VARIAN

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Galaxie™
Report Editor

User's Guide

 Printed in U.S.A. 03-914949-00: Rev 6

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Introduction

Galaxie Report Editor enables you to generate, customize, and print reports from the Galaxie Chromatography Data System.

Galaxie Reports may contain Galaxie Chromatography Data System objects, such as the chromatograms, the Peak Report table, any of the variables, etc. A Galaxie Report may also include Microsoft™ documents, such as images and labels.

In Galaxie Report Editor, all the objects can be placed and sized inside pages as they will be printed.

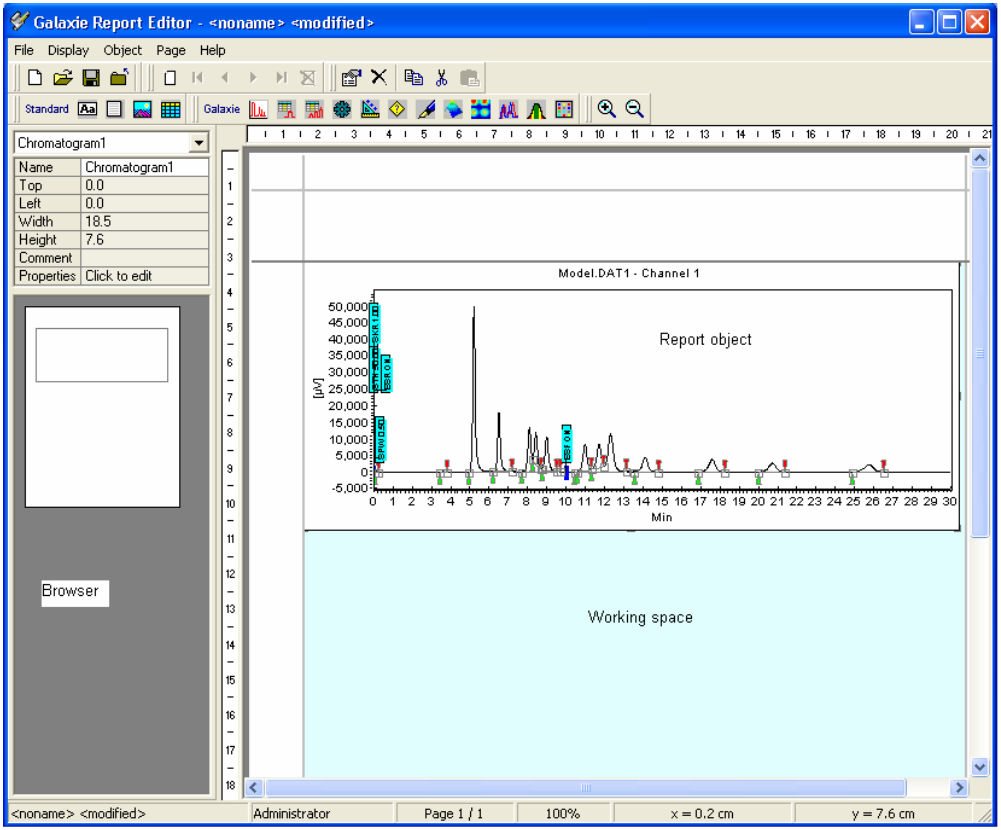
Application Details

The Galaxie Chromatography Data System Report Editor allows you to build customized reports.

For regulatory compliance, a report corresponding to an unsaved data file is printed with a ‘DATA NOT SAVED’ background.

Working Environment

The Galaxie Report Editor graphical environment is composed of a main menu, toolbars, a browser, a working space, and a status bar.



Main Menu

File	Used to manage the report style files (open, close, save, print).
Display	Allows you to configure the zoom level, particularly the browser display.
Object	Allows you to insert an object and edit its properties.
Page	This menu enables you to define the page parameters.
Help	Enables access to the Help file and information about the Galaxie Report Editor version.

File Menu

New style	Creates a new report style in Galaxie Report Editor.
Open	Opens an existing report style.
Save	Saves the current report style.
Save as	Saves the current report style under a different name. (Note that 'Save as' will not allow you to overwrite an existing file.)
Close	Closes the current report style.
Quit	Exits Galaxie Report Editor.

Display Menu

Zoom in	Zooms in on the report.
Zoom out	Zooms out on the report.
Browser	Used to show or hide the browser enabling you to see the contents of each page.

Object Menu

Insert	Inserts a Galaxie object or a standard object. The available Galaxie objects are a chromatogram, a peak or group result table, a method, a calibration report, a suitability tests, an electronic signature, .a 3D chromatogram, a library search, an isoabsorbance, a peak purity or a collection log file. The standard objects are a label, a graphic, a text (including Galaxie variables), or a table. The corresponding object is always added in the left top corner of the page. Refer to "Building the Report Style" to learn how to resize or modify the position of a selected object.
Select	Selects an object.
Delete	Deletes the selected object.
Copy	Copies the selected object.
Cut	Cuts the selected object.
Paste	Inserts the contents of the clipboard.
Properties	Used to display and edit the properties of the selected object.

Page Menu

New Page	Creates a new page in the same report style. The new page is inserted before the active page.
New page at the end	Creates a new page at the end of the report.
Delete Page	Deletes the current page.
Page Break	Inserts a break between pages.
Next Page	Displays the next page.
Previous Page	Displays the previous page.
First Page	Displays the first page of the report.
Last Page	Displays the last page of the report.

Help Menu

Help content	Displays the on-line Help.
About	Provides information about the Galaxie Report Editor.

Toolbars

Several toolbars can be accessed from the Display menu

Pages Toolbar

This toolbar is useful if several pages have been defined:


Displays the first page of the report.


Displays previous page of the report.


Displays next page of the report.


Displays the last page of the report.


Adds a new page at the end of the report.


Deletes the current page.

Standard Toolbar

Creates a new report style.

Opens an existing report style.

Saves the current report style.

Closes the current report style.

Saves the current report style under a different name. (Note that 'Save as' will not allow you to overwrite an existing file)

Uses to cut the selected objects

Copies the selected object.

Inserts the contents of the clipboard.

Object Toolbar

This toolbar allows you to add objects to the report style.

The corresponding object is always added in the left top corner of the page. Refer to "Building the Report Style" to learn how to resize or modify the position of a selected object.

Adds a label, for example the title of the report style, with a special display (colors, shadows, etc.).

Inserts a text object.

Inserts a graphic. Right-click on the graphic and select the image to be added in the report style.

Adds a table which is created and completed by the user.

Adds a chromatogram.

Adds a Peak Report, i.e., a table of the peaks in the chromatogram.

Adds a Group Report, i.e., a table of the groups in the chromatogram.

Adds the Method to the report. Press the right mouse button to choose which properties you want to print.

Prints the Calibration Curve.

Prints the Suitability Tests results.

Prints the Electronic Signature.

Prints the 3D chromatogram.

Prints the Isoabsorbance view.

Prints the Library Search results.

Prints the peak purity results.

Prints the Collection Log File.

Displays the object properties.

Deletes the selected object

Display Toolbar

Zooms in on the report.

Zooms out on the report.

Browser

The browser is displayed on the left side of the screen and is divided into two parts.

The first part (a table) shows properties of the selected objects (i.e., the object name, the location of this object in the page, a comment). Click on the Properties field to open the selected object properties.

The second part gives a preview of all pages of the report style. Click on any page to display it in the Galaxie Report Editor.

Building the Report Style

To create a new report style from Galaxie, select the FILE / NEW / NEW REPORT STYLE menu: Galaxie Report Editor is opened, and a blank report is displayed.

A report style is composed of several pages onto which objects (see below) are added. Each page is divided into a header area, a main area, and a footer area. The header and the footer are common and will be printed at the top and the bottom of all the pages.

The header and the footer areas are delimited with a line. The size of the header and footer can be modified. Click on the line; the cursor appearance is modified. Drag the line to the desired location.

To place objects in the header, the main area, or the footer, select the area with the mouse, then select the object from the toolbar or from the insert menu.

The object is always added in the top left corner of the area. To move and resize the object you can:

- click on the object and drag it to the desired location
- click on the grey squares and drag the borders of the object
- modify its coordinates in the browser

For each object, pop-up menus are available by clicking the right mouse button. These pop-up menus enable access to functions such as delete, copy, cut, paste, and properties.

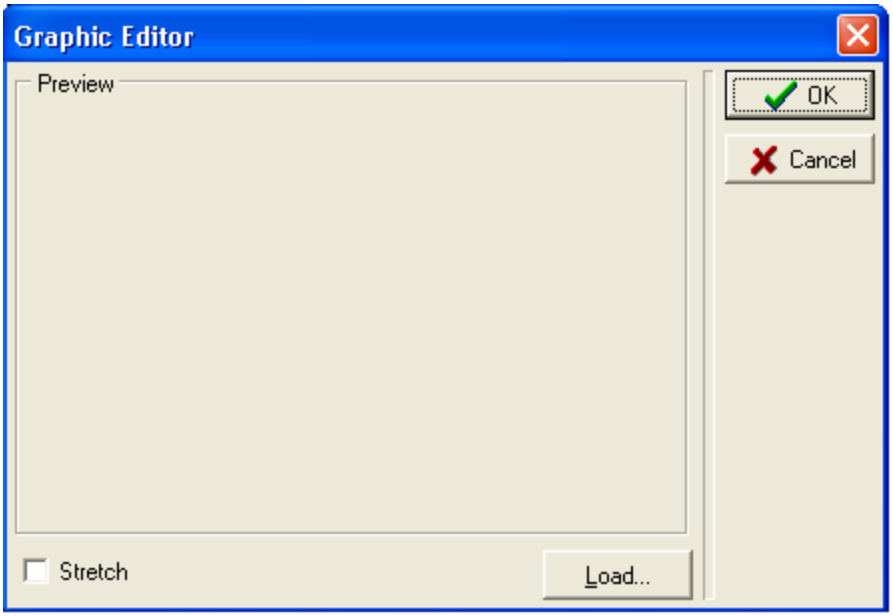
Object Properties

Once the object is added to the report, right-click on the object. A pop-up menu appears. Select PROPERTIES to configure the object.

Graphic Object

This object enables you to display a graphic in the bitmap format. It can be used to insert the company logo, for example.

In the pop-up menu select PROPERTIES to configure the object. The following window appears:

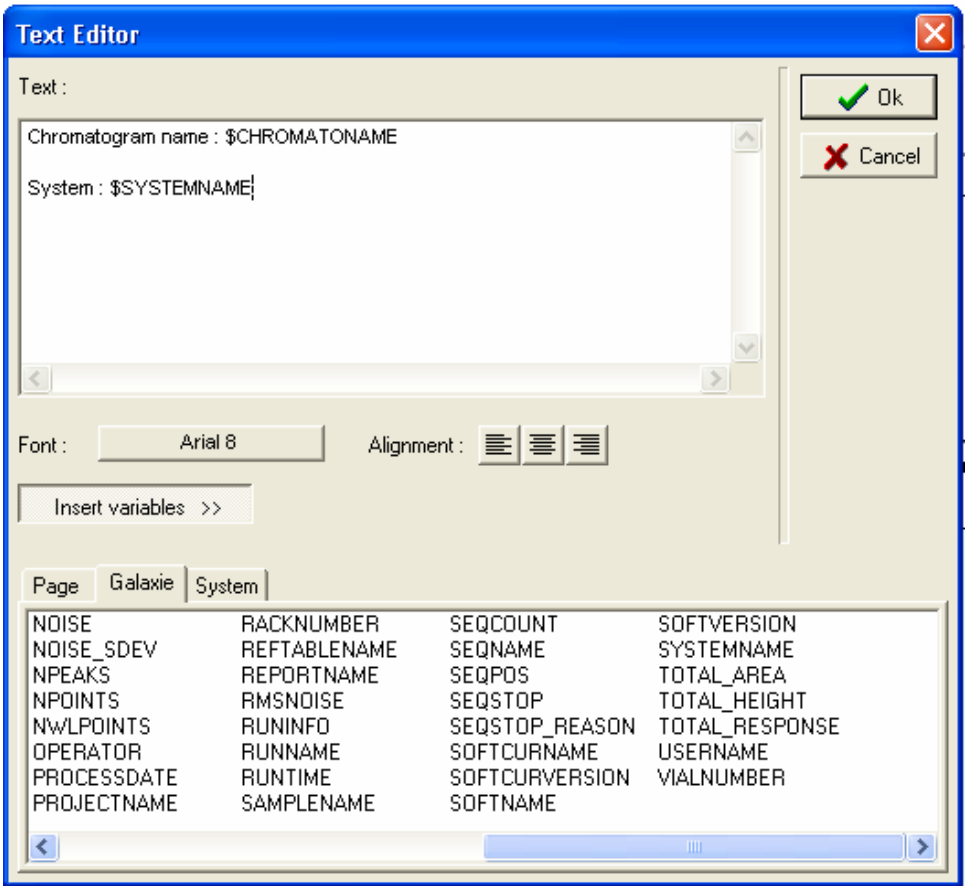


Press the *Load* button to select the image to display. A preview of the selected image is displayed.

Check Stretch to adjust the image to the object size.

Text Object

This object enables you to enter text and variables in the report.



A variable name is always preceded by the symbol $.

You may configure the font style, size, and color. Use the  buttons to modify the text alignment.

Click on the *Insert variables*>> button to choose a type of variable. Three tabs are displayed: Page, Galaxie, and System. Select one of these tabs, then in the associated list, click on the variable you want to add.

The *Page* tab enables you to print the page number, the total page numbers, and the report-guide variable, which associates a unique number with each report.

The *Galaxie* tab enables you to print the Galaxie Chromatography Data System variables. It is also possible to print the Archive number of the chromatogram, by adding the variable $ARCHIVERSION.

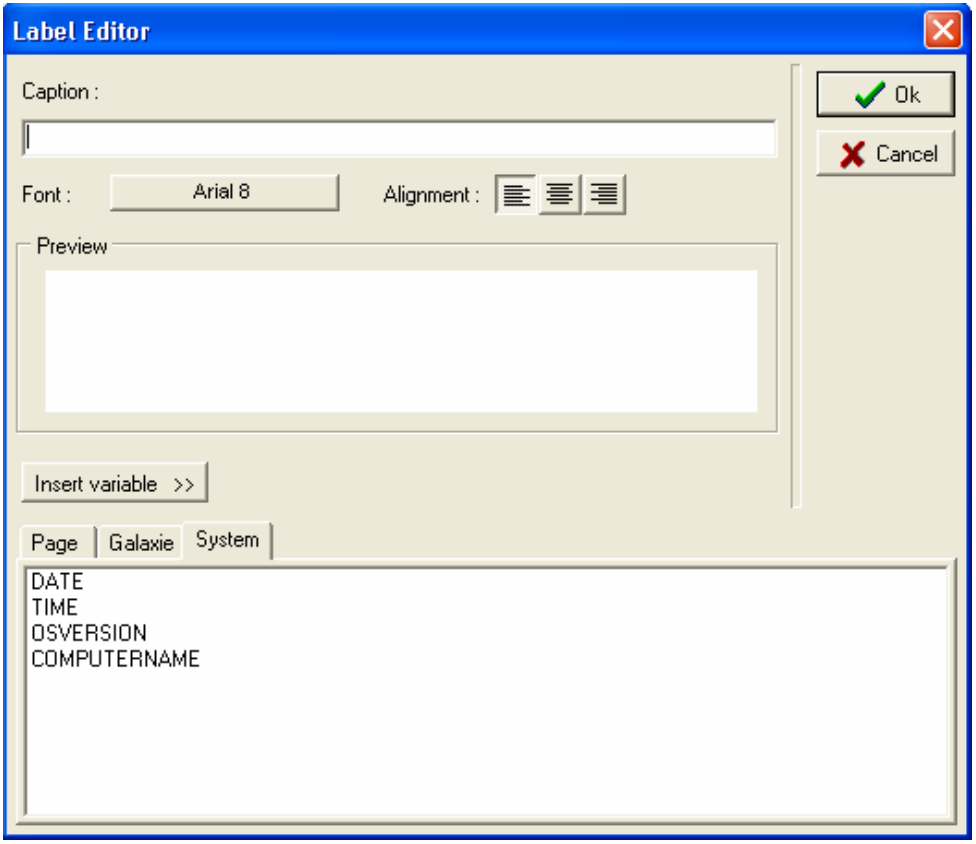
The *System* tab enables you to print system variables such as the printing date and time, the computer's name, and the OS version.

For example, if you type 'The name of the chromatogram is: ' and then you choose the variable CHROMATONAME, the name of the chromatogram will be printed after the words you typed.

Label Object

This object enables you to create and to insert a label, for example, title of the report. You can define the caption font style, size, and color.

In the pop-up menu select PROPERTIES to configure the object. The following window appears:



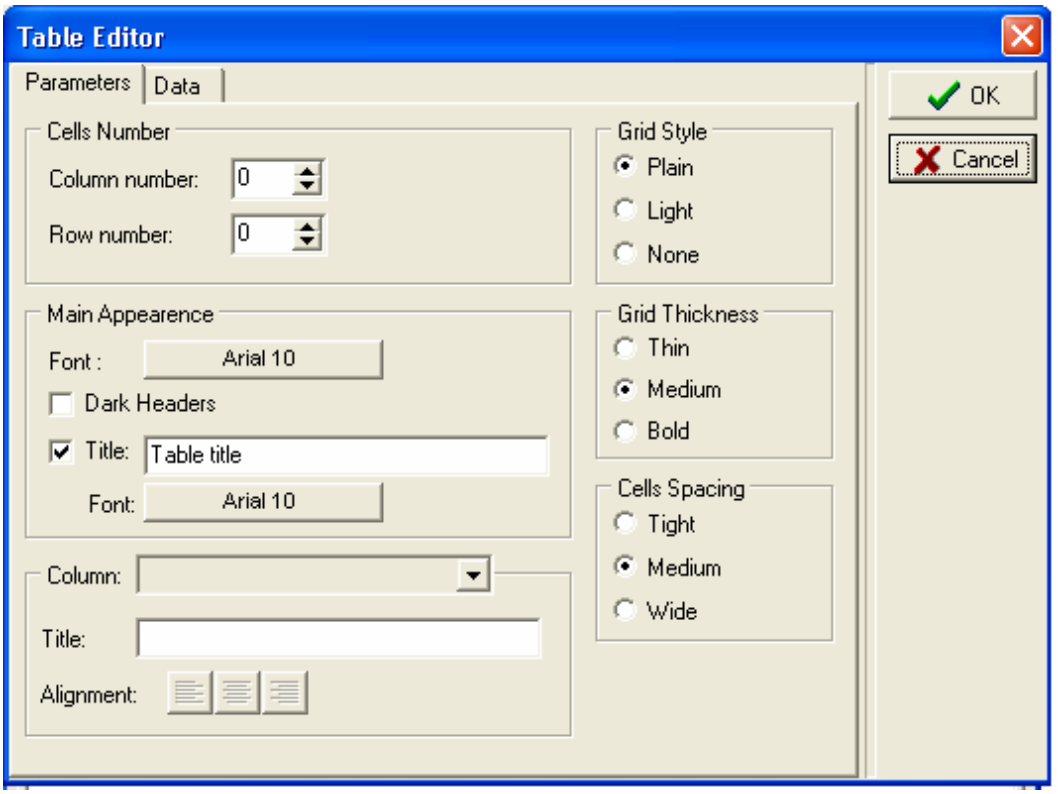
In the Caption area, enter the words to be displayed, e.g., 'Analysis report'. You can also insert a variable (as with the text object) with the *Insert variable>>* button.

Click on the *Font* button to modify the font style, size, and color. Use the  buttons to modify the text alignment.

Table Object

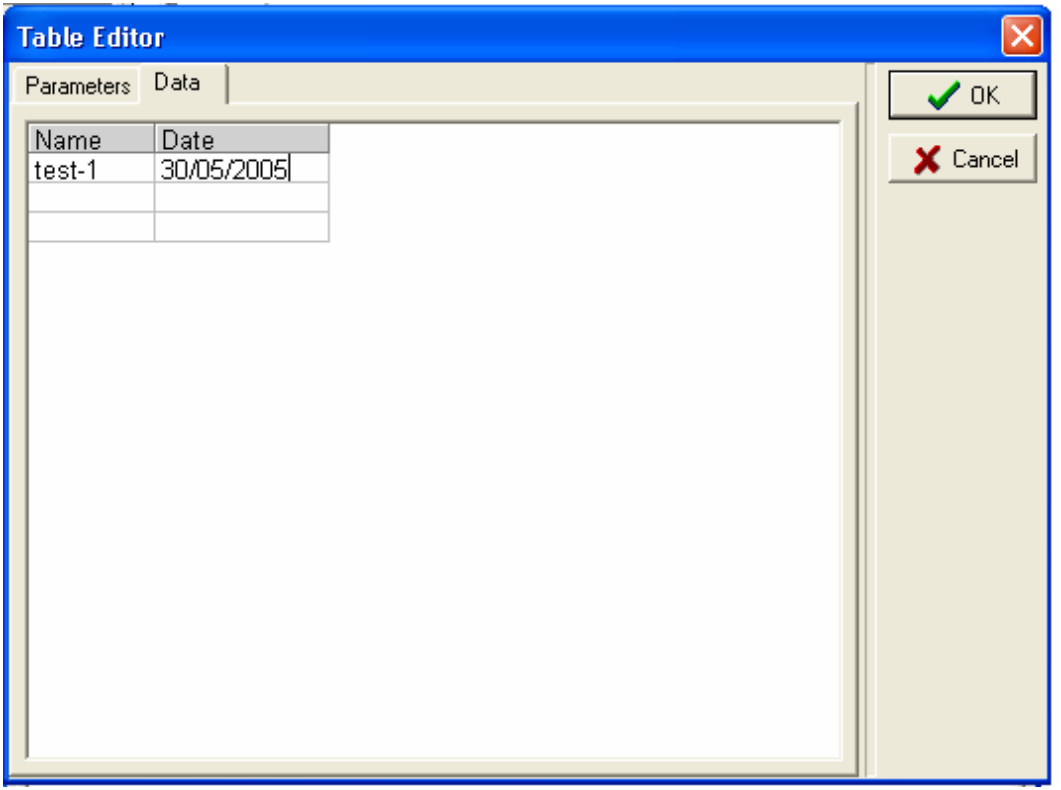
Adds a table.

In the pop-up menu select PROPERTIES to configure the object. The following window appears:



In the Table Editor Parameters tab, you can choose the table size and customize its display (grid style, thickness, cell spacing, and main appearance). You can also name the columns of the table.

Select the Data tab to add data into the table.

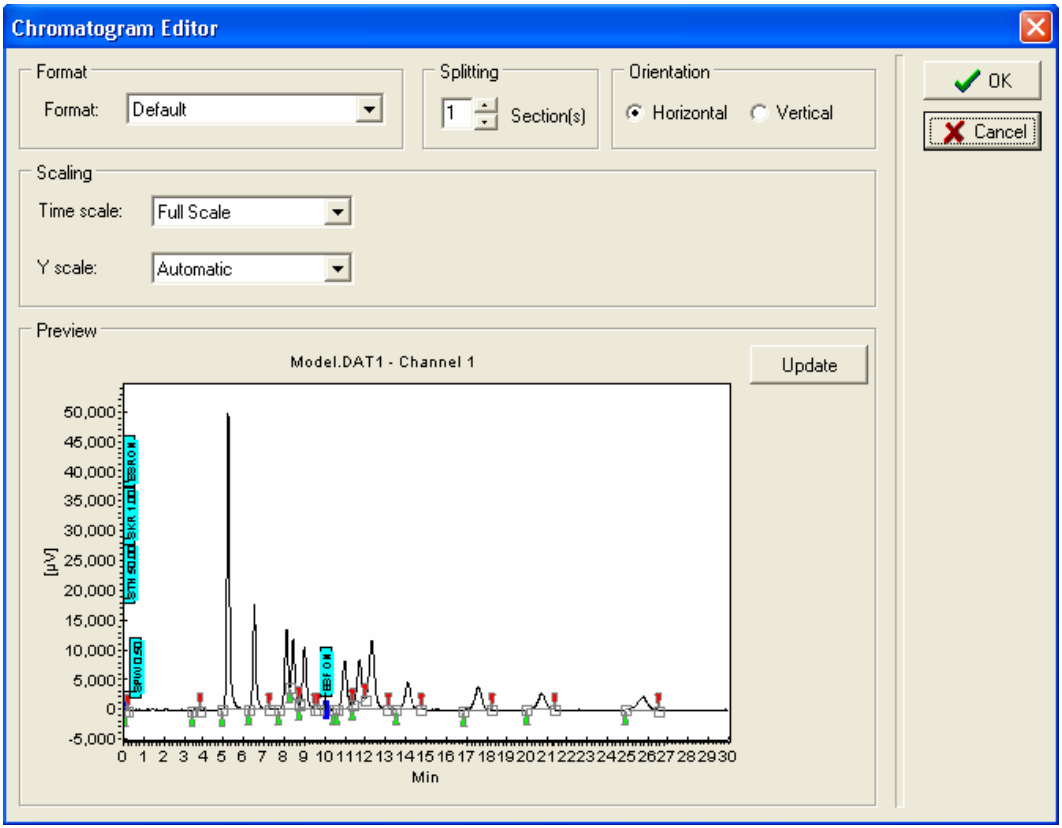


Chromatogram Object

This object enables you to add a chromatogram to the report.

In the pop-up menu select PROPERTIES to configure the object.

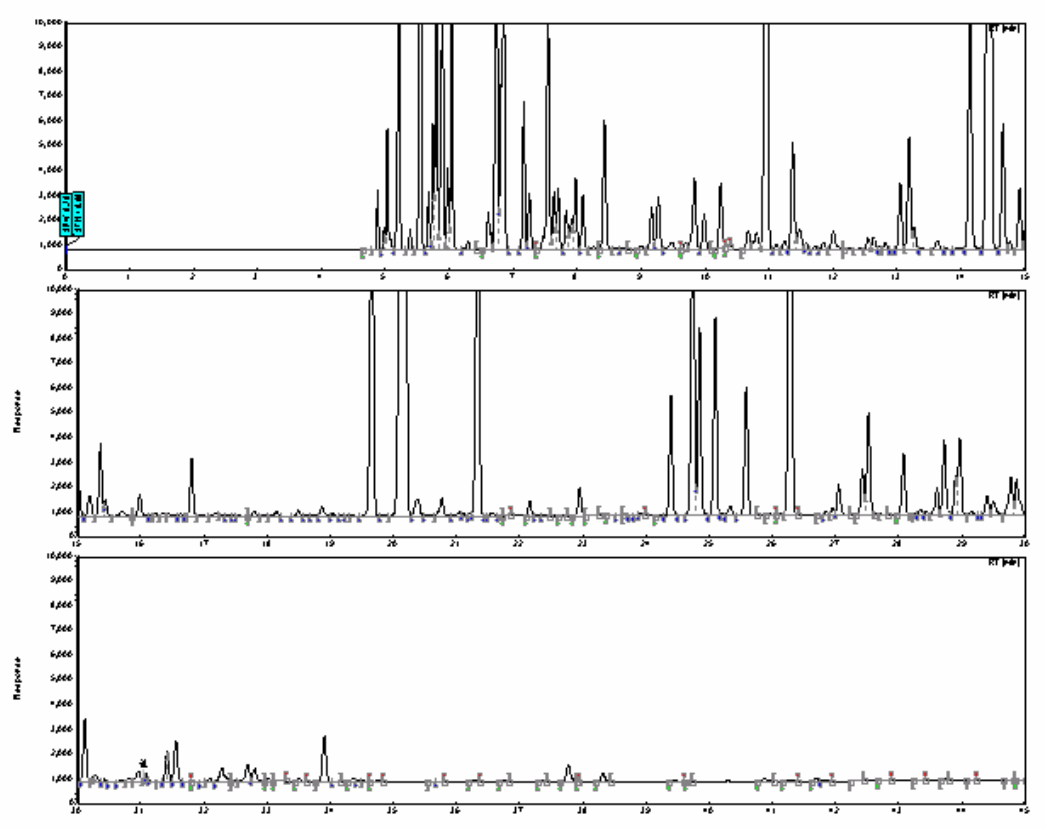
The following window appears:



In the *Format* area, choose the chromatogram format configured in Galaxie (in the format section of the method). The chromatogram can be opened in Galaxie Chromatography Data System with one format and printed with another format.

In the Splitting area, choose the number of sections in which to split the chromatogram.

Example: 3 sections



In the Orientation area, choose if the chromatograms are to be printed horizontally or vertically.

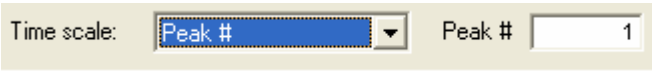
In the Scaling area, you can modify both the time scale and the amplitude scale.

Time Scale: The time range represents the limits of the chromatogram X axis.

Full scale: The chromatogram is printed in maximum scale (from zero to the end of the acquisition).

Custom: Select this option to specify manual limits to the chromatogram. When this option is selected, some edit boxes appear:

Peak # or Named peak: Select this option to print a peak only. User has to choose which peak to print by choosing either its name or its index.



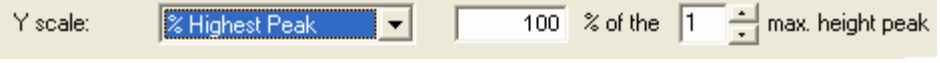
Working scale: Select this option to print the chromatogram in the scale defined in Galaxie Chromatography Data System This scale can be defined in the Quick Start windows (or in the acquisition area of the method), or after the acquisition in the working scale.

Y Scale*:* This amplitude range is the limit of the chromatogram ordinates.

Automatic: The chromatogram is printed with the acquisition scale.

Custom: Select this option to manually specify the limits of the chromatogram amplitude. When this option is selected, the following edit boxes appear:

% highest peak: Select this option to scale the chromatogram according to the height of one of the peaks (defined by its relative height). For example, if you choose to plot the chromatogram up to 200% of the second highest peak, the maximum Y value will be twice the height of the second highest peak.



Named peak: Select this option to scale the chromatogram according to the height of one of the named peaks. For example if you choose to plot the chromatogram up to 200% of the peak

Butane, the maximum Y value will be twice the height of the peak Butane.

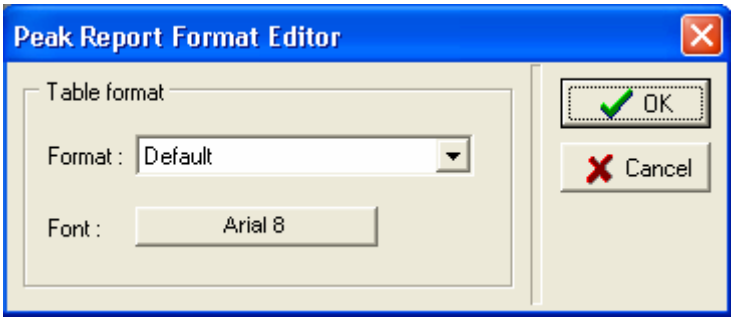
A chromatogram preview allows you to view the chromatogram as it will be printed, according to the chosen options. Click on the *Update* button to take into account the options chosen in the fields of the chromatogram properties.

Peak Results Object

This object enables you to insert the peak results. You can customize the table (font style, size, and color) and select a specific format.

The Peak Report contains all the peaks integrated into the chromatogram. (Select RESULTS / PEAK REPORT in the browser to display the Peak Report in Galaxie Chromatography Data System.)

In the pop-up menu select PROPERTIES to configure the object. The following window appears:



The Peak Table can be printed with a specific format. In the Galaxie Chromatography Data System it is possible to define formats in the method or in the peak table properties (see the Galaxie Chromatography Data System User's Guide). One of these formats can be applied to the printing.

The Peak Table formats are saved with a specific name and a comment in the Galaxie Chromatography Data System. Select

the corresponding name in the Format dropdown list, and the comment will appear.

In the Peak Results properties you can modify the appearance of the table using the *Font* button.

Note that the printed table can have a different format from the one displayed in Galaxie (Results).

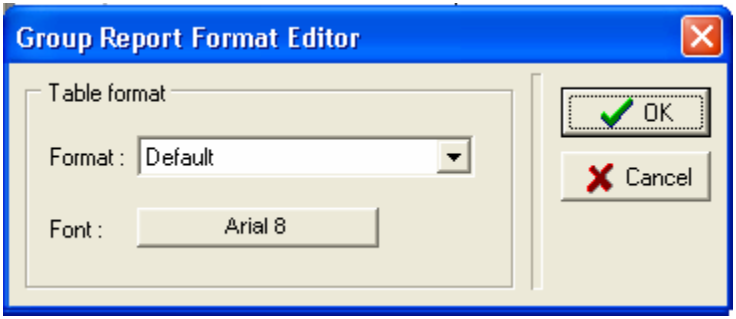
Group Results Object

This object enables you to insert the group results. You can customize the table (font style, size, and color) and select a specific format.

The Group Report is the table containing all the groups defined in the chromatogram. Select RESULTS/GROUP REPORT in the browser to display the Group Report in Galaxie.

The group table can be configured in the same way as the peak table.

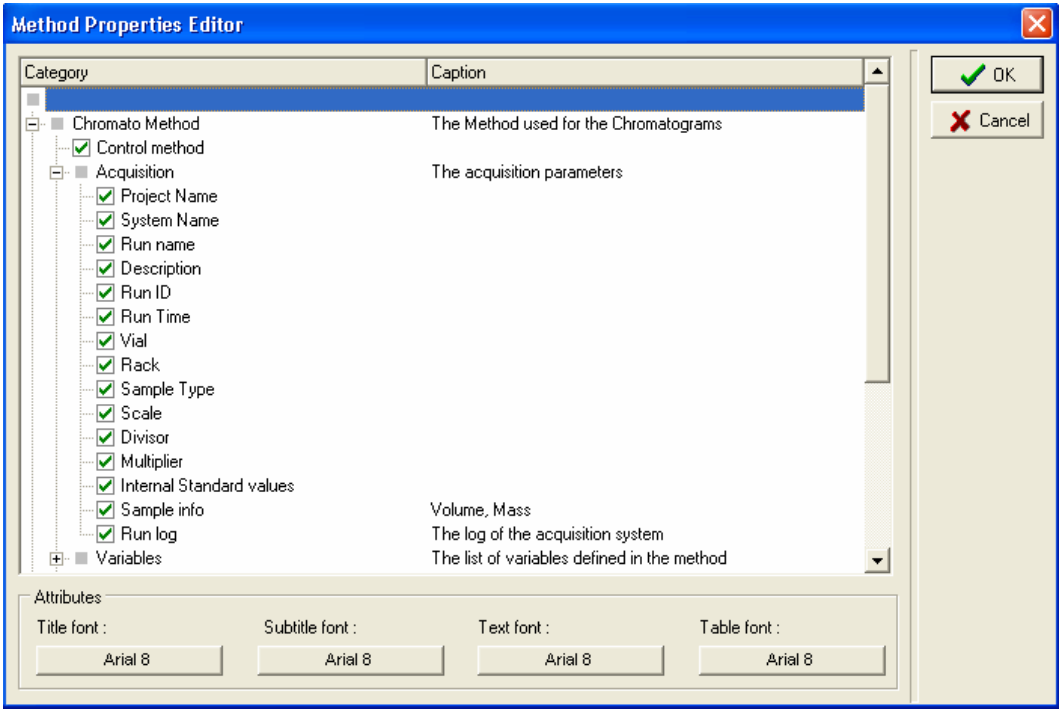
In the pop-up menu select PROPERTIES to configure the object. The following window appears:



Method Object

This object enables you to insert the method.

In the pop-up menu select PROPERTIES to configure the object. The following window appears:



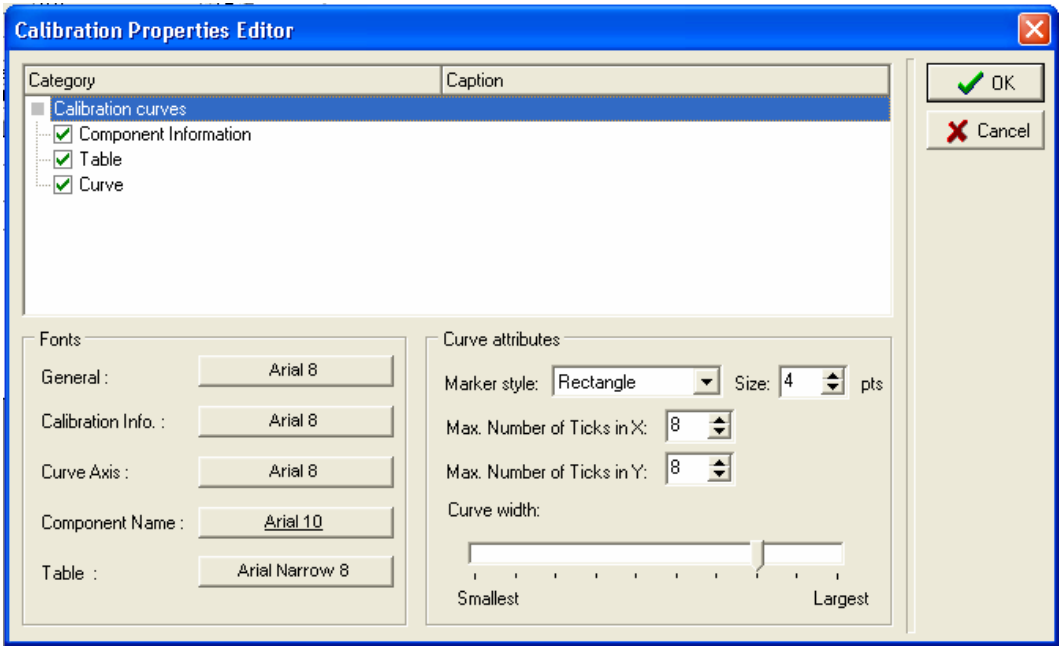
Check the parts of the method to print; uncheck the ones that you do not want to print.

NOTES: The acquisition parameters printed are the ones entered at the acquisition time. If the chromatogram has been reprocessed with different parameters, then they will not be printed in this part. The latest ones are in the global variables available in a text or a label object.

Calibration Report Object

This object enables you to print the Calibration Report.

In the pop-up menu select PROPERTIES to configure the object. The following window appears:



Check the calibration parameters to print; uncheck the parameters you do not want to print.

- **Component information:** prints the mathematical model, the calibration curve equations, the regression coefficients, the weighting, and forcing through (0,0).
- **Table**: prints the calibration point tables displayed in the 'Calibration' tab in Galaxie, the list of the calibration points, their origin, the acquisition date, the name of the user that added the point, etc.
- **Curve:** Prints the calibration curves.

In the Fonts area, you can choose the fonts for the different areas of the Calibration object.

- **General:** name of the calibration curve.
- **Calibration info:** equation, correlation factors.

- **Curve axis:** curve axis names, graduations.
- **Component name:** name of the component.
- **Table:** font used for all table fields.

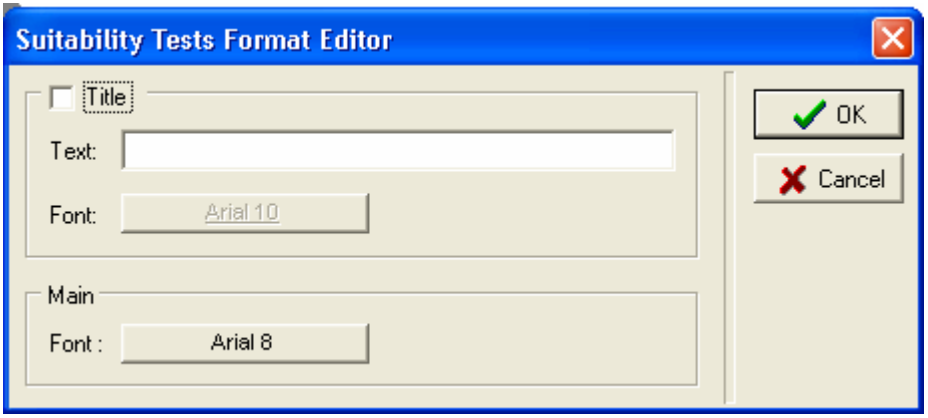
In the ‘Curve attributes’ field you can configure the style of the printed calibration curve displaying: type and size of the marker style, number of ticks in X and Y axis and location of the calibration curve on the page using the curve width bar. The curve is always placed on the right side of the page.

Suitability Tests Object

This object enables you to print the results of the suitability tests.

The suitability tests are defined in the Method.

In the pop-up menu select PROPERTIES to configure the object. The following window appears:

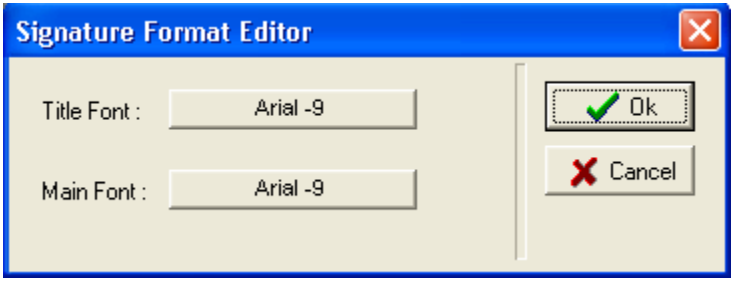


You can define a Suitability Tests title in the dedicated field (check the title box) and define the font style, size, and color.

Electronic Signature Object

This object enables you to print the electronic signature.

In the pop-up menu select PROPERTIES to configure the object. The following window appears:

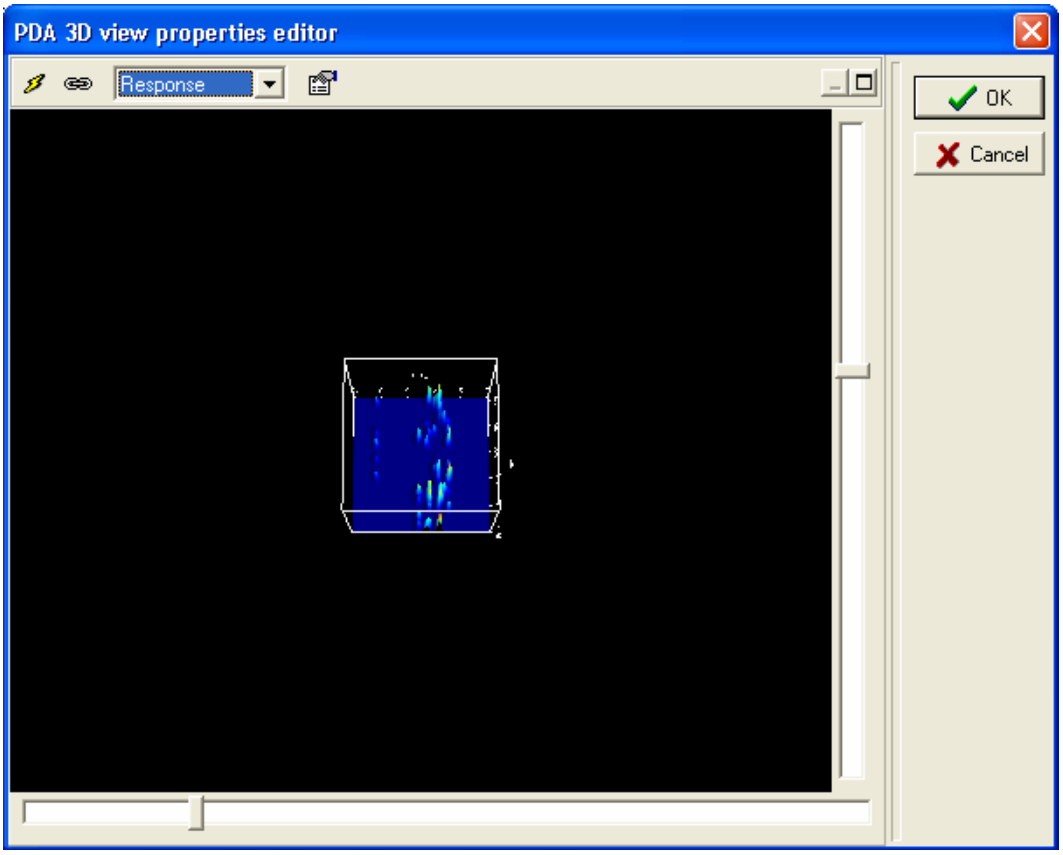


You can define the font displayed in the table: Title Font for the title, Main Font for the content of the table.

The 3D Chromatogram Object

This object enables you to print the 3D chromatogram.

In the pop-up menu select PROPERTIES to configure the object. The following window appears:

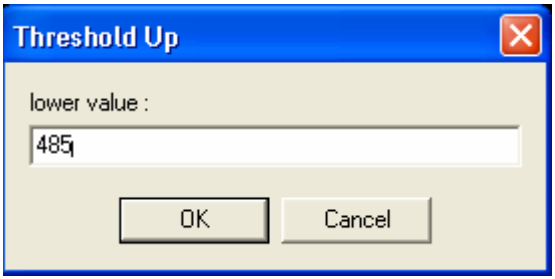


The appearance of the 3D chromatogram can be modified with the scroll bars. The scale of the X-axis can be changed by moving the slider on the horizontal scroll bar. The Y-axis scale is controlled by the slider on the vertical scroll bar. To change the Z-axis orientation (to rotate or tilt the 3D image), click on a corner of the image and drag it with the mouse until the desired orientation is obtained.

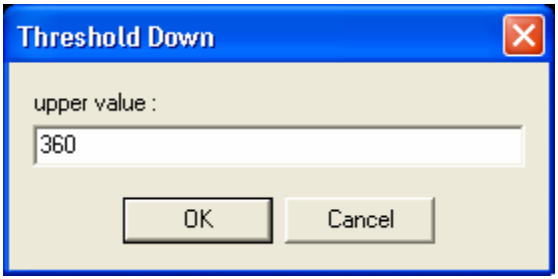
Select the required response type from the drop down list. Four choices are available:

Response: displays the 3D view with all the absorbance levels.

Threshold up: displays all the absorbance levels lower than the limit value (defined in the following screen) with the same color.

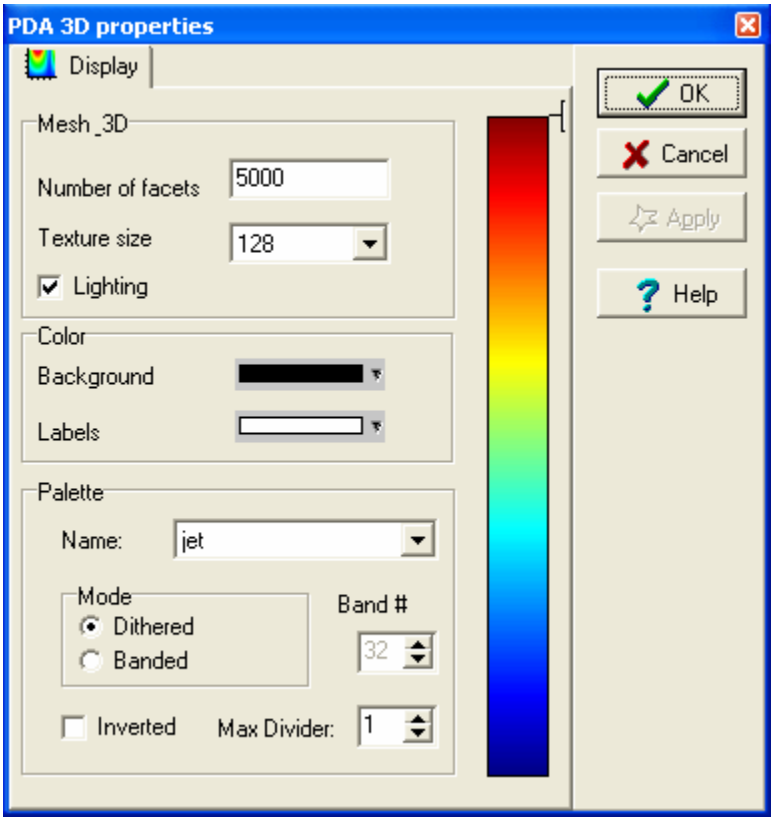


Threshold down: displays all the absorbance levels higher than the limit value (defined in the following screen) with the same color.



Threshold between: displays all the absorbance levels outside of the lower and upper limit values with a unique color.

Click on the  button to display the PDA 3D view properties window:



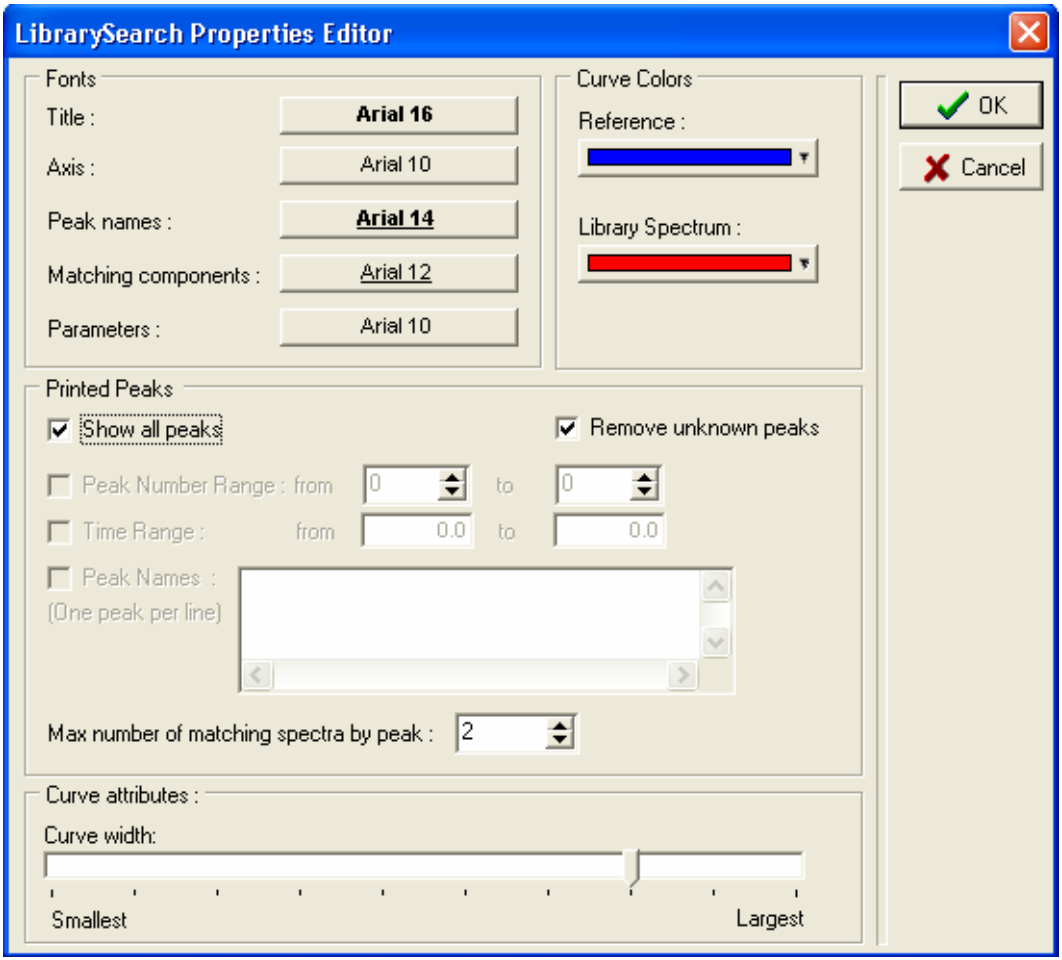
The appearance of the 3D object can be modified.

The number of facets and the texture size can be modified in the Mesh-3D area. The color of the background and the labels can be chosen in the Color area. In the Palette area, the color palette can be chosen. The coloration can be dithered or banded (in this case, you can choose the number of bands. Choose also the Max Divider which emphasizes the little variations of the map when its values are increased

The Library Search Object

This object allows you to print the Library Search results.

In the pop-up menu select *Properties* to configure the object. The following window appears:



In the **Fonts** area, you can define axis and peak name fonts, name of the matching components, and the information field associated with its spectrum.

In the **Curve Colors** area, you can define the colors of the reference and library spectra.

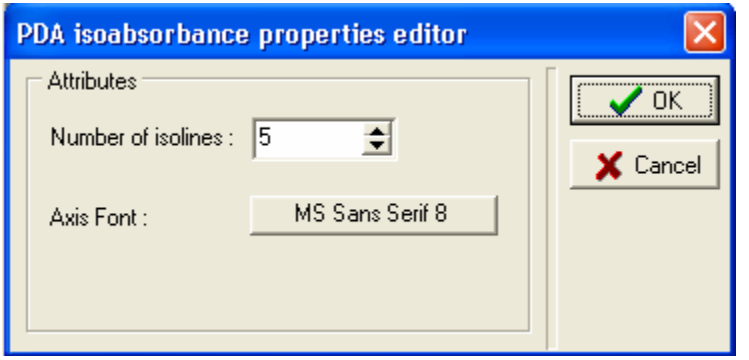
In the **Printed Peaks** area, you can choose which peak(s) to print. The different criteria allowing you to choose the peak to print are the time (Time range), the index (Peak number Range), the name (Peak names) and the named peaks (Remove Unknown peak). All peaks can be printed (Show all peaks).

In the **Curve attributes** area, you can define the size of the spectra.

The Isoabsorbance Object

This object allows you to print the isoabsorbance chromatogram.

In the pop-up menu click on Properties. The following window appears:

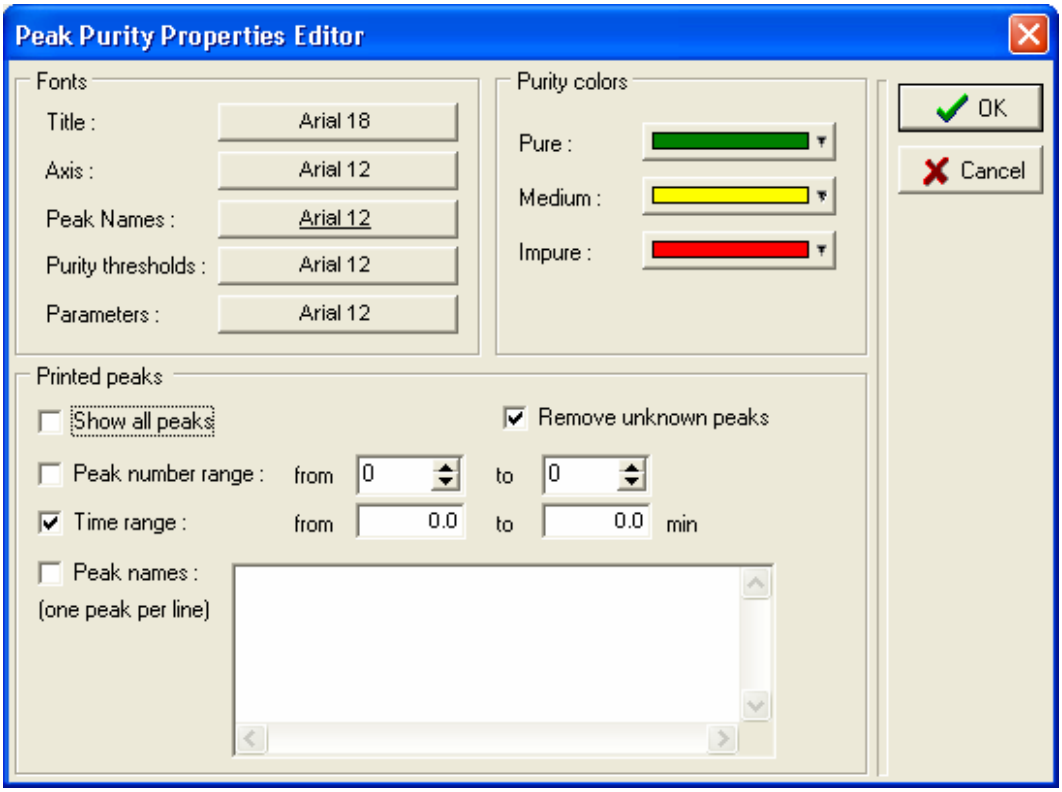


Choose the number of isolines to print and the axis font.

The Peak Purity Object

This object enables you to print the peak purity results.

In the pop-up menu click on Properties. The following window appears:



Fonts: define the axis and the other items names fonts.

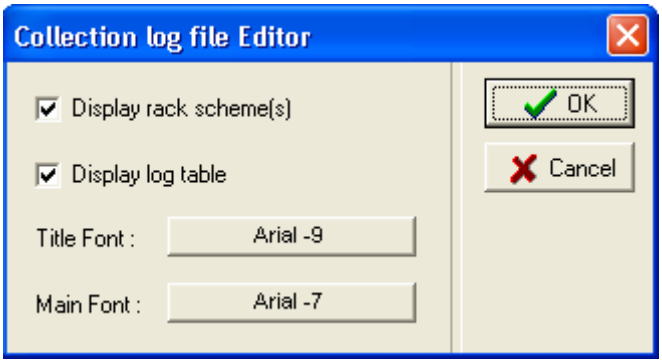
Purity colors: colors indicating the purity level.

Printed Peaks: choose which peak(s) to print. The different criteria allowing you to choose the peak to print are the time (Time range), the index (Peak number Range), the name (Peak names), and the named peaks (Remove Unknown peak). All peaks can be printed (Show all peaks).

The Collection Log File Object

This object enables you to print the collection log file, if using a fraction collection module

In the pop-up menu select PROPERTIES. The following window appears:



The User selects the parameters to print: the rack scheme and/or the log table, as they are displayed in the Collection log file.

Default Reports

Eight default reports are provided in the Galaxie / data folder.

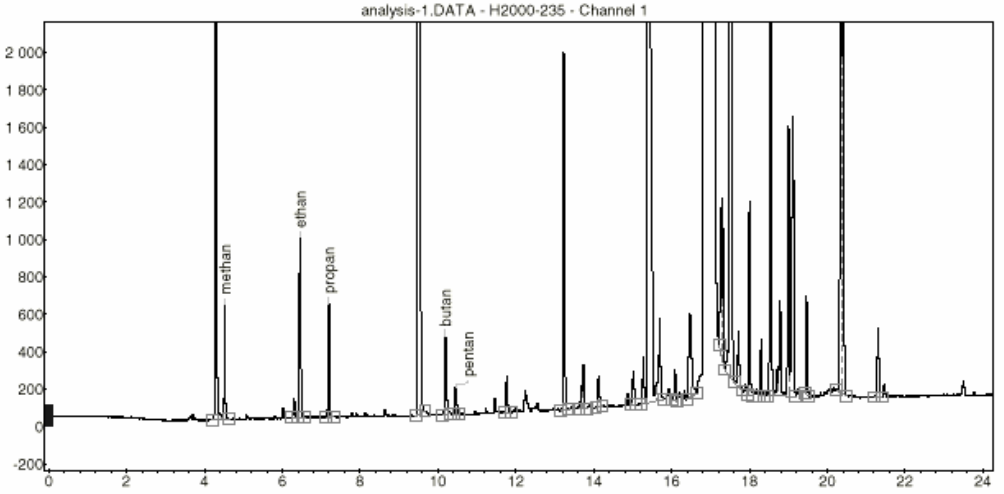
You must copy them into the Group subfolder where you want to use them.

Default_standard.STYL:

Chromatogram : analysis-1_channel1

System : GC_59
Method : sample analysis
User : sv

Acquired : 05/12/00 12:00:50
Processed : 26/04/01 12:04:01
Printed : 26/04/01 12:11:07



Peak results :

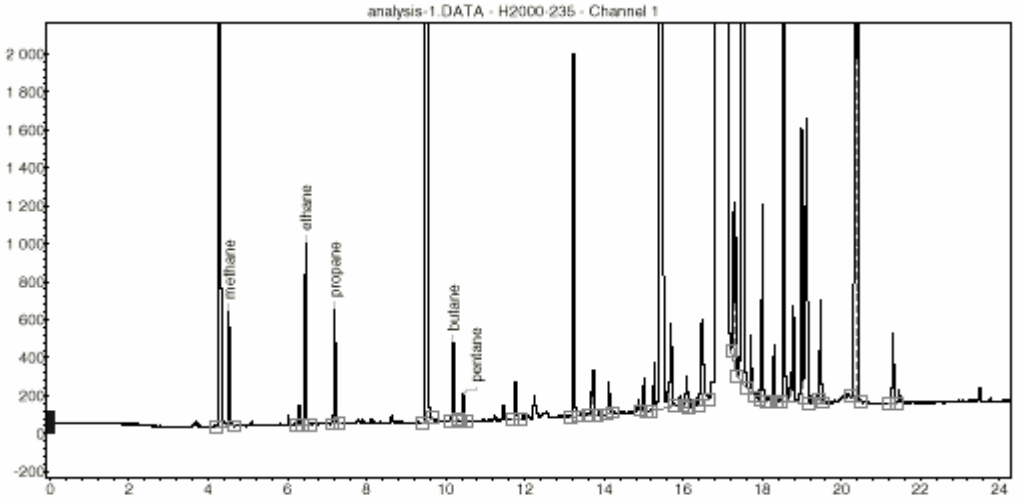
Index	Name	Time	Quantity	Area	Area
		[min]	[mass ratio]	[µV.min]	[%]
2	methan	4.52	0.00	19.3	0.034
4	ethan	6.46	0.00	37.6	0.066
5	propan	7.20	0.00	24.8	0.044
7	butan	10.19	0.00	21.7	0.038
8	pentan	10.46	0.00	7.0	0.012
Total			0.00	56793.2	100.000

Default_group_standard.STYL

Chromatogram : analysis-1_channel1

System : GC_59
Method : sample analysis
User : sv

Acquired : 05/12/00 12:00:50
Processed : 26/04/01 17:15:44
Printed : 26/04/01 17:16:59



Peak results :

Index	Name	Time	Quantity	Area	Area
		[min]	[g/l]	[µV.min]	[%]
2	methane	4.52	5.90	19.3	0.034
4	ethane	6.46	0.00	37.6	0.066
5	propane	7.20	10.23	24.8	0.044
7	butane	10.19	0.00	21.7	0.038
8	pentane	10.46	0.00	7.0	0.012
Total			16.13	56793.2	100.000

Group results :

Index	Name	Area	Area
		[µV.min]	[%]
1	group1	55349.4	97.458
2	group2	1333.4	2.348
Total		56682.7	99.806

Default calibration.STYL

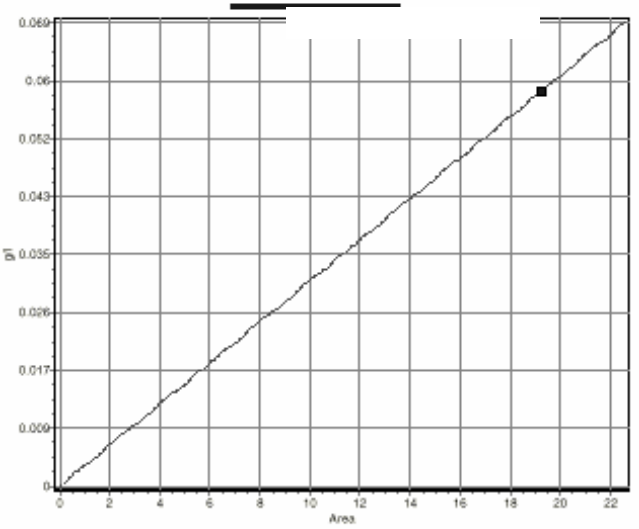
Chromatogram : analysis-1_channel1

System : GC_59
Method : sample analysis
User : sv

Acquired : 05/12/00 12:00:50
Processed : 26/04/01 16:03:03
Printed : 26/04/01 16:11:13

Calibration Report :
File : alkanes

Component : methane
Polynom : y = b x + a
a = 0
b = 3.06394E-003
Correlation Coef. : -1.0000
Weighting : None
Force zero : Yes



Calibration table : methane

#	Used	Name	Area	gl	Chromatogram	Date	gl Precision	Rec %	time [min]	Level	Username
1	1	Point 1	18.26	0.05	analysis-1 - 1	26/04/01 15:47:57	0.06	0.00	4.62	1	sv

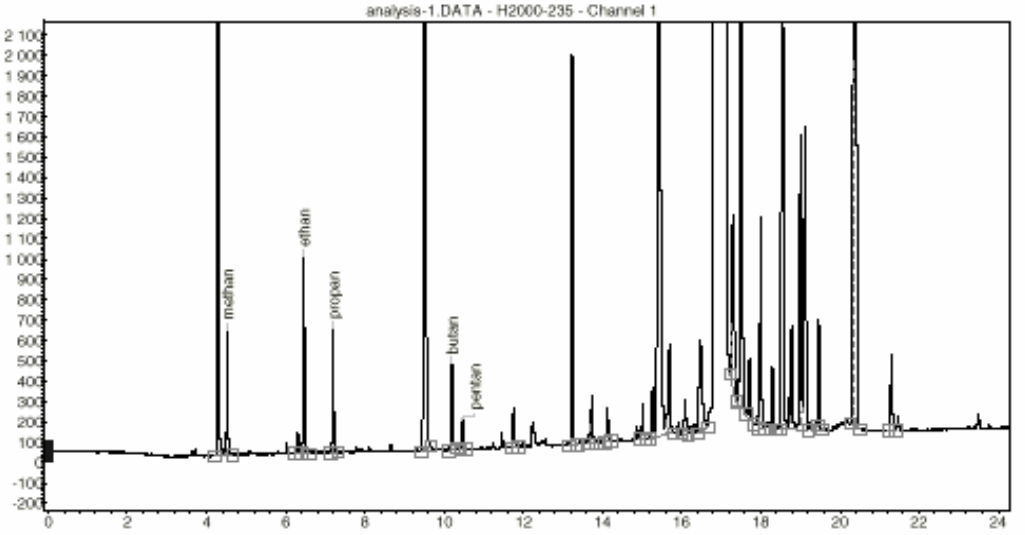
Component : propane
Polynom : y = b x + a
a = 0

Default suitability.STYL

Chromatogram : analysis-1_channel1

System : GC_59
Method : sample analysis
User : sv

Acquired : 05/12/00 12:00:50
Processed : 26/04/01 14:00:24
Printed : 26/04/01 14:00:53



Peak results :

Index	Name	Time	Quantity	Area	Area
		[min]	[mass ratio]	[µV.min]	[%]
2	methan	4.52	0.00	19.3	0.034
4	ethan	6.46	0.31	37.6	0.066
5	propan	7.20	0.00	24.8	0.044
7	butan	10.19	0.18	21.7	0.038
8	pentan	10.46	0.06	7.0	0.012
Total			12.29	56793.2	100.000

Suitability Results :

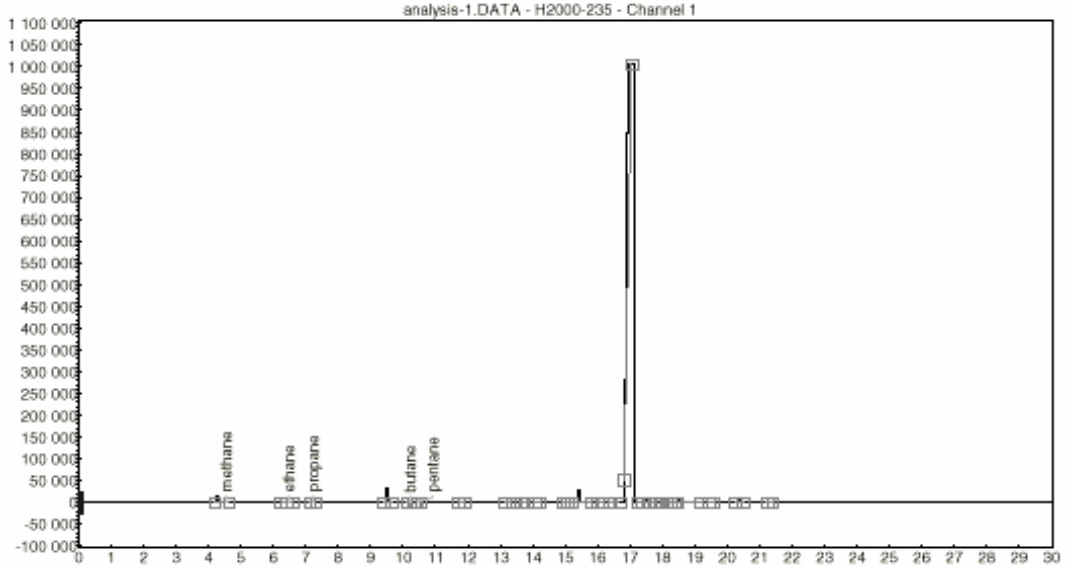
For Peakmethan : if test *AREAP = 10.00 fails then report only: Failed! (production problem)

Default_method.STYL

Chromatogram : analysis-1_channel1

System : GC_59
Method : sample analysis
User : sv

Acquired : 05/12/00 12:00:50
Processed : 26/04/01 16:31:53
Printed : 26/04/01 16:51:40



Results :

Index	Name	Time	Quantity	Area	Area
		[min]	[g/l]	[µV.min]	[%]
2	methane	4.52	5.90	19.3	0.034
4	ethane	6.46	0.00	37.6	0.066
5	propane	7.20	10.23	24.8	0.044
7	butane	10.19	0.00	21.7	0.038
8	pentane	10.46	0.00	7.0	0.012
Total			16.13	56793.2	100.000

Chromatogram : analysis-1_channel1

System : GC_59
Method : sample analysis
User : sv

Acquired : 05/12/00 12:00:50
Processed : 26/04/01 17:24:04
Printed : 26/04/01 17:24:25

CHROMATOGRAM METHOD REPORT :

Acquisition :

Run Time : 30.00
Vial : 0
Rack : 0
Divisor factor : 1.00
Multiplipliер factor : 100.00
Analysis : Sample
Injection volume : 1.00 µl
Injection amount : 12 067.30

Preprocessing :

Blank Subtract :

File:
N.A.

Integration Method :

Reduce Noise : Yes
Spike Parameter : 1
Use Relative Threshold : Yes

Integration Events :

Active	Time	Event	On	Value
Yes	0.00	Set Peak Width		0.2
Yes	0.00	Set Threshold		4

Manual actions :

Manual integration action count : 0

Peak Identification table :

Peak Name	RT [min]	Abs.Window[min]	Window %	Ref ?	Mode	Group
methane	4.53	0.20	0.20		Nearest	
ethane	6.47	0.20	0.20		Nearest	
propane	7.22	0.20	0.20	X	Nearest	
butane	10.21	0.20	0.20		Nearest	
pentane	10.44	0.20	0.20		Nearest	

Resolve with references : Yes

Group Identification table :

Group Name	Group type	Parameters
group1	Calibration grou	p1 range(s)
group2	Calibration grou	p1 range(s)

Calibration Method :

Method type : External Standard
Response : Area
Standard Unit : g/l
Calibration curve file name : alkanes

Factors : Curve
Subtract internal standard mass
Response unit : Curve

Unknown mode : Response Factor
Factor value : 0.025
Internal Standard

Componer	Model	Weighting	Poly Order	(0,0) ?	Level 1
methane	Polynomia	N/A	1	X	5.90

Chromatogram : analysis-1_channel1

System : GC_59
Method : sample analysis
User : sv

Acquired : 05/12/00 12:00:50
Processed : 26/04/01 16:31:53
Printed : 26/04/01 16:51:40

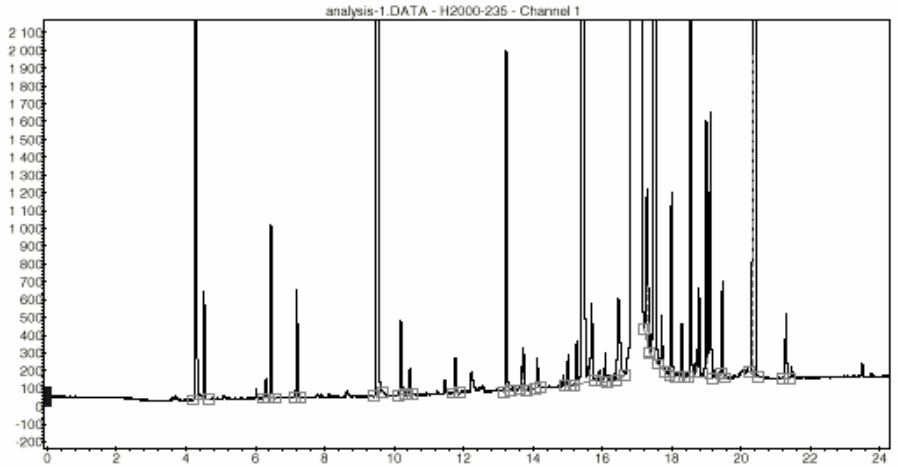
Componer	Model	Weighting	Poly Order	(0,0) ?	Level 1
propane	Polynomia	N/A	1	X	10.23

Default_group_method

Chromatogram : analysis-1_channel1

System : GC_59
Method : sample analysis
User : sv

Acquired : 05/12/00 12:00:50
Processed : 26/04/01 17:24:04
Printed : 26/04/01 17:24:25



Peak results :

Index	Name	Time	Quantity	Area	Area
		[min]	[g/l]	[µV.min]	[%]
2	methane	4.52	5.90	19.3	0.034
4	ethane	6.46	0.00	37.6	0.066
5	propane	7.20	0.00	24.8	0.044
7	butane	10.19	0.00	21.7	0.038
8	pentane	10.46	0.00	7.0	0.012
Total			5.90	56793.2	100.000

Group results :

Index	Name	Area	Area
		[µV.min]	[%]
1	group1	55349.4	97.458
2	group2	1333.4	2.348
Total		56682.7	99.806

Chromatogram : analysis-1_channel1

System : GC_59
Method : sample analysis
User : sv

Acquired : 05/12/00 12:00:50
Processed : 26/04/01 17:24:04
Printed : 26/04/01 17:24:25

CHROMATOGRAM METHOD REPORT :

Acquisition :

Run Time : 30.00
Vial : 0
Rack : 0
Divisor factor : 1.00
Multiplipliier factor : 100.00
Analysis : Sample
Injection volume : 1.00 µl
Injection amount : 12 067.30

Preprocessing :

Blank Subtract :

File:
N.A.

Integration Method :

Reduce Noise : Yes
Spike Parameter : 1
Use Relative Threshold : Yes

Integration Events :

Active	Time	Event	On	Value
Yes	0.00	Set Peak Width		0.2
Yes	0.00	Set Threshold		4

Manual actions :

Manual integration action count : 0

Peak Identification table :

Peak Name	RT [min]	Abs.Window[min]	Window %	Ref ?	Mode	Group
methane	4.53	0.20	0.20		Nearest	
ethane	6.47	0.20	0.20		Nearest	
propane	7.22	0.20	0.20	X	Nearest	
butane	10.21	0.20	0.20		Nearest	
pentane	10.44	0.20	0.20		Nearest	

Resolve with references : Yes

Group Identification table :

Group Name	Group type	Parameters
group1	Calibration group	1 range(s)
group2	Calibration group	1 range(s)

Calibration Method :

Method type : External Standard
Response : Area
Standard Unit : g/l
Calibration curve file name : alkanes

Factors : Curve
Subtract internal standard mass
Response unit : Curve

Chromatogram : analysis-1_channel1

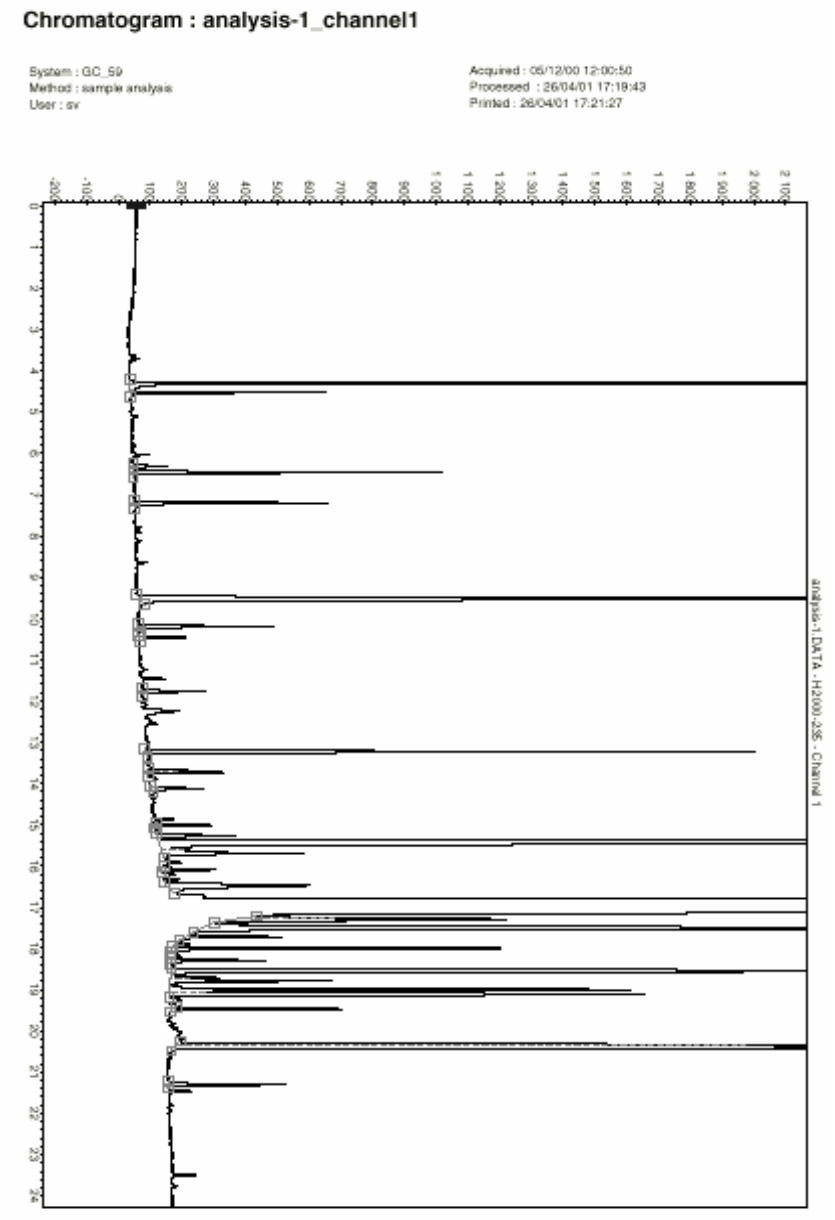
System : GC_59
Method : sample analysis
User : sv

Acquired : 05/12/00 12:00:50
Processed : 26/04/01 17:24:04
Printed : 26/04/01 17:24:25

Unknown mode : Response Factor
Factor value : 0.025
Internal Standard

Componer	Model	Weighting	Poly Order	(0,0) ?	Level 1
methane	Polynomial	N/A	1	X	5.90

Default_WinNT



Chromatogram : analysis-1_channel1

System : GC_59
Method : sample analysis
User : sv

Acquired : 05/12/00 12:00:50
Processed : 26/04/01 17:19:43
Printed : 26/04/01 17:21:27

Peak results :

Index	Name	Time	Quantity	Area	Area
		[min]	[g/l]	[µV.min]	[%]
2	methane	4.52	5.90	19.3	0.034
4	ethane	6.46	0.00	37.6	0.066
5	propane	7.20	0.00	24.8	0.044
7	butane	10.19	0.00	21.7	0.038
8	pentane	10.46	0.00	7.0	0.012
Total			5.90	56709.2	100.000