This operating sequence gives you a general indication to set the correct category according to the sample nature.

The parameters are:

- **Flows** — Flow 1 and Flow 2 are the flows of oxygen. Both can assume the following values: 0.125, 0.250, 0.500, 0.750, 1.000, 1.250, 1.500 L/min (*liters/minute*).
 - *If the sample is rich in fat:*
For these samples it is suggested to set a high enough flow of Oxygen, for example 0.750 L/min.
 - *If the sample is rich in water:*
For these samples the combustion is easy. It is suggested to set a low flow of oxygen and an high **Oxygen Delay** time, for example 25 s.
- **Time Ratio** — Ratio between Time 1 (Flow 1) and Time 2 (Flow 2).
- **Oxygen Caps** — Quantity of Oxygen, in liters, required to oxidize the tin caps. For the 63-mm tin caps it is 0.1 liters.
- **Oxygen Sample** — Quantity of oxygen required to oxidize one gram of sample.
- **Oxygen Delay** — When this time is elapsed, oxygen is injected into the circuit.
- **Purge** — Duration of the sample purge. It depends on the concentration of nitrogen in the sample. If the percentage of nitrogen in the sample is lower than 0.5%, it is suggested to set **Trace Purge**, otherwise the **Standard Purge** is used.
- **Density** — Only available if the autosampler for liquid samples has been configured in Instrument Configuration. See “[Instrument Name and Configuration](#)” on [page 16](#).
Here you must specify the density of the liquid sample. *EagerSmart* corrects the weight in function to the density entered.

A **combustion set-up** is accessible from the Sample Table to help you in the choice of the analytical conditions according to the nature of the sample.

❖ To set up the combustion

1. Open the Sample Table as shown in [Figure 60](#).

Figure 60. Sample Table (1)

	A	Sample name	Filename	Type	Standard nam	Weight (mg)	Protein F.	Category	Sample Vial	Humidity %
1		Mas 4000	test \XL001	Bypass		1		A		0
2		Mas 4000	test \XL002	Bypass		1		A		0
3		Mas4000	test \XL003	Bypass		1		A		0
4		Glucose Blank	test \XL004	Bypass		1002.007		A		0
5		Glucose Blank	test \XL005	Blank		999.51		A		0
6		EDTA	test \XL006	Bypass		502.466		B		0
7		EDTA	test \XL007	Std	EDTA	499.35		B		0
8		EDTA	test \XL008	Std	EDTA	506.363		B		0
9		EDTA	test \XL009	Std	EDTA	507.774		B		0
10		Pasta	test \XL010	Unk		1000.05	6.25	C		0
11		Pasta	test \XL011	Unk		1001.06	6.25	C		0
12	Act.	Pasta	test \XL012	Unk		1000.975	6.25	C		0
13										

- In the **Category** column click the **green arrow**. The window of Figure 61 is visualized.

Figure 61. OxyTune Window (1)

- Click **Combustion Set-up**. The window of Figure 62 is visualized.

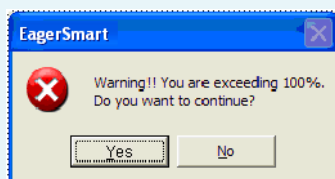
Figure 62. Combustion Assistant Window

- If you know the **nutritional composition** of your sample, select **Nutritional composition** then type proteins, carbohydrates, fibers, fat, and humidity values in the proper box. An algorithm calculates Oxy, Flow 1, Flow 2, Oxy delay, and Purge values suggested for the analysis.
- If you know the **elemental composition** of your sample select **Elemental composition**, then type H, C, S, O, and N percentage values. An algorithm calculates the condition of combustion suggested.

- Click **Calc.** to perform the calculation of the analytical condition.

ATTENTION

If the sum of the percentage values typed are higher than 100%, the following message is visualized:



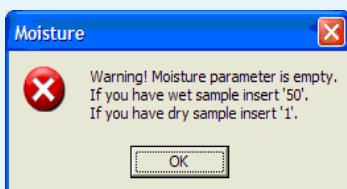
Message 1

Click Yes or No according to your proper answer.



The value of **Oxygen Delay** to use depends on the **Moisture** parameter. Usually Oxygen Delay used is 7 s for dry samples and 25 s for wet samples.

If **Moisture** box is empty, the following message is visualized:



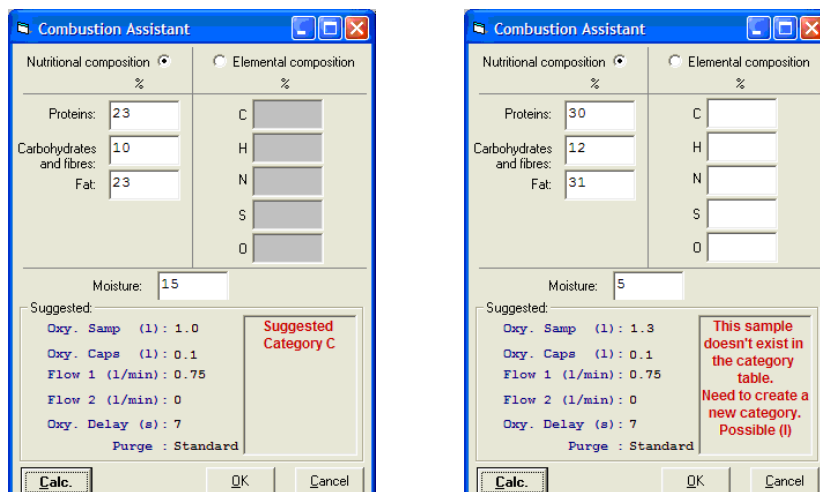
Message 2

Insert the value as suggested in the message.

If you insert a value of 50 for moisture, and the total composition exceeds 100%, the warning message appears. Ignore this message and click **OK** to continue.

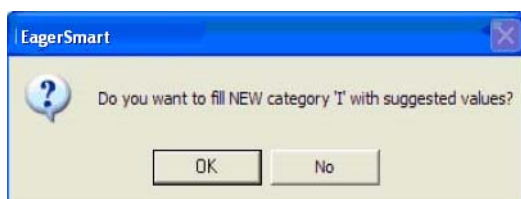
Figure 63 shows an example of calculation.

Figure 63. Example of Analytical Condition Calculation



- If the **analytical parameters are already present** in the Sample Table, **Combustion set-up** suggests to use one of the existing categories. If you desire using the category suggested (in the example the category is C), click **OK**. The category is selected automatically.

If the **category does not exist**, you need to create a new one. Click **OK** if you desire to use the analytical condition suggested by **Combustion set-up**. A free column is available to be filled, and a message as the follows is visualized. Category **I** is reported in the example.



- Clicking **OK**, the column indicates in the example is automatically filled with the calculated analytical condition.
- Click in the column **I** and type the name of the sample in exam, (for example **Chicken**), as shown in the example of [Figure 64](#).

Figure 64. Oxy Tune Window (2)

OxyTune: Automatic Oxygen Dosing

This window provides the sample nature selection for automatic calculation of the oxygen quantity needed for optimal combustion.

Sample # 12 Type Unk Weight (mg): 1000.975

Automatic Oxygen quantity:

Category **I**

Flow 1 (l/min): 0.75 Time 1 (s): 112 Oxy Delay (s): 7

Flow 2 (l/min): 0 ☒ Off Time 2 (s): 0 Purge: Standard

Oxy. Caps (l): 0.1

Oxy. Samp (l): 1.3 Time Ratio: 0

	E	F	G	H	I
1	COCOA	HAM	SALAME	CHEESE	CHICKEN
2					
3					
4					
5					
6					
7					
8					
9					
10					

Combustion Flow 1 = 0.75 Oxy.Caps = 0.1
Set-up Flow 2 = 0 Oxy.Samp = 1.3
Purge = Standard Oxy.Delay = 7

OK Cancel

- Click **OK**, category **I** is shown in the Sample Table as shown in [Figure 65](#).

Figure 65. Sample Table (2)

Standard nam	Weight (mg)	Protein F.	Category	Sar
EDTA	499.35		B	
EDTA	506.363		B	
EDTA	507.774		B	
	1000.05	6.25	C	
	1001.06	6.25	C	
	1000.975	6.25	I	

ATTENTION If all the categories are filled, the following message appears: Click **OK**, Oxy Tune page indicates the suggested conditions, but it is necessary to replace the condition values of one category, and type the new sample name.



Sampler Method

The autosampler method column is only available if the autosampler for liquid samples has been configured in **Instrument Configuration**. See [Instrument Name and Configuration](#) on page 16.

You must specify the sampler method filename to be used for the addressed sample. See [“Edit Sampler Parameters Icon”](#) on page 83.

Vial

Vial column is only available if the autosampler for liquid samples has been configured in Instrument Configuration. See [“Instrument Name and Configuration”](#) on page 16.

You must specify the vial position of the addressed sample (1 to 90, or 1 to 200 according to the type of sampler in use). See [“Edit Sampler Parameters Icon”](#) on page 83.

Humidity

Specifies the percentage of humidity present in the sample.

Wizard Method Development

This chapter provides the instructions for developing the various methods.

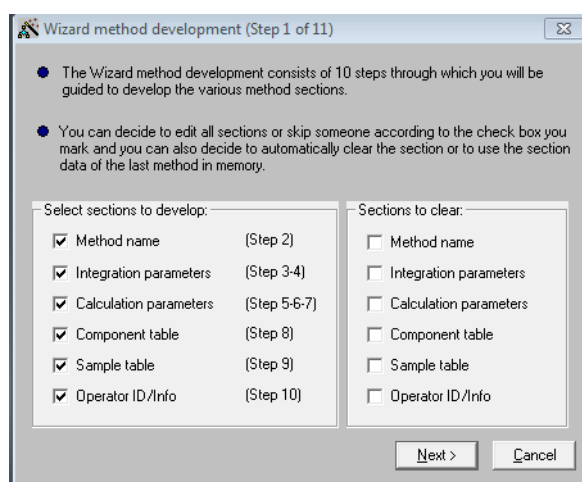
Contents

- [Function Description](#)

Function Description

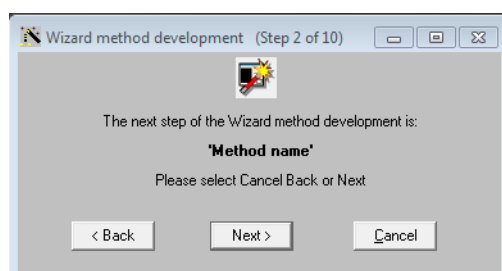
Wizard Method Development allows you to be lead by the system to entirely develop the analytical method. See [Figure 66](#).

Figure 66. Wizard Method Development



An experienced user probably goes directly to the module where a change is needed. For beginners, or when generating a new method, this function helps in entering the different module sections in the right order, and forces to set all parameters used for acquisition, calculation, and reporting. See [Figure 67](#).

Figure 67. Wizard Method Development Step 2 "Method Name"

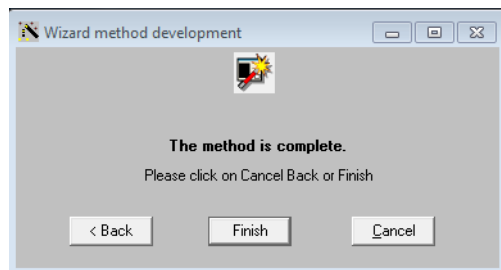


The method development is automatically:

- Interrupted by clicking **Cancel** while leaving a module.
- Continued by clicking **Next >** or **< Back**.

At the end of the method development, the following page is visualized. See [Figure 68](#).

Figure 68. Wizard Method Development Last Step



Click **Finish** to exit.

Edit Elemental Analyzer Method

This chapter provides the instructions for setting the parameters for Flash*Smart*, Flash 2000, Flash 4000, and EA 1110 (USB-A/D) Elemental Analyzer versions.

Contents

- [Edit Flash*Smart*/Flash 2000 Elemental Analyzer Method](#)
- [Edit Flash 4000 Elemental Analyzer Method](#)
- [Edit EA 1110 Elemental Analyzer Method](#)

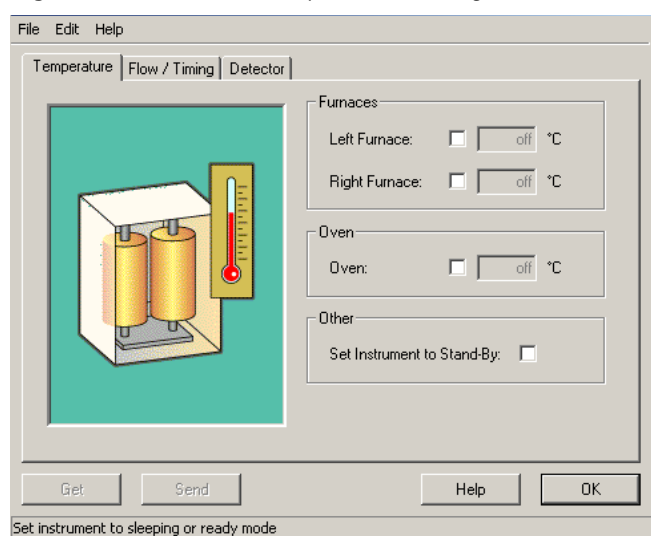
Edit Flash*Smart*/Flash 2000 Elemental Analyzer Method

This section provides information for setting the parameters for Flash*Smart* and Flash 2000 Elemental Analyzers ([Eager*Smart*](#) for FLASH versions).

Introduction

The dialog window shown in [Figure 69](#) sets temperatures and gas flows for the analyzer connected.

Figure 69. Elemental Analyzer Method Page for Flash*Smart* and Flash 2000



Once the parameters are set, they can be sent to the instrument clicking **Send**.

In case the instrument is already correctly set, the parameters can be loaded from the instrument clicking **Get**, and visualized in the window.

The method page is subdivided into three tabs:

- **Temperature**, see [page 98](#)
- **Flow/Timing**, see [page 99](#)
- **Detector**, see [page 100](#)

All the tabs have the following buttons:

Button	Description
Get	Loads the method parameters from the instrument.
Send	Sends the method parameters to the instrument.
Ok	Confirms all modifications done in the current tab. The program returns to the previous tab.
Help	Opens help instruction.

All the parameters can be saved and loaded into a file with extension ***.eam**. This file is also memorized with *EagerSmart* global method with extension ***.mth**.

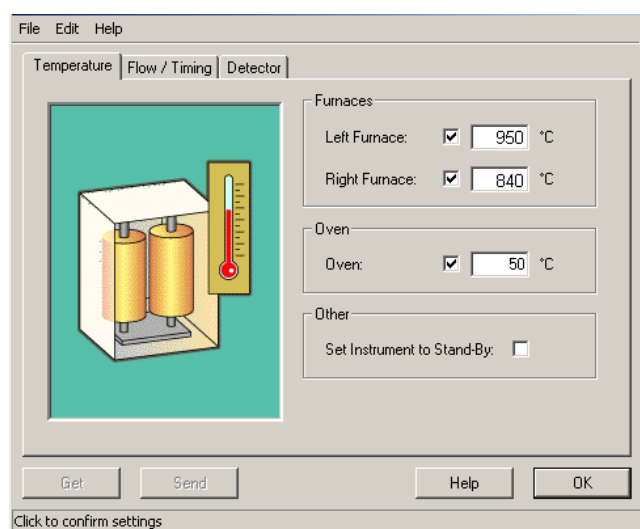
Every time a method with extension ***.mth** is loaded from Main Menu, *EagerSmart* checks if a file with extension ***.eam** has been stored with the method. The system asks whether to send the parameters to the instrument or not.

By clicking **Send parameters to analyzer**, the parameters present in the file with extension ***.eam** are transferred to the instrument. Before running analyses, wait for the instrument to reach the new temperature values.

Temperature

Temperature tab is shown in [Figure 70](#).

Figure 70. EAM Parameters of FlashSmart/Flash 2000 (1)



This tab comprises the following fields:

Furnaces

Set a temperature between 400 °C for **Left furnace** and 1100 °C for **Right furnace**.
If a furnace is not used, clear the relevant box; the furnace is put to **Off**.

Oven

Set a temperature between 40 °C and 190 °C for **Oven**.
If the gas chromatographic column inside the Oven is not used, clear the box; the oven is put to **Off**.

Other

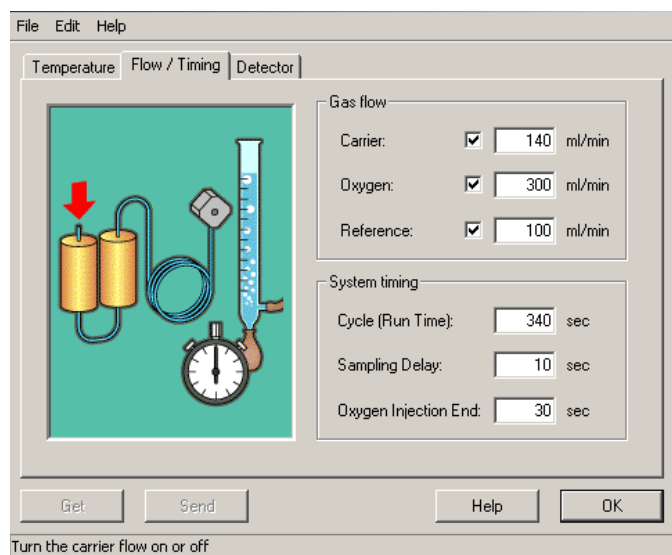
When the instrument is not used for long time, decrease the temperature of the furnaces to save power and extend their life, and also to decrease gas flows to reduce consumption. To do that, select **Set Instrument to Stand-by** box.

Note When a temperature value or the Stand-by condition are changed, nothing occurs inside the instrument until the **Send** button is clicked.
Click **Get** if you want to import into the FLASH Method window the temperatures set in the instrument.

Flow/Timing

Flow/timing tab is shown in [Figure 71](#).

Figure 71. EAM Parameters of FlashSmart/Flash 2000 (2)



This tab comprises the following fields:

Gas Flow

Set a gas flow between 10 mL/min and 300 mL/min for **Carrier**, **Oxygen** and **Reference** gas. To cut off a gas flow, clear the relevant box.

System Timing

This field includes the following functions:

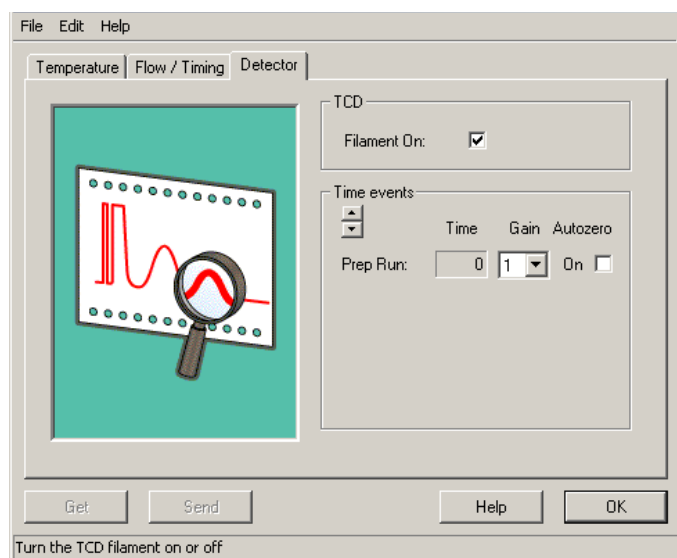
- **Cycle (Run Time)** — Sets a time in seconds between 0 and 1200. The system acquires the chromatogram points within this total time.
- **Sampling Delay** — Sets a time in seconds between 0 and 150.
This time is the delay given to the sampling from the start of oxygen introduction. This delay allows to have the sample fall into the combustion reactor just when oxygen reaches the reactor itself.
- **Oxygen Injection End** — Sets a time in seconds between 0 and 150.
This time defines the end of oxygen injection into the pneumatic circuit. Oxygen must be introduced only for the time required to a good “**FLASH**” combustion and no longer, since oxygen oxidizes copper in the reduction reactor.
In the N/Protein configuration this time is automatically calculated by *EagerSmart* to dose the oxygen amount according to the sample nature and the weight. See “*OxyTune™ Function (for FlashSmart and Flash 2000)*” on page 86.

Note When a flow or time value is changed, it is not transmitted to the instrument until **Send** is clicked. If you want to import temperatures and times already set in the instrument, click **Get**.

Detector

Detector tab is shown in [Figure 72](#).

Figure 72. EAM Parameters of FlashSmart/Flash 2000 (3)



This tab comprises the following field:

TCD

To turn off the filaments of the Thermal Conductivity Detector, clear the box **Filament On** and click **Send**.

During acquisition at a preset time, **Time Event** option amplifies the signal sensitivity by 10 times (**Gain x10**). This can be useful when the percentage of an element present in the sample is very low (traces).

In the **Time box**, set a value in seconds which defines the moment of the gain change. In the **Gain box** select 1 or 10. Select the box **Autozero** if you want to force the signal autozero at the gain change.

When more than one **Gain** change is required, click the **Down Arrow** to add another line of Time Events.

To cancel a line of Time Events, click the **Up Arrow**.

Note Whereas all parameters of the FlashSmart or Flash 2000 Method window can be sent to the instrument memory by clicking Send, the **Time Events** parameters are only managed inside *EagerSmart*. Therefore, Time Events is not part of the data bank stored in the analyzer.

When a new method (*.mth or *.eam) is loaded, **Time Events** function is automatically modified.

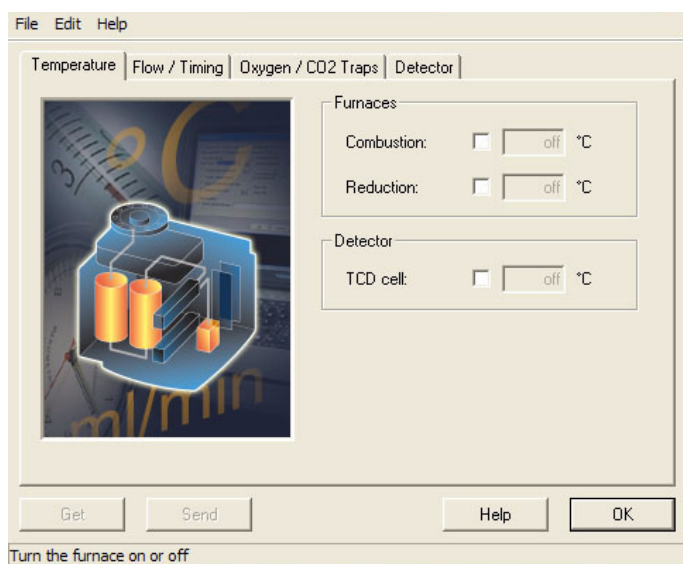
Edit Flash 4000 Elemental Analyzer Method

This section provides information for setting the parameters of the Flash 4000 Elemental Analyzer (*EagerSmart* for FLASH versions).

Introduction

The dialog window shown in [Figure 73](#) allows sets temperatures, gas flows for the connected Flash 4000.

Figure 73. EAM Elemental Analyzer Method Page for Flash 4000



Once the parameters are set, they can be sent to the instrument clicking **Send** button.

In case the instrument is already correctly set, the parameters can be loaded from the instrument clicking **Get** button, and visualized in the window.

The Flash 4000 Method is subdivided into four tags:

- **Temperature**, see [page 102](#)
- **Flow/Timing**, see [page 103](#)
- **Oxygen/CO₂ Traps**, see [page 104](#)
- **Detector**, see [page 105](#)

All the tags have the following buttons:

Button	Description
Get	Loads method parameters from the instrument.
Send	Sends method parameters to the instrument.
Ok	Confirms all modifications done in the current tab and the program returns to the previous tab.
Help	Opens help instruction.

All parameters can be saved and loaded into a file with extension ***.eam**. This file is also memorized with *EagerSmart* global method with extension ***.mth**.

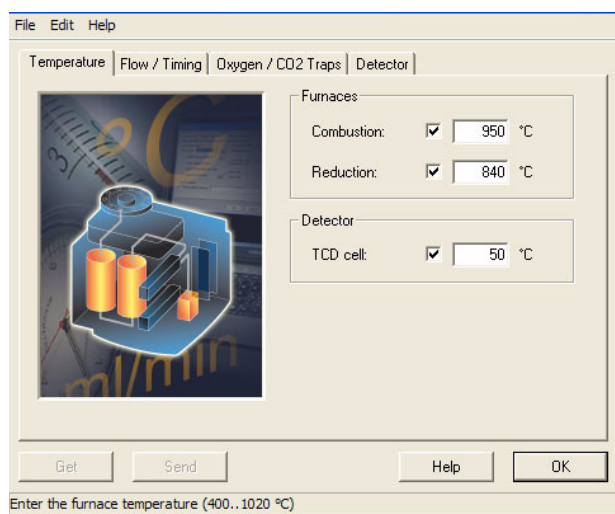
Every time a method with extension ***.mth** is loaded from the Main Menu, *EagerSmart* checks if a file with extension ***.eam** has been stored with the method. The system asks whether to send the parameters to the instrument or not.

Clicking **Send parameters to analyzer**, the parameters present in the file with extension ***.eam** are transferred to the instrument. Before running analyses, wait for the instrument to reach the new temperature values.

Temperature

Temperature tab is shown in [Figure 74](#).

Figure 74. EAM Elemental Analyzer Method Page (1)



This tab comprises the following fields:

Furnaces

Select the relevant check box to enable the **Combustion** and **Reduction** furnaces temperature control and the relevant text box. In the relevant text box set a temperature between 400 °C and 1200 °C.

To put a furnace to **Off**, clear the relevant check box.

Detector

Select this box to enable the **TCD cell** temperature control and the relevant text box. Set a temperature between 40°C and 190°C. To put the TCD cell to **Off**, clear the check box.

Note When a temperature value or the Stand-by condition are changed, nothing occurs inside the instrument until **Send** is clicked.
If you want to import into the Flash 4000 Method window the temperatures set in the instrument, click **Get**.

Flow/Timing

Flow/Timing tab is shown in [Figure 75](#).

Figure 75. EAM Elemental Analyzer Method Page (2)

This tab comprises the following fields:

Carrier

Select the **Carrier On** check box to enable the carrier gas control and the flow text box. In the Flow text box set a flow rate between 10 and 500 mL/min.

To put the carrier gas to **Off**, clear the relevant check box

In the **Pulse time** text box set a time between 0 and 999 seconds. After oxygen introduction, the carrier goes to full scale (500 mL/min) for the time set in this text box. Pulse time restores the pressure of the system as soon as possible for the combustion.

Reference On

Select the **Reference On** check box to enable the reference gas control and the Flow text box. In the **Flow** text box set a flow rate between 10 mL/min and 500 mL/min. To put the reference gas to **Off**, clear the relevant check box.

System Timing

This field includes the following functions:

- **Cycle Run Time** — Sets a time in seconds between 0 and 3600. The system acquires the chromatogram points within this total time.
- **Sampling Delay (-) Oxy Delay (+)** — This time is the delay given to the sampling from the start of oxygen introduction. This delay allows to have the sample fall into the combustion reactor just when oxygen reaches the reactor itself.

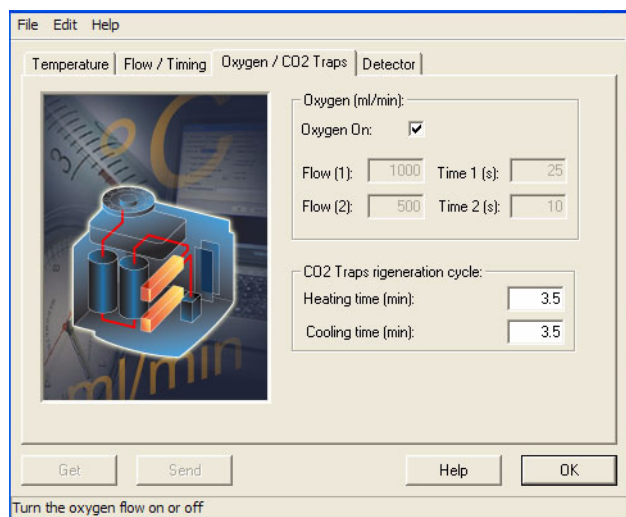
Note When a temperature value or the Stand-by condition are changed, nothing occurs inside the instrument until **Send** is clicked.

If you want to import into the Flash 4000 Method window the temperatures set in the instrument, click **Get**.

Oxygen/CO₂ Traps

Oxygen/CO₂ tab is shown in [Figure 76](#).

Figure 76. EAM Elemental Analyzer Method Page (3)



This tab comprises the following fields:

Oxygen

The **Oxygen On** check box is always selected Both the **Flow** and **Time** text boxes are not editable.

The **Flow 1** and **Flow 2** check boxes visualizes the initial and the final oxygen flows respectively. The flow range is from 0 to 150 seconds.

The **Time 1** and **Time 2** check boxes visualizes the duration of the initial and the final oxygen flows. The range is from 200 mL/min to 1500 mL/min.

CO₂ Traps Regeneration Cycle

This field includes the following functions:

- **Heating Time** — Sets an On time between 3.5 to 9.9 minutes. This time defines the heating time (On) duration of the traps regeneration cycle.
- **Cooling Time** — Sets an Off time between 3.5 to 9.9 minutes. This time defines the heating time (Off) duration of the traps regeneration cycle.

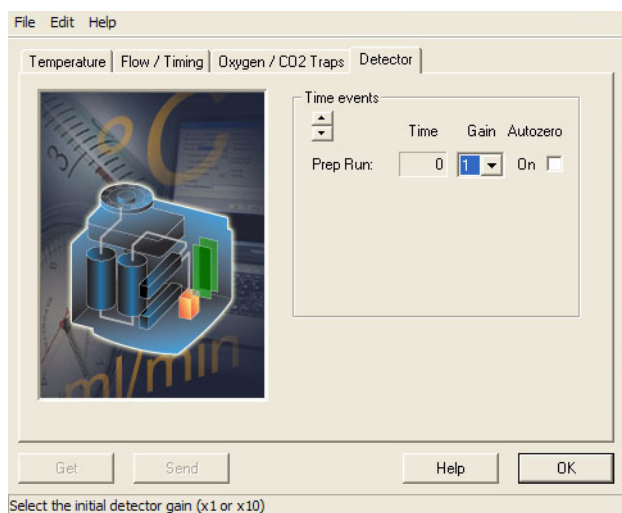
Note When a temperature value or the Stand-by condition are changed, nothing occurs inside the instrument until the **Send** button is clicked.

If you want to import into the Flash 4000 Method window the temperatures set in the instrument, click **Get**.

Detector

Detector tab is shown in [Figure 77](#).

Figure 77. EAM Elemental Analyzer Method Page (4)



This tab comprises the following field:

Time Events

During acquisition at a preset time, **Time Event** option amplifies the signal sensitivity by 10 times (**Gain x10**).

Useful when the percentage of an element present in the sample is very low (traces).

- In the **Time** box set a value in seconds which defines the moment of the gain change.
- In the **Gain** box select 1 or 10. Select the **Autozero** box if you want to force the signal autozero at the gain change.

When more than one **Gain** change is required, click **Down Arrow** to add another line of Time Events. To cancel a line of Time Events, click **Up Arrow**.

Note Whereas all parameters of the Flash 4000 Method window can be sent to the instrument memory by clicking Send, the Time Events parameters are only managed inside *EagerSmart*, and therefore Time Events is not part of the data bank stored in Flash 4000. When a new method is loaded (xxxx.mth or xxx.eam), Time Events function is automatically modified.

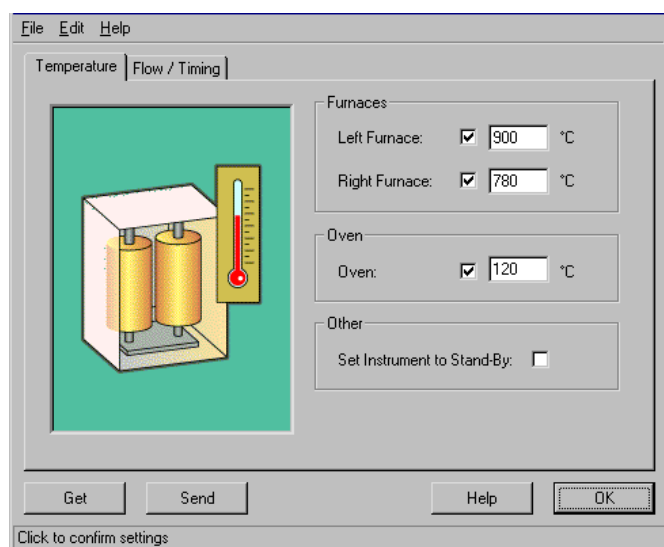
Edit EA 1110 Elemental Analyzer Method

This section provides information for setting the parameters of the EA 1110 Elemental Analyzer (*EagerSmart* USB and A/D version).

Introduction

The dialog window shown in [Figure 78](#) sets temperatures and gas flows for the connected EA 1110.

Figure 78. EAM Elemental Analyzer Method Page for EA 1110



Once the parameters are set, they can be sent to the instrument clicking **Send** button.

In case the instrument is already correctly set, the parameters can be loaded from the instrument clicking **Get** button, and visualized in the window.

The EA 1110 Method is subdivided into two tags:

- **Temperature**, see [page 107](#)
- **Flow/Timing**, see [page 108](#)

All the tags have the following buttons:

Button	Description
Get	Loads method parameters from the instrument
Send	Sends method parameters to the instrument.

Button	Description
Ok	Confirms all modifications done in the current tab, and the program returns to the previous tab.
Help	Opens help instruction.

All parameters can be saved and loaded into a file with extension *.eam. This file is also memorized with EagerSmart global method with extension *.mth.

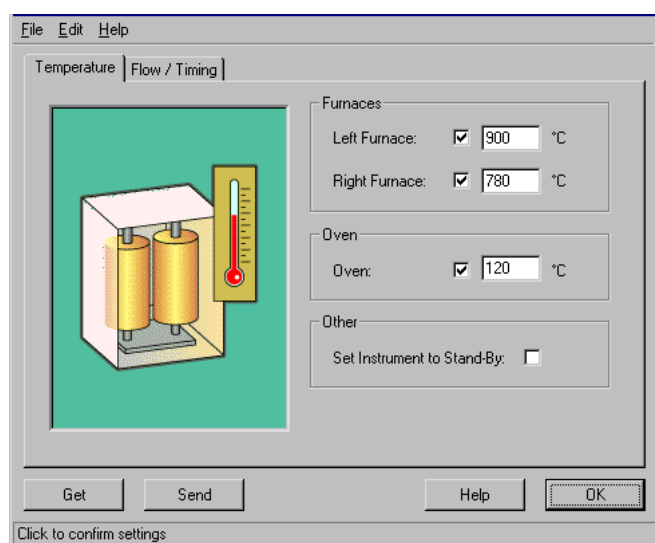
Every time a method with extension *.mth is loaded from the Main Menu, EagerSmart checks if a file with extension “.eam” has been stored with the method. The system asks whether to send the parameters to the instrument or not.

Clicking **Send parameters to analyzer**, the parameters present in the file with extension *.eam are transferred to the instrument. Before running analyses, it is necessary to wait for the instrument to reach the new temperature values.

Temperature

Temperature tab is shown in Figure 79.

Figure 79. EAM Elemental Analyzer Method Page for EA 1110 (1)



This tab comprises the following fields:

Furnaces

Set a temperature between 400 °C and 1100 °C for **Left** and **Right** furnaces. If a furnace is not used, clear the relevant box, and the furnace is put to **Off**.

Oven

Set a temperature between 50 °C and 190 °C for **Oven**. If the gas chromatographic column inside the Oven is not used, clear the box, and the Oven is put to **Off**.

Other

When the instrument is not used for long time, it is possible to decrease the temperature of the furnaces to save power and extend their life, and also to decrease gas flows to reduce consumption: to do that, select the box **Set Instrument to Stand-by**.

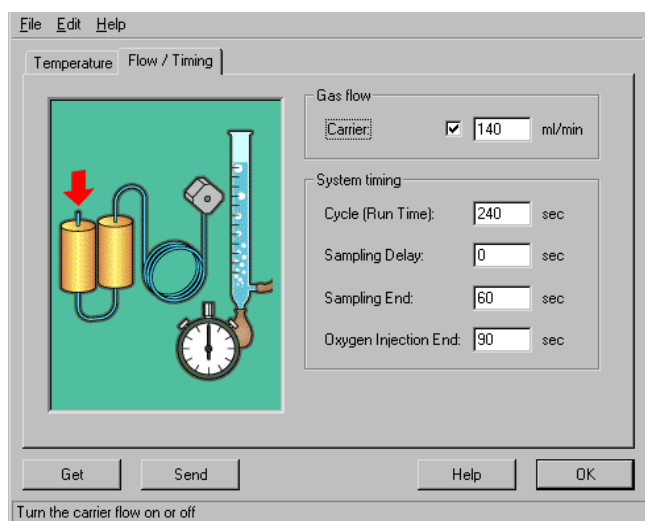
Note When a temperature value or the Stand-by condition are changed, nothing occurs inside the instrument until **Send** is clicked.

If you want to import into the EA 1110 Method window the temperatures set in the instrument, click **Get**.

Flow/Timing

Flow/Timing tab is shown in [Figure 80](#).#

Figure 80. EAM Elemental Analyzer Method Page for EA 1110



This tab comprises the following fields:

Gas Flow

Set a gas flow between 10 mL/min and 300 mL/min for **Carrier**, **Oxygen** and **Reference** gas. To cut off a gas flow, clear the relevant box.

System Timing

This field includes the following functions:

- **Cycle (Run Time)** — Gives you the possibility to change the analytical cycle modifying the value of Cycle Time. Normally set this value lower to **Analysis Time** parameter in **Detector Parameters** page. See "[Analysis Duration Box](#)" on [page 48](#).
- **Sampling Delay** — Sets a time in seconds between 0 and 150.
This time is the delay given to the sampling from the start of oxygen introduction. This delay allows to have the sample fall into the combustion reactor just when oxygen reaches the reactor itself.

- **Sampling End** — Specifies the sample end time. After this time, It allows the autosampler to be ready for the next sampling. Set a time in seconds higher than the **Sampling Delay** time.
- **Oxygen Injection End** — Sets a time in seconds between 0 and 150 (normally 60). This time defines the end of oxygen injection into the pneumatic circuit.

Note When a flow or time value is changed, it is not transmitted to the instrument until **Send** is clicked. If you want to import temperatures and times already set in the instrument, click **Get**.

Edit Sampler Parameters

This chapter provides instructions for setting the parameters for the AI 1310/AS 1310 and AI 3000/AS 3000 II autosampler for liquid samples.

Contents

- [Introduction](#)
- [User Interface](#)
- [Menus Description](#)
- [Evaluate Injection Delay](#)

Introduction

The functions of the autosampler are controlled and programmed through a data system provided by *EagerSmart* installed in the computer, and interfaced with the instrument via serial line RS 232.

This paragraph describes the user interface to program the instrument operating parameters.

User Interface

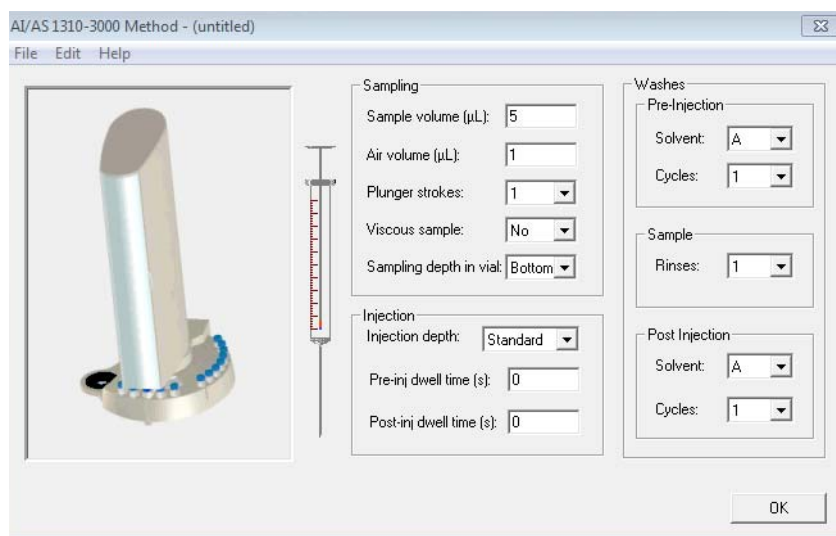
The user interface, shown in the example of [Figure 81](#), is the same for both the AI 1310/AS 1310 and AI 3000/AS 3000 II autosamplers for liquid samples.

The AS 2000 autosampler has a proper user interface.

Set in this page the parameters required for the correct control of the autosampler according to the used syringe and the sample nature.

Note The page is visualized after that an autosampler for liquids has been selected in the Configuration page.

Figure 81. User Interface for AI 1310/AS 1310 and AI 3000/AS 3000 II



The user interface is subdivided into four sections.

Sampling

In this field the autosampler parameters can be set.

- **Sample Volume (μL)** — Specifies the sample volume to be injected as a function of the syringe installed.
 - With a 10 μL syringe, choose a value between 0 and 5 μL in steps of 0.1 μL.
 - With a 250 μL syringe, choose a value between 0 and 125 μL in steps of 5 μL.

It is also possible to use 50 μL and 100 μL syringes.

- **Plunger Strokes** — Specifies the number of plunger strokes to eliminate air bubbles forming during sample drawing. Set a value 0 to 15.
- **Viscous Sample** — Defines the sample drawing speed as a function of the sample viscosity. Choose one of the following options:
 - **No** if the sample has low viscosity (default value).
 - **Yes** if the sample has high viscosity.
- **Sampling Depth in Vial** — Specifies the penetration depth of the syringe needle into the vial. Set the parameter choosing one of the following options:
 - **Bottom** (default value) — The needle goes down to the vial bottom.
 - **Center** — The needle goes down to half vial. Select **Center** if the sample vial may contain solid residues on the bottom.

Injection

In this field the injection parameters are selected.

- **Injection Depth** — Defines the penetration depth of the syringe needle into the injector. Set the parameter choosing one of the following options:

- **Standard** (default value) — The needle goes into the injector to the maximum possible depth.
- **Minimum** — The needle enters the injector and stops immediately beyond the septum. Choose **Minimum** only if injecting with cold needle.

Note When **Minimum** is selected, **Pre-inj. dwell time (s)** and **Post-inj. dwell time (s)** boxes are not enabled.

- **Pre-inj Dwell Time (s)** — Active when the option **Standard** has been selected in **Injection depth:**. Specifies how long the syringe needle must remain inside the injector before injection. This allows the needle to be heated before the sample injection. Set the delay time between 0 and 63 seconds.
- **Post-inj Dwell Time (s)** — Active when the option **Standard** has been selected in **Injection depth:**. Specifies how long the syringe needle must remain inside the injector after injection. This allows the complete evaporation of any residues present inside the needle. Set the delay time between 0 and 63 seconds.

Washes Section

In this field the parameters of pre-washing and post-washing with solvent, and washing with sample are specified.

- **Pre-Injection** — In this box the parameters of pre-washing with solvent are specified.
 - **Solvent** — Sets the vial containing the pre-washing solvent. The autosampler can use up to four different solvents. It is possible to define which solvent, or combination of two solvents, must be used before injection selecting one of the following options:
A, B, C, D, A+B, C+D — If A+B or C+D are selected, the autosampler uses both solvents in sequence. Different combinations from A+B or C+D are not possible.
 - **Cycles** — Sets how many syringe pre-washing cycles with solvent have to be run before injection. Set a number between 0 and 15.
- **Sample** — The parameters of the syringe washing with sample are set in this box.
 - **Rinses** — Sets the number of syringe pre-washing cycles with sample to be run. Select a number between 0 and 15.
- **Post Injection** — The parameters of the syringe post-washing with solvent are set in this box.
 - **Solvent** — Specifies the vial containing the post-washing solvent. The autosampler can use up to 4 different solvents. It is possible to define which solvent, or combination of two solvents, must be used after injection selecting one of the following options:
A, B, C, D, A+B, C+D — If A+B or C+D are selected, the autosampler uses both solvents in sequence. Different combinations from A+B or C+D are not possible.
 - **Cycles** — Sets how many syringe post-washing cycles with solvent have to be run after injection. Set a number between 0 and 15.

Info Line

Displays the range of the selected parameter.

Status Line

Displays the instrument status messages and error messages that may occur during operation.

Menus Description

File Menu

This menu contains the following function:

- **New** — Creates a new method for the autosampler starting from the data currently in memory, or from default parameters previously stored with the function **Save As Default**.
- **Open** — Uploads a pre-existing analytical method for the autosampler from disk to the computer memory.
- **Open Recent...** — Retrieves the last five saved analytical methods.

Note To activate a loaded or modified method, use the command **Send Method to Sampler**.

- **Save (Save as...)** — Saves an analytical method on the hard disk. With the command **Save as...** the method can be saved with a new name.
- **Load from Default** — Uploads a default analytical method.
- **Save as Default** — Saves the current analytical method as a default method for the autosampler (...\\tmp\\AI\\AS3000 **Default method.asm**). The parameters of this method can be retrieved when selecting the function **New**.
- **Get Method from Sampler** — Transfers the autosampler current method to the FLASH elemental analyzer.
- **Send Method to Sampler** — Transfers the method from the computer to the autosampler and makes the method active.
- **Print** — Prints the method.
- **Close** — Closes the method. If modifications have been done, the system asks where to save them in the method.

Edit Menu

This menu gives access to the following function:

- **View Audit Trail** — Displays the log file of the method. Each change to the method parameters is recorded on the log file with the operator's name as well as the date and time of the modification. Using the function **Copy** part or all the log file contents are copied into Windows™. The information can be transferred to other programs if required.

Note Audit trail method log is available only if a protection policy is active in the data system.

Command Menu

This menu gives access to the following functions:

- **Start Clean Cycle** — Starts a washing cycle.
- **Inject Single Sample** — Starts the injection of a single sample.
- **Force Autosampler to Stand-by** — Interrupts any current operation and forces the autosampler to stand-by.
- **Menu Help** — Gives access to the on-line guide.

Evaluate Injection Delay

From Main Menu select **Edit | Evaluate Injection Delay** function. The following window is visualized. See [Figure 82](#).

Figure 82. Injection Delay Window

The figure shows two versions of the 'Injection delay' window. Both windows have a title bar with a bug icon and standard window controls. The main text area contains a description: 'This window provides the ability to evaluate the sample preparation time. According to the Sampler method in use (see 'Actual' sample of Sample Table) this routine evaluates the time spent from start command and the moment the injection take place. The program needs to know exactly the injection moment in order to deliver oxygen at right time for correct combustion.'

The left window is for 'AI/AS 1310-3000'. It features a 'Sampler start/stop' section with a text box 'Method used for test as sample actual 1' and a 'Vial' box set to '1'. Below are buttons 'AI/AS 1310 Start' and 'Stop when Sampler injects'. The 'Delay calculation' section shows the formula 'Delay run = T1-T2+T3' with input fields for 'Sample preparation time (s) (T1): 0', 'Oxygen delay time (s) (T2): 8', and 'Correction for vial 1 (s) (T3):'. The resulting 'Instrument delay run (s): 15' is shown with a 'Calc.' button. At the bottom, it says 'AI/AS 1310-3000', 'Difference of delay time from the vial 1 and the vial 40 (def. 6): 6', and 'Vial used for test: 1'. 'OK' and 'Cancel' buttons are at the bottom right.

The right window is for 'AS2000'. It has a similar layout but with the 'AS2000 Start' button. The 'Delay calculation' section shows the formula 'Delay run = T1-T2' with the same input fields for T1 and T2. The resulting 'Instrument delay run (s): 15' is shown with a 'Calc.' button. 'OK' and 'Cancel' buttons are at the bottom right.

This function calculates the delay to be set for start analysis and allows the autosampler to perform the preliminary sampling operations.

To run a correct analysis, it is important that the sample injection takes place an instant before the oxygen arrival into the combustion zone.

The time elapsing between the start sent to the autosampler for liquids and the actual sample injection into the instrument, is greater than the time required by oxygen to reach the combustion zone. Therefore, the start to the autosampler must be sent before that to the instrument. This window coordinates times in a way to obtain a good sample combustion.

In **Method used for test** box, the directory **Filename** of the autosampler method used for running analyses must be visualized. The directory is the same where the current *EagerSmart* main method (*.mth) is saved. The filename of the autosampler method (*.asm) is drawn from the AS method setting in the **Sample Table** referred to the sample vial marked as **Actual**, or from the number of the vial manually set in the **Vial** box.

In **Oxygen delay time** box enter the delay for oxygen arrival in seconds. Click **AI/AS 1310 Start** (or **AI/AS 3000 Start**), the autosampler performs the sample preparation and introduces the syringe into the injector mounted on the instrument. When the syringe enters the injector, click **Stop** when the autosampler injects.

Note For this test use the vial 01 in the case of the 105-position sample tray, or the vial 08 in the case of the 8-position sample tray.

The time between **AI/AS Start** and **Stop** is entered into **Sample preparation time** box. The difference between **Sample preparation time** and **Oxygen delay time** is entered into the **Instrument run delay** box. Every time **Start analysis** is activated, *EagerSmart* sends the start command to the autosampler, waits for the time set in **Instrument run delay**, and then sends the start analysis command to the instrument.

Note In a sequence of analyses the method used for the autosampler for liquids (**.asm**) may be different from one sample to the other, but the sample preparation must always take place within the time set in this page.

Difference of Delay Time

According to the sample tray used see:

- [105-position Sample Tray](#)
- [8-position Sample Tray](#)

105-position Sample Tray

The tray can contain up to 105 vials numbered 01 to 105 arranged on three circular rows:

- From 01 to 40 into the external row
- From 41 to 80 into the middle row
- From 81 to 105 into the internal row

The delay time between the start command send to the sampler and the sample injection is different if the sample is withdrawn from the vial 01 or from the vial 40. The variation is due to the time that the sampler needs to rotate the tray from the vial 01 to the vial 40. This delay time is about 6 seconds.

Note Because the vial positions are arranged on three circular rows, the delay time between the vial 01 and the vials 40, 80, and 105 is the same.

❖ To verify the correctness of the delay time

1. Place an empty vial in the positions 01 and 40 of the sample tray.
Perform a test simulating the injection of the sample 01 and sample 40 measuring the delay time between the start command is sent to the autosampler and the injection of the sample.
2. Calculate the difference of the delay time of sample 40 respect to sample 01.
3. Enter the obtained value in the **Difference of delay time for the vial 1 and the vial 40 (def. 6)** box. This data is enough to calculate the delay for all the samples from 01 to 105.

To verify the correction of the delay for a specific vial proceed as follows:

1. Enter the number of the vial to verify in **Vial used for test** box.
2. Click **Calc.** (calculate).
3. The delay time calculated for that vial is visualized in the **Correction for vial XX (s) (T3)** box.

Note If you verify the delay time for vials aligned on the same ray of the sample tray, (for example vials 20, 60, and 93), you may note that the calculated times have the same value. This because the rotating time for the vial positioning is the same yet.

8-position Sample Tray

❖ To correct the delay time between the vial 08 and the vial 02

1. Place an empty vial in the positions 01 and 08 of the sample tray.
Perform a test simulating the injection of the sample 01 and sample 08 measuring the delay time between the start command is sent to the auto sampler and the injection of the sample.
2. Calculate the difference of the delay time of sample 01 respect to sample 08.
3. Enter the resulting value in the **Difference of delay time for the vial 1 and the vial 8 (def. 6)** box.

View Sample Being Acquired

This chapter provides the instructions for monitoring the sample currently being acquired.

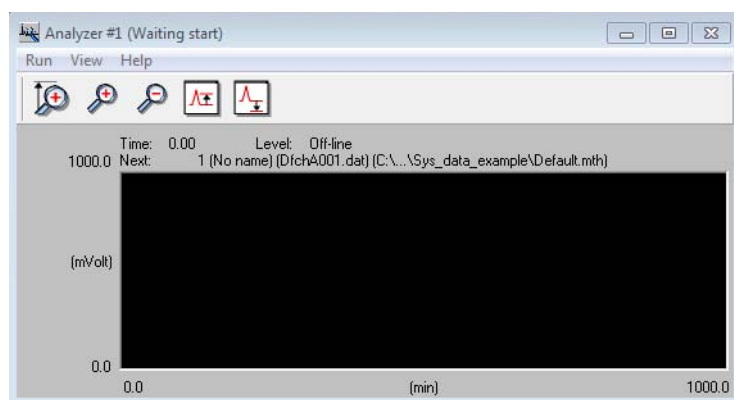
Contents

- [Introduction](#)
- [Run Menu](#)
- [View Menu](#)
- [Last Sample Calculated Results](#)

Introduction

View Sample Being Acquired is a tool to monitor the sample currently being acquired. See [Figure 83](#).

Figure 83. View Sample Being Acquired Page



Note This page shows the real chromatogram being acquired, or the result of the baseline background compensation if the function has been activated in **Integration Parameters** and **Detection Parameters**.

Icon	Description	See on:
	Fit to Higher Peak	page 120
	Expand (scale/2)	page 120

Icon	Description	See on:
	Step Up	page 120
	Step Down	page 120

Icon	Description	See on:
	Shrink (Scale*2)	page 121

Icon	Description	See on:

Run Menu

This menu gives access to the following functions:

- **Start Single Sample Data Acquisition** — Starts the acquisition of single sample of the instrument currently in use. All parameters set in **Detection Parameters** and **Integration Parameters** are used for starting the acquisition.
- **Stop Data Acquisition** — Stops the acquisition of the instrument currently in use. The system, after a confirmation, stops the acquisition saving the chromatogram data up to the moment of the **stop** command, and a report is generated if required.
- **Close Partial and View Chromatogram** — Closes the partial chromatogram being acquired. The portion of chromatogram appears automatically. Moreover, it is possible to integrate the chromatogram being acquired before the end of the sample elution with the function **Detect** in **Integration Parameters**.
- **Peak Threshold Evaluation** — *EagerSmart* evaluates the detector signal and may set, on request, the Peak detection threshold in order to avoid the integration of baseline noise as peaks. Approximately after 20 seconds, the system sets, if confirmed, the new value of peak threshold for the method in memory.
- **Exit Monitor Detector** — Exits from detector monitoring. The program returns to the Main Menu, but the acquisition continues in the background.

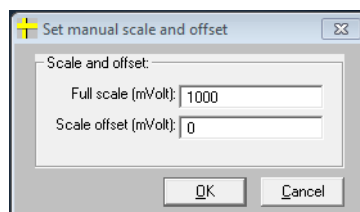
View Menu

This menu gives access to the following functions:

- **Fit to Highest Peak** — Expands or reduces the chromatogram in order to fit all peaks being part of the partially acquired chromatogram centering the signal on the window display. This modification has effect only on the real time display, but it does not affect the integration and the chromatogram printout.
- **Step Up** — Lifts the chromatogram lowering the beginning of the scale by about 1/10 of the full scale. The result is a lift of the chromatogram baseline. This modification has effect only on the real time display, but it does not affect the integration and the chromatogram printout.
- **Step Down** — Lowers the chromatogram increasing the beginning of the scale by about 1/10 of the full scale. This modification has effect only on the real time display, but it does not affect the integration and the chromatogram printout.
- **Expand (scale/2)** — Expands the chromatogram by dividing the full scale in two. The system automatically re-draws the entire chromatogram with the new required scale. This modification has effect only on the real time display, but it does not influence the integration and the chromatogram printout.

- **Shrink (scale*2)** — Reduces the chromatogram by doubling the full scale. The system automatically re-draws the entire chromatogram with the new required scale. This modification has effect only on the real time display, but it does not affect the integration and the chromatogram printout.
- **Set Manual Scale** — Sets manually the values for the beginning and the full scale. You can center the signal on the window display or you can display the signal with a desired attenuation. This modification has effect only on the real time display, but it does not affect the integration and the chromatogram printout. See [Figure 84](#).

Figure 84. Set Manual Scale

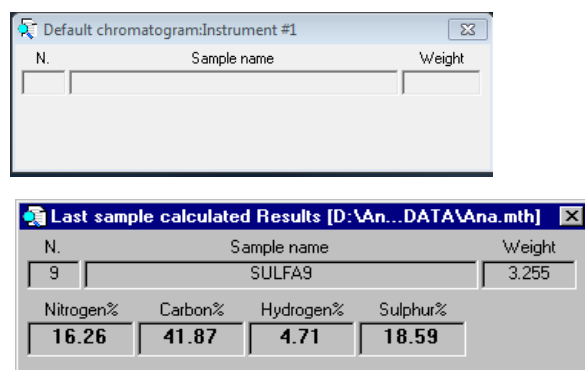


- **Set Focus to Eager Main Menu** — Sets the focus on Main Menu. The function is only used when you want to use the keyboard instead of the mouse. All functions, like in all other Windows™ applications, can be accessed with **Alt** key. After the use of **View chromatogram being acquired**, the function returns the focus on the Main Menu functions.

Last Sample Calculated Results

This window shows the percentages of the elements found. See [Figure 85](#).

Figure 85. Example of Last Sample Calculated Results



Note The results are only shown at the end of an analysis or when a recalculation is performed.

View Calibration Curves

This chapter provides the instructions to see the calibration curve of the method in memory.

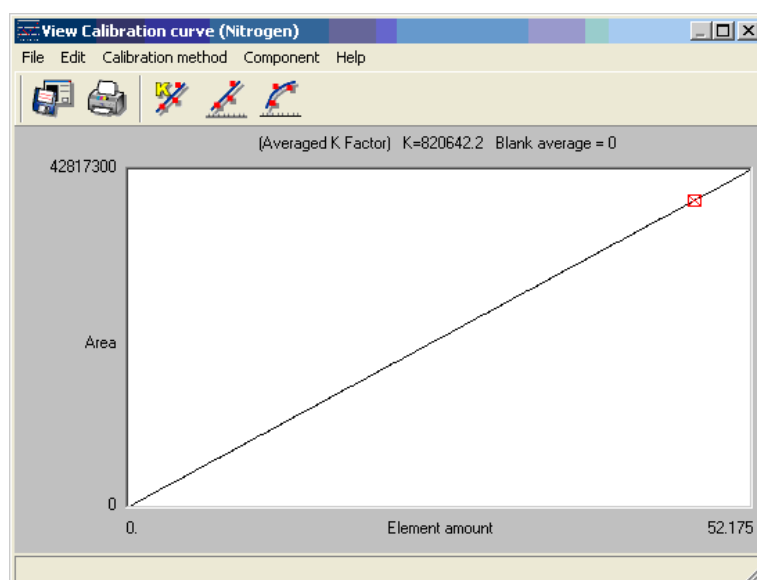
Contents

- [Introduction](#)
- [File Menu](#)
- [Edit Menu](#)
- [Calibration Method](#)
- [Component](#)

Introduction

View Calibration Curve shows the curve of the selected component and the factors in use. See [Figure 86](#).

Figure 86. View Calibration Curve



The standards that appear on the calibration curve are visualized with different colors according to their status:

- ■ **Red** are standards valid and used for calculations.
- ■ **Blue** are standards valid but not participating in the calculation of the equation.

Place the mouse pointer over the standard points. Left-click to change the status of the standard from valid to non-valid so that you can modify the calibration curve accordingly. It is also possible to display the standard data by placing the mouse cursor over the point, and then right-click.

To enlarge a portion of graph, move the mouse pointer to the zone to be enlarged and left-click. To restore the original scale, double-click the button inside the graph.

The system shows also the curve fitting, RF, Linear or Quadratic, and the parameters of the equation of the curve.

Icon	Description	See:
	Save Calibration Factors	"File Menu" on page 124
	Print Calibration Curve	"File Menu" on page 124
	Use Averaged RF	"Calibration Method" on page 126
	Use linear fit	"Calibration Method" on page 126
	Use quadratic fit	"Calibration Method" on page 126

File Menu

This menu gives access to the following functions:

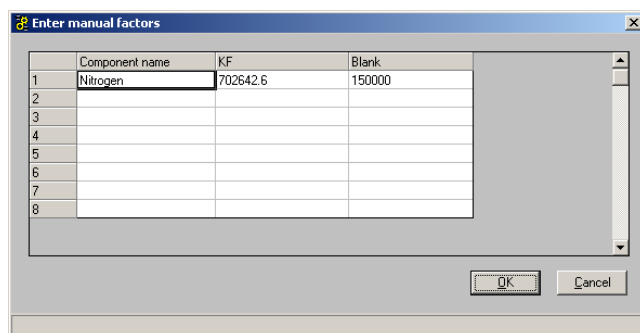
- **Save Calibration Parameters** — Saves the modified **Calibration Factors** onto disk. All K Factors, KA, KB, and KC are saved for future use. Use this function after entering the calibration factors for a method starting with unknown samples without calibration sequence, or to eliminate one or more calibration levels showing bad linearity due to wrong weight.
- **Convert to HPGL Format** — Saves the calibration curve currently shown in to HPGL format. The HPGL format is very flexible and efficient to export curves to third party software like Win-Word, Page-Maker, Ventura, or other desktop publishers.
- **Print Calibration Curve of Single Component** — Prints the calibration curve currently visualized. You can select the different target printer with the **Printer manager** utility, or in **Set Color** module accessible from Main Menu. Moreover, it is possible to print the curve in landscape or portrait mode according to the selection done in **Set Color** module accessible from Main Menu.
- **Print All Component Curves** — Prints the calibration curves of all components of the method. You can select the different printer target with the **Printer Manager** utility, or in **Set Color** module accessible from Main Menu. Moreover, it is possible to print the curve in landscape or portrait mode according to the selection done in **Set Color** module accessible from Main Menu.
- **Quit Calibration Curves** — Exits the view calibration module. If any modification has been made on the calibration factors, the system prompts for **Save Calibration Factors**.

Edit Menu

This menu gives access to the following functions:

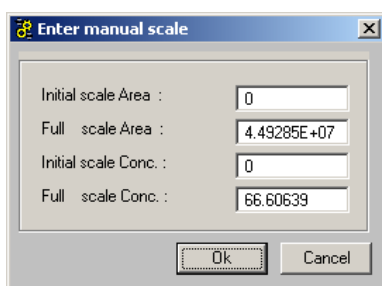
- **Calibration Curve Graph Title** — Enters the title of the graph that is printed on the curve with the functions **Print Calibration Curve of Single Components** and **Print All Components Curves**. See “[File Menu](#)” on [page 124](#).
- **Copy to Clipboard** — Copies the calibration curve or part of it into the clipboard. You can paste the curve sent into the clipboard to Paint, or Write, or any Windows™ program.
- **Enter Manual Factors** — Enters the calibration factors for a method starting with unknown samples without calibration sequence. After clicking this function, a dialog box prompts for the factors of all components of your method, and according to the calibration method in use, you can enter the RF, KA, KB, or KC. See [Figure 87](#).

Figure 87. Manual calibration factor



- **Fill Factor for All Peaks** — Enters the same calibration factors for all components. The factors of the addressed peak are automatically copied into all calibration factors of all peaks present in the Component Table.
- **Restore Original Factors** — Restores the original factors of all peaks. Occasionally after some factor modification there is a need to clear all manually entered factors, this function clears any operation done and restores the original factors.
- **Set Manual Scale and Offset** — The calibration curve visualized is shown with an automatic scale, but through this function, you can manually set any value to better show specific parts of the curve. See [Figure 88](#).

Figure 88. Manual Scale



Calibration Method

EagerSmart allows to select **Average K-Factor**, **Linear Fit** and **Quadratic Fit** for multilevel calibration.

- **Averaged K-Factor** — Select this option for single level calibration. The quantification of the element that has been analyzed (for example Carbon) is determined by comparing the values obtained from the analysis of the sample with the analysis of a suitable standard and the use of a reference factor known as K-Factor.

$$K = \frac{AreaStd - AreaBlank}{(\%Tstd \times Wstd) / 100}$$

Where:

AreaStd = peak area or integral of standard

AreaBlank = peak area or integral of blank

% Tstd = theoretical percentage of standard

Wstd = weight of standard

The calculation of the percentage of element (%) is given by the following equation:

$$Calculated\% = \frac{(AreaUnk - AreaBlk) / K}{Wunk} \times 100$$

Where:

K = Average K-Factor

AreaUnk = peak area or integral of the unknown

AreaBlk = peak area or integral of the blank

Wunk = weight of the unknown

- **Linear Fit** — This method of calculation is based on the analysis of at least three standards. The results are calculated with the aid of the linear regression method by which one variable is analyzed in relation to another one. This method performs a least-square linear regression between integration data (area counts) and known amount of elemental components of the standard, where for each element a linear equation of calibration is applicable.

The regression analysis for the linear function is based on the slope and intercept form of the general linear equation:

$$y = KB \times x + KC$$

Where:

x = concentration

y = area

KB = The coefficient of x term in either regression analysis for component (n).

KC = The Y-axis intercept term in regression analysis.

- **Non Linear Fit** — This method of calculation is based on the analysis of at least three standards. The results are calculated with the aid of a quadratic regression method by which one variable is analyzed in relation to another one. This method performs a least-square quadratic regression between integration data (area counts) and known amount of elemental components of the standard, where for each element a quadratic equation of calibration is applicable.

The regression analysis uses the least-squares fitting of a parabolic (non-linear) shape and is expressed by the quadratic equation:

$$y = KA \times x^2 + KB \times x + KC$$

Where:

x = concentration

y = area

KA = The coefficient of the x^2 term in the nonlinear regression analysis for component (n).

KB = The coefficient of x term in either regression analysis for component (n).

KC = The Y-axis intercept term in regression analysis.

- **Force the Curve Through Zero** — The least squares fit technique of fitting a curve to standard data can force the intercept of the calibration curve through zero.

The equation for **Linear Fit** is: $y = KB \times x$

Where:

x = concentration

y = area

KB = The coefficient of x term in either regression analysis for component (n).

The equation for **Non Linear Fit** is: $y = KA \times x^2 + KB \times x$

Where:

x = concentration

y = area

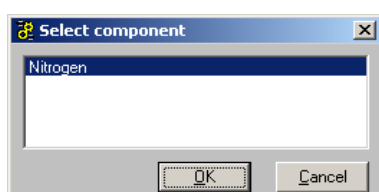
KA = The coefficient of the x^2 term in the nonlinear regression analysis for component (n).

KB = The coefficient of x term in either regression analysis for component (n).

Component

Selects the component name referred to the curve currently visualized. The system shows a dialog box presenting all component names being part of the Component Table. You can click on the component to be shown. See [Figure 89](#).

Figure 89. Select Component Dialog Window



View Chromatograms

This chapter provides the instructions to view or modify the integration of the peaks.

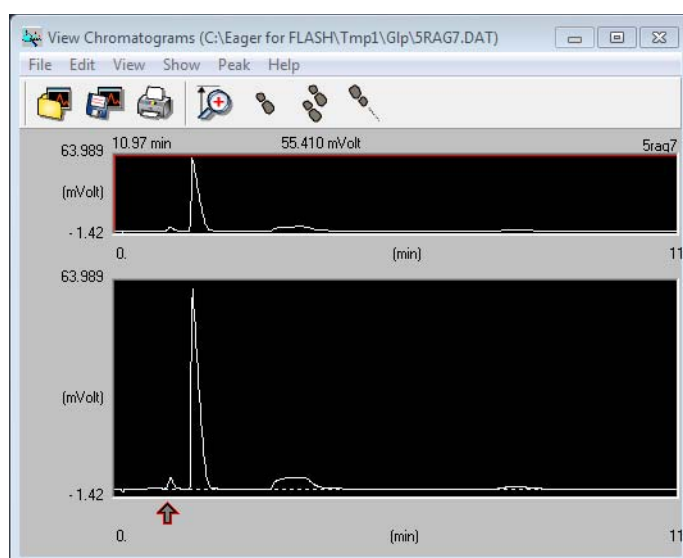
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- [File Menu](#)
- [Edit Menu](#)
- [View Menu](#)
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- [Chromatogram Icons](#)

Introduction

View Chromatograms is a tool to view or modify the integration of the peaks. See [Figure 90](#).

Figure 90. View Chromatograms



The options available permit to modify the peak baseline correction and to view the peak data.

Icon	Description	See on:
	Load chromatogram	page 130
	Save chromatogram	page 130
	Print chromatogram	page 131
	Chromatogram icons	page 136

File Menu

This menu gives access to the following functions:

- **Load Chromatogram** — Loads any chromatogram stored on disk. The system asks for the chromatogram name, showing the chromatogram trace.

Note The names of the peaks are linked to the method currently in memory, therefore the system shows the name of the components currently in memory if required. They can differ from the chromatogram loaded. See also **Peak Name** on [page 132](#).

- **Save Chromatogram** — Saves the modified chromatogram onto disk.
The system asks for the chromatogram name. All data points and baseline correction is saved for future use. Any manual baseline modification should be saved with this function if a recalculation is required using the area or height obtained with the functions available in “[Peak Menu](#)” on [page 133](#).
- **Store Actual Zoom for Signal-to-Noise Evaluation** — *EagerSmart* can calculate the **Signal-to-noise ratio**. Choose the baseline portion on which the noise evaluation should be done. The value of the signal is calculated on the selected peak, and the noise is evaluated for the given initial and final time. According to the found values, the ratio is calculated and reported between the Peak signal value and the peak-to-peak noise.

Signal to noise report

```
-----
Signal peak name      : n3
Signal peak RT       (min): 6.543
Signal value         (uV): 1829.5
Noise eval from/to (min): 7.0-7.1
Peak to peak noise   (uV): 40.0
Signal to noise ratio : 45.7
```

- **Convert to HPGL Format** — Saves the bottom view of the chromatogram in HPGL format. The HPGL format is very flexible and efficient to export chromatogram or part of a chromatogram to third party software like Word, PageMaker, Corel Ventura, or other desk top publishers.
- **Convert to ASCII Format** — Saves the chromatogram in ASCII format.
The ASCII format is very flexible and efficient to export the chromatogram to third party software or customer applications. Upon request of this function, the system requires the number of points to be saved. You can save all points or alternatively one point every 2, 6, 10, 20, 60, 100, or 200 points.

- **Convert to BMP Format** — Saves the bottom view of the chromatogram in BMP format. The BMP format is very flexible and efficient to export chromatogram or part of it to any other Windows™ application through the clipboard. After executing this function, with any other Windows™ application like Paint or Write, it is possible to get the chromatogram trace with the **Paste** function.
- **Print Chromatogram** — Prints the chromatogram or part of it currently visualized in the lower window. You can select the printer target with the Printer manager utility. Moreover, it is possible to print the chromatogram in landscape or portrait mode according to the selection done in **Set Color** module from Main Menu.
- **Quit View Chromatogram** — Exits the View Chromatogram tab. If any modification has been made on the baseline correction, the system prompts for **Chromatogram saving function**.

Edit Menu

This menu gives access to the following function:

- **Copy Lower Window to Clipboard** — Sends to the clipboard the chromatogram, or part of it, currently visualized in the lower window. You can paste to Paint, Write, or any Windows™ program the chromatogram sent to the clipboard.

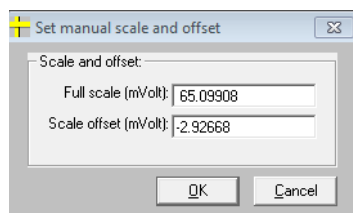
View Menu

This menu gives access to the functions to change the aspect of the chromatogram displayed.

You can select the following functions:

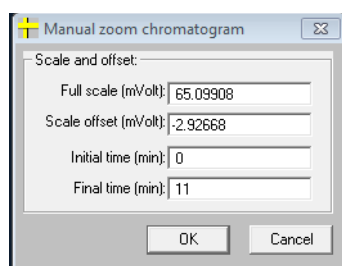
- **Original Scale and Offset** — Restores the original scale and offset after a **Set manual scale and Offset** has been performed. The chromatogram is generally stored with original scale and offset calculated to keep in scale all peaks not exceeding 1000 mV full scale.
- **Set Manual Scale and Offset** — Enters a manual scale to display the chromatogram in the top window. After any manual modification of the scale, it is always possible to restore the original values with the function **Original Scale and offset**. The chromatogram is generally stored with original scale and offset calculated to keep in scale all peaks not exceeding the 1000 mV full scale. See [Figure 91](#).

Figure 91. Manual Scale and Offset



- **Set Manual Zoom** — Enters a manual scale and time to display the chromatogram in the window. See [Figure 92](#).

Figure 92. Manual Zoom



- **Fit to Higher Peak** — Adjusts the scale of the top window to keep in scale any peak being part of the chromatogram. Even peaks with height higher than 1000 mV is automatically in scale.
- **Fit to Higher Peak on Scale** — Adjusts the scale of the top window in order to keep in scale any peak being part of the chromatogram but within 1000 mV of height.
- **Fit to Current Peak** — Adjusts the scale of the bottom window to keep in scale the peak currently selected with the peak pointer. Firstly you should select with the peak pointer, below the bottom window, the peak on which you want modify the starting point. Next, selecting **Fit to Current Peak**, the system adjusts the scale of the bottom window to keep in scale the selected peak.
- **Center to Current Peak** — Adjusts the time frame of the bottom window to keep in center scale the peak currently selected with the peak pointer. Firstly you should select with the peak pointer, below the bottom window, the peak on which you want to modify the starting point. Next, selecting **Center Peak**, the system adjusts the time frame scale of the bottom window to keep in center scale the selected peak.

Show Menu

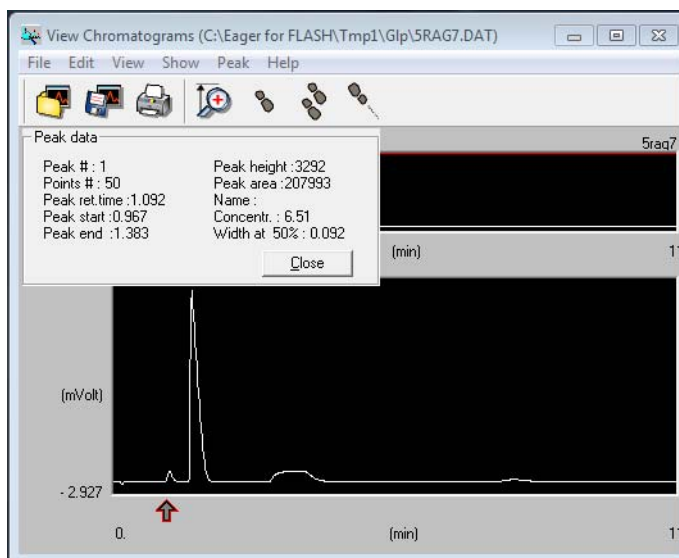
This menu gives access to the functions for changing the aspect of the chromatogram visualized. These functions are:

- **Baseline** — Displays the baseline correction of the chromatogram. If a check mark is shown beside the command, the chromatogram is visualized with a dashed line of the baseline correction, otherwise only the chromatogram data points are shown.
- **Maxima** — Displays a small tick on the top of each peak. If a check mark is shown beside the command, the chromatogram is visualized with small marks indicating the maximum of the peak, and indicating that the peak is integrated.
- **Retention Time** — Displays the retention time of the peaks. If a check mark is shown beside the command, the chromatogram is visualized with the retention time at the maximum of the peak, indicating that the peak has been eluted at the reported time
- **Peak Name** — Displays the name of the components. If a check mark is shown beside the command, the chromatogram is visualized with the name of each component found in the chromatogram.

Note The names of the components are reported only if the chromatogram has been processed, and if the method currently in memory corresponds to the method used for the original sample acquisition.

- **Start/Stop** — Displays the start and stop point of each peak. If a check mark is shown beside the command, the chromatogram is visualized with two small arrows indicating the start and the end point of the peaks.
- **View Peak Data** — Displays the calculated parameter of a desired peak. If a check mark is shown beside the command, the chromatogram is shown with a window indicating all peak information. You should select with the peak pointer, located below the bottom window, the peak of which you want the information. Automatically the system shows all parameters of the peak including column performance parameters. See [Figure 93](#).

Figure 93. Example of Peak Data



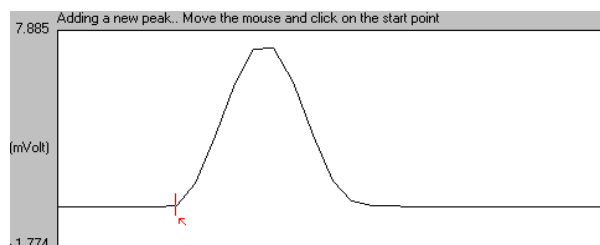
- **None of Above** — Disables all the functions currently selected for the chromatogram display.

Peak Menu

This menu modifies any baseline of the peaks currently being part of the chromatogram. You access the following functions:

- **Add Peak** — Integrates manually a peak. After selecting this function, you should move the mouse over the chromatogram in the bottom window. The system shows a small marker along the chromatogram. See [Figure 94](#).

Figure 94. Chromatogram Marker



Left-clicking, the beginning of the desired peak is traced until a second left-click to confirm the end of the peak.

Note A new peak can be added only in a chromatogram area where there are no peaks.

- **Move Peak Start** — Modifies the beginning of a selected peak. With the peak pointer located below the bottom window, you should select the peak on which you want to modify the starting point. Select **Move Peak Start** function from the pull down menu. Moving the mouse, the system shows the moving baseline of the peak according to the mouse position. Once the appropriate starting point has been reached, left-click and the new peak start is placed at that point.



ATTENTION The beginning of a peak cannot be placed before the end of the previous peak in the chromatogram.

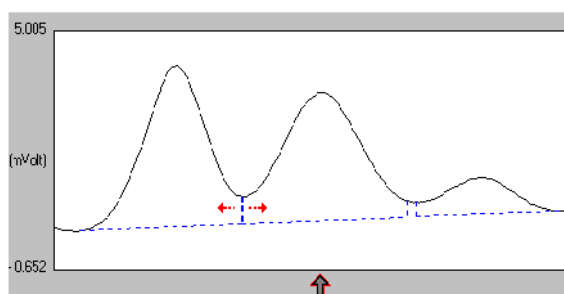
- **Move Peak End** — Modifies the end point of the selected peak. With the peak pointer located below the bottom window, you should select the peak on which you want to modify the ending point. Select **Move Peak End** function from the pull down menu. Moving the mouse, the system shows the moving baseline of the peak according to the mouse position. Once the appropriate end point has been reached, left-click and the new peak end is placed at that point.



ATTENTION The end of a peak cannot be placed after the beginning of the next peak in the chromatogram.

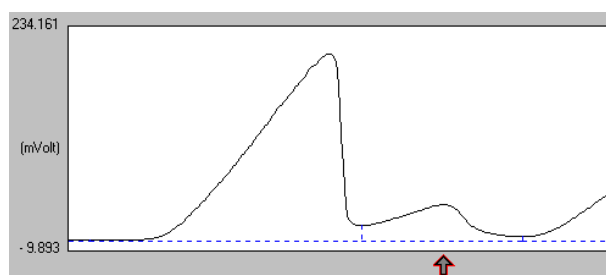
- **Move Perpendicular** — When two adjacent peaks are not well separated, and a “cut” perpendicular to the baseline has been performed, it is possible to move the vertical line that separates the two fused peaks. With the peak pointer, located below the bottom window, you should select the peak on which you want to modify the perpendicular. The peak on the right to the perpendicular should be selected. See [Figure 95](#).

Figure 95. Baseline Correction 3rd Example

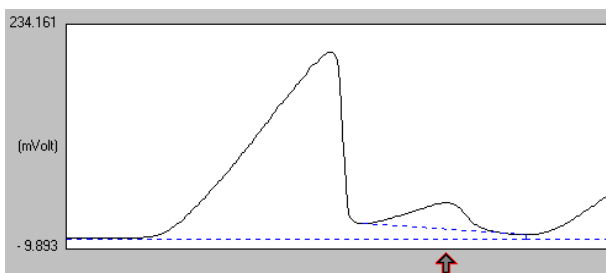


Select **Move Perpendicular** function from the pull down menu; and then moving the mouse, the system shows the moving perpendicular of the peak according to the mouse position. Once the appropriate position has been reached, left-click and the new perpendicular is placed at that point.

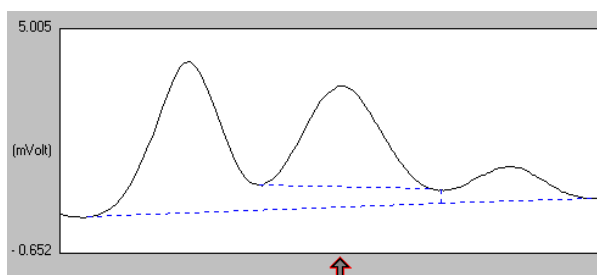
- **Skim Peak** — When two adjacent peaks are not well separated, and a "cut" perpendicular to the baseline has been performed. See [Figure 96](#).

Figure 96. Baseline Correction 1st Example

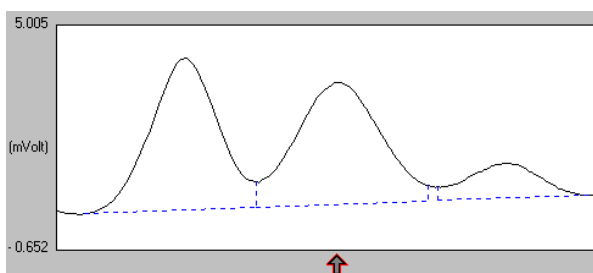
It is possible to correct the tangent of the peak indicated by the pointer in the lower window.



- **Unskim Peak** — If two peaks have been tangentially corrected, it is possible to perform a "cut" between the peaks' valley and the baseline. See [Figure 97](#).

Figure 97. Baseline Correction 2nd Example

The pointer in the lower window must be positioned on the second peak (Carried peak).



- **Delete Peak** — When an undesired peak needs to be eliminated. With the peak pointer, located below the bottom window, you should select the unwanted peak. Select **Delete Peak** function from the pull down menu; the selected peak disappears immediately.

Note The data points of the peak are always available but the areas and retention times are no longer reported

- **Clear Baseline Before Modification** — When a peak modification is performed on the chromatogram, it is possible to clear the baseline of the adjacent peak before starting the manual operation. If a check mark is shown beside the command, the baseline is cleared before any operation.

Chromatogram Icons

The chromatogram icons are a series of functions to manipulate the chromatogram view.

Icon Function	Description
	Restores the chromatogram currently in memory with the original scale and offset. After a number of zoom commands you would like to review the original chromatogram time frame; through this command the system immediately restores the full chromatogram view.
 	Advances the chromatogram view by the same time frame of the actual window or half the actual window.
	Remembers the last 10 chromatogram time-frame views and it restores the last 10 zoom steps.

Overlay Chromatograms

This chapter provides the instructions to view and compare different chromatograms.

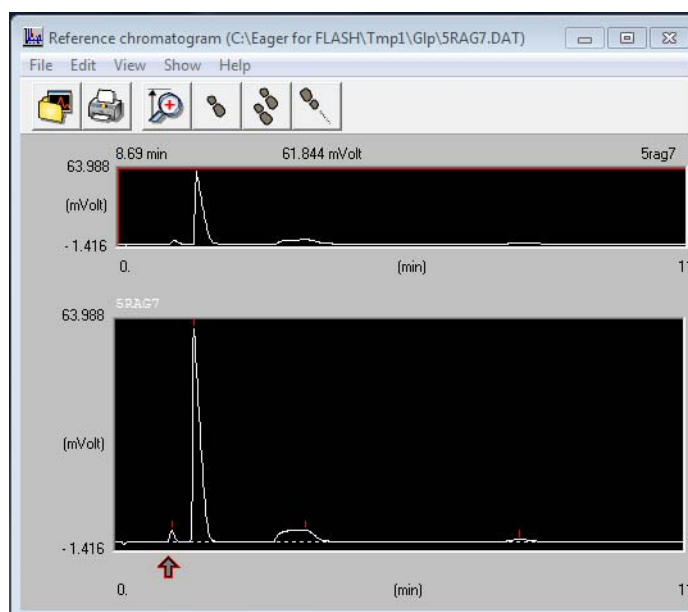
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Introduction

Overlay Chromatograms is a tool to view and compare different chromatograms. See [Figure 98](#).

Figure 98. Overlay Chromatograms



The available options permit to load the Reference and up to four chromatograms to view the peak data differences.

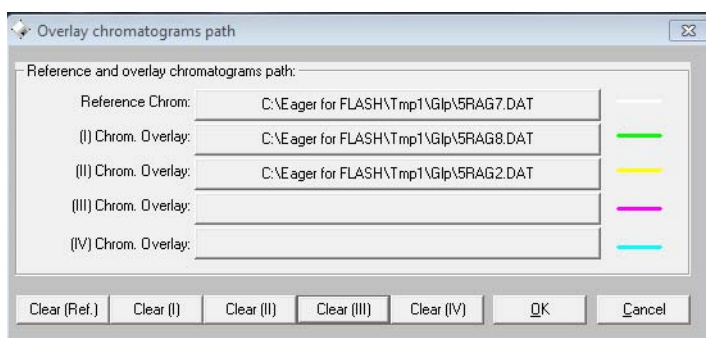
Icon	Description	See on:
	Load chromatogram	page 139
	Save chromatogram	---
	Print chromatogram	page 139
	Chromatogram icons	page 142

File Menu

This menu give the access to the following functions:

- **Load Chromatogram** — Loads any chromatogram stored on disk. See [Figure 99](#).

Figure 99. Overlay Chromatograms Path



The system asks for the reference and the other chromatograms name to be overlaid, showing the chromatograms with or without 3D effect according to the relevant selection.

Note The names of the peaks are linked to the method currently in memory. Therefore, if required the system shows the name of the components currently in memory. They can differ from the chromatogram loaded. See also **Peak Name** in “[Show Menu](#)” on [page 140](#).

- **Store Actual Zoom for Signal-to Noise Evaluation** — Chooses the baseline portion on which the noise evaluation should be done.

The signal value is calculated on the selected peak and the noise is evaluated for the given initial and final time.

According to the found values, the ratio is calculated and reported between the Peak signal value and the peak-to-peak noise.

Signal to noise report

```
-----
Signal peak name      : Nitrogen
Signal peak RT       (sec): 218.0
Signal value         (uV): 22064.8
Noise eval from/to   (sec): 150.0-160.0
Peak to peak noise   (uV): 81.2
Signal to noise ratio : 271.7
```


- **Convert to BMP Format** — Saves the bottom view of the chromatograms in BMP format. The BMP format is very flexible and efficient to export chromatograms, or part of chromatograms, to any other Windows™ application through the clipboard. After executing this function, with any other Windows™ application like Paint or Write, it is possible to get the chromatogram trace with the **Paste** function.
- **Print Chromatogram** — Prints the chromatogram, or part of it, currently visualized in the lower window. You can select the different target printer with the **Printer manager** utility. Moreover, it is possible to print the chromatogram in landscape or portrait mode according to the selection done in **Set Color** module from Main Menu.
- **Quit Overlay Chromatograms** — Exits the overlay chromatograms module.

Edit Menu

This menu gives access to the following function:

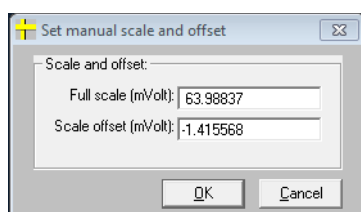
- **Copy Lower Window to Clipboard** — Sends to the clipboard the chromatogram, or part of it, currently visualized in the lower window. You can paste to Paint, Write, or any Windows™ program the chromatogram sent to the clipboard.

View Menu

This menu gives access to the functions for changing the aspect of the chromatogram displayed. You can select the following functions:

- **Original Scale and Offset** — Restores the original scale and offset after a **Set Manual Scale** has been performed. The chromatogram is generally stored with original scale and offset calculated to keep in scale all peaks not exceeding 1000 mV full scale.
- **Set Manual Scale and Offset** — Enters a manual scale to display the chromatogram in the top window. After any manual modification of the scale, it is always possible to restore the original values with the function **Original Scale and Offset**. See [Figure 100](#).

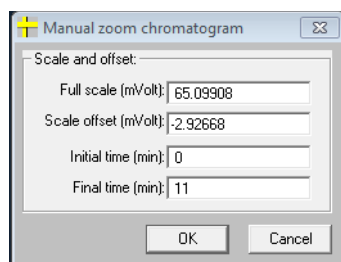
Figure 100. Chromatogram Scale and Offset



The chromatogram is generally stored with original scale and offset calculated to keep in scale all peaks not exceeding the 1000 mV full scale.

- **Set Manual Zoom** — Enters a manual scale and time to display the chromatogram in the window. See [Figure 101](#).

Figure 101. Manual Zoom



- **Fit to Highest Peak** — Adjusts the scale of the top window to keep in scale any peak being part of the chromatogram. Even peaks with height higher than 1000 mV are automatically in scale.
- **Fit to Highest Peak on Scale** — Adjusts the scale of the top window to keep in scale any peak being part of the chromatogram but within 1000 mV of height.
- **Fit to Current Peak** — Adjusts the scale of the bottom window to keep in scale the peak currently selected with the peak pointer. With the peak pointer, located below the bottom window, you should select the peak on which you want to modify the starting point. After selecting **Fit to Current Peak**, the system adjusts the scale of the bottom window to keep in scale the selected peak.
- **Center to Current Peak** — Adjusts the time frame of the bottom window in order to keep in center scale the peak currently selected with the peak pointer. With the peak pointer, located below the bottom window, you should select the peak on which you want to modify the starting point. After selecting **Center Peak**, the system adjusts the time frame scale of the bottom window in order to keep in center scale the selected peak.

Show Menu

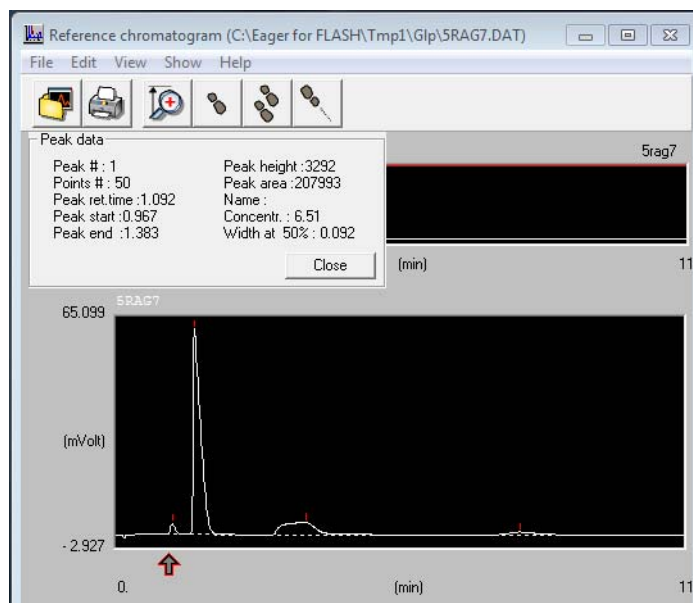
This menu gives access to the functions for change the aspect of the chromatogram display. You can select the following functions:

- **Peak Baseline** — Displays the baseline correction of the chromatogram. If a check mark is shown beside the command, the chromatogram is visualized with a dashed line of the baseline correction. Otherwise, only the chromatogram data points are shown.
- **Peak Maxima** — Displays a small tick on the top of each peak. If a check mark is shown beside the command, the chromatogram is visualized with small marks indicating the maximum of the peak, and indicating that the peak is integrated.
- **Retention Time** — Displays the retention time of the peaks. If a check mark is shown beside the command, the chromatogram is visualized with the retention time at the maximum of the peak, indicating that the peak has been eluted at the reported time
- **Peak Name** — Displays the name of the components. If a check mark is shown beside the command, the chromatogram is visualized with the name of each component found in the chromatogram.

Note The names of the components are reported only if the chromatogram has been processed, and if the method currently in memory corresponds to the method used for the original sample acquisition.

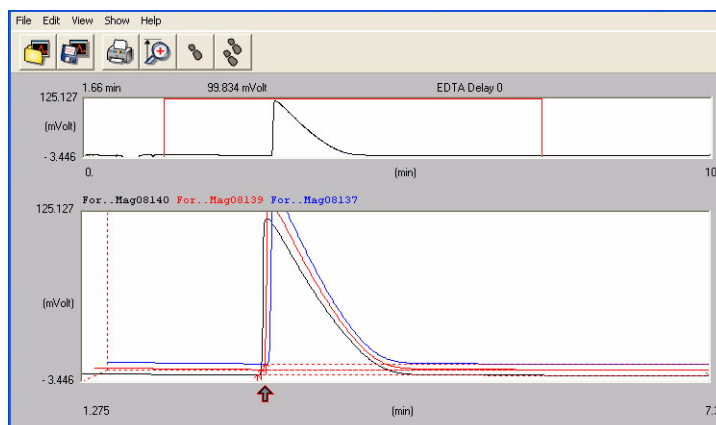
- **Peak Start/Stop** — Displays the start and stop point of each peak. If a check mark is shown beside the command, the chromatogram is visualized with two small arrows indicating the start and end point of the peaks.
- **View Peak Data** — Displays the calculated parameter of a desired peak. If a check mark is shown beside the command, the chromatogram is shown with a window indicating all peak information. With the peak pointer, located below the bottom window, you should select the peak of which you want the information. Automatically the system shows all parameters of the peak including column performance parameters. See [Figure 102](#).

Figure 102. Example of Peak Data



- **Swap Reference <-> Overlay** — Swaps the reference chromatogram with any of the overlaid chromatograms. The peaks data currently visualized are always referred to the reference chromatogram. Therefore, if you wants to compare the peak data of an overlaid chromatogram, the reference must be swapped first.
- **3D Display** — Views the chromatograms overlaid with or without 3D effect. Disables all the functions currently selected for the chromatogram display. See [Figure 103](#).

Figure 103. 3D Display



Chromatogram Icons

The chromatogram icons are a series of functions to manipulate the chromatogram view.

Icon Function	Description
	Restores the chromatogram currently in memory with the original scale and offset. After a number of zoom commands you would like to review the original chromatogram time frame; through this command the system immediately restores the full chromatogram view.
	Advances the chromatogram view by the same time frame of the actual window or half the actual window.
	Remembers the last 10 chromatogram time-frame views and it restores the last 10 zoom steps.

Operate on Chromatograms

This chapter provides the instructions to operate on the chromatograms.

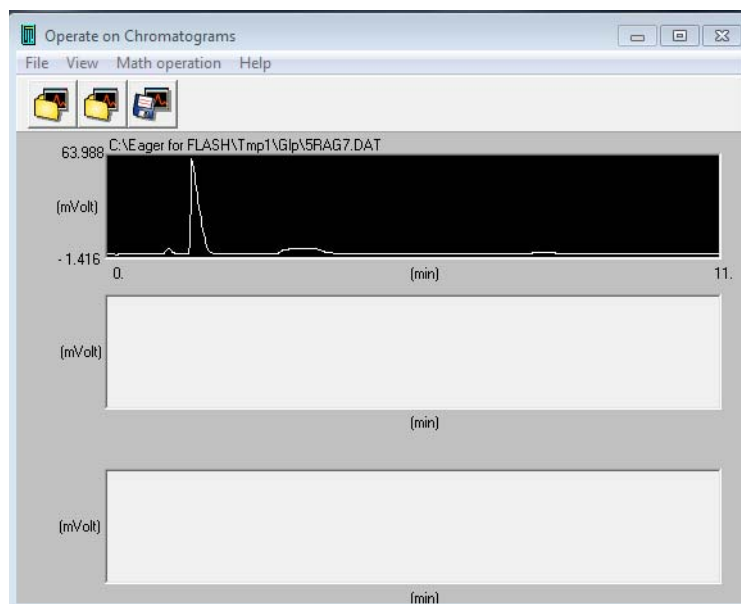
Contents

- [Introduction](#)
- [File Menu](#)
- [View Menu](#)
- [Math Operation](#)

Introduction

Operate on Chromatograms is a tool to perform addition, subtraction, smoothing, and many other operations on chromatogram data points. See [Figure 104](#).

Figure 104. Operate on Chromatograms



Note All modified chromatograms saved by this module are marked. When the report is generated, a message is printed to inform you that the data points have been manipulated.

Icon	Description	See on:
	Load 1st Chromatogram	page 144
	Load 2nd Chromatogram	page 144
	Save Chromatogram Result	page 144

File Menu

This menu gives access to the following functions:

- **Load 1st Chromatogram** — Loads in the first window any chromatogram stored on disk. The system asks for the name of the chromatogram to be used as the first operator for all mathematical operations permitted by this module.
- **Load 2nd Chromatogram** — Loads in the second window any chromatogram stored on disk. The system asks for the name of the chromatogram to be used as the second operator for all mathematical operations permitted by this module.
- **Save Chromatogram Result** — Saves on disk the result of the last operation performed. The system generates a chromatogram as visualized in the result box; it is saved with a supplied name.

Note All the chromatograms generated with this module are manipulated chromatograms. The system prints a message every time a manipulated chromatogram is used to generate a report.

- **Quit Operate on Chromatogram** — Exist Operate on Chromatograms module.

View Menu

This menu gives access to the functions for changing the aspect of the chromatogram displayed. You can select the following functions:

- **Autoscale 1st Chromatogram** — Restores the automatic scale and offset after a **Manual Scale 1st Chromatogram** has been performed. The chromatogram is generally stored with automatic scale and offset calculated to keep in scale all peaks not exceeding 1000 mV full scale.
- **Manual Scale 1st Chromatogram** — Enters a manual scale to display the chromatogram in the 1st window. After any manual modification of the scale, it is always possible to restore the original values with the function **Autoscale 1st Chromatogram**.
- **Autoscale 2nd Chromatogram** — Restores the automatic scale and offset after a **Manual Scale 2nd Chromatogram** has been performed. The chromatogram is generally stored with automatic scale and offset calculated to keep in scale all peaks not exceeding 1000 mV full scale.

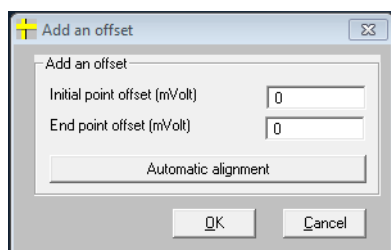
- **Manual Scale 2nd Chromatogram** — Enters a manual scale to display the chromatogram in the 2nd window. After any manual modification of the scale, it is always possible to restore the original values with the function **Autoscale 2nd Chromatogram**.
- **Autoscale Result Chromatogram** — Restores the automatic scale and offset after a **Manual Scale Result Chromatogram** has been performed. The chromatogram is generally stored with automatic scale and offset calculated to keep in scale all peaks not exceeding the 1000 mV full scale.
- **Manual Scale Result Chromatogram** — Enters a manual scale to display the chromatogram in the result window. After any manual modification of the scale, it is always possible to restore the original values with the function **Autoscale Result Chromatogram**.

Math Operation

This menu gives access to the functions to perform mathematical operations:

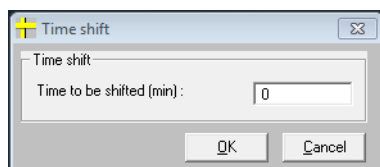
- **Add Chromatogram** — Performs the addition point to point of the two chromatograms. The chromatogram result is visualized in the result window.
- **Subtract Chromatogram** — Performs the subtraction point to point of the two chromatograms. The chromatogram result is visualized in the result window.
- **Add an Offset** — Adds a constant offset or to correct with a linear function all the chromatogram data points. See [Figure 105](#).

Figure 105. Add an Offset



- **Time Shift** — Shifts in time the entire chromatogram. See [Figure 106](#).

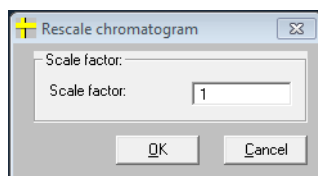
Figure 106. Time Shift



Possible delay in data acquisition can be easily adjusted shifting in time the chromatogram data points.

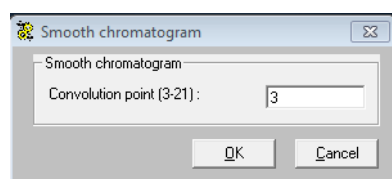
- **Rescale Chromatogram** — Re-scales all the chromatogram data points. You can specify a constant by which the system re-scales the entire chromatogram. See [Figure 107](#).

Figure 107. Rescale Chromatogram



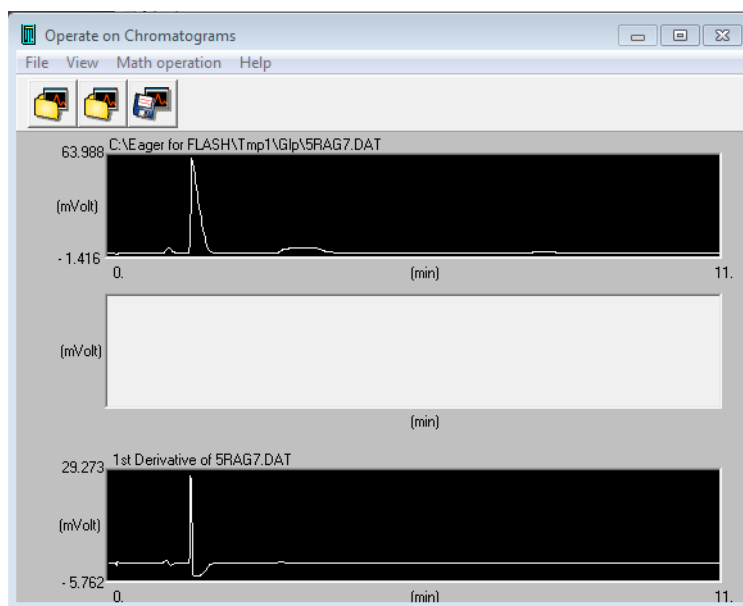
- **Smooth Chromatogram** — Smooths noisy chromatograms through a weighted average of the original data points. You can specify the number of points on which the average is calculated. This number is introduced in the box named **Convolution points**. See [Figure 108](#).

Figure 108. Smooth Chromatogram



- **1st Derivative** — Generates a graphic curve representing the 1st derivative calculation performed on the original chromatogram. See [Figure 109](#).

Figure 109. 1st Derivative



Compare Chromatograms

This chapter provides the instructions to compare chromatograms.

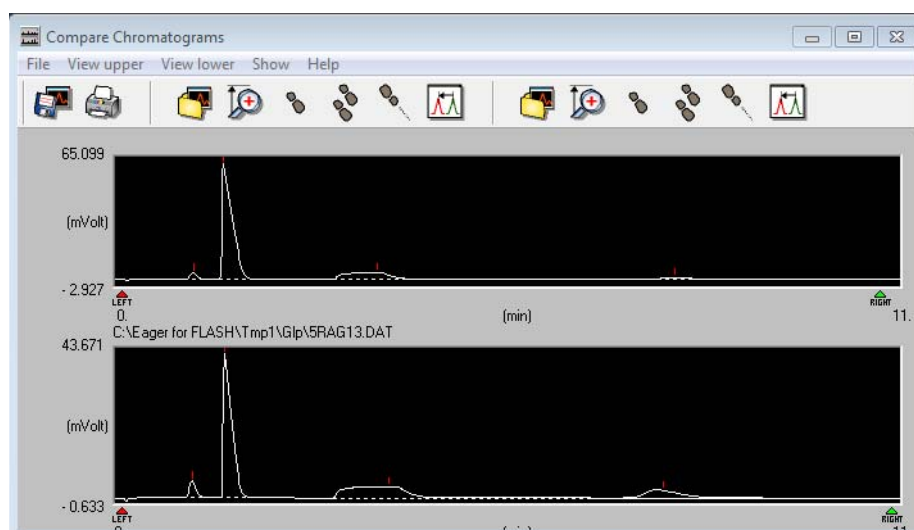
Contents

- [Introduction](#)
- [File Menu](#)
- [View Upper/View Lower Menu](#)
- [Show Menu](#)
- [Chromatogram Icons](#)

Introduction

The complete chromatogram is visualized on the screen top window, while a second chromatogram is visualized on the bottom window. See [Figure 110](#).

Figure 110. Compare Chromatogram



Using the mouse or the computer keyboard arrow keys, you can easily enlarge or reduce the chromatograms. You can compare peaks with a vertical marker. On request, EagerSmart can generate a stretched chromatogram as a result of the **Left** and **Right** markers position.

Icon	Description	See on:
	Stretch and save	page 148
	Print chromatograms	page 148
	Load upper chromatogram	page 148
	Load lower chromatogram	page 148
	Equalize chromatogram	page 149
	Chromatogram icons	page 150

Marker	Description
	Left marker sets the initial point for stretching chromatogram. See Stretch and Save on page 148 .
	Right sets the final point for stretching the chromatogram. See Stretch and Save on page 148 .

Note After selecting Left or Right marker function, the system shows a vertical marker on the window. You should move the mouse left or right on the window, and by left-clicking, the final point for stretching is selected.

File Menu

This menu gives the access to the following functions:

- **Load Upper Chromatogram** — Loads any chromatogram stored on disk. The system asks for the chromatogram name, showing in the upper window the chromatogram trace.
- **Load Lower Chromatogram** — Loads any chromatogram stored on disk. The system asks for the chromatogram name, showing in the lower window the chromatogram trace.
- **Stretch and Save** — Performs the stretching operation according to the **Left marker** and **Right marker** previously placed on the **Upper** and **Lower Chromatograms**. The result of the operation is stored on disk under the required name.
- **Print Chromatograms** — Prints the two chromatograms currently visualized. Two different chromatograms can be loaded into the top and bottom windows.
With the left and right limits, the top window can be assigned to display a desired time frame of the first chromatogram. In the same way, the second chromatogram can be visualized with a desired time frame, eventually corresponding to the reference chromatogram area in the top window. The two areas of the two chromatograms may be different to eventually adjust the difference on retention time of the two chromatograms. This operation compares chromatograms with different retention time but stretched on the screen.

Note The Print option is only available when both chromatograms are loaded in memory.

- **Quit Compare Chromatograms** — Exits the compare chromatograms module.

View Upper/View Lower Menu

This menu gives access to the functions for changing the aspect of the chromatogram displayed on the upper or lower window. You can select the following functions:

- **Original Scale and Offset** — Restores the original scale and offset after a **Set Manual Scale** has been performed. The chromatogram is generally stored with original scale and offset calculated to keep in scale all peaks not exceeding the 1000 mV full scale.
- **Set Manual Scale and Offset** — Enters a manual scale to display the upper or lower chromatogram in the window. After any manual modification of the scale, it is always possible to restore the original values with the function **Original Scale and Offset**. The chromatogram is generally stored with original scale and offset calculated to keep in scale all peaks not exceeding 1000 mV full scale.
- **Set Manual Zoom** — Enters a manual zoom scale and zoom time to display the chromatogram.
- **Fit to Highest Peak** — Adjusts the scale of the top window in order to keep in scale any peak being part of the chromatogram. Even peaks with height higher than 1000 mV is automatically in scale.
- **Fit to Highest Peak on Scale** — Adjusts the scale of the top window in order to keep in scale any peak being part of the chromatogram but within 1000 mV of height.
- **View Left / Right Limits** — Sets the time scale used for the chromatogram visualized, with the **Left** and **Right limits**.
- **Equalize Zoom** — Sets the scale used for the chromatogram visualized on the upper window, the same as the scale currently used to display the chromatogram in the lower window from **View upper** menu or vice-versa from **View lower** menu.

Show Menu

This menu gives access to the functions for changing the aspect of the chromatogram displayed. You can select the following functions:

- **Peak Baseline** — Displays the baseline correction of the chromatogram. If a check mark is shown beside the command, the chromatogram is visualized with a dashed line of the baseline correction, otherwise only the chromatogram data points are shown.
- **Peak Maxima** — Displays a small tick on the top of each peak. If a check mark is shown beside the command, the chromatogram is visualized with small marks indicating the maximum of the peak, and indicating that the peak is integrated.
- **Retention Time** — Displays the retention time of the peaks. If a check mark is shown beside the command, the chromatogram is visualized with the retention time at the maximum of the peak, and indicating that the peak has been eluted at the reported time

- **Peak Name** — Displays the name of the components. If a check mark is shown beside the command, the chromatogram is visualized with the name of each component found in the chromatogram.

Note The names of the components are reported only if the chromatogram has been processed, and if the method currently in memory corresponds to the method used for the original sample acquisition.

- **Start/Stop** — Displays the start and stop point of each peak. If a check mark is shown beside the command, the chromatogram is visualized with two small arrows indicating the start and end point of the peaks.
- **None of Above** — Disables all the functions currently selected for the chromatogram displayed.
- **Vertical Marker** — Displays a vertical marker on the two windows. Through this vertical marker you can compare the retention times of the two chromatograms. See **Redraw**.
- **Redraw** — Clears all **Vertical Marker** traced on chromatograms.

Chromatogram Icons

The chromatograms icons are a series of functions to manipulate the chromatogram view.

Icon Function	Description
	Restores the chromatogram currently in memory with the original scale and offset. After a number of zoom commands you would like to review the original chromatogram time frame. Through this command the system immediately restores the full chromatogram view.
	Advances the chromatogram view by the same time frame of the actual window or half the actual window.
	Remembers the last 10 chromatogram time-frame views and it restores the last 10 zoom steps.

Elemental Analyzer Status

This chapter provides the instructions to visualize the status of the Elemental Analyzer in *EagerSmart* for *FlashSmart*, Flash 2000, Flash 4000, and EA 1110 (USB or A/D) versions.

Contents

- [Status of the FlashSmart and Flash 2000 Elemental Analyzers](#)
- [Status of the Flash 4000 Elemental Analyzer](#)
- [Status of the EA 1110 Elemental Analyzer](#)

Status of the FlashSmart and Flash 2000 Elemental Analyzers

FlashSmart and Flash 2000 Status comprises the following tabs:

- “General” on [page 152](#)
- “Detector” on [page 153](#)
- “Auto-Ready” on [page 154](#)
- “Special Functions” on [page 155](#)

All the pages have the following buttons and status bars:

Button	Description
Step sampler tray position	Performs the MAS Plus Autosampler maintenance. Refer to the <i>FlashSmart Operating Manual</i> or <i>Flash 2000 Operating Manual</i> .
Ok	Confirms all modifications done in the current tab and the program returns to the previous tab.
Help	Opens help instruction.

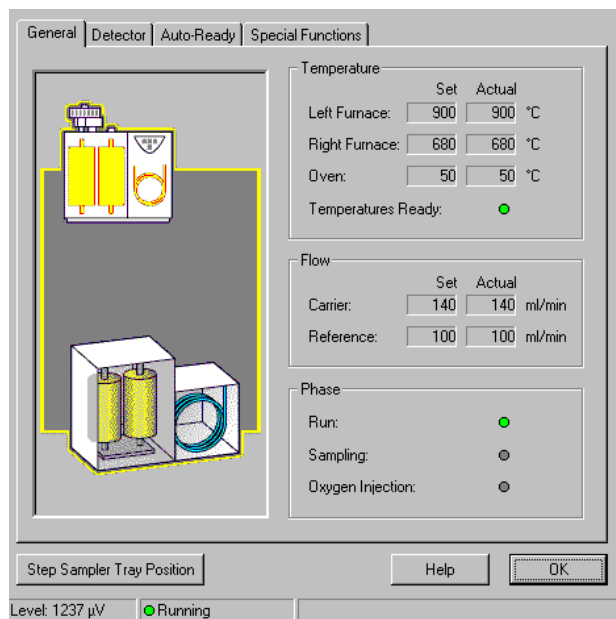
Bar	Description
Level μV	Indicates the signal level in micro Volt. In Ready status, and in absence of peaks, the signal must generally be about 1000 μV . If the level is far from this value, adjust the signal level in “Detector” on page 153 .
Instrument Condition	Indicates the instrument condition: Ready for analysis, Not Ready, Running , and so on.

Bar	Description
Error Message	Displays messages of possible errors occurred inside the instrument For example: Oxygen pressure too low, Furnace over limit...

General

This tab shows temperatures, flows, and status of the connected instrument. See [Figure 111](#).

Figure 111. *FlashSmart* and Flash 2000 General Status Tab



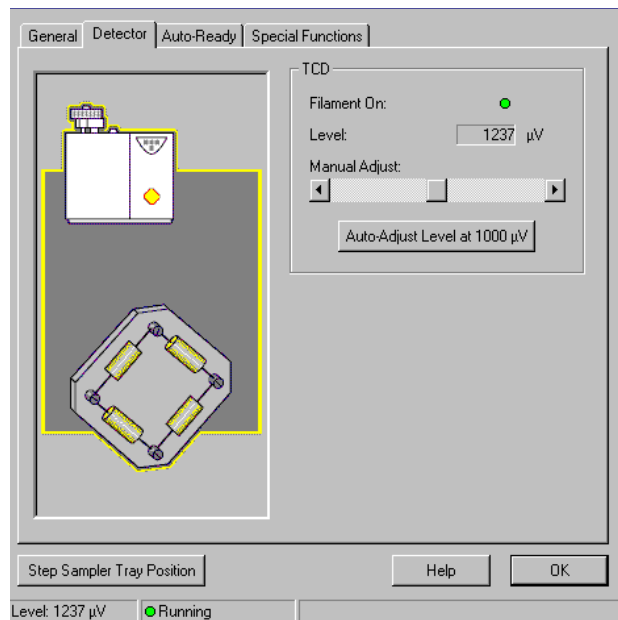
This tab comprises the following fields:

- **Temperature** — Reports the set temperatures (column **Set**), and the currently read values (column **Actual**). The indicator beside **Temperature Ready** is green when the actual temperatures of furnaces and oven reach the set value.
- **Flow** — Reports the set flows (column **Set**), and the currently read values (column **Actual**).
- **Phase** — Includes three LEDs:
 - **Run** = When **green**, the instrument is acquiring data.
 - **Sampling** = When **green**, the sample is dropped into the combustion reactor.
 - **Oxygen Injection** = When **green**, Oxygen is entering the carrier pneumatic circuit.

Detector

The Detector tab is shown in Figure 112.

Figure 112. FlashSmart and Flash 2000 Detector Status tab



This tab comprises the following field:

TCD

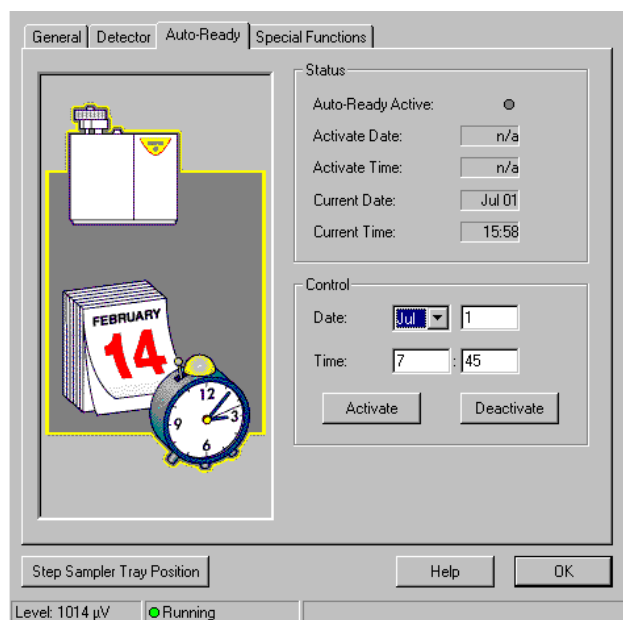
This field shows the following LED, bar and buttons:

- **Filament On** — Indicates the status of the detector filament. The **green** light indicates that the detector filament is active.
- **Level** — Indicates the signal actual value in μV . In the **Ready** status and in absence of peaks, the signal must generally be about 1000 μV . If the level is far from this value, adjust it by moving the cursor of the **Manual Adjust** scroll bar, or by clicking **Auto-Adjust Level at 1000 μV** .
- **Manual Adjust Scroll** — See **Level**.
- **Auto-Adjust Level At 1000 μV** — See **Level**.

Auto-Ready

Resets the operating conditions of temperature and flows on the date and time specified in this tab. See [Figure 113](#).

Figure 113. *FlashSmart* and Flash 2000 Auto-Ready Status tab



This tab comprises the following fields and buttons:

- **Status** — Indicates the activate time and data to start running analyses, and the current time and data. These indication are not editable.
See “[Operations](#)” on [page 154](#).
- **Control** — Includes appropriate boxes to set date and time for instrument **Auto-Ready**.
- **Activate** — Sends to the instrument the set date and time for Auto-Ready, and the current date and time of your computer.
- **Deactivate** — Gives up the Auto-Ready.

Operations

When the instrument is not used for some time, it is possible to decrease the temperature of the furnaces to save power and extend their life. It is also possible to decrease the flow of gases to reduce consumption; see [Chapter 7](#).

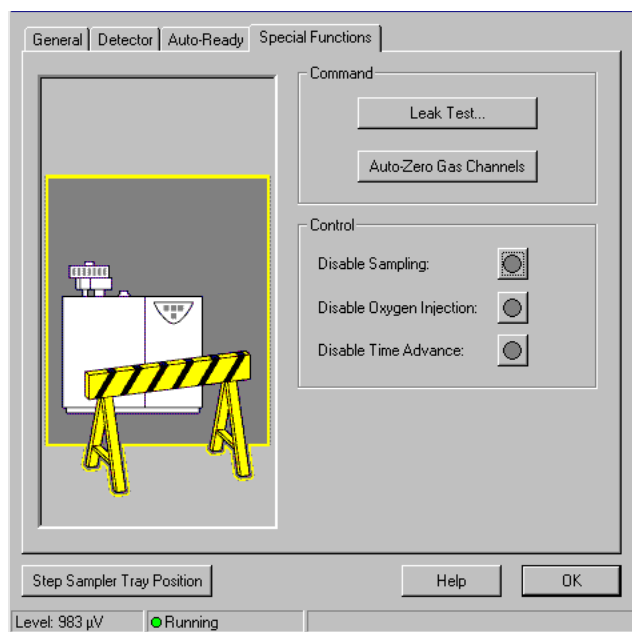
If the date and time to start running analyses again are known, it is possible to have the instrument restore operating temperatures and be in the Ready condition on the specified date and time. To do this, put the instrument in Stand-by condition. In the **Control** box of this page, set month, day, time (hours and minutes), when the instrument must exit Stand-by condition. Then click **Activate** for sending to the instrument the set date and time for Auto-Ready, and the current date and time of your computer. To give up Auto-Ready, click **Deactivate**.

In the **Status** section, the green indicator means that Auto-Ready is active. The boxes below show month/day and hours/minutes of activation as well as month/day and hours/minutes currently set in the instrument.

Special Functions

This tab contains special functions, such as **Leak Test** and **Autozero Gas**. It also disables sampling and oxygen injection, and stops time progress during acquisition. See [Figure 114](#).

Figure 114. FlashSmart and Flash 2000 Special Functions tab

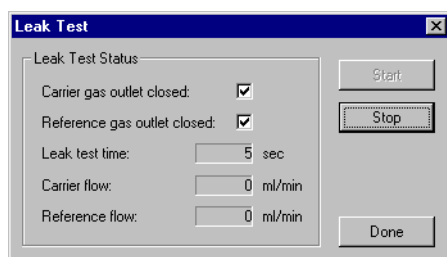


This tab comprises the following fields:

Command

- **Leak Test** — Checks for leakage the Carrier and Reference pneumatic circuits. See [Figure 115](#).

Figure 115. Leak test



In practice, solenoid valves shut the gas outlets of the two channels.

- If there is a gas leak in the circuit, the flow controller can let some gas flow to the circuit, whereas on the contrary.
- If the circuit is leak free, no gas can come from the regulator.

To perform the leak test, refer to the following operating sequence.

- **Auto-Zero Gas Channels** — Calibrations to zero the flow controllers. The gas inlet solenoid valves of the Carrier and Reference channels are closed, and the flow reading is set to zero.

❖ To perform a leak test

1. Press **Start** to begin the operation.

2. When starting **Leak Test**, the system asks if the zero of flow controllers has to be calibrated, reply **Yes** to this question. This operation takes place in less than one minute.
3. Then gas outlets are closed by the solenoid valves. Wait for some time, according to the instrument configuration, to let the gas circuit reach the equilibrium pressure. From now, the values of **Carrier flow** and **Reference flow** must remain at about 0 mL/m (max 3 mL/m). This means that the circuit is leak-free.

Note Leaks in the system are generally due to incorrect closure of the reactors and filters locking nuts. Rarely, leaks may be due to the autosampler.

4. To terminate the leak test, and restore the flow operating values, click **Stop** and **Done**.

Control

Button	Description
Disable Sampling	Disables the autosampler progress.
Disable Oxygen Injection	Disables the oxygen introduction into the carrier circuit.
Disable Time Advance	Stops the time progress during sample acquisition.

Status of the Flash 4000 Elemental Analyzer

Flash 4000 Status comprises the following tabs:

- “General” on [page 157](#)
- “Detector” on [page 157](#)
- “Stand-by/Wake-up” on [page 158](#)
- “Traps Functions” on [page 160](#)
- “Special Functions” on [page 160](#)

All the pages have the following buttons and bars:

Button	Description
Ok	Confirms all modifications done in the current tab, and the program returns to the previous tab.
Help	Open the help instruction.

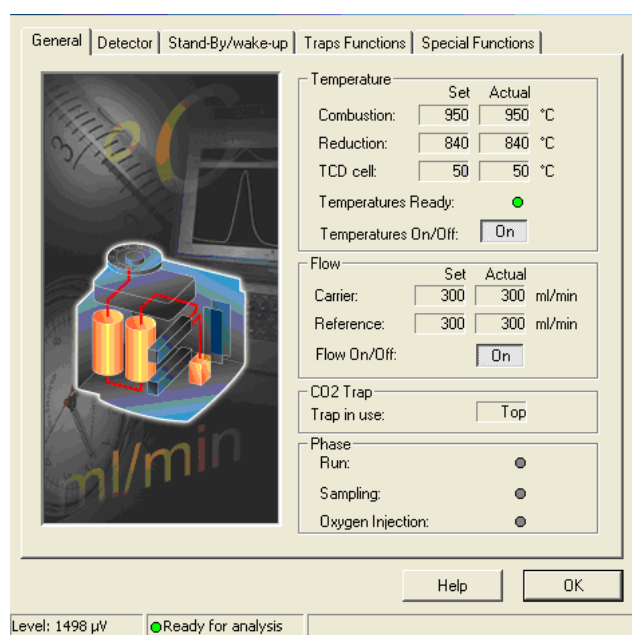
Bar	Description
Level μV	Indicates the signal level in μV . In Ready status, and in absence of peaks, the signal must generally be about 1000 μV . If the level is far from this value, adjust the signal level in “Detector” on page 157 .
Instrument Condition	Indicates the instrument condition: Ready for analysis , Not Ready , Running , and so on.

Bar	Description
Error Message	Displays messages of possible errors occurred inside the instrument. For example: No Connection , Oxygen pressure too low , Furnace over limit...

General

This tab shows temperatures, flows, traps, and status of the connected instrument.
See [Figure 116](#).

Figure 116. Flash 4000 General Status Tab



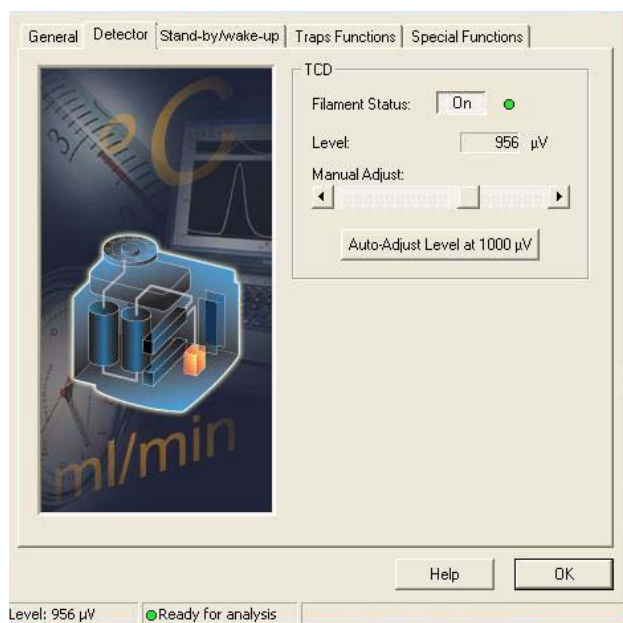
This tab comprises the following fields:

- **Temperature** — Reports the set temperatures (column **Set**), and the currently read values (column **Actual**). The indicator beside Temperature Ready is green when the actual temperatures of reactors and TCD cell reach the set value. It is possible to switch on and off its function with the proper button.
- **Flow** — Reports the set flows (column **Set**), and the currently read values (column **Actual**). It is possible to switch on and off its function with the proper button.
- **CO₂ Trap Box** — Specifies the top or bottom trap currently in use.
- **Phase** — Includes three LEDs:
 - **Run** = When **green**, the instrument is acquiring data.
 - **Sampling** = When **green**, the sample is dropped into the combustion reactor.
 - **Oxygen Injection** = When **green**, oxygen is entering the carrier pneumatic circuit.

Detector

The Detector tab is shown in [Figure 117](#).

Figure 117. Flash 4000 Detector Status Tab



This tab comprises the following field:

TCD

Displays the following LED, bar and buttons:

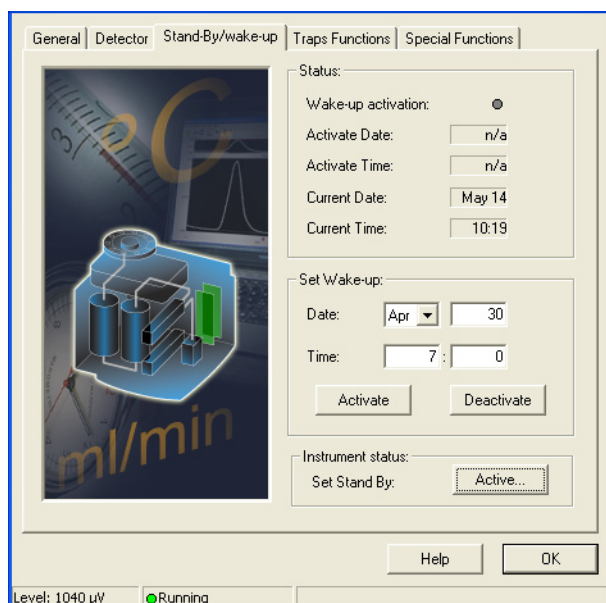
- **Filament Status On/Off LED** — Sets the TCD filaments **On** or **Off**.
- **Filament Status LED** — Indicates the status of the detector filament. The **green** light indicates the detector filaments are active.
- **Level** — Indicates the signal actual value in μV . In the Ready status and in absence of peaks, the signal must generally be about 1000 μV .
If the level is far from this value, adjust it by moving the cursor of the **Manual Adjust** scroll bar, or by clicking **Auto-Adjust Level at 1000 μV** .
- **Manual Adjust Scroll** — See **Level**.
- **Auto-Adjust Level At 1000 μV** — See **Level**.

Stand-by/Wake-up

These are timed functions which can be programmed to minimize dead times.

These functions reset the operating conditions of temperature and flows on the date and time specified in this tab. See [Figure 118](#).

Figure 118. Flash 4000 Stand-by/Wake-up Tab



This tab comprises the following fields and buttons:

- **Status** — Indicates the activate time and data to start running analyses, and the current time and data. These indication are not editable. See “Operations” on page 159.
- **Set Wake-up** — Includes appropriate boxes to set date and time for instrument Wake-up.
- **Activate** — Sends to the instrument the set date and time for Wake-up, and the current date and time of your computer.
- **Deactivate** — Gives up Wake-up.
- **Instrument Status** — Indicates the current state of the instrument.
- **Active/Stand-by** — Puts the instrument in stand-by, or active condition.

Operations

When the instrument is not used for some time, it is possible to decrease the temperature of the furnaces to save power and extend their life. It is also possible to decrease the flow of gases to reduce consumption; see [Chapter 7](#).

If the date and time to start running analyses again are known, it is possible to have the instrument restore operating temperatures, and be in the Ready condition on the specified date and time. To do this, put the instrument in Stand-by condition, then in the **Set Wake-up** box of this page, set month, day, time, (hours and minutes), when the instrument must exit Stand-by condition. Then click **Activate** for sending to the instrument the set date and time for auto-ready, and the current date and time of your computer. To give up the Wake-up, click **Deactivate**.

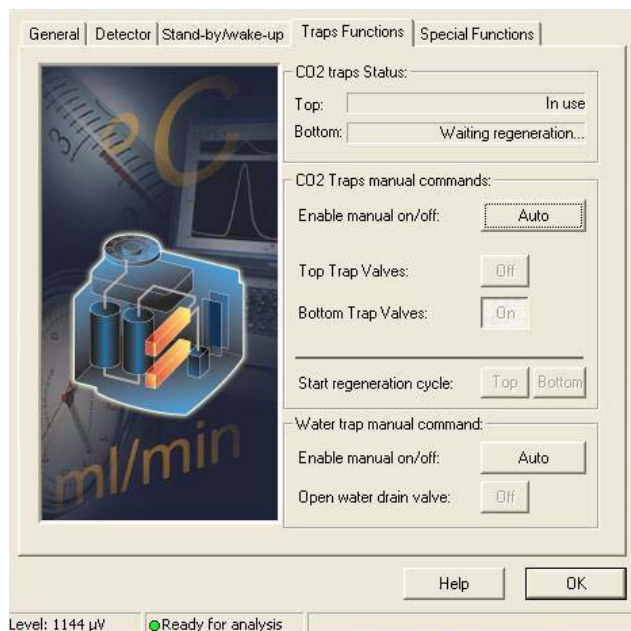
In the **Status** section, the green indicator means that Wake-up is active.

The boxes below show month/day and hours/minutes of activation as well as month/day, and hours/minutes currently set in the instrument.

Traps Functions

This tab contains the functions for the automatic and manual control of the adsorption filters (traps), and of the water condensate drainage. See [Figure 119](#).

Figure 119. Flash 4000 Traps Functions Tab



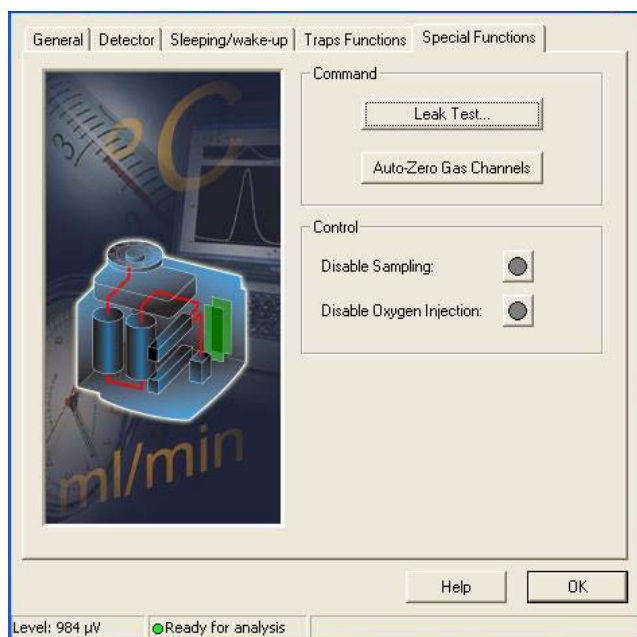
This tab comprises the following fields and buttons:

- **CO₂ Traps Status** — The status of the top and bottom traps are visualized. The status of the traps may be: **In use**, **Heating**, **Cooling**, **Complete** and **Wait to regeneration**. Note that when a trap is **In use**, the other is under regeneration.
- **CO₂ Traps Manual Command** — Enables Manual **On/Off** button:
 - **Auto**: This is the default condition. The traps are automatically controlled by the instrument. All the functions available in the box are non selectable.
 - **Manual**: This condition is used for diagnostic scope. All the functions available in the box are selectable for the manual On/Off control of the top and bottom trap valves and trap heating. Moreover, it is possible to start the regeneration cycle for the top or bottom trap.
- **Water Trap Manual Command** — Enables Manual **On/Off** button:
 - **Auto**: This is the default condition. The water trap is automatically controlled by the instrument; the function **Open water drain valve** is non selectable.
 - **Manual**: This condition is used for diagnostic scope. The function **Open water drain valve** is selectable for its manual On/Off control.

Special Functions

This tab contains special functions, such as **Leak Test** and **Autozero Gas**, disables sampling and oxygen injection, and stops the time progress during acquisition. See [Figure 120](#).

Figure 120. Flash 4000 Special Functions Tab

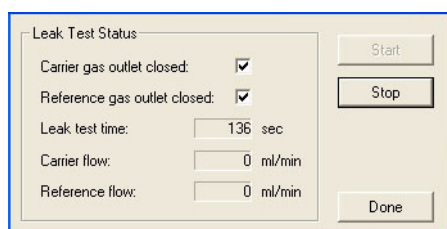


This tab comprises the following fields:

Command

- **Leak Test** — Checks for leakage the Carrier and Reference pneumatic circuits. In practice, solenoid valves shut the gas outlets of the two channels. See [Figure 121](#).

Figure 121. Leak test



- If there is a gas leak in the circuit, the flow controller can let some gas flow to the circuit, whereas, on the contrary.
- If the circuit is leak free, no gas can come from the regulator.

To perform the leak test, refer to the following operating sequence.

- **Auto-Zero Gas Channels** — Calibrates to zero the flow controllers: the gas inlet solenoid valves of the Carrier and Reference channels are closed, and the flow reading is set to zero.

❖ To perform a leak test

1. Press **Start** to begin the operation. A window appears where you are requested to perform the leak test with the **CO₂ trap regeneration** on the last use.
2. A second window appears where you are requested to perform the Autozero.
3. Then gas outlets are closed by the solenoid valves. Wait for some time, according to the instrument configuration, to let the gas circuit reach the equilibrium pressure.

From now, the values of **Carrier flow** and **Reference flow** must remain at about 0 mL/min and 5mL/min. This means that the circuit is leak-free. Higher values indicate that the system is not leak-free.

Note Leaks in the system are generally due to incorrect closure of the reactors locking nuts.

4. To terminate the leak test and restore the flow operating values, press **Stop** and **Done**.

Control

Button	Description
Disable Sampling	Disables the autosampler progress.
Disable Oxygen Injection	Disables the oxygen introduction into the carrier circuit.

Status of the EA 1110 Elemental Analyzer

EA 1110 Status comprises the following pages:

- “General” on [page 163](#)
- “Detector” on [page 164](#)
- “Auto-Ready” on [page 164](#)
- “Special Functions” on [page 165](#)

All the pages have the following buttons and bars:

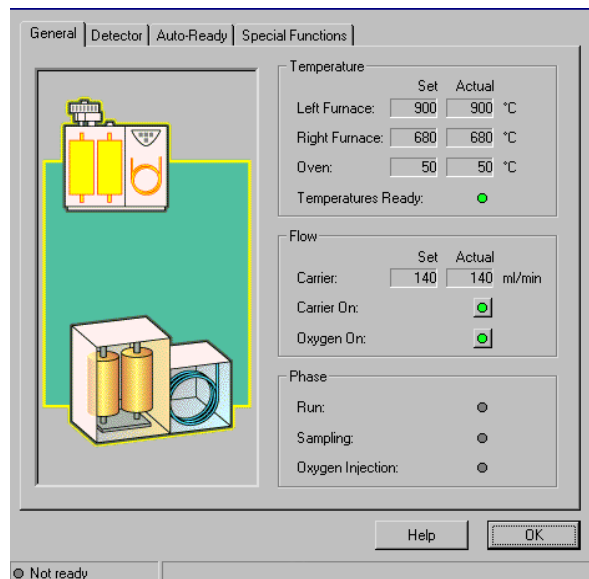
Button	Description
Ok	Confirms all modifications done in the current tab and the program returns to the previous tab.
Help	Opens help instruction.

Bar	Description
Instrument Condition	Indicates the instrument condition: Ready for analysis , Not Ready , Running and so on.
Error Message	Displays messages of possible errors occurred inside the instrument. For example Oxygen pressure too low , Furnace over limit...

General

This page shows temperatures, flows, and status of the connected instrument. See [Figure 122](#).

Figure 122. EA 1110 General Status Tab



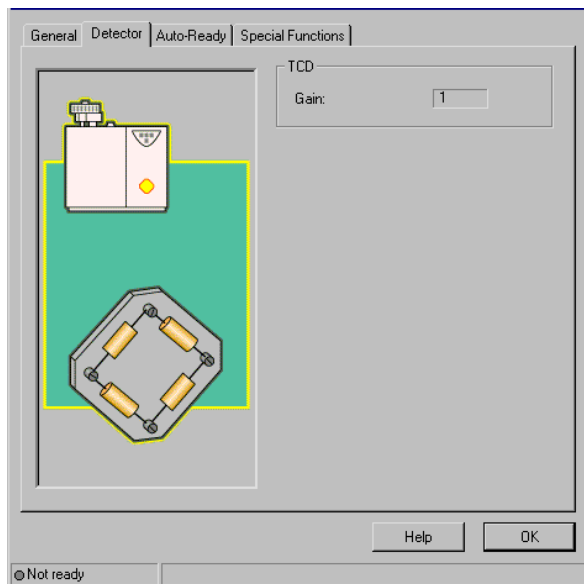
This tab comprises the following fields:

- **Temperature** — Reports the set temperatures (column **Set**), and the currently read values (column **Actual**). The indicator beside **Temperature Ready** is green when the actual temperatures of furnaces and oven reach the set value.
- **Flow** — Reports the set carrier flow (column **Set**), and the currently read value (column **Actual**). The following buttons and LEDs are also included.
 - **Carrier On** button — When selected, the helium line is closed. Helium flows through a calibrated restrictor that reduces the flow to 10-20 mL/min. Therefore saving on gas consumption is achieved without putting the instrument in Stand-by mode.
 - **Carrier On** LED — When green colored, the helium line is open. By closing the line, the LED gets red colored. See the relevant button.
 - **Oxygen On** button — When pressed, the oxygen line is closed.
 - **Oxygen On** LED — When green colored, the oxygen line is open. By closing the line, the LED gets red colored. See the relevant button.
- **Phase** — Includes three LEDs:
 - **Run** = When green, the instrument is acquiring data.
 - **Sampling** = When green, the sample is dropped into the combustion reactor.
 - **Oxygen Injection** = When green, oxygen is entering the carrier pneumatic circuit.

Detector

This tab is shown in [Figure 123](#).

Figure 123. EA 1110 Detector Status Tab



TCD

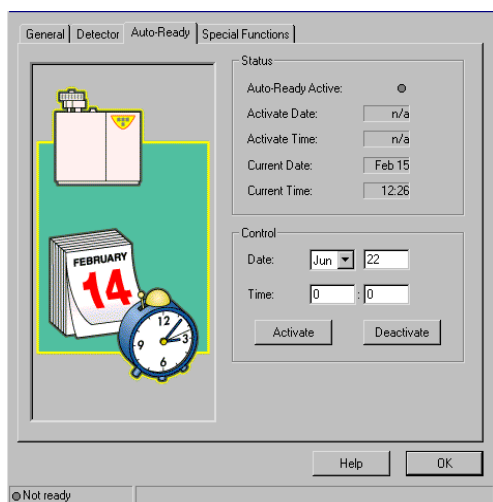
This field shows the following box:

- **Gain** — When the Gain is equal to 10, it means that the signal coming from the detector is amplified by ten times, whereas it is not when the Gain is equal to 1.

Auto-Ready

Resets the operating conditions of temperature and flows on the date and time specified in this page. See [Figure 124](#).

Figure 124. EA 1110 Auto-Ready Status Tab



This tab comprises the following fields and buttons:

- **Status** — Indicates the activate time and data to start running analyses, and the current time and data. These indication are not editable. See “Operations” on page 165.
- **Control** — Includes appropriate boxes to set date and time for instrument **Auto-Ready**.
- **Activate** — Sends to the instrument the set date and time for Auto-Ready and the current date and time of your computer.
- **Deactivate** — Gives up Auto-Ready.

Operations

When the instrument is not used for some time, it is possible to decrease the temperature of the furnaces to save power and extend their life. It is also possible to decrease the flow of gases to reduce consumption. See [Chapter 7](#) .

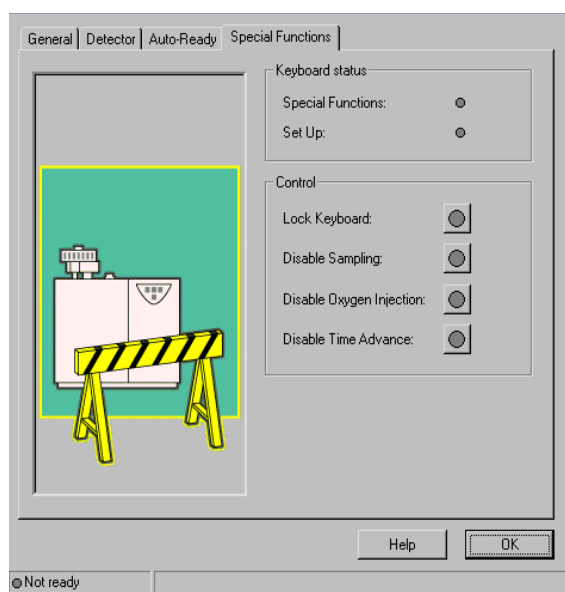
If the date and time to start running analyses again are known, it is possible to have the instrument restore operating temperatures, and be in the Ready condition on the specified date and time. To do this, put the instrument in Stand-by condition. In the **Control** box of this page, set month, day, time (hours and minutes), when the instrument must exit Stand-by condition. Click **Activate** for sending to the instrument the set date and time for Auto-Ready, and the current date and time of your computer. To give up Auto-Ready, click **Deactivate**.

In the **Status** section, the green indicator means that Auto-Ready is active. The boxes below show month/day and hours/minutes of activation as well as month/day and hours/minutes currently set in the instrument.

Special Functions

This tab contains special functions, and it also allows to disable sampling and oxygen injection, and to stop time progress during acquisition. See [Figure 125](#).

Figure 125. EA 1110 Special Functions Tab



View Maintenance

This chapter provides the instructions to view and set-up the instrument maintenance program.

Contents

- [Introduction](#)
- [View Menu](#)
- [Edit Menu](#)

Introduction

Each reactor, filter, and relevant fillings need to be replaced according to the analytical configuration used. For each configuration, an average life of its components has been established.

The **View Maintenance** option indicates when the different components must be replaced.

This window allows you to set counters analyses, to display alarm messages for replacing catalyst and adsorption filters, or removing ashes. When the lifetime values previously set are reached, an alarm message is visualized on Main Menu, and monitor the sample actually being acquired pages.

This program prompt shows all the active components of the current instrument configuration with their lifetime situation, namely the number of runs until next maintenance, those since last maintenance, and those before the warning message is visualized. The examples of [Figure 126](#) and [Figure 127](#) show the analytical circuit components for which the maintenance routine is required.

Figure 126. Example of Maintenance Program Schedule (1)

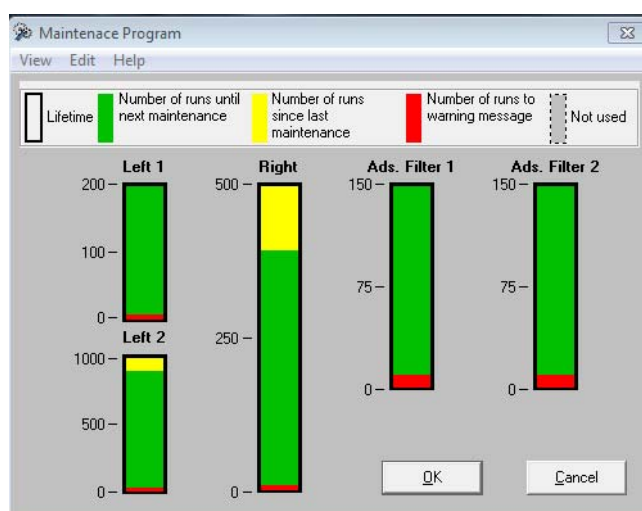
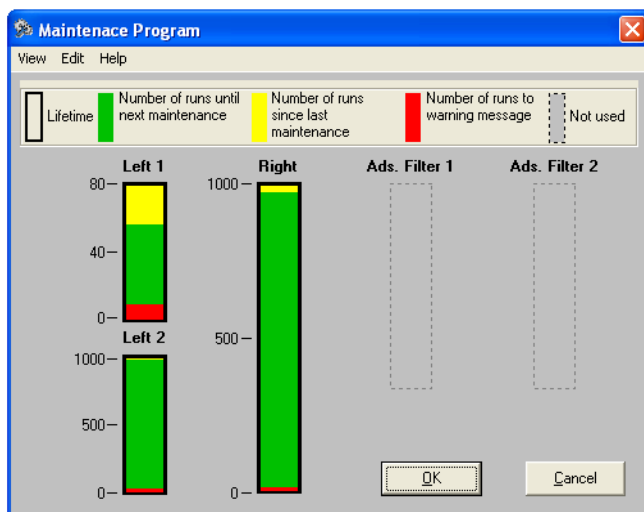


Figure 127. Example of Maintenance Program Schedule (2)



This program prompt shows all the active components of the current instrument configuration with their lifetime situation, namely the number of runs until next maintenance, those since last maintenance, and those before the warning message is visualized.

The examples of [Figure 126](#) and [Figure 127](#) show the analytical circuit components for which the maintenance routine is required.

Component	Description
Left	Represents the oxidation reactor. In Figure 126 and Figure 127 Left 1 represents the crucible or ashes, while Left 2 represents the oxidation reactor.
Right	Represents the reduction o pyrolysis reactor.
Ads Filter 1	Represents the first adsorbent filter. (Not present for Flash 4000)
Ads Filter 2	Represents the second adsorbent filter. (Not present for Flash 4000)

In the diagram the active components are indicated with colored areas. The numerical scale of their lifetime are shown on the left. The meaning of each colored area is indicated in the upper section of the diagram.

The components not present in the concerned instrument configuration are indicated by a dashed line.

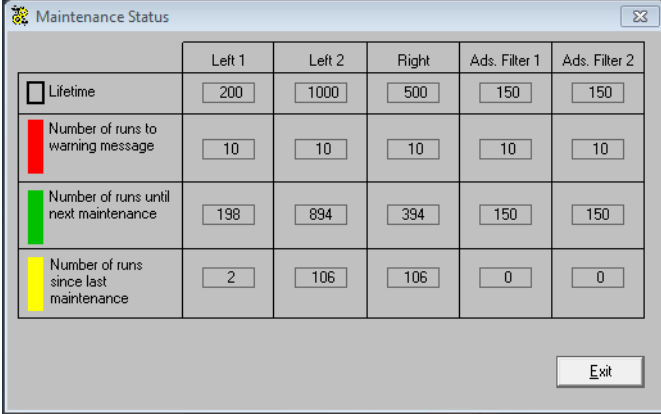
Button	Description
Cancel	Clears all modifications done in the current section, and the program returns to the previous tab.
OK	Confirms all modifications done in the current tab, and the program returns to the previous tab.

View Menu

Show Maintenance Status

This program section visualizes the instrument maintenance status as shown in the example of [Figure 128](#).

Figure 128. Example of Maintenance Status Tab



	Left 1	Left 2	Right	Ads. Filter 1	Ads. Filter 2
☐ Lifetime	200	1000	500	150	150
 Number of runs to warning message	10	10	10	10	10
 Number of runs until next maintenance	198	894	394	150	150
 Number of runs since last maintenance	2	106	106	0	0

- **Life time** — Indicates the preset maximum number of analyses each individual component can perform.
- **Number of runs to warning message** — Indicates that when any of the components still have to run only 10 analyses to reach the number set in **Lifetime**, each program page shows the message **Check Maintenance**. If the message is ignored and analyses are continued, the message **Alarm** is visualized when the preset number of runs is reached. This does not stop the analytical cycle.
- **Number of runs until next maintenance** — Indicates the number of analyses to be performed before next maintenance.
- **Number of runs since last maintenance** — Indicates the number of analyses performed after last maintenance.

Edit Menu

This menu allows to view in detail the default conditions of the components of the concerned instrument configuration, and to create a different maintenance program from the default one.

Set Maintenance

It is possible to set the maintenance program either entering in a manual mode the lifetime values more suitable to your needs, or using the default ones.

- **Manual** — [Figure 129](#) shows an example of **Edit Maintenance Table**.

Figure 129. Example of Manual Maintenance Program

	Left 1	Left 2	Right	Ads. Filter 1	Ads. Filter 2
☐ Lifetime	200	1000	500	150	150
☒ Number of runs to warning message	10	10	10	10	10
☒ Number of runs until next maintenance	198	894	394	150	150
☒ Number of runs since last maintenance	2	106	106	0	0

OK Cancel

For inserting the component lifetime value, click on the proper box of the first line, then type in the value your analytical method requires.

In the second line of this table you should enter the number of analyses to be run before the warning message is visualized for expiry of the component lifetime.

Note After typing a lifetime value, always press the **Enter** key.
Before abandoning this program section click **OK** command box if you want to confirm the set value, or **Cancel** if you do not want it.

- **Default** — Sets the maintenance program according to the instrument configuration selected. See [Figure 130](#).

Figure 130. Example of Default Maintenance Program (1)

	Left 1	Left 2	Right	Ads. Filter 1	Ads. Filter 2
☐ Lifetime	200	1000	500	150	150
☒ Number of runs to warning message	10	10	10	10	10
☒ Number of runs until next maintenance	198	894	394	150	150
☒ Number of runs since last maintenance	2	106	106	0	0

OK Cancel

Reset Maintenance

Resets the lifetime of the component as reactor, filter, and ashes, that has just been replaced. For example, the adsorption filters lifetime is usually shorter than the tubes. Therefore, after the adsorption filters maintenance, only the lifetime of the latter must be reset but not that of the reactor. See [Figure 131](#).

Figure 131. Example of Default Maintenance Program (2)

	Left 1	Left 2	Right	Ads. Filter 1	Ads. Filter 2
☐ Lifetime	200	1000	500	150	150
Number of runs to warning message	10	10	10	10	10
Number of runs until next maintenance	200	894	394	150	150
Number of runs since last maintenance	0	106	106	0	0

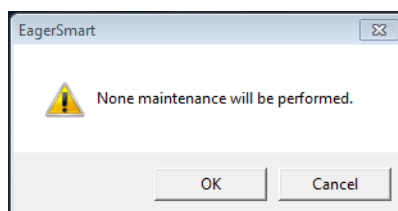
Reset Reset Reset Reset Reset

OK Cancel

Button	Description
Reset	Resets the lifetime of the component that has just been replaced.

Exclude Maintenance

Disables the Maintenance Program.



Recalculation

This chapter provides the instructions to recalculate sample batches.

Contents

- [Recalculation Dialog Box](#)

Recalculation Dialog Box

The Recalculation dialog box recalculates sample batches. *EagerSmart* performs the recalculation of the samples first-last (included) using the selected option. See [Figure 132](#).

Figure 132. Recalculation Dialog Box

Recalculation

Integration options:

- ☒ Reintegrate
- ☒ Identify peaks
- ☒ Review Integration
- ☐ Review Identification
- ☒ Save after Integration
- ☐ Review report text
- ☐ Review report publisher

Chromatogram source:

- ☒ Sample sequence
- ☐ Single sample (out of seq)

Recalculate sample(s) from Sample Sequence:

First sample: Last sample:

Recalculate sample out of Sample Sequence:

Data filename:

Weight: Protein Factor:

OK Cancel

The available options for recalculation are:

- [“Integration Options” on page 174](#)
- [“Chromatogram Source” on page 174](#)
- [“Recalculate Sample\(s\) from Sample Sequence” on page 174](#)
- [“Recalculate Sample\(s\) not in Sample Sequence” on page 175](#)

Integration Options

- **Reintegrate** — Includes/excludes the peak integration during the recalculation process. This option must be disabled when a manual peak modification has been performed. The reintegration would cancel any manual modification replacing the original peak results.
- **Identify** — Includes/excludes the peak identification during the recalculation process. This option must be enabled when a modification has been entered in the Component Table.
- **Review Integration** — Includes/excludes the manual modification of the peak baseline during the recalculation process. Enabling this function, after the automatic integration of the peaks, the system enters the module showing the chromatogram, and offering the possibility to manually modify any peak start/stop, and the baseline correction.
- **Review Identification** — Includes/excludes the manual modification of peak identification during the recalculation process. Enabling this function, after the automatic identification of the peaks, the system enters the module showing the chromatogram, and offering the possibility to manually modify any peak retention time and window. This function is very helpful for chromatograms that have a significant peak drifting. Every sample can be manually adjusted for best peak identification before report generation.
- **Save after Reintegration** — A **Save Chromatogram** after the calculation option includes/excludes the save function during the recalculation process. Enabling this function, after the calculation and report, *EagerSmart* saves the chromatogram peak data on disk.
- **Review Report Text** — Include/exclude the manual modification of the report during the recalculation process. Enabling this function, after the automatic report generation, the system enters the module showing the report, and offering the possibility to manually modify any report line. The system also imports comments or part of pre-defined text, and it is possible to generate reports with different layout easily.
- **Review Report Publisher** — Include/exclude the manual modification of the report publisher. See [Chapter 19, “Report Publisher.”](#)

Chromatogram Source

EagerSmart can recalculate any chromatogram previously stored on disk.

The chromatogram can be part of the sample sequence of the method in memory, or it can be any other chromatogram acquired with any other method. This box informs the system on which chromatogram has to be reprocessed.

- **Sample Sequence** — You should supply the first-last sample to be reprocessed. See [“Recalculate Sample\(s\) from Sample Sequence”](#) on [page 174](#).
- **Single Sample (out of seq.)** — You can enter a **Single Sample** that is reprocessed out of the sequence with the response factor or calibration curves of the method in memory. See [“Recalculate Sample\(s\) not in Sample Sequence”](#) on [page 175](#).

Recalculate Sample(s) from Sample Sequence

When **Sample Sequence** has been selected in **Chromatogram Source** box:

- **First Sample** — Enters the first Sample to be reprocessed.

- **Last Sample** — Enters the last Sample to be reprocessed.

Recalculate Sample(s) not in Sample Sequence

When **Single Sample** has been selected in **Chromatogram Source** box:

- **Data Filename** — Enters the data filename that is reprocessed with the response factor, or calibration curve of the method in memory.
- **Weight** — Enters the weight of the sample.
- **Protein Factor** — Enters the protein factor.



ATTENTION The reprocessing of a Single Sample not in Sample Sequence does not generate any information for summarize data-base; it can be only an unknown sample, never a calibration.

Summarize Results

This chapter provides the instructions to view the results of a batch of sample.

Contents

- [Introduction](#)
- [File Menu](#)
- [Select Results Menu](#)
- [View Menu](#)
- [Print Menu](#)
- [Summarize Results Grid](#)
- [Elemental Formula Calculator](#)

Introduction

Summarize Results Dialog Box is a tool to view the results of a batch of samples. See [Figure 133](#).

Figure 133. Summarize Results Dialog Box

	Group	Sample name	Filename	Nitrogen
4	0	pasta	december004	2.12
5	0	pasta	december005	2.09
6	0	tin cup	december006	0.00
7	0	pasta	december007	2.07
8	0	glucose	december008	0.00
9	0	tin cap	december009	0.00
10	0	glucose	december010	0.00
11	0	pasta	december011	2.10
12	0	glucose	december012	0.00

You should create the summary internal data base by setting the option “[Append To Summarize](#)” on [page 59](#). Automatically EagerSmart generates all results in a special format available at the end of the sample sequence for statistical calculation.

Summarize Results generates short reports with averages, standard deviations and trend plot of the entire sequence with up to 200 samples.

Icon	Description	See on:
	Load Original Summary Data	page 178
	Save Summarize File	page 179
	Export to Excel File	page 178
	Show Summary Data (Statistical Calculation)	page 184
	Show Summary Graph (Graphic Trend)	page 182
	Print	page 185
	Show Summary Sheet of Selected Group	page 180
	Show Summary Sheet of All Groups	page 180
	View Chromatogram	page 184
	Elemental Formula Calculator	page 185

File Menu

This menu gives access to the following options:

- **Load Original Summary File** — Loads the original summarize file. You can enter new groups of samples for calculation of averages and standard deviation. It is always possible eliminate any entered group modification by loading the original summarize file.

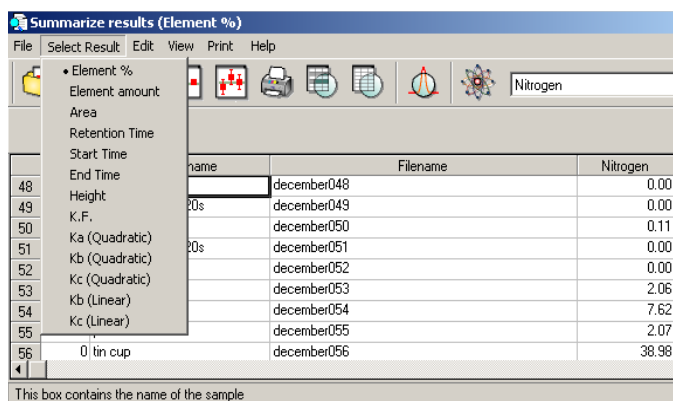
Note Loading original summarize file clears any modification of groups' column done in this section.

- **Save Summarize File** — Saves the modified summarize file. You can enter new groups of samples for calculation of averages and standard deviation. Use this function to save permanently the entered group modification. When selecting **Quit**, if any group modification has been done, the system prompts for the automatic save function of the summarize file.
- **Export to Excel File** — Saves summarize file into Excel file format.
- **Export to Text File** — Saves summarize file into text file format.
- **Quit** — Exits the Summarize Results module.
If any modification has been made on the sample groups, the system prompts for **Save Summarize File**.

Select Results Menu

This menu allows to select the type of result to visualize in the column of the elements. See [Figure 134](#).

Figure 134. Select Results Menu



Even the summarize files created with *EagerSmart* can be converted, load the method and recalculate the whole samples.

Edit Menu

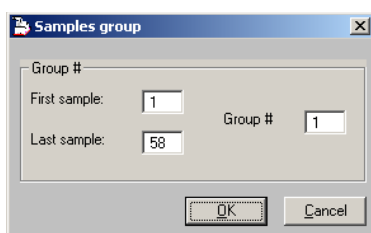
This menu includes the function to clear the group column and the function to fill group of samples with the same group number. Moreover, it includes the function to change the cells format.

- **Cell Format** — Sets the format of each cell. Firstly you should select the cell or the cells you want to change, then with this function, you can set the number of decimal digits to be used for the selected cells.
 - Clicking on the name of the column, the entire column is automatically selected.
 - Clicking on the cell in the upper left corner, the entire summarize grid is affected by the new cell format.

The function **Reset Cells Format** can eventually be used to cancel any cell format modification.

- **Reset Cell Format** — Resets the format of all cells of the summarize grid. Upon requesting this function, all cells are visualized with free format according to the number to be represented. Any previous **Cells Format** is cleared.
- **Insert Group** — Enters the group number for a batch of samples. Upon requesting this function the system shows a box for selecting the first compile, the last sample, and the group number to be assigned. See [Figure 135](#).

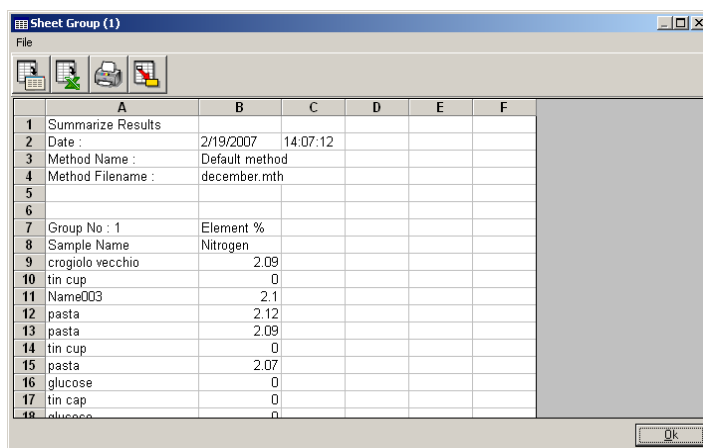
Figure 135. Sample Group Tab



The group number is the key point of the summarize calculation. All operations are performed on the selected group. For example, the average is calculated on all samples having the same group number. See also **Input Box**.

- **Delete All Groups** — Clears all sample groups. Upon requesting this function the system requires a confirmation and then all sample groups is set to zero, ready for entering a new set of groups.
- **Summary Sheet Icons** — The  and  icons shown the summary sheet of selected group and of all the groups respectively. See [Figure 136](#).

Figure 136. Example of Summary Sheet



	A	B	C	D	E	F
1	Summarize Results					
2	Date :	2/19/2007	14:07:12			
3	Method Name :	Default method				
4	Method Filename :	december.mth				
5						
6						
7	Group No : 1	Element %				
8	Sample Name	Nitrogen				
9	crogiolo vecchio	2.09				
10	tin cup	0				
11	Name003	2.1				
12	pasta	2.12				
13	pasta	2.09				
14	tin cup	0				
15	pasta	2.07				
16	glucose	0				
17	tin cap	0				
18	glucose	0				

The page of [Figure 136](#) is visualized only if a batch of samples has been selected with the **Insert Group** command in “**Edit Menu**” on [page 179](#).

- **Copy to Clipboard** — As with most Windows™ applications that use the Clipboard to transfer text, graphics, and other data, you can copy and move text from *EagerSmart* into different applications.

To copy text between *EagerSmart* and another application proceed as follows:

- Select the cells you want to copy.
 - From the Edit menu choose **Copy**.
 - Switch to the other application:
 - If the other application is not open, start the other application.
 - If the other application is already open, press CTRL+ESC, and then choose the application from the Task List.
 - Position the insertion point where you want to insert the text.
 - From the **Edit** menu, choose **Paste** (ALT, E, P).
- **Select Reference Compounds** — Selects a reference compound in the table. See [Figure 137](#).

Figure 137. Compound of Reference Selection Table

	Name	Nitrogen	±%	Carbon	±%	Hydrogen	±%	Sulphur	±%	Oxygen	±%
1	Acetanilide	10.36	0.99	71.09	0.43	6.71	1.33	0	0	11.84	0
2	Atropine	4.84	1.52	70.56	0.43	8.01	1.2	0	0	16.59	0
3	BBOT	6.51	1.35	72.53	0.42	6.09	1.39	7.44	1.26	7.43	1
4	Benzoic acid	0	0	68.85	0.44	4.95	1.5	0	0	26.2	0
5	CEDFNI	20.14	0.98	51.79	0.58	5.07	1.49	0	0	23	0
6	Cystine	11.66	0.99	29.99	0.97	5.03	1.5	26.69	0.97	26.63	0
7	Diphenyltiourea	12.27	0.99	68.39	0.45	5.3	1.47	0	0	14.04	0
8	Methionine	9.39	1.06	40.25	0.73	7.43	1.26	21.49	0.98	21.45	0
9	Nicotinamide	22.94	0.98	59.01	0.51	4.95	1.5	0	0	13.01	0
10	Sulphanilamide	16.27	0.98	41.84	0.71	4.68	1.53	18.62	0.98	18.58	0
11	Triouracile	21.86	0.98	37.49	0.78	3.15	1.68	25.02	0.97	12.48	0
12	Urea	46.65	0.64	20	0.98	6.71	1.33	0	0	26.64	0
13	edta	9.59	1.04	0	0	0	0	0	0	0	0
14	beans	4.03665	2.15	0	0	0	0	0	0	0	0

The reference selection table shows a few substances with percentages of elements and limits admitted for comparison.

To add a new substance in the table, enter the name in the first column and in the elements columns (N, C, H, S, and O) the known percentage of the elements. Tolerance is calculated by the system when **OK** is selected. The tolerance assigned by the system is indicative and it can be increased.

If you want to add a sample you have analyzed in the reference compound table, select the sample line in the **Summary table** and then in the **Edit** menu enable the function **Add compound to reference library**.

When a reference compound is selected, *EagerSmart* compares the percentage of each element of the addressed sample in the **Summarize Result Tab** with the percentage of each element of the reference compound.

If the difference between the two values is within admitted limits, a green LED indicator suggests the good correspondence of the values for each of the elements found. On contrary, the not correspondence is indicated by a red LED indicator. See [Figure 138](#).

Figure 138. Example of Compounds Comparison

Group	Sample name
1	crogiolo vecchio
2	tin cup
3	Name003
4	pasta

Group	Sample name
50	glucose
51	glucose PULSE 20s
52	glucose
53	pasta

- **Add Component to Reference Library** — Adds the data of the addressed sample of the **Summary table** to the reference **Compound table**. Sample name is entered in the Name column, the percentages of the elements calculated for the sample are entered in the elements columns, and the system automatically assigns the admitted tolerance, which however can be modified by you.

View Menu

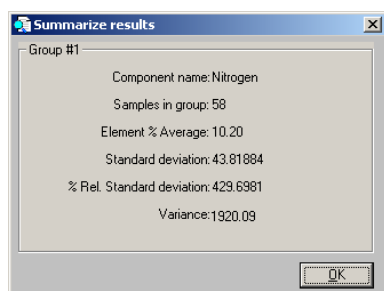
This menu gives access to the functions for:

1. Changing the aspect of the **Samples Grid**.
2. Performing a statistical calculation on a sample group.
3. Viewing graphic trend.
4. Viewing a chromatogram of the addressed sample in the grid.

The available functions are:

- **View Sample Information** — Displays the grid of the samples including or excluding the specific sample information according to this function.
 - If this function is selected, the sample grid includes Filename, Date and Time of injection, and the sample type.
 - When this function is off, the sample grid contains only the sample name and the results.
- **Statistical Calculation** — Performs statistical calculation on the selected group of samples. See [Figure 139](#).

Figure 139. Sample Information Tab



After the component selection, address the group number required by clicking on the sample grid in any column of one sample line. By this function the calculation is started and a box shows average, standard deviation, relative standard deviation, and variance for the specific group of samples.

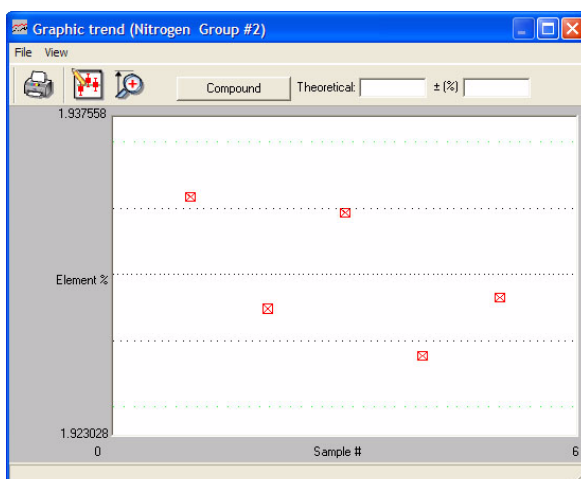


ATTENTION The file EAGER.INI contains a variable to change the **Variance** calculation mode.

Variance Calculation = 0

- Set to 0 for Variance calculation. $\text{Variance} = (\text{Ex}^2 - (\text{Ex})^2/n)/(n-1)$
- Set to 1 for Variance calculation. $\text{Variance} = (\text{Ex}^2 - (\text{Ex})^2/n)/(n)$

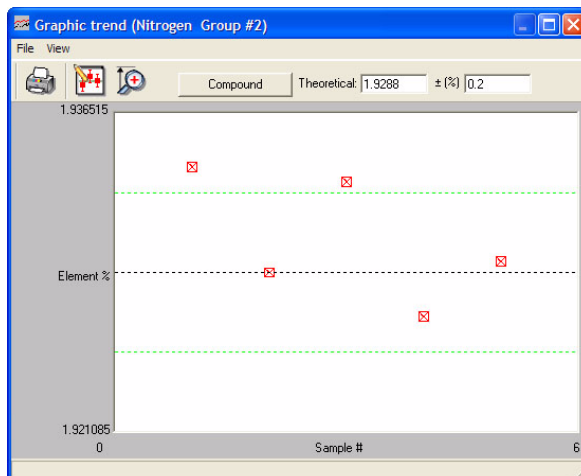
- **Graphic Trend** — Displays a graphic trend for the selected group of samples.
After the component selection, address the group number required by clicking on the sample grid in any column of one sample line. By this function, the calculation is started, and a graphic form shows the results graph trend for the specific group of samples. See [Figure 140](#).

Figure 140. Example of Summarize Graphic (1)

The dashed line in the middle of the graph represents the arithmetical average of the percentages of the element considered for samples of the same group.

The two closer dashed lines define the samples whose percentage is lower than the standard deviation.

To compare the results of the group samples with a reference compound, click **Compound**. In the visualized table select one of the reference compounds. See [Figure 141](#) and “[Select Reference Compounds — Selects a reference compound in the table.](#) See [Figure 137.](#)” on [page 180](#).

Figure 141. Example of Summarize Graphic (2)

The middle dashed line in the graph represents the percentage of the of the considered element, assigned in **Compound Reference Table**.

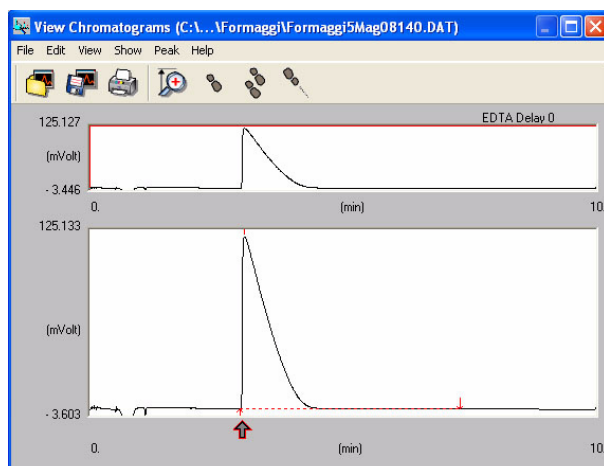
The two other dashed lines define the samples whose percentage is lower than permitted tolerance. The two values are reported in the input-boxes located near the button bearing the name of the reference compound.

It is possible enter directly a theoretical percentage and an error in the two input-boxes, and obtaining the corresponding graph.

To go back to the graph plotted with arithmetical average and standard deviation, enter 0 (zero) in the input-box **Theoretical**.

- **View Chromatogram** —Views the chromatogram trace of the sample currently addressed. You should address the sample required by clicking on the sample grid in any column of one sample line. By this function, the system chains the module to show the chromatogram. See [Figure 142](#).

Figure 142. Example of View Chromatogram



- **Elemental Formula Calculator** — See “[Elemental Formula Calculator](#)” on [page 185](#).
- **Compare to Reference Compound** — Views the result obtained by comparing the results of a sample addressed in the Summary table with a reference compound. See “[Select Reference Compounds — Selects a reference compound in the table. See Figure 137.](#)” on [page 180](#).

When a reference compound is selected, EagerSmart compares the percentage of each element of the sample addressed in the Summary table with the percentage of each element of the reference Compound. If the difference between the two values is within admitted limits, a **green** LED indicator suggests the good correspondence of the values for each of the elements found.

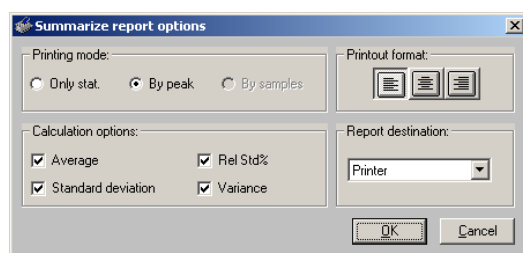
- **Search for Nearest Compounds** — Views the name of the compound whose percentage of the element more approaches the results of the sample addressed in the Summary table. With a **green** LED it indicates the elements within the admitted limits for the compound found.

Print Menu

This menu gives access to the following functions:

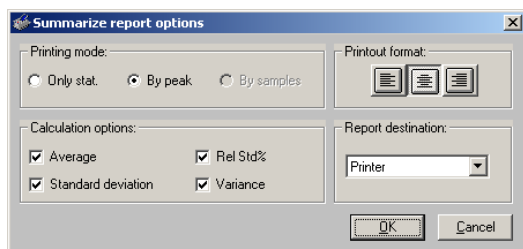
- **Print Single Group** — Prints the sample results of a single group. You should address the group required by clicking on the sample grid in any column of one sample line. By this function, the system shows a box for the print options. See [Figure 143](#).

Figure 143. Print Single Group Options



- **Print Single Group Options** — A large selection of print options tailors different requirements of format and destination of the summarize report.
- **Print All Group** — Prints the sample results of all the group in a sample grid. By this function the system shows a box for the print options. See [Figure 144](#).

Figure 144. Print All Group Options



A large selection of print options tailors different requirement of format and destinations of the summarize report.

- **Print Sheet** — Prints the Summary table as visualized on the screen.
- **Print Selected Area** — Prints the area selected inside the Summary table.

Summarize Results Grid

The sample grid contains all sample information. Scroll up and down, right and left with the arrows located in the corners for showing the part of samples of interest.

All cells in the grid are read only except the group number where it is possible to enter any number in the range 1-32 to inform the system about samples of the same nature to be grouped for calculation.

The group number can be placed in any order even non sequentially; the system automatically performs the calculation on the samples having the same group number.

You should address the sample required by clicking on the sample grid in the group column of a sample line.

The cursor automatically addresses the input box, ready to accept the new group value.

Once the new value has been entered and confirmed by pressing **Enter** key, the system updates the group column. Alternatively, you can address the box by a double click, in this case the system edits the previous content of the box.

Elemental Formula Calculator

The Elemental Formula Calculator is an additional device of *EagerSmart* that gets the elemental formula of a chemical compound analyzed by the instrument.

The samples are supposed to be pure compounds. Any impurities affects all the elemental percentages determined by the instrument.

The percentages written in the boxes C-H-N-S and the sample number/name are derived from the sample selected in the grid of the summary.

There are two different modes of use of this EFC:

- “Calculating Formula Mode” on page 186
- “Calculating% Mode” on page 188

Use **F >>%** button to exchange mode.

Calculating Formula Mode

The formula mode is shown in Figure 145.

Figure 145. Calculating Formula Mode

There are two possibilities:

1. You already know the formula of the molecule you expect to get by your organic synthesis, and you need to confirm you have got it
2. You simply do not know which kind of compound you may have obtained. You know just the elements present in it.

Water% Corrector

If the water content of a compound is known, it is possible to turn the percentage (%) of the wet sample determined by the instrument into the percentage of the dry sample.

Insert the water percentage in the proper box.

- If you click $\Rightarrow$ in the boxes on the right, the percentages of the dry compound are visualized.
- If you click **Calculate**, the elemental formulas corresponding to the dry percentages is calculated.

Calculation with Total Molecular Weight

❖ To perform calculation with TMW

1. In one of the seven available **combo-boxes**, insert the name of the elements that should be present in the compound, and that were not determined by the instrument. By clicking the arrow on the right, you are able to select any element among all those existing in the periodic table.

You can also click the arrow and then type the element symbol. The system automatically finds it.

Other known elements						
S	O	Cl	I			
0	0	0	0			
Atoms number of element						

If you put the cursor on the box below the **name of the atom**, you gets the **atomic mass** of the selected element. You can also write the **number of atoms** present in the compound for each element. The software gives as a result only the compounds containing exactly those numbers of atoms.



ATTENTION The system does not accept anything you type without clicking on the arrow.

2. Insert the **Total Molecular Weight** in the proper box.
3. Set the **Tolerance**.
The tolerance is defined as the window of acceptability for the TMW found by the software. For example, if you set TMW=500 AMU and Tolerance=2, the system finds only the molecules with TMW within the range 498-502. Since the calculation is based on a precise TMW, we suggest to set Tolerance=1.
4. Click **Calculate**. During the calculation time you see the bar getting full. At the end, the results are visualized in the bottom space.
5. Click  (**Print Preview**). You see all the molecular formulas found with their elemental percentages and TMW. Then you can print them by clicking **Print**.

Example: You need to confirm you have got the pesticide $\text{C}_{10}\text{H}_{19}\text{ClNO}_5\text{P}$, after getting C = 40.35%, H = 6.45%, N = 4.62%.

Insert as other unknown elements Cl, O, P.

Insert TMW = 299.69 and Tolerance = 1.

The result is the expected molecule.

C H N S						
Water%	%	40.35	6.45	4.62		
	>					
Other known elements						
Cl	O	P				
0	0	0				
Atoms number of element						
Total Molecular Weight:		299.69	+			
Tolerance:		1			CALCULATE	
Calculated Molecular Weight:		153.2668	C-H-N-S			
C H N S						
%	40.078	6.39	4.6737		Found	
					1	
C H N Cl O P	299.6906					
10 19 1 1 5 1						

Calculation Without Total Molecular Weight

❖ To perform the calculation without total molecular weight

1. In one of the seven available **combo-boxes**, insert the name of the elements that should be present in the compound and that were not determined by the instrument.

By clicking the arrow on the right, you are able to select any element among all those existing in the periodic table. You can also click the arrow and then type the element symbol. The system automatically finds it.

Other known elements					
S	O	Cl	I		
0	0	0	0		
Atoms number of element					

If you put the cursor on the box below the name of the atom, you get the atomic mass of the selected element.



ATTENTION The system does not accept anything you type without clicking the arrow.

2. Set the **Tolerance**.

The Tolerance is defined as the window of acceptability for the TMW found by the software. The higher the Tolerance is, the broader is the range of TMW investigated by the software. According to the tests performed so far, we suggest to set Tolerance=15. This is valid for the majority of the compounds. If you would like to get more results, try to increase this value up to 50, and repeat the calculation.

- Click **Calculate**. During the calculation time you see the bar getting full. At the end, the results are visualized in the bottom space.
- In this way you have obtained a possible compound at a possible TMW. In order to go on with the research, press **+** button. The software automatically goes on with the research, till it find compounds compatible with the experimental data. Only results with Carbon and Hydrogen percentages within the FLASH technical specifications is delivered at the end of the calculation.
- Click  **Print Preview**. You see all the molecular formulas found with their elemental percentages and TMW. Then you can print them by pressing the **Print** button.

Example: You need to find all the possible compounds matching the results C=40.35%, H=6.45%, N=4.62%. Insert as other unknown elements Cl, O, and P. Set Tolerance=15.

The results are $C_{10}H_{19}ClNO_1P_3$, $C_{10}H_{19}ClNO_3P_2$, $C_{10}H_{19}ClNO_5P_1$.

By clicking  **Print Preview**, it is possible to get the elemental percentages of all the calculated compounds. In this case, the compounds found by the software are all in the range of 297-300 AMU as a TMW. If you would like to extend the research up to 50 as a Tolerance, you get the same compounds. In this example, as in the majority, any further compounds have been found with the broader **Tolerance**.

Calculating% Mode

In this mode the program shows the percentage of the elements and the Total Molecular Weight present in a compound typed in the proper space. See [Figure 146](#).

Figure 146. Calculating% Mode

Sample #11 Metionine11

	C	H	N	S
%	36.21	7.81	8.45	19.33
	40.233	7.435	9.389	21.478

Other known elements

Atoms number of element

Insert Elemental Formula(ex:C12N1BR3)

C5H11N1S1O2

Water%

10

[%Corrected]

C%=40.248 [36.223]
 H%=7.43 [7.806]
 N%=9.387 [8.449]
 S%=21.49 [19.941]
 O%=21.445 [28.182]

Total Molecular Weight: 149.2134

Buttons: % > F, Help, Ok

Example:

Type **C10H19N1Cl1O5P1** and click **Calculate**. The following results are visualized:

C% = 40.07801

H% = 6.389958

N% = 4.673721

Cl% = 11.82987

O% = 26.6932

P% = 10.33525

Total Molecular Weight: 299.6906

Note The number 1 has always to be typed to indicate the presence of only 1 atom of any element.

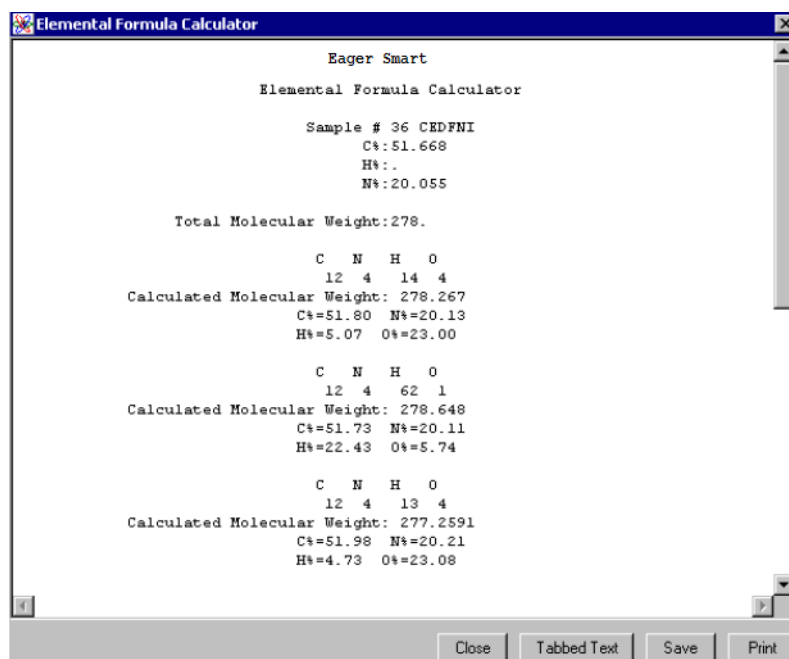
Water% Corrector

It is possible to calculate the elemental composition of a wet compound, providing the water% is known. Type the compound formula and the water% in the proper boxes, then click **Calculate**. The chemical composition of both the dry and the wet compounds are visualized.

Print Preview

Clicking , you see all the molecular formulas found with their elemental percentages and TMW. See [Figure 147](#).

Figure 147. Print Preview Report



The following buttons are available:

Button	Description
Print	Prints the report currently visualized in the page.
Save	The system asks for the report filename (default name is extracted to sample filename), and save the report currently visualized in the page (Normal or Tabbed Mode) on *.txt format.
Tabbed Text	The report is switched in tabbed format, for resume the normal text press another time this button. Now the label of this button is Normal Text. The tab format is useful to export the report in the programs of type Sheet (Excel...), to do this, use the clipboard. For capture the tabbed text in the clipboard you select full or partial text, then right-click and select Copy option. Otherwise, press Ctrl+Ins on the PC keyboard. Through the Paste option in the Sheet program, the selected text is exported of suitable format.
Close	To close this page and return to Elemental Formula Calculation .

Report Publisher

This chapter provides the instructions to create or modify the file report layout.

Contents

- [Introduction](#)
- [File Menu](#)
- [Edit Menu](#)
- [Zoom In or Zoom Out of a Document](#)

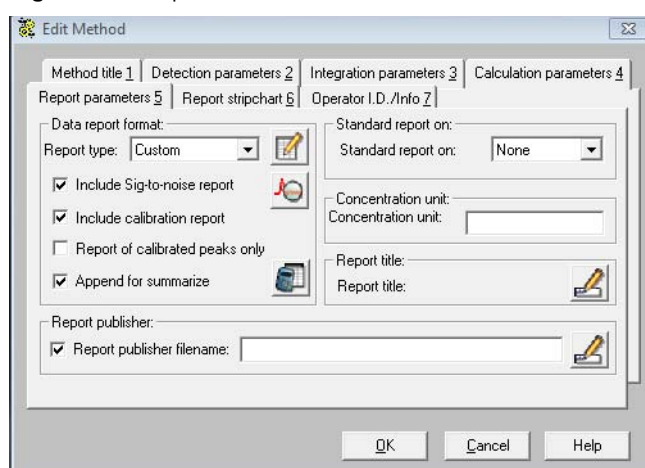
Introduction

Report Publisher is the tool to create or modify the file report layout with extension ***.rep**. EagerSmart generates a report with the objects and size decided by you.

To enter in this tool proceed as follows:

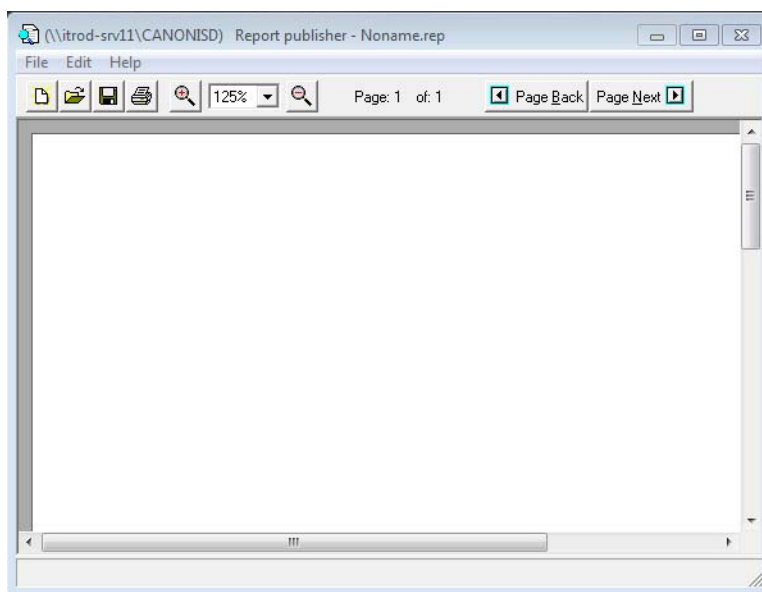
1. From Main Menu select **Edit | Report Parameter**, then select in **Report Publisher** the **Report publisher filename**. See [Figure 149](#).

Figure 148. Report Publisher (1)

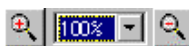


2. Click the  icon. The window of is visualized.

Figure 149. Report Publisher (2)



The stripchart, the calculated peaks data, a title, text comment, and graphic logo (*.bmp) can be positioned with the desired dimension on the final report page.

Icon	Description	See on:
	New report	page 192
	Load report	page 192
	Save report	page 193
	Printer setup	page 193
	Zoom option	page 195

File Menu

This menu gives access to the following functions:

- **New Method** — Clears the report layout currently in memory. All objects are cleared, their position and size are set to default values.

Note If any modification has been made on the report in memory, before proceeding the system asks for saving the report in memory.

- **Load Method**— Loads any report layout previously generated. The system asks for the report file name, showing the report layout.

Note The filename of the report selected is also used by *EagerSmart* for the report generation.

- **Save** — Saves the report layout currently being edited onto disk. The system asks for the report filename. All selected objects, their size and position is saved for future use.
- **Save as...** — The system asks for the report filename. All selected objects, their size and position is saved for future use.
- **Printer Setup** — Displays a dialog box for setting up the printer before printing a job.
- **Print** — Prints the report currently visualized in the page.
- **Exit** — Exits Report Publisher. If any modification has been made on the report layout currently in memory, the system prompts for Save report

Edit Menu

This menu enables or disables the printout of the various objects on the report generated by *EagerSmart*. The available options are:

- **Enable Title Object** — Enables or disables the printout of the title. If a check mark is shown on the left of this function, the corresponding object is visualized on the report layout. You can modify the size and the position of the object until the desired effect is found.

Object size and position:

- First of all you should click on the object.
The object is immediately replaced by a window with the title of the object name.
- Now the size of the object and the position can be changed with the standard Windows functions.
- Right-click in the chromatogram box for additional options.

- **Enable Chromatogram Object** — Enables or disables the printout of the stripchart. If a check mark is shown on the left of this function, the corresponding object is visualized on the report layout. You can modify the size and the position of the object until the desired effect is found.

Object size and position:

- First of all you should click on the object.
The object is immediately replaced by a window with the title of the object name.
- Now the size of the object and the position can be changed with the standard Windows functions.
- Right-click in the chromatogram box for additional options.

- **Enable Report Header Object** — Enables or disables the report header. If a check mark is shown on the left of this function, the corresponding object is visualized on the report layout. You can modify the size and the position of the object until the desired effect is found.

Object size and position:

- First of all you should click on the object.
The object is immediately replaced by a window with the title of the object name.

- Now the size of the object and the position can be changed with the standard Windows™ functions.
- Right-click in the report header box for additional options.
- **Enable Report Data Object** — Enables or disables the printout of the peaks data.
If a check mark is shown on the left of this function, the corresponding object is visualized on the report layout. You can modify the size and the position of the object until the desired effect is found.

Object size and position:

- First of all you should click on the object.
The object is immediately replaced by a window with the title of the object name.
- Now the size of the object and the position can be changed with the standard Windows functions.
- Right-click in the report data box for additional options.

Note If the report data is too long to fit the object size, the system prints one or more pages for the rest of the report. The additional pages are printed with the standard report format.

- **Enable Additional Test Box Object** — Enables or disables the printout of a user text.
If a check mark is shown on the left of this function, the corresponding object is visualized on the report layout. You can modify the size and the position of the object until the desired effect is found.

Object size and position:

- First of all you should click on the object. The object is immediately replaced by a window with the title of the object name.
- Now the size of the object and the position can be changed with the standard Windows functions.
- Right-click in the text box for additional options.

- **Enable Bitmap Object** — Enables or disables the printout of the bitmap picture.

The bit map picture is a graphic file ***.bmp** that may contain the logo of the company.

Any graphic program like paintbrush (included in Windows™ package), or a scanner system can generate a file with extension ***.bmp**.

If a check mark is shown on the left of this function, the corresponding object is visualized on the report layout. You can modify the size and the position of the object until the desired effect is found.

Object size and position:

- First of all you should click on the object.
The object is immediately replaced by a window with the title of the object name.
- Now the size of the object and the position can be changed with the standard Windows™ functions.
- Right-click in the bitmap box for additional options.

The system offers the possibility to select the **Picture Filename** of the bitmap picture file.

- **Picture Filename** — The filename specified by this function is used to load in memory the bitmap picture. All files with extension ***.bmp** can be loaded by this function and the corresponding picture is immediately visualized in the Bit map picture object.
- **Enable Page Number Object** — Enables or disables the printout of the page numbers. If a check mark is shown on the left of this function, the corresponding object is visualized on the report layout. You can modify the size and the position of the object until the desired effect is found.

Object size and position:

- First of all you should click on the object. The object is immediately replaced by a window with the title of the object name.
- Now the size of the object and the position can be changed with the standard Windows™ functions.
- Right-click in the page number box for additional options.
- **Delete Page** — Deletes the current page visualized and all its contents after your confirmation. Click Yes or No.
- **Insert Page** — Adds a page at the current page visualized after your confirmation. Click Yes or No.
- **Copy Page** — Copies a page. See Paste Page.
- **Paste Page** — Pastes a page copied. See Copy Page.
- **Add Pages to fit long report data.**

Zoom In or Zoom Out of a Document

You can **Zoom In**  to get a close-up view of your document, or **Zoom Out**  to see the page in a reduced size. You can selecting the size in the Zoom Control box



Custom Report Editor

This chapter provides the instructions to generate a report designed by you.

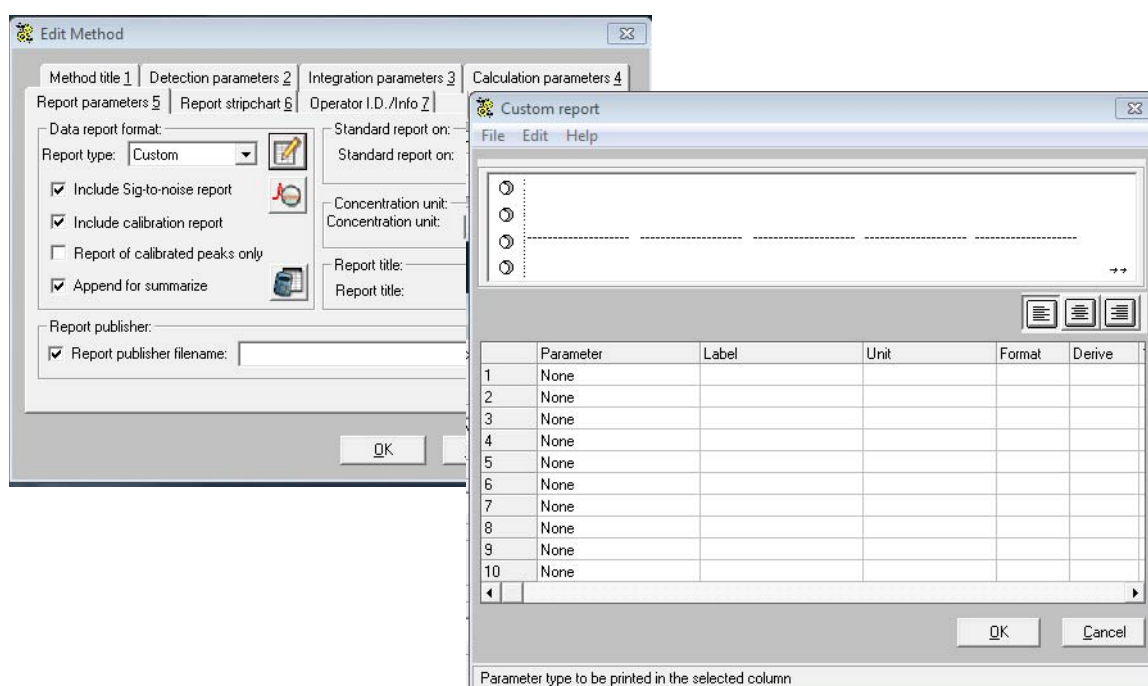
Contents

- “Introduction” on page 197
- “File Menu” on page 198
- “Edit Menu” on page 198
- “Custom Report Editor Input Box” on page 199
- “Custom Report Editor Grid” on page 199

Introduction

Custom Report Editor is the section of the analytical method that contains the information to generate a report designed by you. The editor page is available from the **Report Parameter** tab by selecting the report type as **Custom**, and by clicking on the icon . See [Figure 150](#). and “[Report Parameters](#)” on [page 55](#).

Figure 150. Custom Report Editor



Button	Description
	Changes the aspect of the Custom Report Grid. Right, Centered, and Left are the available options. According to the selection, the custom report information visualized in the Component Grid are justified as required.
Cancel	Clears all modifications done in the current section and the program returns to Main Menu.
OK	Confirms all modifications done in the current tab and the program returns to Main Menu.

EagerSmart offers you a graphical way to layout in a few seconds the report you desire. All columns of the report are selected through a fast and simple dialog box. It offers 23 different columns result with the possibility to customize the title, the format, and eventually to derive the results multiplying and adding constants.

The custom report is printed only if **Custom Report** is selected in **Report Type of Report Parameters**. See paragraph “[Report Parameters](#)” on [page 55](#).

File Menu

This menu gives access to the function **Exit** to leave Custom Report Editor. **Exit** function confirms all modifications done in the current section and the program returns to the **Report Parameters**.

Note All modifications are stored in the method actually in memory but to save permanently the modifications you should use **Save Method** command.

Edit Menu

This menu gives access to the functions to set or delete the Custom Report Editor.

The following functions can be selected:

- **Default Custom Report** — Compiles the custom report automatically with default parameters for file columns of the final report.
- **Clear Custom Report** — Clears all the parameters entered for the five columns of the final report. At this command the system clears the table and the report header.
- **Copy Table to Clipboard** — As with most Windows™ applications that use the **Clipboard** to transfer text, graphics, and other data, you can copy and move text from *EagerSmart* into different applications.

❖ To copy text between *EagerSmart* and another application

1. Select the cells you want to copy.
2. From **Edit** menu choose **Copy**.
3. Switch to the other application.

- If the other application is not open, start the other application.
 - If the other application is already open, press CTRL+ESC, and then choose the application from the Task List.
4. Position the insertion point where you want to insert the text.
 5. From **Edit** menu, choose **Paste** (ALT, E, P).

Custom Report Editor Input Box

The input box is where new custom report information can be entered.

1. First, you should address the report column of interest by clicking on the custom report grid in any line.
2. Second, the cursor automatically addresses the input box, ready to accept the new value.
3. Once the new value has been entered and confirmed by pressing the **Enter** key, the system updates the custom report. Alternatively, you can address the box by double click, in this case the system edits the previous content of the box.

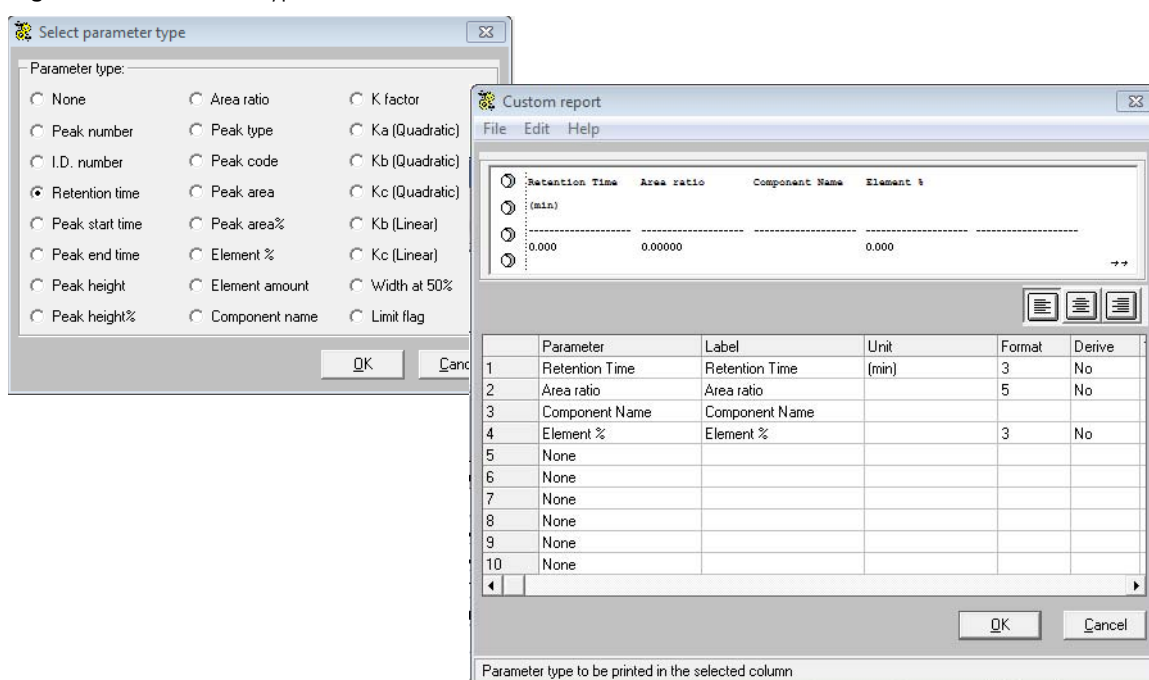
Custom Report Editor Grid

Custom Report Editor Grid contains all the information to layout the desired peak report. You can select up to ten columns for the desired report.

Parameter Type

This box contains one of the possible result of the sample report. See [Figure 151](#).

Figure 151. Parameter Type Selection



You can select any of the possible choices to be printed in the desired column.

- **Label** — Changes the aspect of the **Custom Report Editor** column. You can enter the label to be printed for the parameter assigned to this column.
- **Units** — Changes the aspect of the **Custom Report Editor** column. You can enter the units to be printed for the parameter assigned to this column.
- **Format** — Changes the aspect of the **Custom Report Editor** column. You can specify the number of decimals to be printed for the parameter assigned to this column. When this column is set to (-1) the system uses the free format **0.xxxxxExx**.
- **Derive** — Calculates new data from the results printed in the standard [EagerSmart](#) report.

To do so, enter **Yes** in this column. The system enables you to enter the **Report Derive Parameters**.

The specific calculation performed is:

$$\text{Result} = [(\text{Orig. Parameter} + \text{1st Offset}) * (\text{1st Multiplier} + \text{2nd Offset})] * \text{2ndMultiplier}$$

Peaks Detection

This chapter provides the instructions to test the entered parameters of a stored chromatogram.

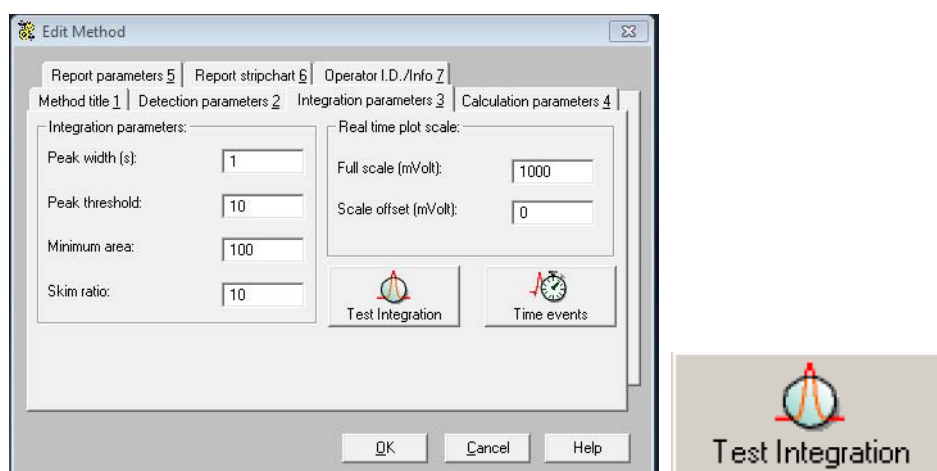
Contents

- [Introduction](#)
- [File Menu](#)
- [View Menu](#)
- [Show Menu](#)
- [Detect Menu](#)
- [Chromatogram Icons](#)

Introduction

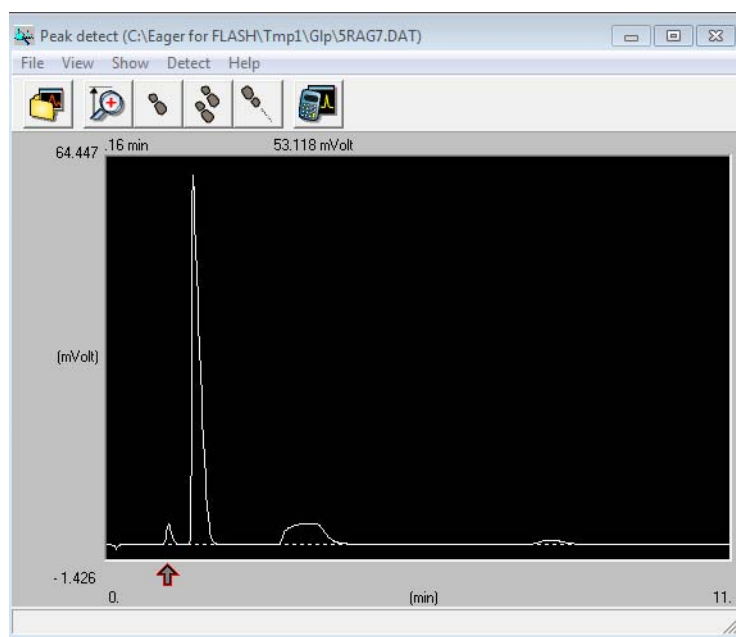
Peak detection tests the entered parameters of a stored chromatogram. The system offers the opportunity to load different chromatograms and to force the immediate integration using the selected parameters. You can modify the integration parameters until the desired integration is achieved. Enter **Peak Detection Page** menu clicking **Test Integration** in **Integration Parameter** tab as shown in [Figure 152](#). Also see “[Integration Parameters](#)” on [page 49](#).

Figure 152. Integration Parameter Tab



The Peak Detection page is visualized as shown in the example of [Figure 153](#).

Figure 153. Peak Detection Page



Icon	Description	See on:
	Load chromatogram	page 203
	Chromatogram icons	page 205
	Test integration (Detection Menu)	page 204

File Menu

This menu gives access to the following functions:

- **Load Chromatogram** — Loads any chromatogram stored on disk. The system asks for the chromatogram name, showing the chromatogram trace.

Note The names of the peaks are linked to the method currently in memory. Therefore, the system shows the name of the components currently in memory, and they can differ from the chromatogram loaded. See also **Peak Name** on [page 204](#).

- **Save Chromatogram** — Saves the integrated chromatogram onto the disk. The system asks for the chromatogram name. All data points and baseline correction is saved for future use.
- **Store Actual Zoom for Signal-to-Noise Evaluation** — *EagerSmart* can calculate the **Signal-to-noise ratio**. Chooses the baseline portion on which the noise evaluation should be done.

The signal value is calculated on the selected peak and the noise is evaluated for the given initial and final time. According to the found values, the ratio is calculated and reported between the peak signal value and the peak-to-peak noise.

Include Signal-to-Noise report.

The calculated **signal-to-noise ratio** chooses the peak of interest and the baseline portion on which the noise evaluation should be done.

You should check this option and the report is automatically generated:

```
Signal to noise report
-----
Signal peak name      : Nitrogen
Signal peak RT       (sec): 218.0
Signal value         (uV): 22064.8
Noise eval from/to   (sec): 150.0-160.0
Peak to peak noise   (uV): 81.2
Signal to noise ratio : 271.7
```

The value of the signal is calculated on the selected Signal Peak ID, and the noise is evaluated for the given Initial Time and Final Time. According to the found values, the ratio is calculated and reported between the peak signal value and the peak-to-peak noise.

- **Quit Peak Integration** — Exits the peak detection module.

View Menu

This menu gives access to the functions for changing the aspect of the chromatogram displayed.

- **Original Scale and Offset** — Restores the original scale and offset after a **Set Manual Scale** has been performed. The chromatogram is generally stored with original scale and offset calculated to keep in scale all peaks not exceeding 1000 mV full scale.
- **Set Manual Scale and Offset** — Enters a manual scale to display the chromatogram in the window. After any manual modification of the scale it is always possible to restore the original values with the function **Original Scale and Offset**. The chromatogram is generally stored with original scale and offset calculated to keep in scale all peaks not exceeding 1000 mV full scale.
- **Set Manual Zoom** — Enters a manual scale and time to display the chromatogram in the window.
- **Fit to Highest Peak** — Adjusts the scale of the window in order to keep in scale any peak being part of the chromatogram. Even peaks with height higher than 1000 mV is automatically in scale.
- **Fit to Highest Peak on Scale** — Adjusts the scale of the window in order to keep in scale any peak being part of the chromatogram but within 1000 mV of height.

Show Menu

This menu gives access to the functions for changing the aspect of the chromatogram display. You can select the following functions:

- **Baseline** — Displays the baseline correction of the chromatogram. If a check mark is shown beside the command, the chromatogram is visualized with a dashed line of the baseline correction, otherwise only the chromatogram data points are shown.
- **Maxima** — Displays a small tick on the top of each peak. If a check mark is shown beside the command, the chromatogram is visualized with small marks indicating the maximum of the peak, and indicating that the peak is integrated.

- **Retention Time** — Displays the retention time of the peaks. If a check mark is shown beside the command, the chromatogram is visualized with the retention time at the maximum of the peak, and indicating that the peak has been eluted at the reported time
- **Peak Name** — Displays the name of the components. If a check mark is shown beside the command, the chromatogram is visualized with the name of each component found in the chromatogram.

Note The names of the components are reported only if the chromatogram has been processed, and if the method currently in memory corresponds to the method used for the original sample acquisition.

- **Start/Stop** — Displays the start and stop point of each peak. If a check mark is shown beside the command, the chromatogram is visualized with two small arrows indicating the start and the end point of the peaks.
- **View Peak Data** — Displays the calculated parameter of a desired peak. If a check mark is shown beside the command, the chromatogram is shown with a window indicating all peak information.

First of all, select with the peak pointer, located below the bottom window, the peak of which the user wants the information. Automatically the system shows all parameters of the peak.
- **None of Above** — Disables all the functions currently selected for the chromatogram display.

Detect Menu

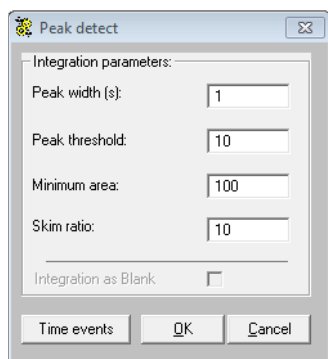
This menu gives access to the following functions:

- **Peak Integration** — Applies the entered integration parameter to the chromatogram currently visualized.

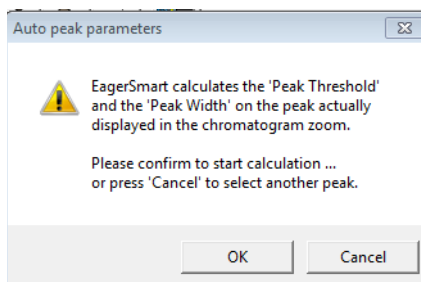
The system performs the complete chromatogram integration, shows the baseline correction, and peak start/stop information.

Clicking on the **Integration as Blank** check box, you may set integration parameters dedicated to samples of blank.

Figure 154. Peak Integration



- **Wizard Peak Integration** — Calculates the **Peak Width**, the **Peak Threshold** and the **Minimum Area** to be used for a correct integration of your chromatogram. Just isolate the smallest peak you would like to be integrated, and then upon requesting this function the system calculates the right parameters for you.



Chromatogram Icons

Icon Function	Description
	Restores the chromatogram currently in memory with the original scale and offset. After a number of zoom commands you would like to review the original chromatogram time frame. Through this command the system immediately restores the full chromatogram view.
	These functions advance the chromatogram view by the same time frame of the actual window or half the actual window.
	Remembers the last 10 chromatogram time-frame views and it restores the last 10 zoom steps.

Time Events

This chapter provides the instructions to improve the integration of different peak shape.

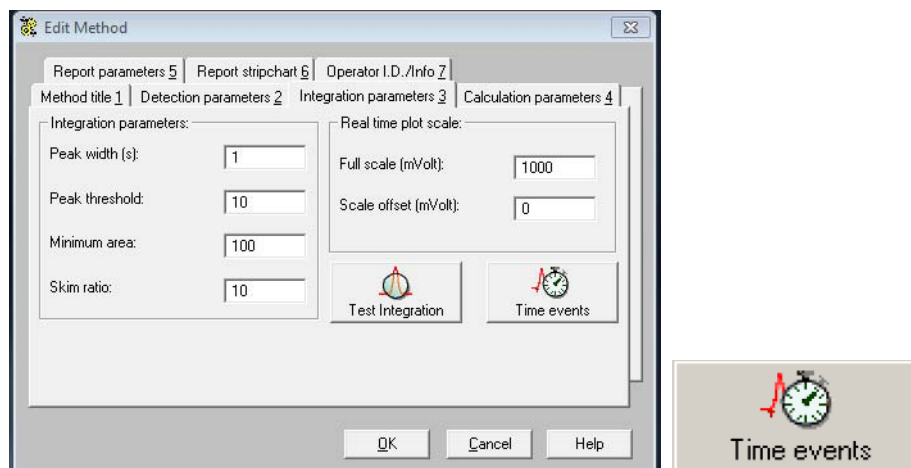
Contents

- [Introduction](#)
- [File Menu](#)
- [Edit Menu](#)
- [View Menu](#)
- [Show Menu](#)
- [Time Events Grid](#)
- [Sort Icon](#)
- [Chromatogram Icons](#)

Introduction

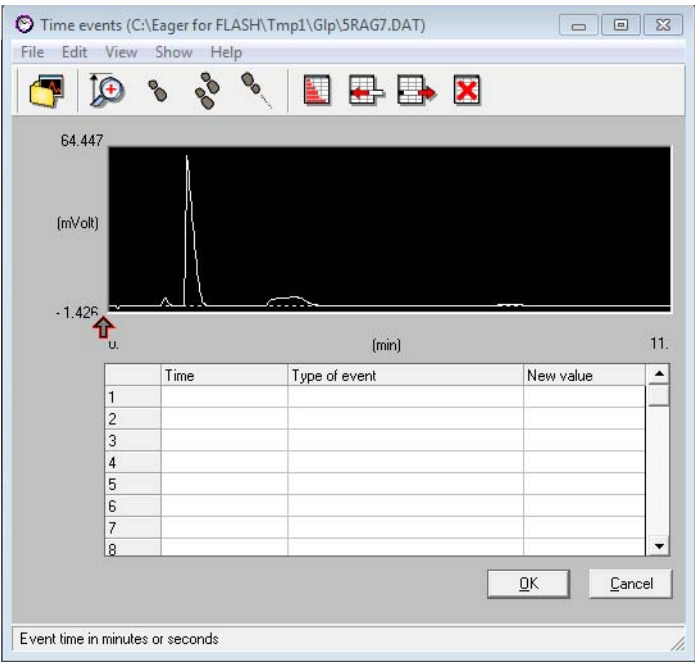
Time Events module is the section of the analytical method that contains all the parameters that need to be changed to improve the integration of different peak shape. Enter Time Events menu by clicking **Times Events** in **Integration Parameter** as shown in [Figure 155](#). Also see the section “[Integration Parameters](#)” on [page 49](#).

Figure 155. Integration Parameter Tab



Time Events table is visualized as shown in the example of [Figure 156](#).

Figure 156. Example of Time Events Table



Peak Width, **Peak Threshold**, and many others, are the parameters you can enter after selecting this function. Usually these parameters are entered by the **Integration parameters** module but, in many occasions, it is necessary to change some parameters during the run. This analytical section enters the time at which a parameter should change and to set its new value.

Icon	Description	See on:
	Load chromatogram	page 209
	Chromatogram icons	page 213
	Retention time sorting	page 209
	Insert line	page 209
	Delete line	page 209 and Chapter 5
	Delete all time events	page 213

Button	Description
Cancel	Clears all modifications done in the current section and the program returns to Main Menu.
Ok	Confirms all modifications done in the current section and the program returns to Main Menu.

Note All modifications are stored in the method currently in memory but to save them permanently you should use the **Save Method** command.

This table provides the following functions:

File Menu

The Time Events table offers a number of tools to enter the time and the parameter to be changed in the chromatogram shown on the upper part of the window. You can load any chromatogram previously acquired just supplying the name of the desired chromatogram.

- **Load Chromatogram** — Loads any chromatogram stored on disk.
The system asks for the chromatogram name, showing the chromatogram trace.
- **Exit Times Events** — Exits the time events table.

Edit Menu

This menu gives access to the functions for filling or deleting Time Events table.
You can select the following functions:

- **Insert Line** — Creates room for a new time event and all time events in memory beyond the pointer are moved down by one step.
- **Delete Line** — Clears the time, the parameter type and the new value of the currently addressed event.
- **Clear Time Events** — Clears completely the time events table currently in memory.
- **Copy to Clipboard** — As with most Windows™ applications that use the Clipboard to transfer text, graphics, and other data, you can copy and move text from *EagerSmart* into different applications.

❖ To copy text between *EagerSmart* and another application

1. Select the cells you want to copy.
2. From **Edit** menu choose **Copy**.
3. Switch to the other application.
 - If the other application is not open, start the other application.
 - If the other application is already open, press CTRL+ESC, and then choose the application from the Task List.
4. Position the insertion point where you want to insert the text.
5. From **Edit** menu, choose **Paste** (ALT, E, P).

View Menu

This menu gives access to the functions for changing the aspect of the chromatogram display. You can select the following functions:

- **Original Scale and Offset** — Restores the original scale and offset after a **Set Manual Scale** has been performed. The chromatogram is generally stored with original scale and offset calculated to keep in scale all peaks not exceeding 1000 mV full scale.
- **Set Manual Scale and Offset** — Enters a manual scale to display the chromatogram in the top window. After any manual modification of the scale it is always possible to restore the original values with the function **Original Scale and Offset**. The chromatogram is generally stored with original scale and offset calculated to keep in scale all peaks not exceeding 1000 mV full scale.
- **Set Manual Zoom** — Enters a manual scale and time to display the chromatogram in the window.
- **Fit to Highest Peak** — Adjusts the scale of the top window in order to keep in scale any peak being part of the chromatogram. Even peaks with height higher than 1000 mV is automatically in scale.
- **Fit to Highest Peak on Scale** — Adjusts the scale of the top window in order to keep in scale any peak being part of the chromatogram but within 1000 mV of height.

Show Menu

This menu gives access to the functions for changing the aspect of the chromatogram display. You can select the following functions:

- **Baseline** — Displays the baseline correction of the chromatogram. If a check mark is shown beside the command, the chromatogram is visualized with a dashed line of the baseline correction, otherwise only the chromatogram data points are shown.
- **Maxima** — Displays a small tick on the top of each peak. If a check mark is shown beside the command, the chromatogram is visualized with small marks indicating the maximum of the peak, and indicating that the peak is integrated.
- **Retention Time** — Displays the retention time of the peaks. If a check mark is shown beside the command, the chromatogram is visualized with the retention time at the maximum of the peak, and indicating that the peak has been eluted at the reported time
- **Peak Name** — Displays the name of the components. If a check mark is shown beside the command, the chromatogram is visualized with the name of each component found in the chromatogram.

Note The names of the components are reported only if the chromatogram has been processed, and if the method currently in memory corresponds to the method used for the original sample acquisition.

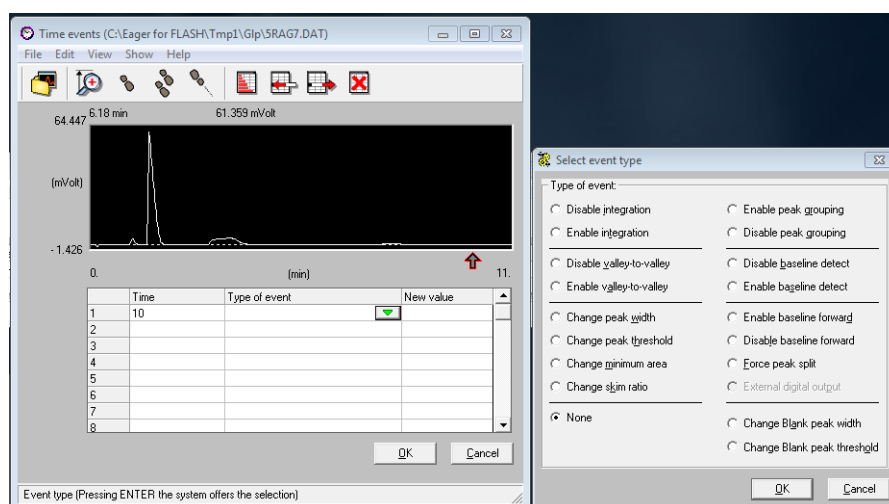
- **Start/Stop** — Displays the start and stop point of each peak.
If a check mark is shown beside the command, the chromatogram is visualized with two small arrows indicating the start and end point of the peaks.
- **None of Above** — Disables all the functions currently selected for the chromatogram display.

Time Events Grid

The time events grid contains all the information to change the integration parameters at the desired time along the chromatogram. The time event is based on the following parameters:

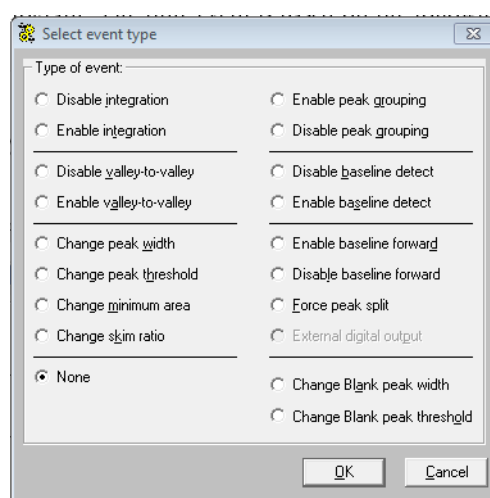
- **Time** — Enters the time at which you want to change a specific parameter. Alternatively, you may use the pointer  under the chromatogram.
- **Type of Event** — Selects the event type you want to change at the specified time as shown in Figure 157.

Figure 157. Type of Events



- **New Value** — Enters the new value to be assigned to the specified parameter. Once the new value has been entered and confirmed by pressing **Enter** key, the system updates the value. Alternatively, you can address the box by a double click; in this case the system edits the previous content of the box.

List of the Events



The available events are the follows:

- **None** — This type of event is not having any effect. It is used to disable an event without deleting the line.

- **Enable/Disable Integration** — Eliminates the peak integration of part of the chromatogram. Firstly, place a Disable peak integration event, then place an Enable peak integration where you want to restart to have integrated peaks.
- **Enable/Disable Valley to Valley** — Integrates the found peaks with a baseline correction drawn from valley to valley of each of the peaks.
- **Enable/Disable Baseline Detect** — Eliminates the baseline search algorithm. Sometime it is required to draw the baseline from one point to the end of a big peak grouping without finding any intermediate baseline point; this can be accomplished by disabling the baseline detection.
- **Enable/Disable Peak Grouping** — Groups all peaks eluted within a specified time. You can enable at the specified time the peak grouping, and until the event **disable peak group** is encountered, all peaks are summed together in a single peak.
- **Change Peak Width** — Specifies the width of the peaks to be integrated. Sometimes for the analyses having large peaks but collected with fast sampling rate, the integration may have difficulties. The best way to overcome those problems is to enter here the width of the peak to be integrated. This parameter can be changed during the analysis through this timed event.
- **Change Peak Threshold** — Sets the threshold in micro volts for peak recognition. This value is used by the integration algorithm to discriminate the peaks from the baseline or the signal noise. Increasing this value, the system becomes less sensitive. Decreasing the value, more peaks is found. This parameter can be changed during the analysis through this timed event.
- **Change Minimum Area** — The peak integration is performed using the parameters **Peak Width** and **Peak Threshold**. The peaks having an area below the entered value are not rejected. This parameter can be changed during the analysis through this timed event.
- **Change Skim Ratio** — If the ratio between the height of two or more consecutive peaks is higher than the entered value, a tangent correction on the carrier peak is performed. This parameter can be changed during the analysis through this timed event.
- **External Digital Output** — EagerSmart sets/resets eight external events along the run. You can select any time to set **on** or **off** any of the eight events. Moreover, you can enter the most appropriate name for the specific use of any of the eight external TTL digital outputs by modifying the **WCC.INI** file.
- **Enable/Disable Baseline Forward** — EagerSmart forces the baseline forward. When enabled, this function projects the baseline from the initial point of the peak up to the end of the peak regardless of the input level. When disabled, the standard baseline detection is used for peak separation.
- **Force Peak Split** — EagerSmart forces the peak split at any desired time. At the given time the integration system separates the current peak forcing an immediate end of the peak. This is used for not separated peaks that need to be divided into fractions.
- **Internal Standard to Be Used...** — EagerSmart uses up to five internal standards. In Component Table on (see [Chapter 5](#)) you may define up to five standards, and with **Time Events** you can program the use of the different standards on a time base. With the event **Internal std to be used...** you divide the entire run into the desired sections where each of the declared internal standards has to be used.

Example:

You declare 3 Internal standards in **Component Table** at 10 min, 20 min, and 30 min.

- From 15 to 24.9999 min, all peaks are referred to the second internal standard (20 min).
- From 25 to the end of the run, all the peaks are calculated with the third internal standard (30 min)

Sort Icon

These functions change the order of the entered time events. The events may be entered with a wrong sequence; it is possible to sort in ascending way all time events.

Chromatogram Icons

The chromatogram icons are a series of functions to manipulate the chromatogram view.

Icon Function	Description
	Restores the chromatogram currently in memory with the original scale and offset. After a number of zoom commands you would like to review the original chromatogram time frame. Through this command the system immediately restores the full chromatogram view.
	Advances the chromatogram view by the same time frame of the actual window or half the actual window.
	Remembers the last 10 chromatogram time-frame views and it restores the last 10 zoom steps.

Use of Eager Simplified User Interface

This chapter provides the instructions for the use of the simplified user interface of *EagerSmart* for *FlashSmart*, *Flash 2000* and *Flash 4000* versions.

The possibility of using a simplified version of *EagerSmart* is mainly addressed to users who do not possess a specific expertise in the instrumental field. However, this option also concerns those who, having to run every day analyses of samples of the same nature, do not need any special functions of *EagerSmart*. For this purpose the software is provided with a **password** system, which makes the application of its functions more or less extended. Normally the password is dedicated to the laboratory head, which allows the use of the entire software, besides one or more passwords dedicated to the operator or operators of the instrument. In this way the laboratory head has the possibility to prevent the operator from using the appropriate software functions he deems and to act in any moment in case of need.



ATTENTION The use of the simplified user interface is NOT available with *EagerSmart* USB and A/D versions.

Note Before using Simplified User Interface, see [System Administration In Compliance with CFR 21 Part 11 Regulation](#).

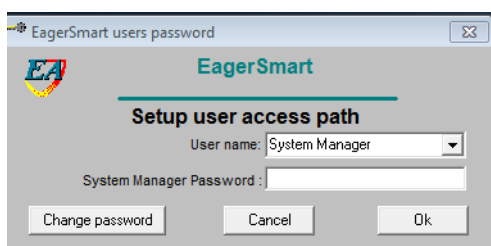
To use the simplified version of *EagerSmart*, do what described in the following operating sequence.

❖ To use the simplified user interface

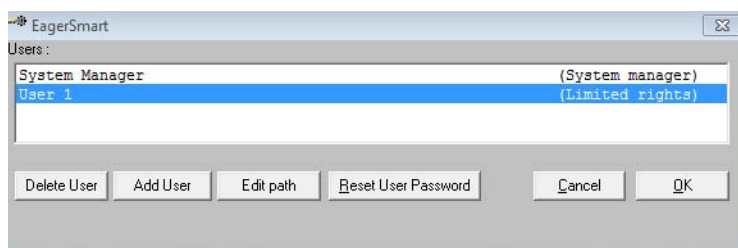
Note The procedure is the same also for higher *EagerSmart* software versions than 1.4.

1. In Main Menu, select **File | System administration**. The following window is visualized, where the System Manager password must be entered.

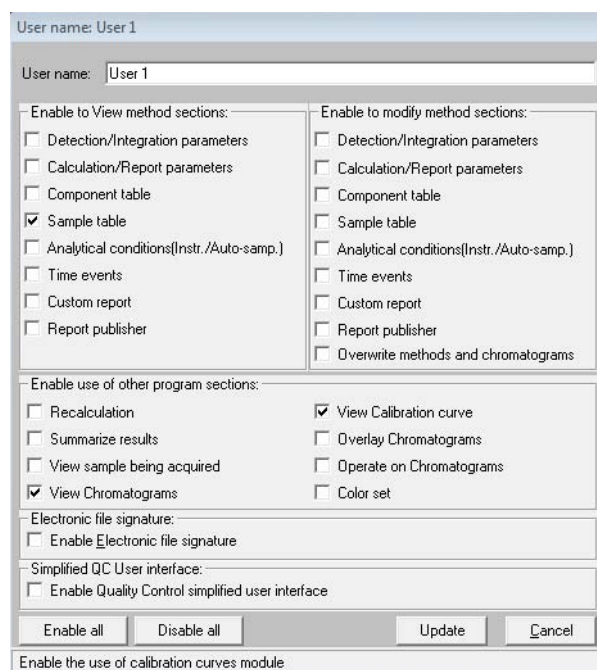
Figure 158. User Password Window (1)



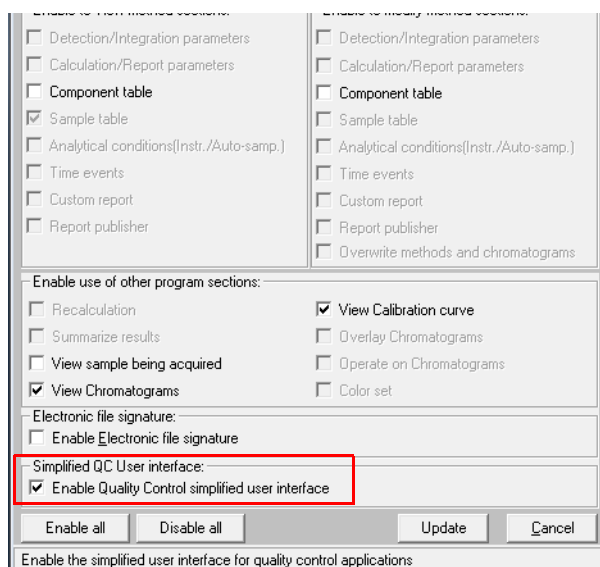
2. After entered the password the following page is visualized.

Figure 159. User Password Window (2)

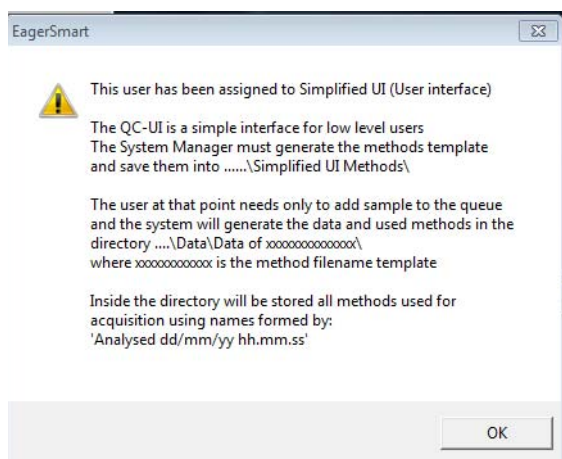
- To exclude the functions that have not to be available to the operator, click **Edit Path**. The following window of is visualized.

Figure 160. User Path Window

- Select the functions that have to be available by ticking the relevant available boxes.
- Select the option **Enable Quality Control simplified user interface** by ticking the appropriate check box.



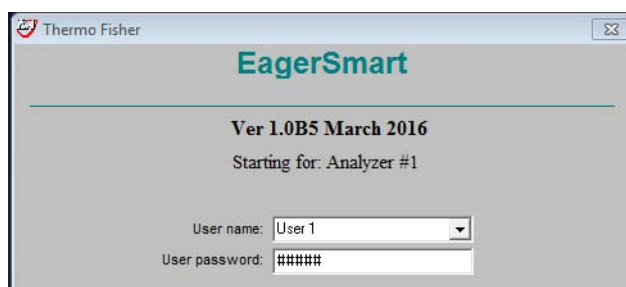
6. Click **Update**. In the page visualized, it is requested to generate a directory for this application.



7. Click **OK**. The following page is visualized.

❖ **to start the simplified user interface**

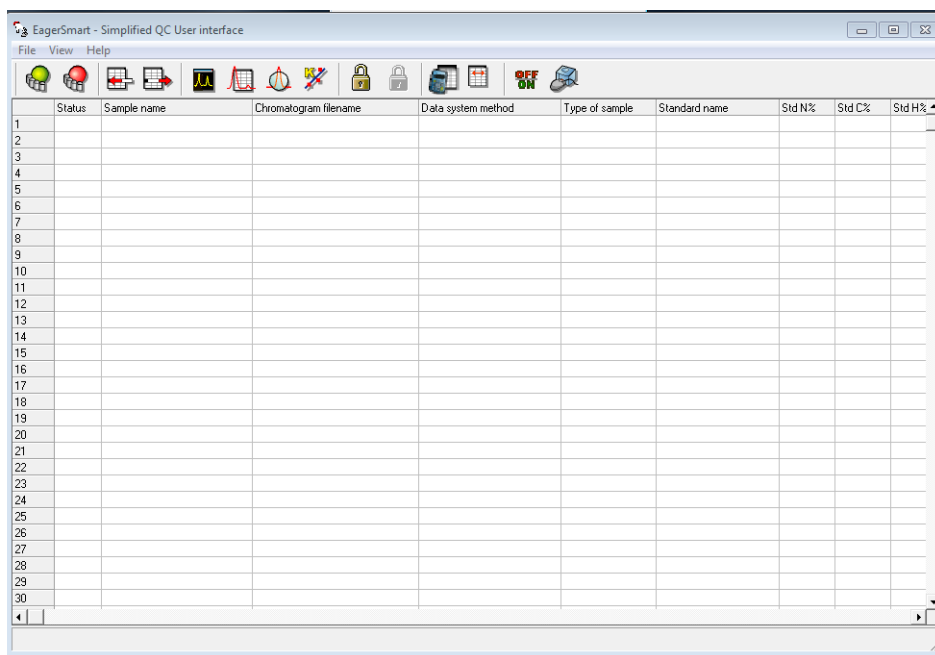
1. From Main menu select **File | Exit Eager Smart** to exit the program.
2. Start *EagerSmart* again selecting **Start | Programs | Eager Smart**. The system ask for the password.



3. Click **OK** to return to Main Menu. Only the function selected in **Edit Path** page is active.

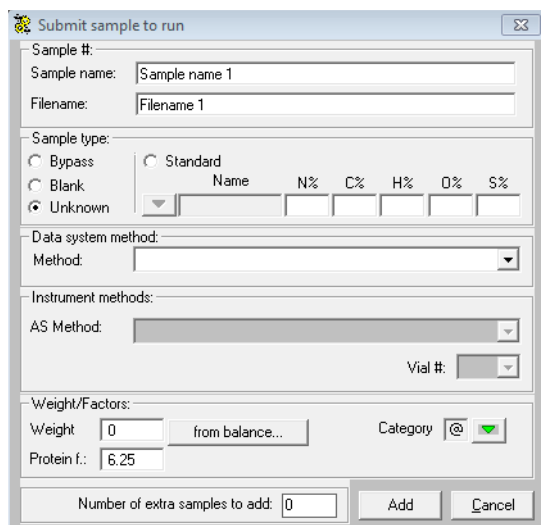
Note The number of icons in the window corresponds to the previously selected functions.

The following window shows an example of Sample Table of the Simplified User Interface

Figure 161. Sample Table of the Simplified User Interface (1)


	Status	Sample name	Chromatogram filename	Data system method	Type of sample	Standard name	Std N%	Std C%	Std H%
1									
2									
3									
4									
5									
6									
7									
8									
9									
10									
11									
12									
13									
14									
15									
16									
17									
18									
19									
20									
21									
22									
23									
24									
25									
26									
27									
28									
29									
30									

4. In the following window select the  *Submit new sample to analyze* icon to edit the sample table. A window like the one below is visualized.

Figure 162. Window of Submit Sample to Run


Submit sample to run

Sample #:

Sample name:

Filename:

Sample type:

☐ Bypass ☐ Standard

☐ Blank ☐ Unknown

Name N% C% H% O% S%

Data system method:

Method:

Instrument methods:

AS Method:

Vial #:

Weight/Factors:

Weight from balance... Category

Protein f.:

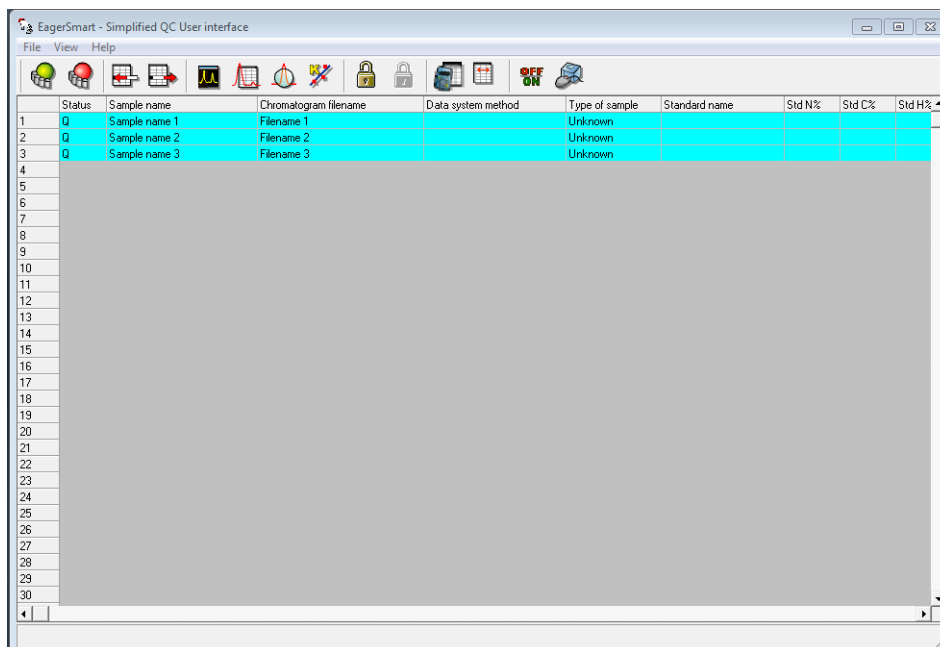
Number of extra samples to add:

Add Cancel

- Enter the **Sample name** and the **chr filename**, followed by a number. Then the filenames and the sample names continue to be progressively numbered.
- Select the type of the sample to be analyzed: **Sample type**.
- In the section **Instrument** select, in **Data Method**, one of the methods previously saved in the folder **Simplified UI Method**.
- Enter the sample **Weight** and, in case of N/Protein and N-Brew configurations, the multiplying factor **Protein f:** and the sample **Category**. Click **Add**.

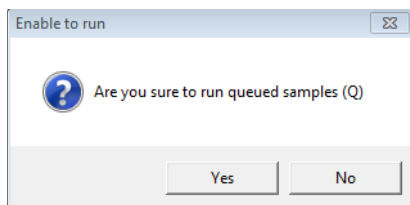
9. Edit the table for all samples to be analyzed. At the end of editing, the Sample Table is visualized filled with all information previously entered, as shown in the following example. The boxes of the **Status** column show a **Q** (Queue).

Figure 163. Sample Table of the Simplified User Interface (2)



	Status	Sample name	Chromatogram filename	Data system method	Type of sample	Standard name	Std N%	Std C%	Std H%
1	Q	Sample name 1	Filename 1		Unknown				
2	Q	Sample name 2	Filename 2		Unknown				
3	Q	Sample name 3	Filename 3		Unknown				
4									
5									
6									
7									
8									
9									
10									
11									
12									
13									
14									
15									
16									
17									
18									
19									
20									
21									
22									
23									
24									
25									
26									
27									
28									
29									
30									

10. To send the start to the instrument select the  icon and reply **Yes** to the question **Are you sure to run queued samples?**. At the end of the analytical sequence the instrument automatically stops.



11. To view the results, choose **View | View only result of sheet**.

Note If at the end of each analysis you want to read directly the result, in the menu *View* enable the function *Last sample calculated results*. If for any reason you need to stop the analytical cycle, click the icon named *Put sample on queue (no run)*.

Electronic File Signature

This chapter provides the instructions to authenticate an analytical method in compliance with the CFR 21 Parts 11 regulation.

EagerSmart includes the feature for method authorization. Once the method is signed, it can be approved, and from that moment on, it is protected from any change. Only copies of the method can be used for further acquisition and process, but signed methods can't be modified. The signed method cannot be overwritten nor modified.

When enabled the **Electronic file signature**, *EagerSmart* protects the method, and chromatogram files from any external corruption or tampering. Each file is constantly monitored by checksum calculation and the result is compared whenever a load is requested. If the method calculated checksum does not match the last checksum when the file was saved, then the method or chromatogram load is denied.

Note Before using Electronic File Signature, see [System Administration In Compliance with CFR 21 Part 11 Regulation](#).

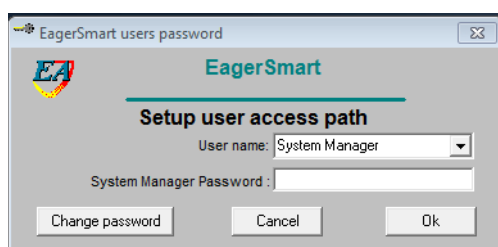
This section provides the instructions for signing and approving a method.

❖ To sign and approve a Method file

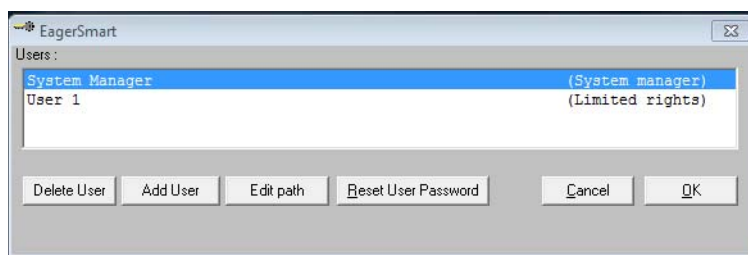
Note The procedure is the same also for higher *EagerSmart* software versions than 1.4.

1. In the Main Menu, select **File | System Administration**. The following window is visualized where the password must be entered.

Figure 164. User Password Window (1)



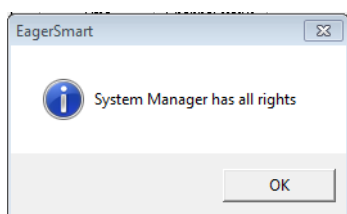
2. After entered the password the following page is visualized.

Figure 165. User Password Window (2)

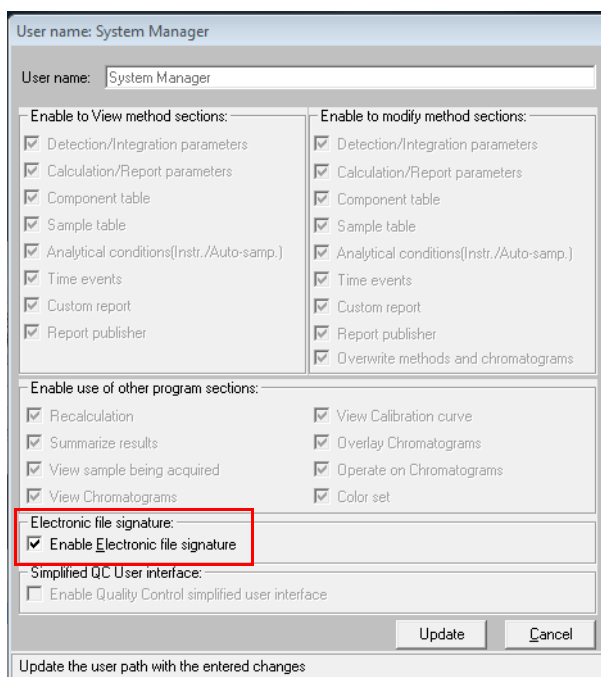
The first line is dedicated to the **laboratory head** (*System Manager*). The **laboratory head** is considered the person responsible of the laboratory or a delegated person. See the step **a**.

The second line is dedicated to the **User** (*Limited rights*). See the step **b**.

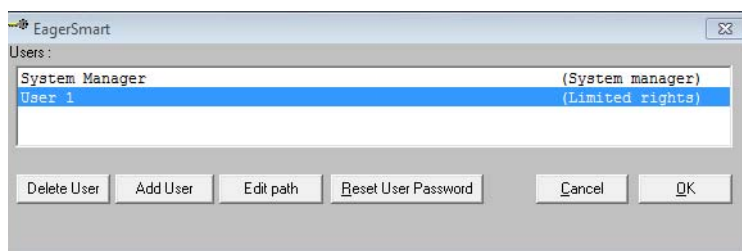
- a. To enable the electronic signature as **Laboratory Head**, highlight the line **System Manager**, and press **Edit Path**. The following window is visualized.



- i. Click **OK**. The following window is visualized.

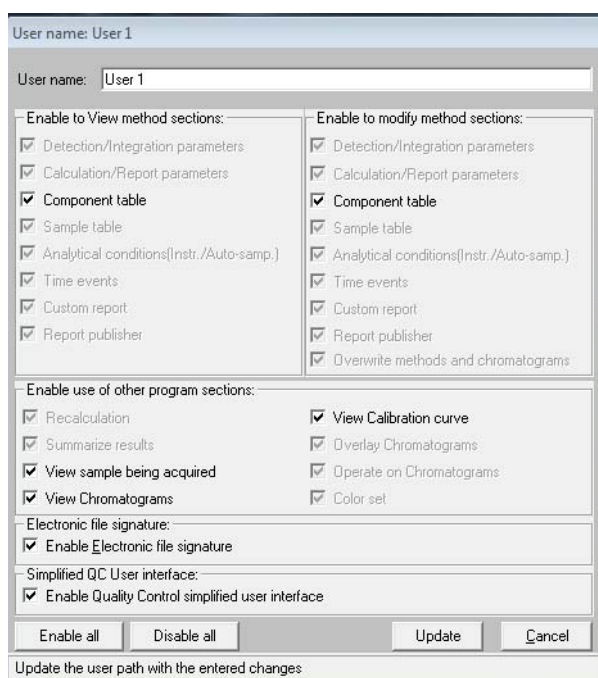
Figure 166. User Path Window (1)

- ii. Select the option **Enable Electronic File Signature** by ticking the appropriate check box.
- iii. Click **Update**. The following window is visualized.



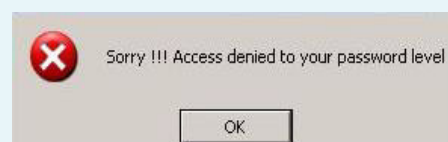
- b. To enable the electronic signature as **User** (*Limited rights*), highlight the line **User**, and click **Edit Path**. The following page is visualized.

Figure 167. User Path Window (2)

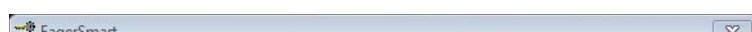


- i. Select the option **Enable Electronic File Signature** ticking the appropriate check box.
- ii. Enable the functions that the user can use by ticking the relative boxes. The functions not enabled are blocked.

Note The user can access only the functions for which he has been enabled to use. Any user's operation without the necessary authorization is not accepted and a window containing a message of denial is visualized as shown in the following message.

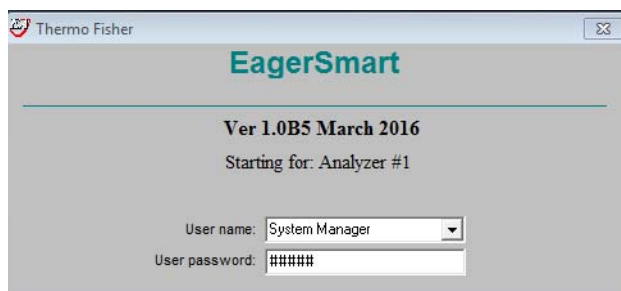


- iii. Click **Update**. The following window is visualized again.



- iv. To enable the electronic signature for eventual other users (*Limited rights*), repeat the procedure from the step **b**.

3. Close and reboot **EagerSmart**. The following window is visualized. Select the name of the user in the **User Name text box** and digit the relevant password in the **User Password text box**.

Figure 168. EagerSmart Users Password (1)

It is possible to enter in the system as follows:

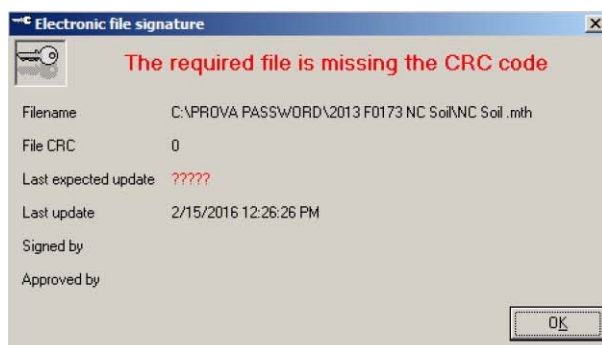
- a. Specific user (operator) “*User*”. See [Enter in the System As User](#)
- b. Laboratory head “*System Manager*”. See [Enter in the System As System Manager](#)

❖ Enter in the System As User

1. Enter in the system as user (for example User1) and digit the appropriate password.

Note The current example supposes that the user has had all the necessary privileges from System Manager.

If loading a predefined method, a window as that shown below is visualized, it means that it is necessary creating a new method, and saving it in a directory with the relative filename.

Figure 169. Required File Missing (1)

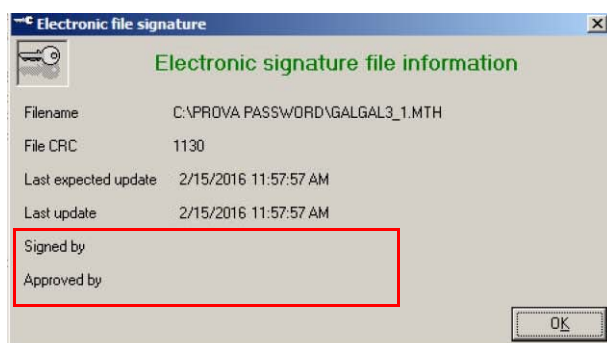
Note CRC code (Cyclic Redundancy Check is an algorithm) that prevents any modification. Each method saved and signed is identified by a checksum calculation and the result is compared whenever a load is requested. The loading of the method is denied if the calculated checksum does not match the last checksum when the method was saved. The solution is the creation of a new method including a sequence of analysis (Sample table), Component table and analytical conditions.

2. Create a new method.
Perform analysis, modifications, recalculation...and so, then save the method in a directory under a specific filename, for example **GALGAL3**.
The options of **File** menu that can be used for saving the method are two: **Save Method** and **Save and Sign Method**. To get the signed method use the option **Save and Sign Method**.



ATTENTION If a method, for example **GALGAL3**, is saved with the option **Save Method** rather than **Save and Sign Method**, that method cannot be saved and signed anymore. The system does not allow the overwriting of a method. For this reason, the method cannot be saved with the same name but with a different name, for example **GALGAL3_1**.

To verify the status of the method from Main Menu select **File | Audit trail method log**. The page **Audit trail** is visualized. In **View** menu select the option **View File Status**. The following window is visualized.

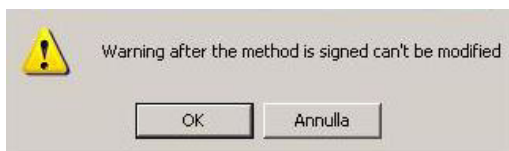


The method results saved with the indication of the last updating but not signed and approved; in fact, the lines **Signed by** and **Approved by** are empty.

- Click **OK** to return to the page **Audit trail** and exit by using the option **Quit Audit trail in File** menu. The Main Menu is visualized. To sign the method, **User** must load the method, and save it by using the option **Save and Sign Method**.

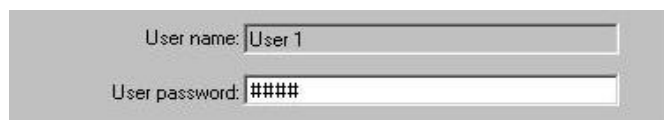
Sign the Method

- Selecting the option **Save and Sign Method** the following message is visualized:

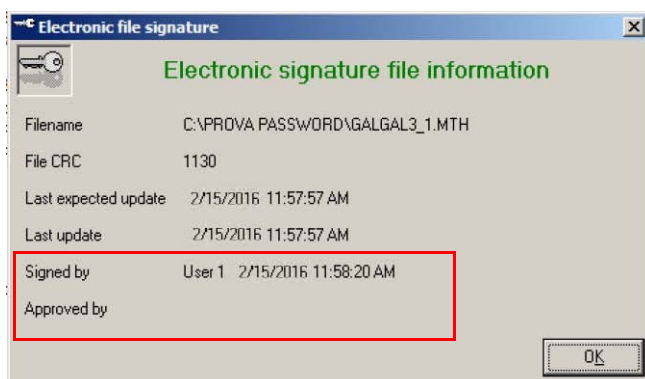


- The message indicates that once the method is signed, it cannot be modified anymore. Click **OK** to confirm the choice. The system asks for the password of the **User1** as shown in the following figure.

Figure 170. EagerSmart Users Password (2)

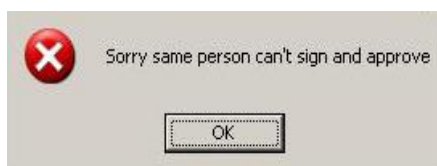


- Digit the password and press **Enter**. Main Menu is visualized.
- To verify that the method have been signed, load the file, and select the option **Audit trail method log** in **File** menu. The page Audit trail is visualized in which all the processes of revision of the method in use are recorded. In substance it is the chronicle of the method. In **View** menu, select the option **View File Status**. The following window is visualized.

Figure 171. Electronic Signature File Information (1)

The page shows that the method is saved and signed but not approved. The line **Signed by** reports who has signed the method, the date, and the time of the event. The line **Approved by** is empty.

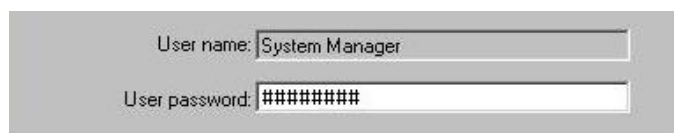
8. Click **OK** to return to the page **Audit trail** and exit by using the option **Quit Audit trail** in **File** menu. The Main Menu is visualized.
9. To approve the method, load the method, and select **File | Approve method**. Answer **OK** to the window that appears. The system again asks the password. Digit the password, and press **Enter**. The following message indicating that the same person cannot sign and approve the method is visualized.



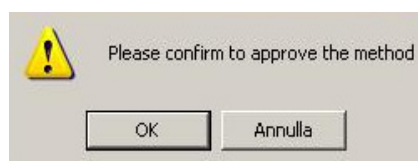
- In the case of **User**, the approval of the method must be carried out by the **System Manager** operating as follows:

Approve the Method

10. Exit from *EagerSmart* and enter again in the system as **System Manager**. The system asks for the password of the **System Manager** as shown in the following window.

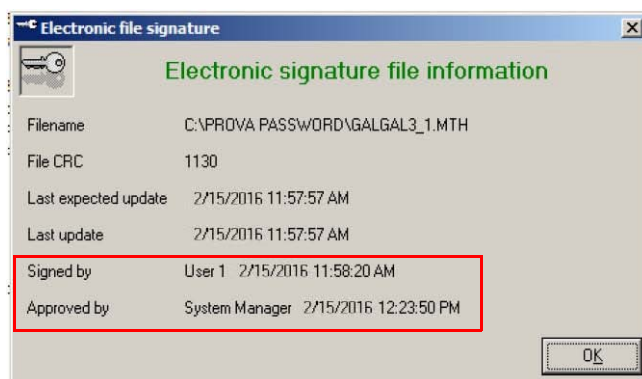
Figure 172. EagerSmart Users Password (3)

11. Digit the password and press **Enter**, Main Menu is visualized. Load the method.
12. The laboratory head can approve the method through the option **Approve method** in **File** menu. Note that the option **Save and Sign method** is non available. The following window is visualized.

Figure 173. Method Approval Confirmation (1)

13. Click **OK**. The system asks for the password again. Digit the password and press **Enter**; Main Menu is visualized.
14. To verify the status of the method, select the option **Audit trail method log** in File menu. The page **Audit trail** is visualized. In the **View** menu select the option **View File Status**. The following window is visualized.

Figure 174. Electronic Signature File Information (2)

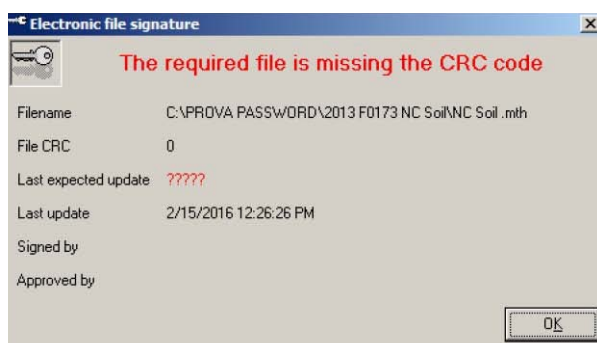


15. The page shows that the method is saved, signed and approved.
 - The line **Signed by** reports who has signed the method, the date and the time of the event.
 - The line **Approved by** indicates who has approved the method, the date and the time of the event.
16. Click **OK** to return to **Audit trail** page and exit by using the option **Quit Audit trail** in **File** menu. The Main Menu reappears.

❖ Enter in the System As System Manager

1. Enter in the system as **System Manager**, and digit the appropriate password. If loading a predefined method, a window as that shown below is visualized, it means that it is necessary creating a new method, and saving it in a directory with the relative filename.

Figure 175. Required File Missing (2)



Note CRC code (Cyclic Redundancy Check is an algorithm) that prevents any modification. Each method saved and signed is identified by a checksum calculation and the result is compared whenever a load is requested. The loading of the method is denied if the calculated checksum does not match the last checksum when the method was saved. The solution is the creation of a new method including a sequence of analysis (Sample table), Component table and analytical conditions.

2. Create a new method.

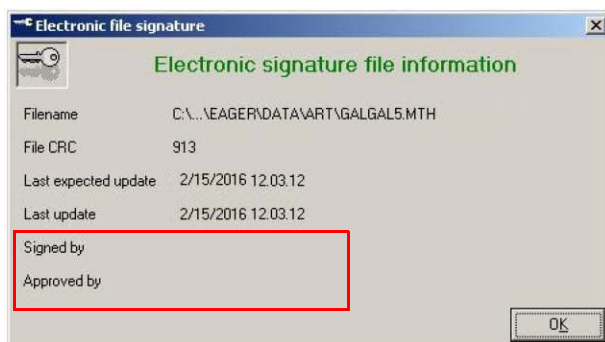
Perform analysis, modifications, recalculation...and so on, then save the method in a directory under a specific filename, for example **GALGAL5**. The options of the **File** menu that can be used for saving the method are two: **Save Method** and **Save and Sign Method**.

To get the signed method use the option **Save and Sign Method**.



ATTENTION If a method (for example **GALGAL5**) is saved with the option **Save Method** rather than **Save and Sign Method**, that method cannot be saved and signed anymore. The system does not allow the overwriting of a method. For this reason, the method cannot be saved with the same name but with a different name (for example **GALGAL5_1**).

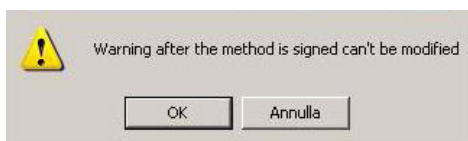
3. To verify the status of the method from Main Menu select **File | Audit trail method log**. The page **Audit trail** is visualized. In **View** menu select the option **View File Status**. The following window is visualized.



4. The method results saved with the indication of the last updating but not signed and approved. In fact, the lines **Signed by** and **Approved by** are empty.
5. Click **OK** to return to the page **Audit trail** and exit by using the option **Quit Audit trail in File** menu. The Main Menu is visualized. To sign the method **System Manager** must load the method, and save it by using the option **Save and Sign Method**.

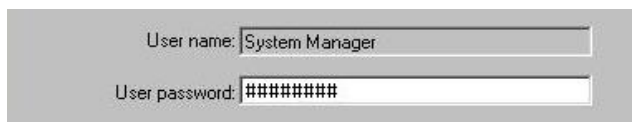
Sign the Method

6. Load the method to sign. Select the option **Save and sign method**, the following message is visualized:



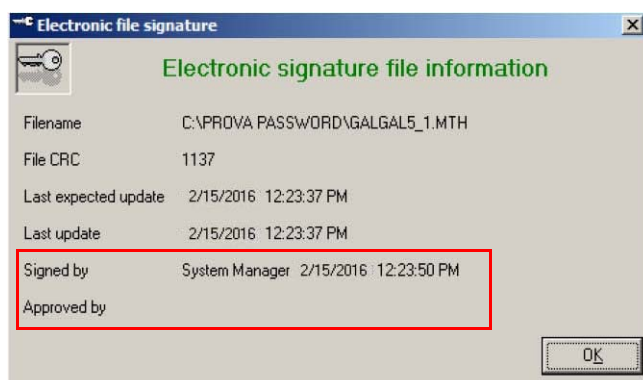
7. The message indicates that once the method is signed, it cannot be modified anymore. Click **OK** to confirm the choice. The system asks for the password of the **System Manager** as shown in the following figure.

Figure 176. EagerSmart Users Password (4)



8. Digit the password and press **Enter**, Main Menu is visualized.
9. To verify that the method have been signed, load the file, and select the option **Audit trail method log** in **File** menu. The page **Audit trail** is visualized. In the **View** menu select the option **View File Status**. The following window is visualized:

Figure 177. Electronic Signature File Information (3)



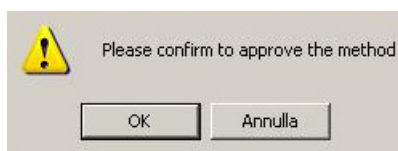
The page shows that the method is saved and signed but not approved. The line **Signed by** reports who has signed the method, the date, and the time of the event. The line **Approved by** is empty.

10. Click **OK** to return to the page **Audit trail** and therefore exit by using the option **Quit Audit trail** in **File** menu. The Main Menu reappears.

Approve the Method

11. To approve the method, load the method and select **File | Approve method**. Note that the option **Save and Sign method** is not available. The following window is visualized.

Figure 178. Method Approval Confirmation (2)



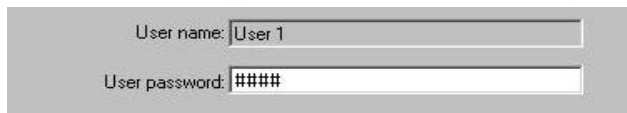
12. Click **OK**. The system again asks for the password. Digit the password and press **Enter**. The following message indicating that the same person cannot sign and approve the method is visualized.



The approval of the method must be carried out from a third person.

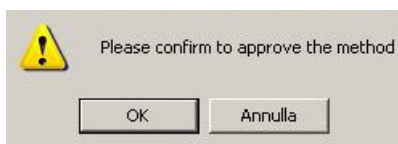
13. Exit from Eager and reenter in the system as **User**. The system asks for the password of the **User** as shown in the following figure.

Figure 179. EagerSmart Users Password (5)



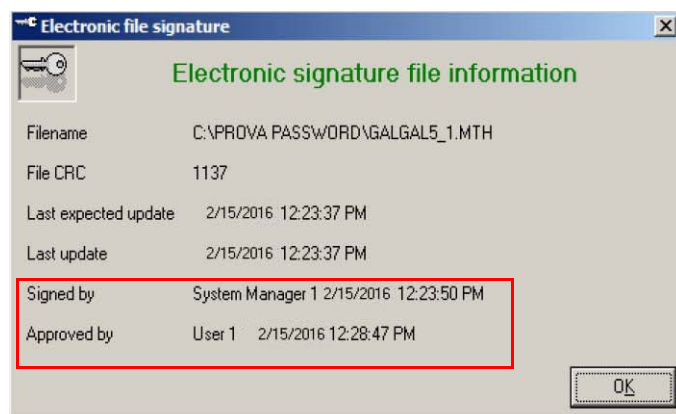
14. Digit the password and press **Enter**. Main Menu is visualized. Load the method to approve.
15. Approve the method by using the option **Approve method** in **File** menu. Note that the option **Save and Sign method** is not available. The following window is visualized.

Figure 180. Method Approval Confirmation (3)



16. Click **OK**. The system ask again for the password of the **User**. Digit the password and press **Enter**. Main Menu is visualized.
17. To verify the status of the method select the option **Audit trail method log** in **File** menu. The page **Audit trail** is visualized. In the **View** menu select the option **View File Status**. The following window is visualized.

Figure 181. Electronic Signature File Information (4)



18. The page shows that the method is saved, signed and approved.
 - The line **Signed by** indicates who has signed the method, the date and the time of the event.
 - The line **Approved by** indicates who has approved the method, the date and the time of the event.
19. Click **OK** to return to the page **Audit trail**, then exit by using the option **Quit Audit trail** in **File** menu. The Main Menu reappears.