

Chromatography Data System

GCsolution version 2.4

Instruction Manual

Operation

Read the instruction manual thoroughly before you use the product.
Keep this instruction manual for future reference.

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Important

- If the user or usage location changes, ensure that this Instruction Manual is always kept together with the product.
- To ensure safe operation, contact your shimadzu representative if product installation, adjustment, or re-installation (after the product is moved) is required.

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Introduction

Thank you very much for purchasing the GCsolution software for Shimadzu gas chromatograph workstations (hereafter called "GCsolution").

GCsolution allows you to control the gas chromatograph (hereafter called "GC") from your personal computer, acquire chromatograms and other different kinds of data, and reanalyze the acquired data under different parameters on your personal computer.

This manual has been put together in order to familiarize you with the basic knowledge required to operate GCsolution. Be sure to read it through before using this software. After reading the manual, keep it in a safe place so that it can be accessed whenever necessary.

The "Reference Manual" and "Administration Manual" for GCsolution for Shimadzu gas chromatograph workstations are attached as on-line manuals.

The Reference Manual covers the on-line help information in PDF format. The Administration Manual covers the information on the features useful for system administration such as the support features for GLP/GMP or FDA 21CFR Part11, a set of regulations for electronic records and electronic signature. For more information on the functions of GCsolution, refer to these on-line manuals.

This manual assumes that the reader is knowledgeable of basic operations of Windows®. For the operation of Windows®, refer to the instruction manual that comes with that product.

Items included in the GCsolution package

The GCsolution product package contains the following items.

Item name	Qty.	Remarks
GCsolution CD-ROM	1	Contains the GCsolution program and the instruction manual for GCsolution (PDF versions of the Reference and Administration manuals).
Operation manual for GCsolution	1	Describes how to acquire and analyze data using GCsolution.
Software License Agreement	1	It is a software use permission contract. Please read it through.
RS-232C cable	1	This cable is used to connect the gas chromatograph to your personal computer.

Note: If this product package comes with any product set, its contents may be slightly different. Refer to the instruction manual accompanying that product set.

Using the instruction manual

Kinds of instruction manuals

The GCsolution package contains the following information that describes the operational procedures and functions.

Name	Media	Description
Operation manual for GCsolution	Printed Document	Explains the operational procedures for data acquisition and analysis using GCsolution.
On-line help	GCsolution program	Provides detailed information on parameters and setting ranges. This is accessible from the Help menu in GCsolution. (For using the on-line help, refer to section 12.1.1 Using Help p.107 in this instruction manual.)
Operation manual for GCsolution(PDF version)	CD-ROM disk for installation	Provides the operations volume of the instruction manual as a PDF file so that it can be viewed on your personal computer. It is accessible from the Help menu in GCsolution. (For using this PDF, refer to section 12.1.2 Using the Online Manual p.108 in this instruction manual.)
Quick manual for GCsolution (PDF version)	CD-ROM disk for installation	Provides the Quick manual as a PDF file so that it can be viewed on your personal computer.
Reference manual for GCsolution (PDF version)	CD-ROM disk for installation	Provides the Reference manual as a PDF file so that the on-line help can be printed out. The general table of contents is available, including all the instruction manuals (PDF versions). This is the common manual for both GCsolution and GCsolution Lite.
Administration manual for GCsolution (PDF version)	CD-ROM disk for installation	Explains the operational procedures and basic idea of system administration and data management using GCsolution. This manual is provided as a PDF file so that it can be referred to on-line whenever operations related to system administration are needed. The general table of contents is available, including all the instruction manuals (PDF versions). This is the common manual for both GCsolution and GCsolution Lite.

Legends for instruction manual

This manual uses the following legends:

Legend	Meaning
❗	Gives you tips.
< >	Shows a window or view name; e.g., <Data Acquisition> window or <Method> view.
[]	Shows a parameter, tab, column, cell, bar name, menu command, that can be selected from the menu bar.
[]-[] command	Shows a sequence of selecting the menu in the first [] and then selecting the command in the second []. For example, [File]-[Print] command means that you should click on the File menu and then select the Print command from the displayed list of commands.

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Contents of Administration Manual

Contents of Reference Manual



1.1

Features

1 What is GCsolution?

❖ 32-bit software using the latest Windows technology

GCsolution runs on WindowsNT/2000 Professional/XP Professional/Vista Business/7 Professional, and its advanced security and multi-task features are supported. It allows you to use long file names and the drag & drop function.

❖ A variety of functions are available through simple operations

- Assistant bar: Guides you so you can easily perform analysis even if you are a novice user.
- Data explorer: Allows you to perform file management through intuitional operations.
- Simple Instrument Parameter Setting view: By offering two configuration modes, this normal (simplified) mode and the advanced mode, GCsolution has improved its operability while still supporting a variety of analysis conditions.
- Batch table wizard: Allows you to easily create a batch table for series of analysis.
- Compound Table Wizard: Provides support for creating a compound table.

In addition, other functions that improve the operability are effectively laid out so that you can make the best use of them.

❖ Reliable GLP/GMP support features

- Security support: Provides the proper security for diverse business flows through the system administration function.
- Audit trail support: Stores all the information on data acquisition and processing, and manages the updating history.
- Validation support: Provides support for hardware, software, and method validation.

For FDA 21CFR Part11 compliance, CLASS-Agent is needed.

❖ Compatible with network environment

- All-in-one file structure (=compound structure system): Has all the data-related information (analytical conditions and report formats) in the data file, allowing you to easily perform data analysis outside the analysis laboratory using the LAN.
This feature is also useful for GLP/GMP file management.
- LAN-enabled system administration: Allows you to share the system administration information by GCsolution software on multiple computers on the LAN.
- GC-LAN connect Option: With this optional software, communication device can be replace from RS-232C to Ethernet between PC(=GCsolution) to GC Instruments.
- GCsolution Agent Option: This optional software provides data archiving and management functions for GCsolution with using Client/Server type database system. The data archiving feature is enhanced to satisfy the FDA 21CFR Part11 requirements.

❖ Applicable for high-throughput analysis of a large number of data

- Applicable for high-speed analysis: Allows you to acquire data in a minimum sampling time of 4 msec. (in case of GC-2010/2014/2025)
- Applicable for analysis of a large number of data: Allows you to simultaneously analyze two samples in the dual line configuration.

The maximum configuration for analysis supports 2 lines with 4 detectors.(excepts for GC-2025)



❖ File compatibility

- Compatibility with CLASS-GC10 format: Allows you to load CLASS-GC10 method files and data files without converting them.
- Compatibility with CLASS-VP4 format: Allows you to use CLASS-VP4 method files and data files by converting them into the GCsolution format.
- Compatibility with the AIA ANDI format: Allows you to read and write files in the AIA ANDI format, which is one of the international standard data formats.

Note: This feature also allows you to pass data files in the GCsolution format to the CLASS-GC10.

Data may be saved in text format so that it can be used on other commercially available software. In addition to that, GCsolution supports the function to save reports in the PDF that satisfies the FDA 21CFR Part11 requirements in combination with Adobe® Acrobat®.*

* You need to install Acrobat® additionally.

❖ Various functions for identification and quantitative processing

- A variety of quantitative calculation methods: Supports 6 different calculation methods, including the external and internal standard methods.
- A variety of calibration curves: Supports 7 different kinds of calibration curves, including straight line, line graph, and exponential calculation curves.
- Flexible creation of calibration curves: Allows you to manually add or delete data in addition to creating data through series or batch analysis.
- Algorithm with established reputation: Uses the peak integration algorithm of the Chromatopac series.

❖ Report format with high flexibility

The Microsoft Word-like report format allows you to create flexible custom reports easily and efficiently.

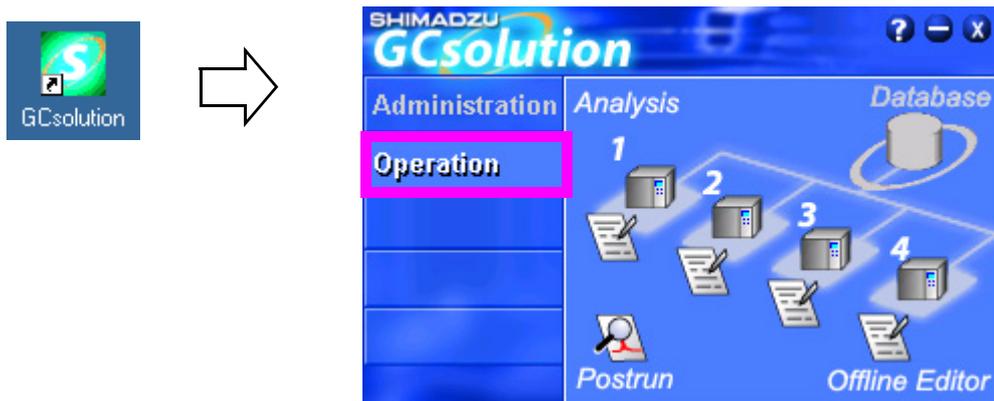
2 Software Overview

2.1 GCsolution Basics

This software consists of three applications: <GC Real Time Analysis>, <GC Postrun>, and <GC Analysis Editor>

2.1.1 GCsolution Applications

Installing this software into the personal computer, the [GCsolution] icon appears on the screen (desk top). Double clicking the icon starts <GCsolution Launcher>.



Note: [Database] icon is enabled when CLASS-Agent (optionally available) is installed.

❖ Icons included in [Operation] tab

	←	<p>Clicking this icon starts an application that is used to control instruments and devices, and to perform a single or batch run.</p>
	←	<p>Clicking this icon starts an application that is used to read acquired analysis data and to perform data re-processing or calibration.</p>
	←	<p>Clicking this icon starts an application that is used to, during analysis, edit a method file or batch file that is not used for analysis.</p>

Note: The [GC Real Time Analysis #] and [GC Analysis Editor #] icons are enabled for the number of GCs that are currently connected to your personal computer.

Note: The [GC Analysis #] and the [GC Analysis Editor #] icons are given instrument name registered on <System Configuration> as "Tool Tips" with focusing by mouse cursor.

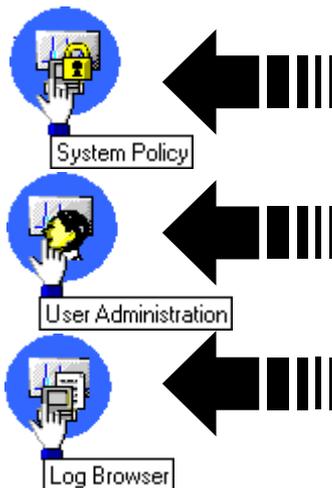


This document does not cover the operations/functions available from the [Administration] tab. It includes following programs.



Note: Settings in the [Data Reg. Settings] is for registering data to CLASS-Agent (optionally available) database.

❖ Icons included in [Administration] tab



To use the system administration function in this software, set the policies like login method and password limitations.

Used to register users or periodically change passwords. Also used to specify the groups on operational rights.

Allows you to search a log of operation history or the like under the advanced search conditions and then list the hit items.

For further details of the icons included [Administration] tab, refer to Administration Manual "2.2 Using the System Administration Tools to Set Available Items".



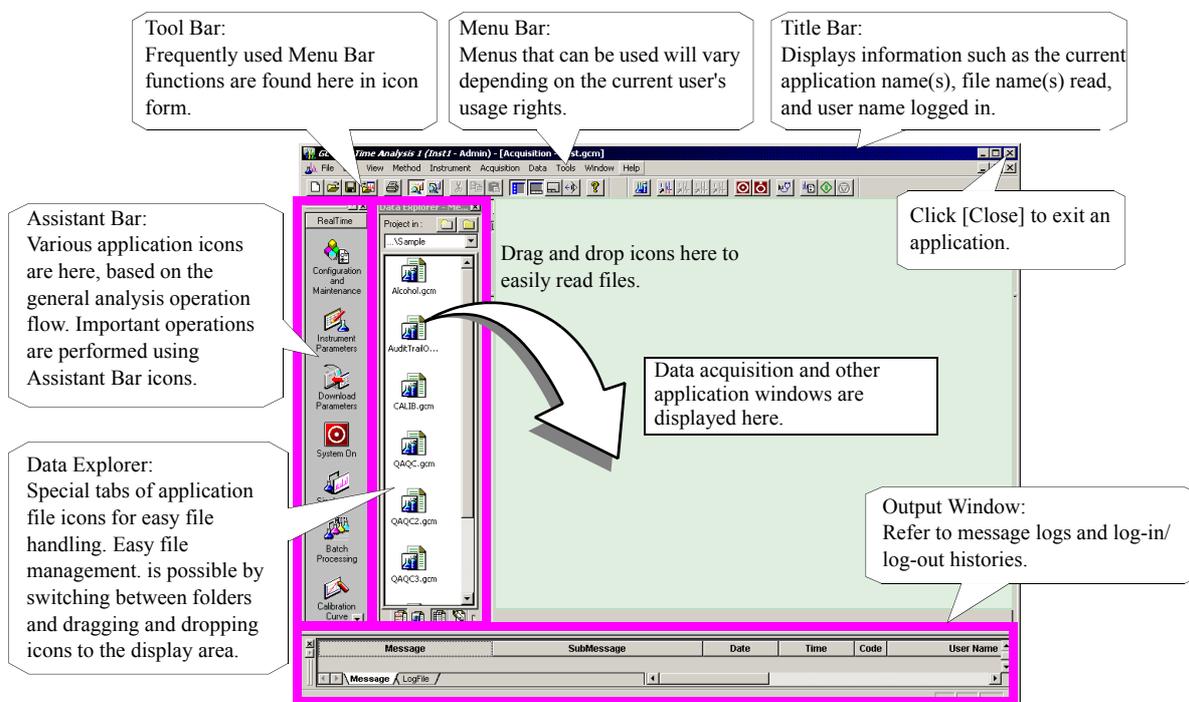
Double-click the icon to start up the program. The following <Login> screen will appear. Enter your user ID and password to log into the program.



Note: Before you start up the <GC Real Time Analysis>, be sure to turn on the GC instrument. When you start up <GC Analysis Editor> or <GC Post-run> it is not necessary.

Note: Just click the [OK] button without entering a password when you start up the program for the first time, for no password has been assigned at that time.

The following is the configuration of the program windows.





2.1.2 File Types and Data Explorer File Tabs

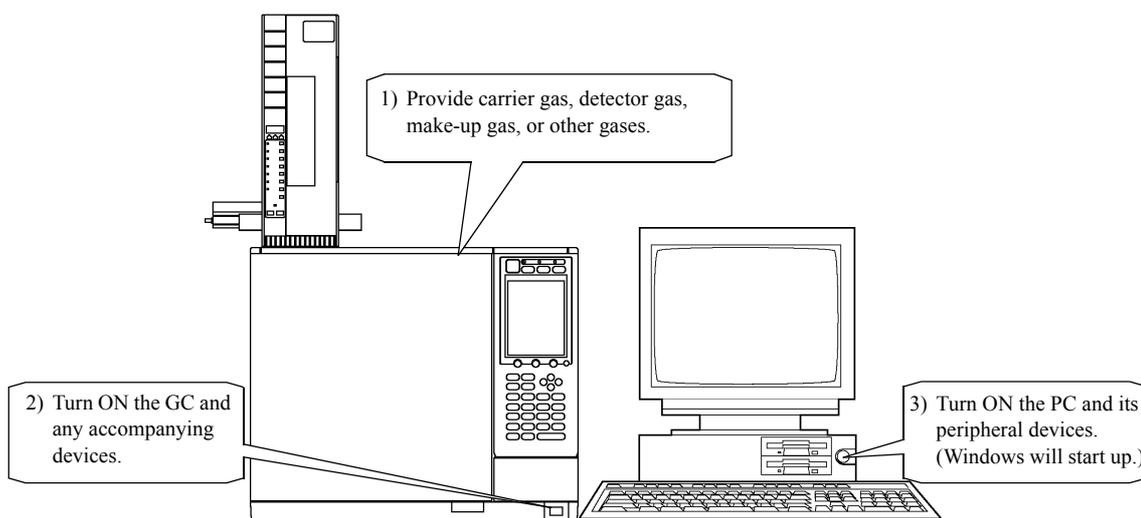
File Type	File Contents
<p>Data File (extension = 'gcd')</p> 	<p>Stores the following information;</p> <ul style="list-style-type: none"> - Chromatogram data: - Calculation results such as area and concentration values - Status information such as oven temperatures and errors during data acquisition. - Method file data that has been used for analysis (including analysis system configuration used) - Report format file data (when report data is output) - Batch file data (when batch processing is performed)
<p>Method File (extension = 'gcm')</p> 	<p>Stores the analysis conditions used for data acquisition, the data processing conditions such as peak integration parameters and compound tables, and the plotted calibration curves. Also, records the system configuration used when editing a method, and this data will be checked against the current system configuration when reading method file data.</p>
<p>Batch File (extension = 'gcb')</p> 	<p>Stores batch table data used to perform series of analyses or post-run analyses. The same file can be used on both <GC Real Time Analysis> and <GC Postrun> screens.</p>
<p>Report Format File (extension = 'gcr')</p> 	<p>Stores report format information such as layouts to be used for report output and detailed report settings. The <Report> window is used on both <GC Real Time Analysis> and <GC Postrun> screens.</p>

3 Performing an Analysis

3.1 Preparing for Analysis

To analyze samples and acquire data using the GC unit, start the <GC Real Time Analysis> application.

3.1.1 Turning on the instrument and logging in to <GC Real Time Analysis>



Then start the <GCsolution Launcher>, click the icon for the instrument to use to start the <GC Real Time Analysis> application. The login screen will appear for you to enter your user ID and password.

<Login>

1) Click [GC Real Time Analysis 1].

2) Click [OK] button.

3) The GC analysis program starts up and the <GC Real Time Analysis> main screen appears.

<GC Real Time Analysis>

GC Real Time Analysis 1 (Instrument1 - Admin) - [Acquisition - Untitled]

File Edit View Method Instrument Acquisition Data Tools Window Help

Ready

Line1-Ch1(DET1): Monitor: 5.62min 3365uV Cursor: 0.79min 4085uV

Chromatogram

Note: To either set up a password for an "Admin" level user, or to add user(s), use the <User Administration> Window (Reference Manual page.522).

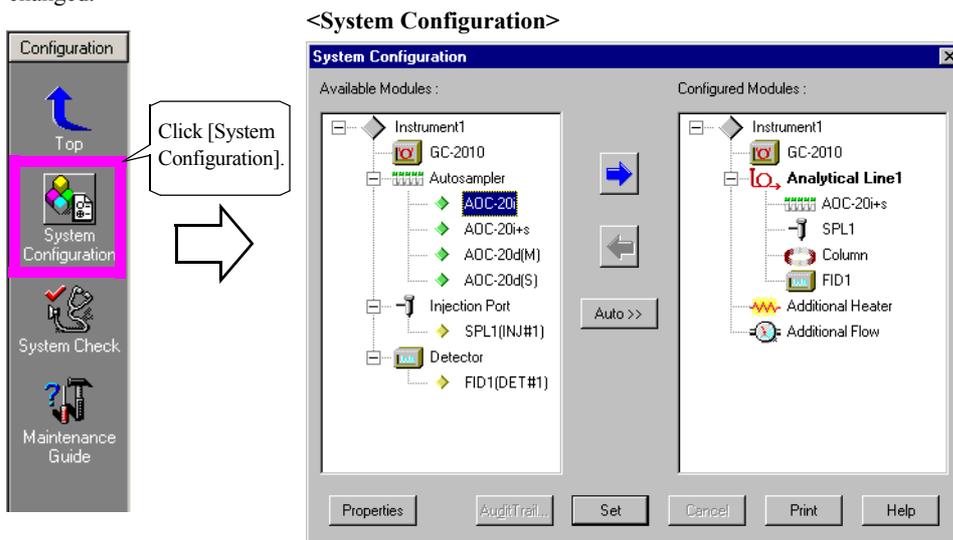
Note: When the <Data Acquisition> window opens, the previously used method file will automatically be read in. To create a new method file before performing any settings, click the [New] button on the toolbar. To edit an existing method file, drag and drop the desired method file from the <Data Explorer> window to the <Data Acquisition> window.



3.1.2 Setting Unit Conditions Used on the <System Configuration> Screen

Click the [Configuration and Maintenance] then click the [System Configuration] icon on the Assistant Bar to set up the GC devices configuration such as the column information.

You need not set up [Configuration] every time you run the program because the previous configuration has been saved. Change the configuration only when it is necessary such as that the column has been replaced or any component has been changed.



[Available Modules] shows all the units connected to the GC. (As for autosampler, all the models you can connect to the GC are displayed.)

Select units you wish to use from [Available Modules] and set to [Configured Modules], in which all the devices used to build the GC system are listed.

To add a unit to [Configured Modules], select the unit by clicking it in the [Available Modules] tree and click the right-arrow button in the center area.

After adding all the necessary units to [Configured Modules], double-click the unit name or select it and click the [Properties] button to set up the detailed configuration for each unit such as carrier gas type and column information.

For more about system configuration, refer to "12.2.6 System Configuration Settings".

For more about column information settings, refer to "4.7 Registering Column Information".



3.1.3 Operation Example Analysis Conditions

Here, the operation flow is shown using the following system configuration and each instrument's analysis conditions.

◆ System Configuration

Gas chromatograph GC-2010
Auto-sampler - AOC-20i
Capillary column: DBWAX
12 m × 0.53 mm LD, 3 µm-thick film
Split/Splitless
Injection unit (SPL)
Flame ionization detector (FID)

◆ Instrument Conditions

Column oven temperature.:
55 °C (3 min. hold.), -120 °C (rate: 10 °C/min.)
Injection Temperature.: 200 °C
Injection mode: Split
(Split ratio 1 : 50)
Detector Temperature.: 200 °C

◆ Analysis Samples

Components contained in ethanol are used as standard samples.

Standard Sample	Concentration
n-propanol	200 ppm
Isobutyl alcohol	200 ppm
Isoamyl alcohol	200 ppm

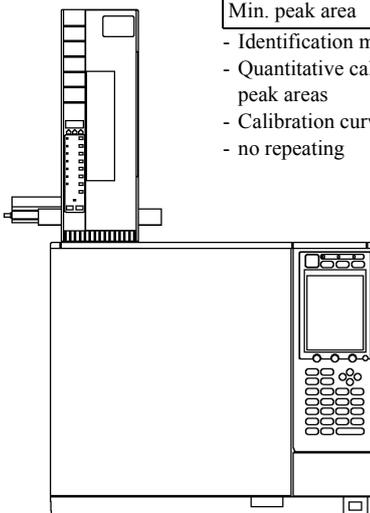
◆ Data Processing Conditions

Use the following parameters to detect peaks and perform data processing.

- Peak integration parameters

Parameter	Setting Value
Slope	1,000 µV/min.
Width	3 sec.
Drift	Auto (Set to 0)
T.DBL	1,000 min.
Min. peak area	1,000 counts (Min.Area)

- Identification method: Absolute RT
- Quantitative calculation method: External standard using peak areas
- Calibration curve: One calibration point
- no repeating



Set up parameters on <Data Acquisition>.

<Data Acquisition>

1) Click [Instrument Parameters].

2) Click [Auto-sampler] tab.

3) Enter "1 μ l" for the [Injection Volume]. All other parameters use default values.

4) Click [Injection unit] tab.

5) [Temperature] = 200 °C
[Flow Control Mode] = Linear Velocity [Linear Velocity] = 30 cm/sec.
[Split Ratio] = 50 (1:50)
[Total Flow] and [Column Flow] will be recalculated based on these settings. All other parameters ([Split Mode] = Split [Carrier Gas] = He) use default values.

Monitor: 23.38min 476uV Cursor: 15.43min 209715200uV
PeakMax : 52,485,180 C
Slope Test
Zero Adjust
Snapshot
Download

Analysis Time : 10.50 min Normal Ac

ADC-20i SPL1 Column FID1

Injection Volume : 1.0 μ L

of Rinses with Solvent(Pre-run) : 0
of Rinses with Solvent(Post-run) : 1
of Rinses with Sample : 2
Plunger Speed(Suction) : High Middle Low
Viscosity Comp. Time : 0.2 sec
Plunger Speed(Injection) : High Middle Low
Syringe Insertion Speed : High Low
Injection Mode : Normal Set...
Advanced...

Temperature : 25.0 C
Injection Mode : Split
Sampling Time : 1.00 min
Carrier Gas : He
Flow Control Mode : Linear Velocity
Pressure : 50.1 kPa
Total Flow : 87.2 mL/min
Column Flow : 1.65 mL/min
Linear Velocity : 30.0 cm/sec
Purge Flow : 3.0 mL/min
Split Ratio : 50.0

INJ. Program Purge Flow Redraw

	Rate	Flow	Hold Time
0	-	3.0	0.00
1	0.00	0.0	0.00
2	0.00	0.0	0.00
3	0.00	0.0	0.00

Total Program Time : 0.00 min
Advanced...

Column Information (0.091 0.05 0.050)

Length : Advanced Setting Thickness : 0.50 μ m
 Link Oven Program and AcquisitionTime.

You can switch the display to the [Normal]/[Advanced] screen by selecting it in the right-click popup menu.
The [Normal] screen shows only frequently changed items. For a newly created method, set up all the items using the [Advanced] setup screen first and then use the [Normal] screen afterward.



3 Performing an Analysis

3.1 Preparing for Analysis

6) Click [Column] tab. [Temperature] (i.e., initial temperature) is set to 55 °C.

8) Click [Redraw] to display the set temperature program data on the graph.

7) Enter temperature program here.
Initial temp. hold time: 3 min.,
Program rate: 10 °C/min.,
Final temperature.: 120 °C,
Retention. time: 1 min.

9) Click [Detector] tab.

10) [Temperature] = 200 °C

By default, the stop time of detector is linked to the stop time of column oven specified in the temperature program.

You can disable the link by deselecting the link option on the menu popped up by right-clicking in the window. Then the stop time can be set independently.

11) Click [General] tab.

11) Click [General] tab.

By [Auto Flame On], detector flame can be ignited automatically at when the GC become ready status.

12) Check [Auto Flame On]

3.1.4 Starting Up the GC

Specified device parameters are sent to the GC when [Download Parameters] is clicked. Then GC will start up when [System On] is clicked.

If you wish to change the temperature or pressure after GC startup, change the parameter for it and click the [Download Parameters] button. Every time the [Download Parameters] button is clicked, changed parameters are sent to the GC.

1) Click [Download Parameters].

2) Click [System On].

3) GC will start up using the downloaded instrument parameter values.

4) Instrument monitor will automatically appear. Confirm [GC System] is ON and wait for [GC Status] to change to Ready.

GC System ON System OFF

GC Status Not Ready

ADC-20HS
Vial#: 0

SPL1
Carrier Gas: OFF ON
Temperature: 0.0 / 25.0 C
Pressure: 0.0 / 100.0 kPa
Total Flow: 0.0 / 50.0 mL/min
Purge Flow: OFF ON
0.0 / 3.0 mL/min

Column
Temperature: 0.0 / 25.0 C

FID1(Ch1)
Detector: OFF ON
Flame: OFF ON
Temperature: 0.0 / 25.0 C

Line1 Relay

Check monitor/setting values for each unit. Since GC startup is controlled in flow rate order --> temperature --> detector, temperature control may not start up or detector may not turn ON immediately after GC starts up.

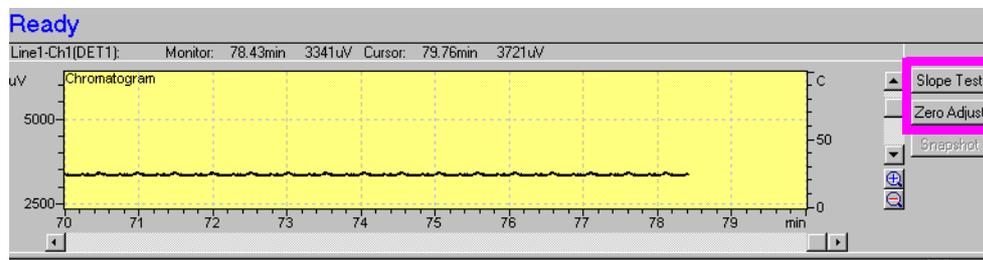
The instrument monitor display can be switched between displayed and hidden using the [Instrument Monitor] button on the toolbar.

For more about GC actions when starting up, refer to "4.3 Setting Up GC Start/Stop Actions".



3.1.5 Performing Detector Signal Zero Adjustment and Slope Testing

When the baseline has come to a stabilized state, run [Zero Adjust] then [Slope Test].

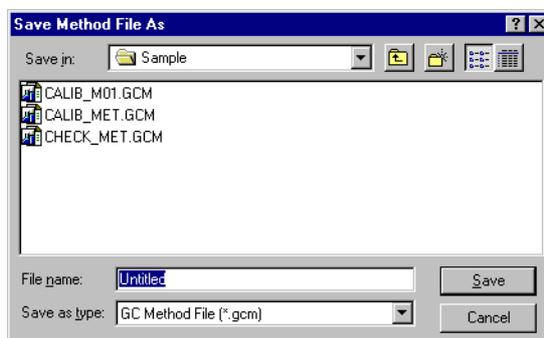


As the result of a slope test will be set to the method as the value for integration parameter "Slope", it should be done once before a sequential analysis is started, you do not need to do the slope test for every analysis.

Refer to "4.2 Slope Test and Snap Shot Button" on p.32, and "4.6 When the Baseline is Unstable", on p.39.

3.1.6 Saving Method File

Save your settings in a method file by selecting [File]-[Save Method File As].



A method file holds data processing parameters and QA/QC parameters as well as the device parameters described in this chapter.

Note: When <GC Real Time Analysis> is activated next time, the method file loaded the last time will be loaded automatically. To create a new method file, click the [New Method File] button on the toolbar before making any settings.

Note: A method file is created based on the configuration of the current device settings. If you load the existing method file after changing the current configuration, a warning is displayed. If you proceed loading the method file, the settings in it will be automatically modified in accordance with the current configuration.

3 Performing an Analysis

3.2 Performing Single-run Analysis

This section describes how to perform a single-run analysis (analyzing samples one by one) using the auto-sampler.

For the manual injection case, a simpler data acquisition method is also available. Refer to "4.9 Acquisition start from instrument".

3.2.1 Setting Single-run Conditions

Prior to starting data acquisition, register sample information by <Sample login>.

1) Click [Single Run]

2) Click [Sample Login].

3) Though [Sample Name] and [Sample ID] can be skipped, be sure to enter [Data File] name.

4) Enter [Vial #] = 1.

5) Click this check and specify report format file to print a report.

6) Click [OK] to complete.

Note: Click  to view existing files.

Note: If folder name is not specified, acquired data is saved in the project folder in which the currently loaded method file is located.

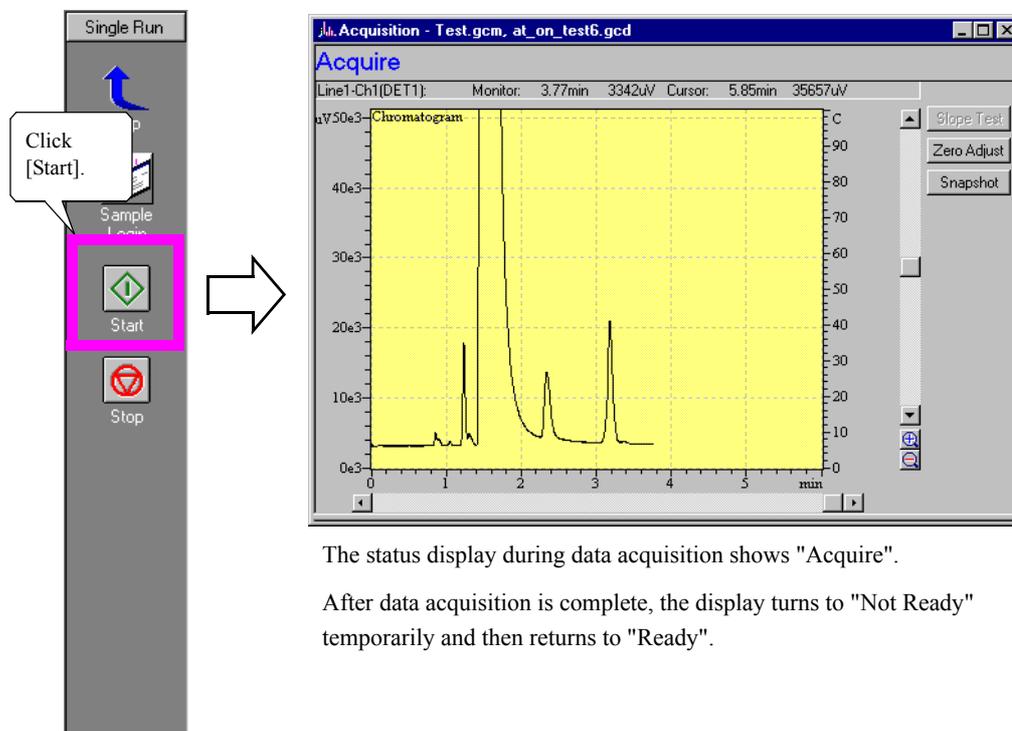
Note: If a data file should not be overwritten by a data acquisition, [Auto increment] adds serial number to end of each file name.

For more about the relationship between file name designation and storage location, refer to "11.2.2 What is a Project?"



3.2.2 Starting an Analysis

In this example, set a standard sample alcohol mixture vial (200 ppm) in the AOC-20i's sample vial number 1 position.



The status display during data acquisition shows "Acquire".

After data acquisition is complete, the display turns to "Not Ready" temporarily and then returns to "Ready".

AOC-20i will inject a sample and begin analysis. At analysis start, screen display changes to plot start.

To perform an analysis by manual sample injection, after clicking the [Start]  icon on the Assistant Bar, inject a sample to the GC and press the [Start]  button on the GC instrument.

If you only press the [Start]  button on the GC without clicking the [Start]  icon for GCsolution, the GC program will start, but data acquisition will NOT be performed.

About changing the analysis time, refer to "4.1.1 Changing Data Acquisition Stop Time During Analysis".

Note: During data acquisition, if [Snapshot] button is clicked, temporary chromatogram data is read to <GC Postrun> - <Data Analysis> from analysis start to clicked points.

Note: Using [File] - [Open Reference Data File], the existing chromatogram data can be read as a <Chromatogram> view area's background.

3 Performing an Analysis

3.3 Checking Analysis Results

3.3.1 Starting up <GC Postrun> - <Data Analysis>

To start <GC Postrun> - <Data Analysis> and check the results, double-click the data file in the <Data Explorer> that was acquired using data acquisition.

<GC Real Time Analysis> - <Data Acquisition>

The screenshot shows two windows from the GC Postrun software. The left window, titled 'GC Real Time Analysis 1 (Instrument1 - Admin) - Data - [Acquisition - Alcohol.gcm]', displays a 'Data Explorer' with a file named 'Alcohol001.g' highlighted. A yellow starburst with the text 'Double-click.' points to this file. The right window, titled 'GC Postrun (Admin) - [Data Analysis - Alcohol002(STD for Calib Curve).gcd Line1 Channel1 FID1]', shows the 'Data Analysis' interface. It features two chromatograms: the top one shows a full run with peaks at 2.505, 2.284, and 19.052 minutes; the bottom one is a zoomed-in view of the peak at 2.284 minutes. Below the chromatograms is a 'Results - Peak Table' with the following data:

Peak#	Ret. Time	Area	Height
1	2.324	59797.3	11335
2	3.170	73157.3	9721
3	5.089	75154.3	15726

Integration parameters are also visible: Width: 3 sec, Slope: 1624 uV/min, Drift: 0 uV/min, T. DBL: 1000 min.

<GC Postrun> - <Data Analysis>

Clicking the [GC Postrun Analysis] icon on the [Operation] tab can also be used to start the <GC Postrun> screen.

<GC Postrun> - <Data Analysis>

The diagram illustrates the steps to start the GC Postrun Data Analysis screen. A hand icon points to the 'GC Postrun' icon on the 'Operation' tab. A callout box lists three steps:

- 1) Click [GC Postrun Analysis] icon on the [Operation] tab.
- 2) Click [Data Analysis].
- 3) Drag and drop file icon to open the data.

The background shows a screenshot of the software interface with the 'Data Analysis' icon highlighted in pink and the 'Alcohol001.g' file icon being dragged towards the 'Data Explorer' window.



3.3.2 Operations in the <Data Analysis> Window

There are various functions to review and re-process a data in the <Data Analysis>.

Drag mouse over <Chromatogram> view area and select lower area's chromatogram display range.

Use right-click menu in <Chromatogram> view area to select [Display Settings] window.
<Display Settings> (Reference Manual page 82)
<Properties> (Reference Manual page 562)

Increases/Decreases intensity axis range.

Changes [View/Edit] mode. Reprocessing is automatically performed if mode is changed from [Edit] to [View].

The screenshot shows the <Data Analysis> window with the following components:

- Chromatogram View:** Two chromatograms are displayed. The top one is zoomed in on a peak at 6.703 minutes. A right-click menu is open over this peak, with 'Display Settings...' highlighted.
- Peak Table:** A table with 5 rows and 5 columns: ID#, Name, Ret. Time, Conc., Units.
- Method - Peak Integration Parameters:** A panel with fields for Width, Slope, Drift, and T. DBL, each with a numerical input and a unit.

ID#	Name	Ret. Time	Conc.	Units
1	Nonane	2.072	100.00000	ppm
2	Decane	2.732	100.00000	ppm
3	Undecane	3.659	100.00000	ppm
4	Dodecane	4.803	100.00000	ppm
5	Tridecane	6.065	100.00000	ppm

<Data Analysis> (Reference Manual p189)

<Data Analysis> can handle only one data file. To process another data file simultaneously, start another <GC Postrun> - <Data Analysis> to open the second data file.

Click [Data in Report] on the Assistant Bar to print the data file content.

After completing operations in <Data Analysis>, be sure to save the data file and/or method file using the [File] menu. Please note that if you exit <Data Analysis> without saving the file, the result of data reprocessing will be lost.

Note: You can copy chromatograms in <Data Analysis> or <Data Comparison> using the right-click popup menu and paste them to other software as graphic images. Please note that, when the multiview mode is selected in <Data Comparison>, the copy function is not available.

Note: A method shown in the <Method> view is the one in the active data file. Please note that it's not method in a standalone method file.

3.3.3 Changing Peak Integration Parameters and Performing Data Post-run

The procedure for editing integration parameters in the <Method> view is described here. You can see post-run analysis results on the <Result> view.

Unnecessary small peaks are also detected.

Check threshold between area/height values of necessary and unnecessary peaks (values designated to be used for quantitation).

Click **Edit** to enter Method Edit mode.

Click [Integration] tab.

Enter "5,000" for the [Min. Area/Height] value.

Click **View** to return to Method View mode.

Data will automatically be re-analyzed when changing from [Edit] to [View] mode, detecting only necessary peaks.

Peak#	Ret. Time	Area	Height
1	2.152	1348.3	354.8
2	2.324	59797.3	11335.2
3	3.170	73157.3	9721.8
4	3.371	1320.0	469.8
5	5.089	75154.3	15726.7

After a method is edited and the screen returns to the Display mode, data is automatically reanalyzed and the result is shown on the <Result> view and <Chromatogram> view. Check the results shown on them. If necessary, modify the method and run a post-run analysis on the data again.

Also data is automatically reanalyzed after quantification parameters and such are modified in the Edit mode and the screen return to the Display mode.

After you have found satisfactory setting values, save the setting as a file by selecting [Save Data and Method File] from the [File] menu.

Note: If reprocessing has not been performed in [Edit] mode, the entered data can be undone to the previous data. (Right-click the <Method> view area to display a pop-up menu, and then select [Cancel Edit].)

About the peak integration parameters, refer to Reference Manual "16.1 Peak Integration Parameters and Peak Integration".

If peaks cannot be detected correctly, refer to Reference Manual "16.5 Problems with Incorrect Peak Integration".

3 Performing an Analysis

3.4 Creating Calibration Curves

When you already have a standard sample data file(s), you can create a calibration curve by reanalyzing the data in the <Batch Table> or <Calibration Curve> screen. When you have no standard sample data file or wish to create or update the calibration curve when data is acquired, analyze your sample with setting its sample type to "Standard".

Here describes a procedure that a calibration curve is created using the Compound Table wizard in the <Calibration Curve> screen of <GC Real Time Analysis>.

Note: The Compound Table wizard is a tool for creating a compound table in a simplified manner. You can use it from the <Data Analysis> and <Calibration Curve> screens of <GC Postrun> also.

3.4.1 <Calibration Curve> on <GC Real Time Analysis>

Click [Calibration Curve] on the Assistant Bar of <GC Real Time Analysis> to show the <Calibration Curve> screen. It shows the content of the method file loaded in the <Acquisition> screen.

In the <Calibration Curve> screen of <GC Real Time Analysis>, a calibration curve is created for the method file used in the analysis (data acquisition), so you can use the calibration curve as it is for analyzing unknown samples for quantitation from the next time.

On the <GC Real Time Analysis>, <Acquisition> and <Calibration Curve> always load the same method file.

<GC Real Time Analysis>

The screenshot shows the GC Real Time Analysis software interface. The main window is titled "Calibration Curve - Alcohol.gcm" and displays a chromatogram with a single peak at 6.18 min. The Acquisition Time is 10.50 min. The temperature profile shows a ramp from 200.0 C to 55.0 C. The chromatogram shows a single peak at 6.18 min. The interface includes a menu bar, a toolbar, and a sidebar with various icons. The main window displays the Calibration Curve for "Alcohol.gcm" with a peak at 6.18 min. The Acquisition Time is 10.50 min. The temperature profile shows a ramp from 200.0 C to 55.0 C. The chromatogram shows a single peak at 6.18 min.

Rate	Temperature	Hold Time
0	55.0	3.00

3.4.2 Selecting Data Files for Calibration Curve

Add data files onto the <Data File Tree> by drag and drop and use them as calibration curve data.

The screenshot shows the 'Calibration Curve - CALIB.gcm Line1 Channel1 FID1' window. It features a 'Calibration Curve' plot for Dodecane with a linear fit equation $Y = aX + b$, where $a = 1.080704e-002$, $b = 2.346902$, $R^2 = 0.9999899$, and $R = 0.9999950$. Below the plot is a table of calibration points:

Level	Conc.	Area
1	100.00	9,087
2	200.00	18,222
3	500.00	46,066

The 'Data File Tree' view shows a list of files including CALIB01.gcm, CALIB02.gcm, and CALIB03.gcm. A 'Data file' icon is being dragged into the tree. A right-click menu is open over a file, with options: 'Data File Properties...', 'Full Path', 'Add...', and 'Delete'. A chromatogram is displayed for the selected file, showing a peak at 4.546 minutes.

- 1) Drag and drop data file onto the level # of the data file tree to add data as calibration point.
- 2) Use right-click menu in <Data File Tree> view area to delete a data file from calibration points.
- 3) Check chromatogram of currently focused file in <Data File Tree> view area.

Note: A data file analyzed as standard sample by a single or a batch analysis is automatically added to the <Data File Tree> view at the end of the analysis. Use the above procedure when you add data files analyzed as unknown sample to the <Data File Tree> view later.

Note: You cannot add data files that do not include the currently displayed channel data to the <Data File Tree>.

3.4.3 Start [Calibration Curve Wizard]

The Compound Table wizard lets you create a compound table using the data selected in the <Data File Tree> view. For you cannot activate the wizard when no data is selected in the view, be sure to click the data of your choice first.

Click the [Compound Table Wizard] icon  on the Assistant Bar. The wizard will start up.

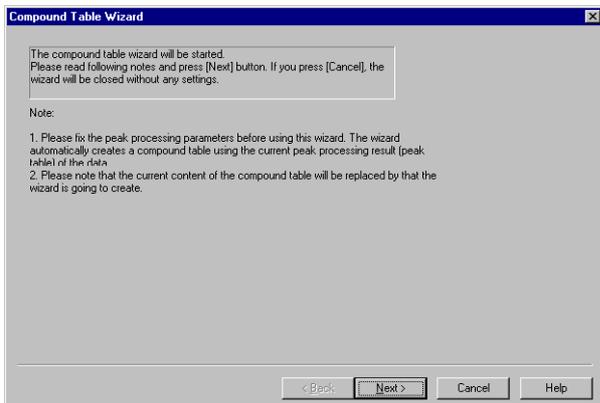
Note: When you are starting the wizard from <GC Postrun> - <Data Analysis>, you need not select data before starting up the Compound Table wizard because a compound table will be created using the data file that has been already loaded.



3 Performing an Analysis

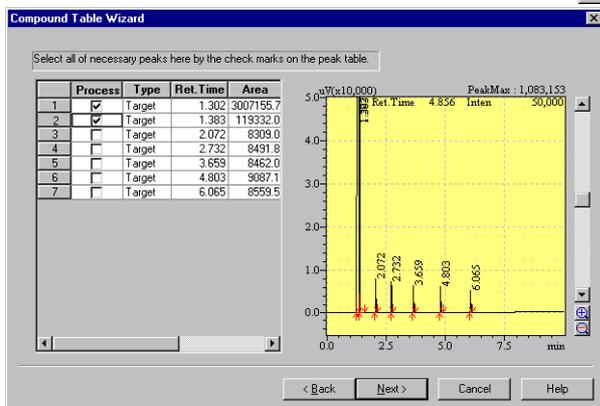
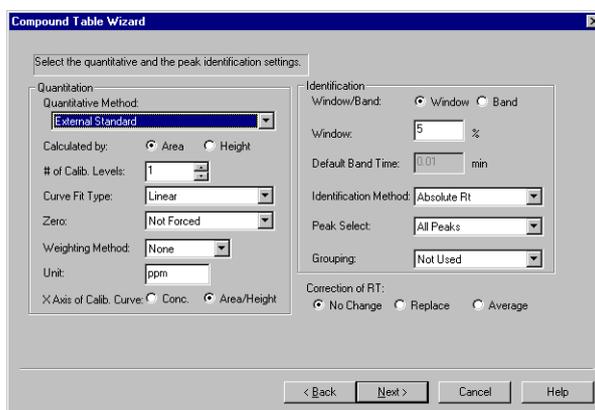
3.4 Creating Calibration Curves

On the wizard set parameters as follows in this chapter;



- 1) After reading the notice, click the [Next] button. (Existing compound table will be overwritten by the wizard.)

- 2) Select "External standard" method and "Calculated by"- "Area".
Number of Calib. Level = 1
Concentration unit = ppm
Leave other values as they are.

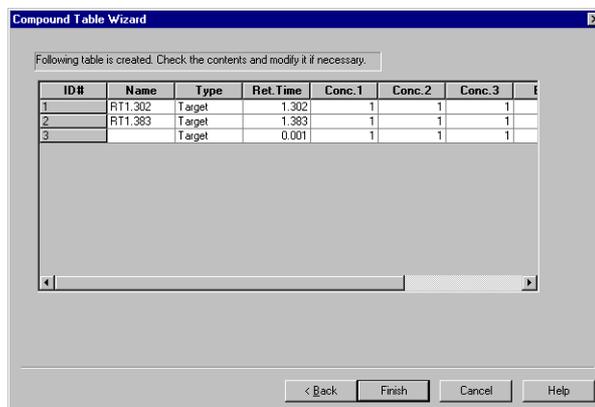


- 3) Select peaks of your target component by check-marking the [Process] check box. (You can zoom up the chromatogram by dragging the mouse.)

- 4) Enter data as follows:

Standard Sample	Retention Time	Concentration
n-propanol	2.324 min.	200 ppm
Isobutyl alcohol	3.170 min.	200 ppm
Isoamyl alcohol	5.089 min.	200 ppm

Click [Finish] to complete the settings.



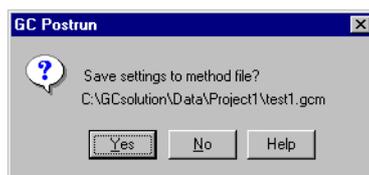
These parameters and the table will displayed on the <Method> view.

About all the quantitation and identification parameters, refer to Reference Manual "16.2 Peak Identification", "16.3 Quantitation Method".

About the settings for each quantitative method and grouping, refer to "6 Quantitation Parameter Settings".

Note: The [Type] field allows you to specify the internal standard substance (ISTD) used in the internal standard method or the reference component used as the reference peak for peak identification using relative retention time. Since our example in this chapter uses the external standard method to specify the target component, leave it to the default value "Target".

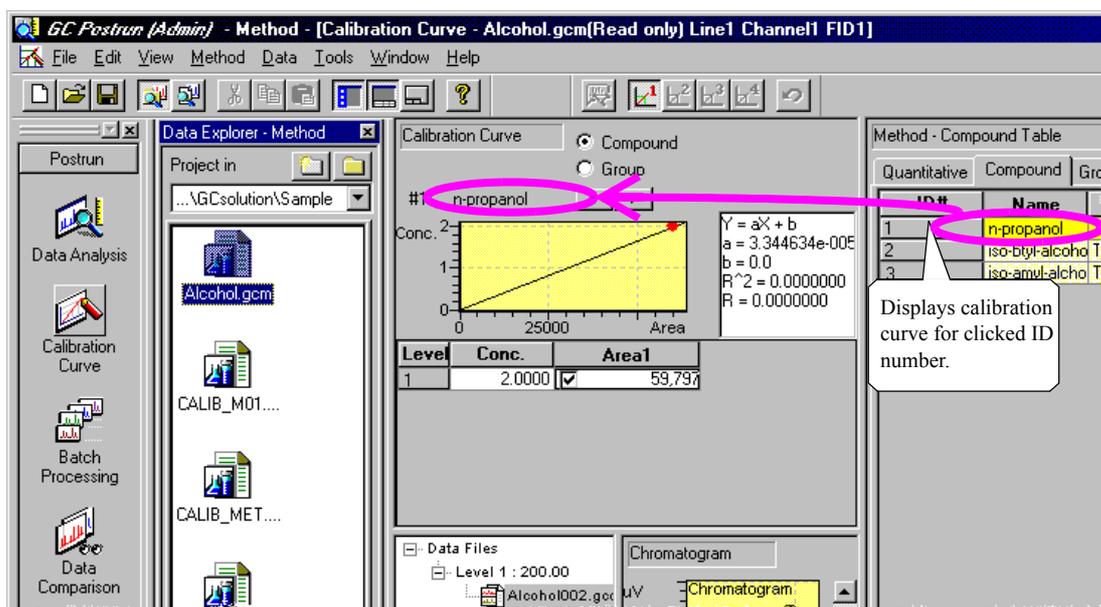
Note: If you have started the Compound Table wizard from <Data Analysis>, a confirmation message will appear when you click the [Finish] button to ask you whether to save the created compound table to the method file or not. If you click [Yes] here, the compound table as well as other data processing parameters are saved in the method file.



3.4.4 Creating Calibration Curve

After the wizard is completed, the <Method> view is in the Edit mode. Check the table settings and make changes if necessary.

If you set the <Method> view to the Display mode, a calibration curve is worked out and displayed on the screen.



After checking the calibration curve created, save the method file using the [File] menu. At this time, the data file used by the calibration curve is modified accordingly and saved.

If you wish to create a multi-level calibration curve, set the [# of Calib. Levels] quantitative parameter and set the concentration for each level in the compound table. Then, you can create a multi-level calibration curve by adding a data file for each level to the <Data File Tree> view.

Although we used the <Calibration Curve> screen to create a calibration curve here, you may also create calibration curves



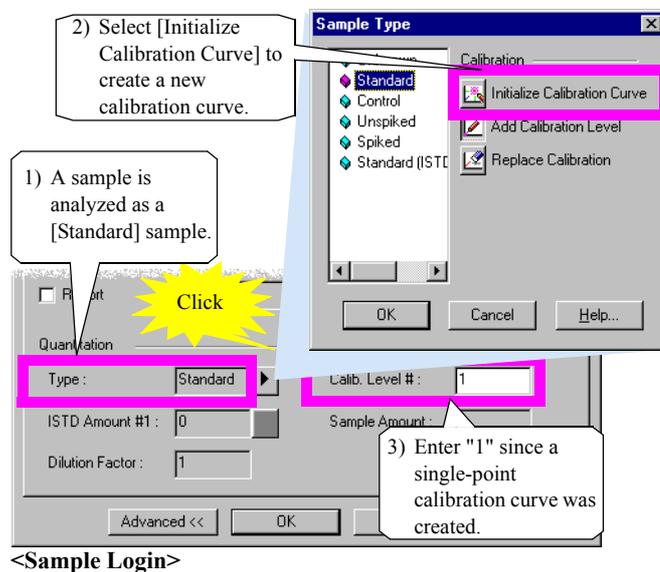
3 Performing an Analysis

3.4 Creating Calibration Curves

by performing a single-run analysis or batch analysis (real-time or post-run analysis) using a method file containing a compound table.

Note: When you have edited a method in <GC Postrun> - <Data Analysis>, export the method as a method file and use the file for analysis.

In a single-run analysis, click the [Advanced] button in <Sample Login> and set the sample type and level number.



On the <Batch Table> set the table as follows;

To initialize a calibration curve, select [Standard] - [Initialize Calibration Curve] in first row and clear current calibration curve.

Set combination of calibration point level and data file.

File #	Sample Type	Level#	Data File	Method File	Rs	
1	STD-Sample	0001	1:Standard:(I)	1	DEMO1_D01.GCD	Test.gcm
2	STD-Sample	0002	1:Standard	2	DEMO1_D02.GCD	Test.gcm
3	STD-Sample	0003	1:Standard	3	DEMO1_D03.GCD	Test.gcm

Note: [Level #] is the number of concentration level of 1-16 on the compound table.

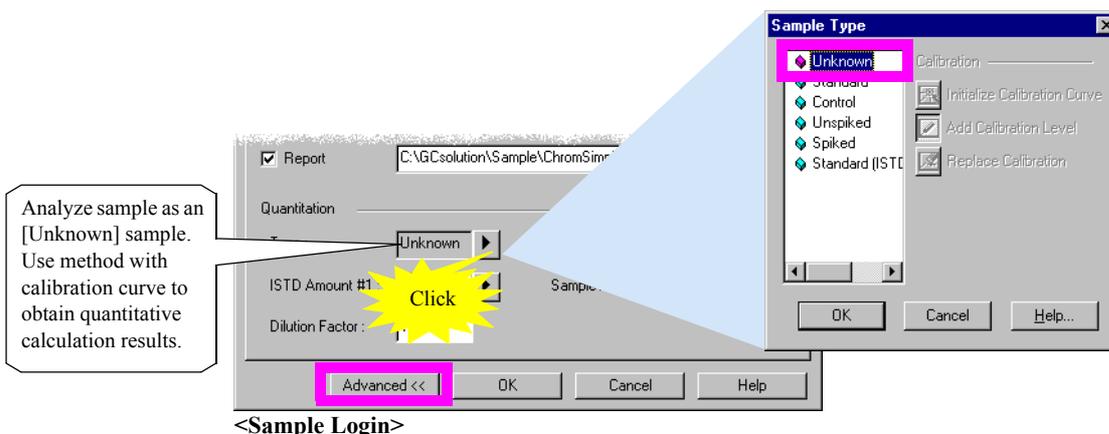
3 Performing an Analysis

3.5 Quantitative Analysis

Using a method that has a calibration curve created for it, analyze an unknown sample by real time analysis or post-run analysis, and then obtain quantitative results.

3.5.1 Quantitative Analysis by Real Time Analysis

To make quantitation using a single-run analysis, load the method for which a calibration curve has been created into the <Acquisition> screen and acquire data using the same operational procedure for "3.2 Performing Single-run Analysis". At this time, be sure to set the sample type to unknown sample in <Sample Login>.



To make quantitation using a batch analysis, specify the method file name with which a calibration curve is created in the batch table and run the analysis with the sample type set to unknown sample.

3.5.2 Quantitative Analysis by Post-run Analysis

When a data file is loaded into the <Data Analysis> screen, the result of quantitation is shown on the <Result> view as compound concentrations. If you wish to quantitate data which has not been quantitated using a method file for which a calibration curve has been created, you need to import that method file.

To import a method file, click [File] - [Load Method]. The data is automatically reanalyzed using the imported method and the quantitation result is shown in the <Result> view.

If you wish to quantitate data using batch post-run analysis, specify the method file name of your choice for which a calibration curve has been created and the data file name which you wish to quantitate in the batch table, and then run post-run analysis with the sample type set to unknown sample.

3 Performing an Analysis

3.6 Performing Sequential Analysis (Batch Analysis)

To perform sequential data acquisition for multiple samples, use the <Batch Table> on the <GC Real Time Analysis> screen.



When the <GC Real Time Analysis> screen has not started yet, click the [GC Real Time Analysis 1] icon on the [Operation] tab.

3.6.1 Opening the <Batch Table>

When you open the <Batch Table>, only one blank row is displayed in it. You can load here existing batch files for editing or create a new table used for running analysis.

The screenshot shows the software interface. On the left, the 'RealTime' sidebar has a 'Batch Processing' icon highlighted with a pink box and a callout: 'Click [Batch Processing] icon.'. An arrow points from this icon to the 'Batch' sidebar, which contains various control buttons like 'Top', 'Settings', 'Wizard', 'Start', 'Pause', 'Stop', and 'Browse Data'. To the right, the '<Batch Table>' window is open, displaying a table with columns: Vial#, Sample Name, Sample ID, Sample Type, Method File, Data File, Baseline Data File, Level#, and ISTD A. The table contains one row with values: 1, , 0:Unknown, , , , 1, 1. A right-click context menu is open over the table, listing various editing commands. A callout points to the menu: 'Select necessary editing commands from right-click menu.'

Vial#	Sample Name	Sample ID	Sample Type	Method File	Data File	Baseline Data File	Level#	ISTD A
1		0:Unknown					1	1

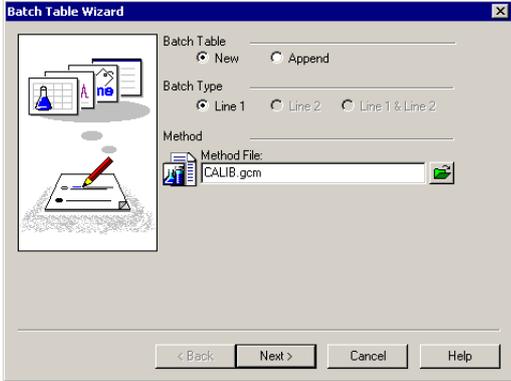
Each row (batch row) corresponds to one data acquisition (single-run analysis).

Complete a batch table by entering a method file name, data file name, and other required items to each batch row. Although you can create a batch table by entering values to the table directly, you can create one much more easily using the wizard.

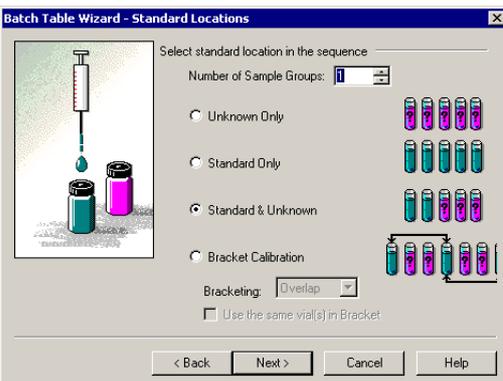
3.6.2 Creating Batch Tables Using the Batch Table Wizard

Although you can create a batch table by filling all the items in each row, you can set up multiple rows of settings easily if you use the Batch Table wizard.

<Batch Table Wizard> (Reference Manual p356)

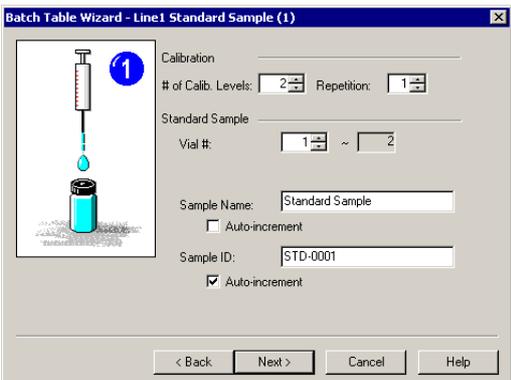


1) Select [New] and enter method file name to use.

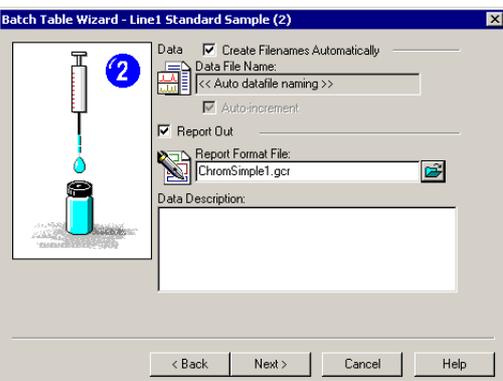


2) For [Number of Sample Groups], specify the number of repetitions of analyses with the same pattern. Set '1' and select [Standard & Unknown] then press [Next] button.

3) Setup for the standard samples. For [# of Calib. Levels], the setting of the method file is shown automatically.



4) Specify the data file name for the standard samples. Checking [Create Filenames Automatically] automatically specifies the data file name according to the setting on the <Setting>-[Data File] tab. Check [Report Out] and specify a report format file, if report output is needed after an analysis.

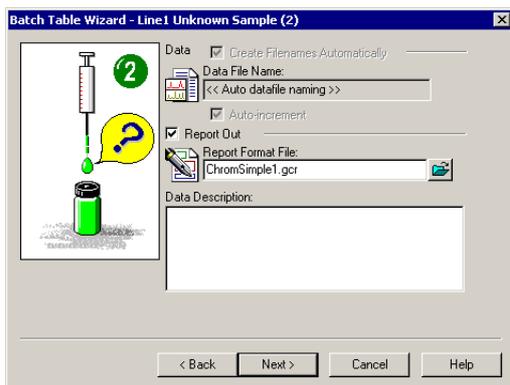
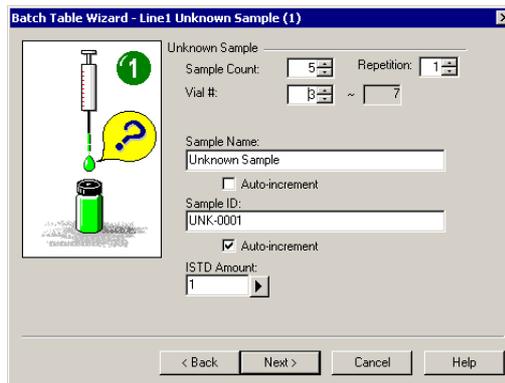




3 Performing an Analysis

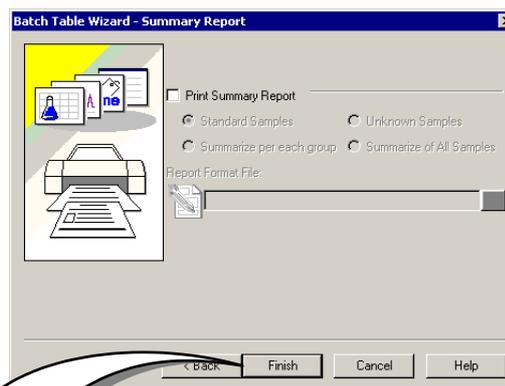
3.6 Performing Sequential Analysis (Batch Analysis)

- 5) Setup for the unknown samples.
Set the number of unknown samples to analyse ([Sample Count]).



- 6) Specify the data file name for the unknown samples.
The setting of [Create Filenames Automatically] is depends on the standard sample settings.

- 6) At the end, specify the summary report settings.
Press [Finish] to generate a batch table.



<Batch Table>

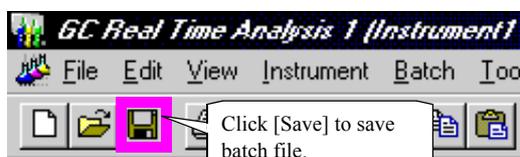
	Vial#	Sample Name	Sample ID	Sample Type	Method File	Data File
1	1	Standard Sample	STD-0001	1:Standard:(I)	CALIB.gcm	
2	2	Standard Sample	STD-0002	1:Standard	CALIB.gcm	
3	3	Unknown Sample	UNK-0001	0:Unknown	CALIB.gcm	
4	4	Unknown Sample	UNK-0002	0:Unknown	CALIB.gcm	
5	5	Unknown Sample	UNK-0003	0:Unknown	CALIB.gcm	
6	6	Unknown Sample	UNK-0004	0:Unknown	CALIB.gcm	
7	7	Unknown Sample	UNK-0005	0:Unknown	CALIB.gcm	

When auto file name creation function is selected, file name cannot be entered into that cell.

The content set up by the wizard is shown in the batch table. If you need to modify it, enter your desired values to cells in the table.

Note: If you have specified the number of repeated injections in the Batch Table Wizard, multiple batch rows are automatically generated for the same vial. This is because this software generates batch rows by assigning one row to one sample injection.

Before running the edited batch table, save it as a batch file using the [File] menu.

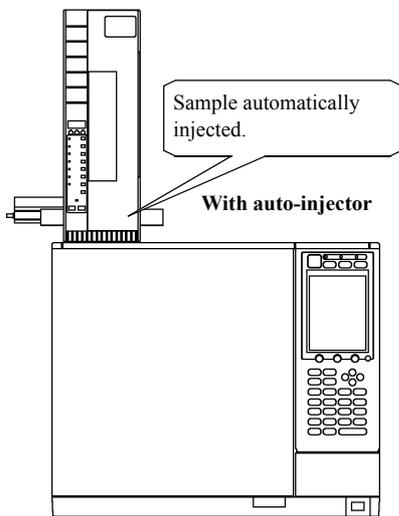


3.6.3 Starting Batch Analysis

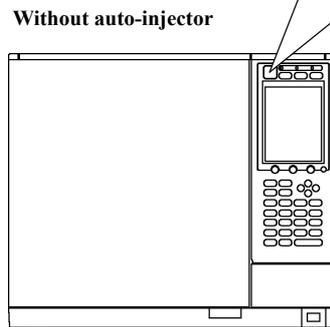
After the batch table settings have been completed, perform batch processing.

The screenshot shows the GC Real Time Analysis software interface. On the left is a vertical toolbar with buttons for Top, Start, Pause, Stop, Browse Data, and Instrument Parameters. The 'Start' button is highlighted with a pink box and a callout bubble that says 'Click [Start]'. An arrow points from this button to the main software window. The main window has a menu bar (File, Edit, View, Instrument, Batch, Tools, Window, Help) and a toolbar. Below the menu bar is a '<Batch Table>' window showing a table with columns: Vial#, Sample Name, Sample ID, Sample Type, Meth, Inj. Volume, Multi-Inj, and ISTD Amount. The table contains two rows of data. Below the batch table is a 'Data Explorer - Method' window showing a file tree with 'AT_on.gcm', 'Mine.gcm', 'Test.gcm', and 'temp.gcm'. To the right is the 'Acquire' window showing a chromatogram plot with a y-axis labeled 'AU' (0 to 45000) and an x-axis labeled 'min' (0 to 5). A callout bubble over the plot says '<Data Acquisition>'. At the bottom of the software window is a 'Message' log table.

Message	SubMessage	Date	Time	Code	User Name	Application Name
Stop Batch Processing (Data Acquisition)	C:\GCsolution\data\Project\test0.gcb	3/13/00	10:56:28 AM	0x1301	Admin	GC Real Time Analysis
End Batch Processing (Data Acquisition)	C:\GCsolution\data\Project\test0.gcb	3/13/00	10:56:28 AM	0x1302	Admin	GC Real Time Analysis
Start Batch Processing (Data Acquisition)	C:\GCsolution\data\Project\test0.gcb	3/13/00	10:56:37 AM	0x1300	Admin	GC Real Time Analysis



After confirming GC status is "Ready", in <Data Acquisition> window press GC unit's [START]  /  key while injecting sample.



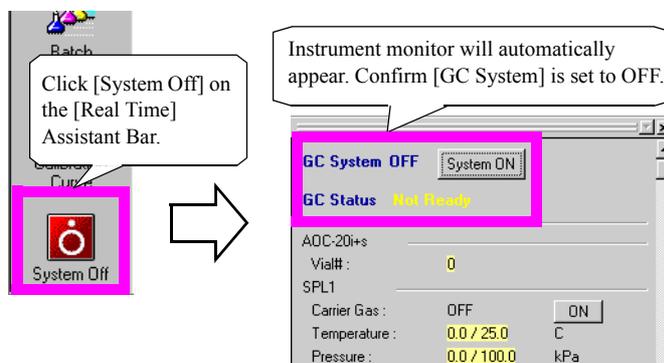
3 Performing an Analysis

3.7 Shutting Down the System

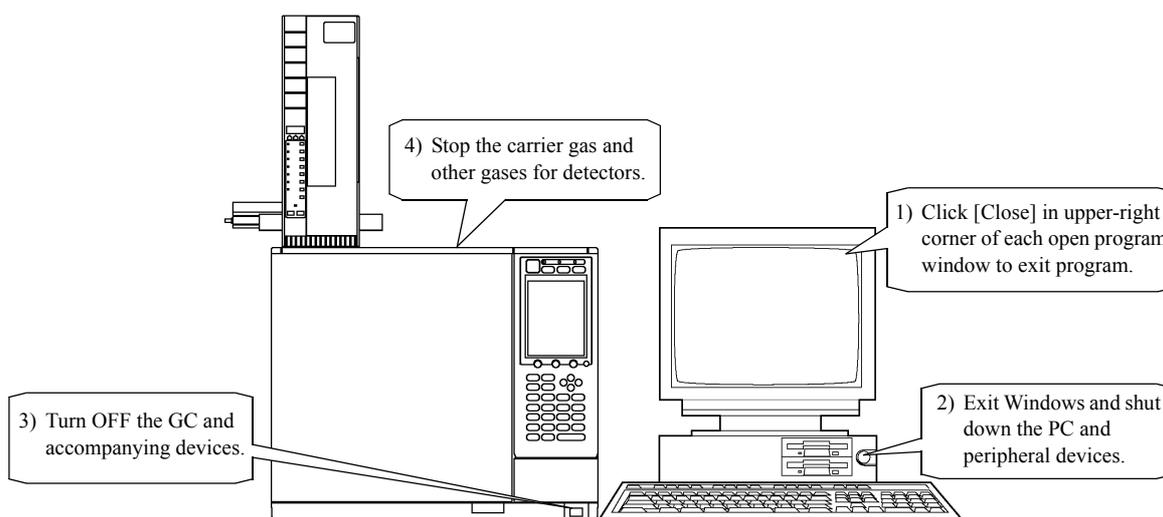
3.7.1 Turning the GC System Off

Click [System Off] to turn the GC system off, then wait for the column oven temperature has decreased low enough.

About GC action settings, refer to "4.3 Setting Up GC Start/Stop Actions".



3.7.2 Exiting GCsolution and Turning Off



Note: Wait for the column oven to cool down before turning off the GC. If the GC is equipped with the flow controller, the column oven gets damaged due to the high temperature, since the GC stops supplying carrier gas when it is turned off.

Note: By specifying [FLOW OFF TIME] in the environment setting, you can make the GC to supply carrier gas for the specified period of time after the GC is turned off.



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4 Next Step - Data Acquisition

4.1 Changing Analysis Stop Time

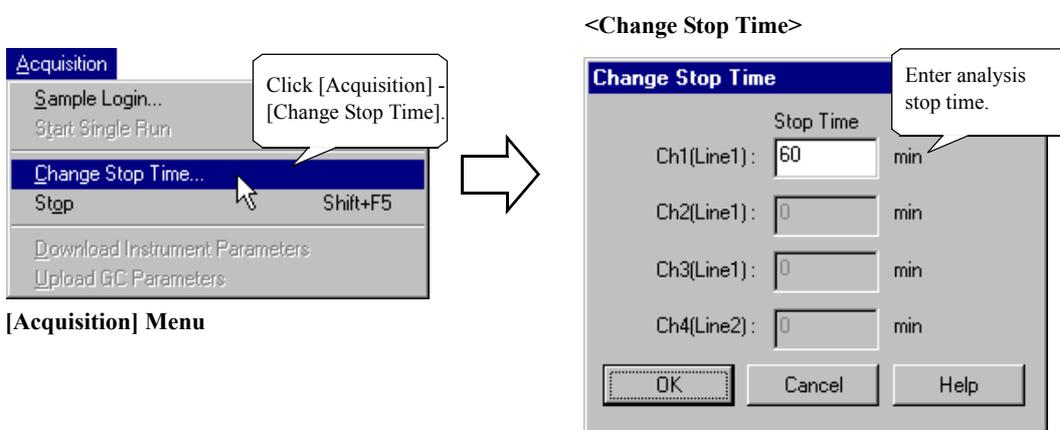
The time required for running a single analysis is set to the longest among the data acquisition completion time and times coded in device-control programs such as one for oven temperature control.

4.1.1 Changing Data Acquisition Stop Time During Analysis

You can change the data acquisition stop time even after the analysis has started.

After data acquisition has started, the setting fields in the <Instrument Parameters> view are set to read-only state so you cannot change the [Stop Time] field any more in it.

During data acquisition, use the <Change Stop Time> screen to change the completing time.



If the set analysis time is shorter than the current analysis time, data acquisition will stop at that time and a data file will be created. After that the confirmation window will come up to save the new analysis time into method.

Note: The time you can change here is only the data acquisition ending time for detectors. You cannot change the running time for GC programs such as temperature programs for the column oven.

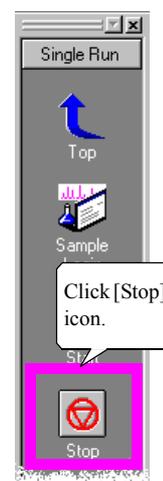
Note: During a batch analysis, click on the <Acquisition> screen to show the [Acquisition] menu on the menu bar.

4.1.2 Stopping the Analysis

While performing a single-run analysis, click the [Stop] icon on the [Single Run] Assistant Bar. At this point data acquisition will stop, and a dialog box will appear asking if you want to stop the GC program, such as for temperature programming. Data obtained before the analysis is stopped is then stored in a data file.

When performing batch data acquisition, click the [Stop] icon on the [Batch] Assistant Bar, and a dialog box will appear asking if you want to immediately stop the current data acquisition (in which case, another dialog box will ask if you want to stop the GC program), or if you want to stop the entire batch acquisition after the current data acquisition has completed.

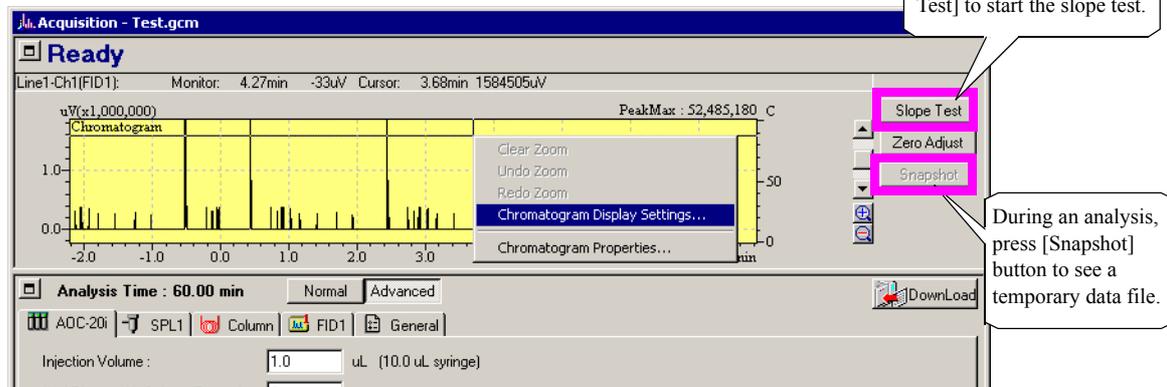
Note: Click  icon on the toolbar in the active <Data Acquisition> window that is displayed during batch data acquisition, and a dialog box will appear asking if you want to stop the current batch row's data acquisition, or if you want to stop the entire batch data acquisition.



4 Next Step - Data Acquisition

4.2 Slope Test and Snap Shot Button

<GC Real Time Analysis> - <Data Acquisition>

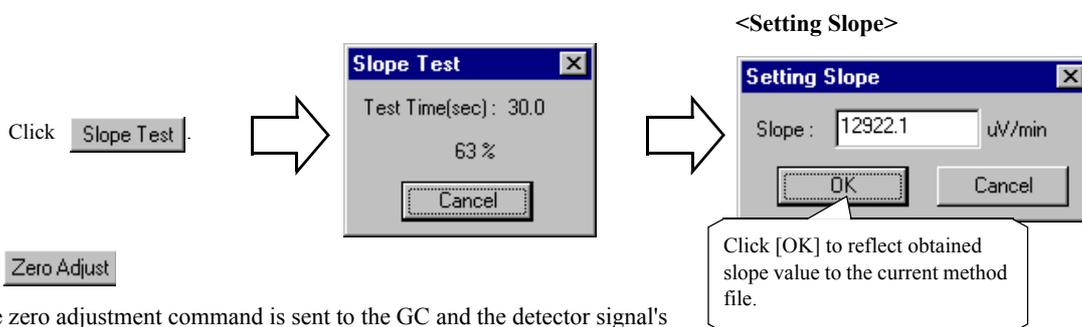


4.2.1 Slope Test

❖ Slope Test

Before starting an analysis (data acquisition), press [Slope Test] button to start the slope test.

The slope value is one of the peak integration parameters used to determine chromatogram peak detection sensitivity. Using the slope test, noise on the signal baseline can be measured and the optimum slope value obtained.



❖ Zero Adjust

The zero adjustment command is sent to the GC and the detector signal's baseline level is adjusted to zero.

4.2.2 Snap Shot

❖ Snapshot

During an analysis (data acquisition), if this button is pressed, a temporary data file is created with chromatograms obtained from the start of analysis to clicked points, and is read into <GC Postrun> - <Data Analysis>. Using this feature, the peak area and other data can be checked during analysis. The data read can be saved under another name, if necessary.

4 Next Step - Data Acquisition

4.3 Setting Up GC Start/Stop Actions

4.3.1 Setting GC Start/Stop Parameters

Parameters related to starting/stopping the temperature control and carrier gas control at GC startup/shutdown can be set.

Configuration

- Top
- System Configuration**
- System Check

<System Configuration>

Available Modules : Autosampler, AOC-20i, AOC-20i+s

Configured Modules : Instrument1, GC-2010, Analytical Line1

Double-click

GC-2010

General | CRG/Relays | Device Information | Units Position

of Analytical Lines : 1

Gas Pressure units : kPa

Save Monitored Values :
Sampling Period : 1000 msec

Atmosphere compensation

GC System On When turning on the power

System On/Off Parameters

START TIME : 0 min

STOP TIME : 0 min

SLEEP TIME : 9999 min

FLOW OFF TIME : 9999 min

System On Mode : Flow/Temp>Det

OK Cancel Apply Help

<GC-2010>

If check-marked, GC monitored values (carrier gas pressure, column oven temperature, etc.) are recorded in the data file.

Click this check box when starting the GC to start up with parameters used when GC was last stopped.

Check whether detector is ON when starting up the GC.

To protect the column, enter time required from starting carrier gas flow to starting temperature control.

Enter time required from clicking [System Off] to stopping temperature control.

Enter time required from stopping temperature control to restarting the GC.

Enter time required from stopping temperature control to stopping carrier gas flow.

4.3.2 Performing GC Automatic Startup/Shutdown

After analysis has completed, the GC can automatically be shut down, or the GC can be started up or shut down on a specified day.

Tools

- Auto System OFF/ON...**
- Audit Trail for Instrument Configuration...
- Check the Program Files...
- Check Raw Data...
- Option...

[Tools] Menu

Click [Set] after entering auto system stop/start conditions.<Auto System OFF/ON> will stay on the screen.

<Auto System OFF/ON>

Auto System OFF/ON

Auto System OFF

After Analysis

2000 07 17 11:1

Auto System ON

2000 07 17 21:1

Set Cancel Help

Note: The GC-14B only allows automatic startup. Automatic shutdown is not supported.

Note: To perform GC auto-shutdown settings during batch analysis, click the <Data Acquisition> window on the screen. The program menu will then become active for the <Data Acquisition> window. Then, set the [After Analysis] using the above procedure. That sets the GC to automatically shut down after the batch-run is finished.

4 Next Step - Data Acquisition

4.4 Changing the Data Sampling Interval

The data sampling interval is designated here based on the peak shapes of the chromatogram to be acquired.

The smaller the data sampling interval is set, the sharper peak shapes the chromatogram data can process. However, if an excessively small sampling rate is designated, the data file size will become unnecessarily large, wasting system resources.

4.4.1 Parameters Related to Data Sampling

The parameters related to the chromatogram data sampling interval are as follows:

❖ <Analysis Line> - [Detector] tab - [Base Period]

Based on the thinnest column that could possibly be used, the basic unit of the chromatogram sampling interval is designated.

Initial Value	40 msec (GC-2010, GC-2014, GC-2025) 100 msec (GC-17A, GC-1700, GC-14B/C)
Options	4, 8, 20, 40, 60, 80, 100, 200, 500, 1,000 msec (GC-2010, GC-2014) 20 to 1,000 msec (GC-17A, GC-1700, GC-14B/C)
Recommended Values	Regular capillary analysis, etc.: 40 to 80 msec. High-speed analysis using narrow bore column: 4 to 8 msec.

Note: For any GC model other than the GC-2010, GC-2014 or GC-2025, if a value smaller than 100 is specified for the base period, the resolution of input signals deteriorates. Avoid using a value smaller than 100 unless otherwise required in a special case.

❖ <Instrument Parameters> view area - [Detector] tab - [Sampling Rate]

The chromatogram sampling interval is designated based on the column and analysis conditions.

Initial Value	System configuration - each detector's base period
Options	Base period 4 to 80 msec.: 1 to 20 times the base period Base period 100 or more msec.: 1 to 10 times the base period
Recommended Values	Analysis using packed column: 400 to 480 msec. Regular capillary analysis: 40 to 160 msec. High-speed analysis using narrow bore column: 4 to 16 msec.

Note: The smaller the designated sampling rate, the larger the data file capacity. When the peak width is larger, set the sampling rate larger.

❖ <Data Processing Parameters> - [Integration] tab - [Width]

This parameter is used to perform chromatogram peak integration. To detect a peak, set a peak half value.

Recommended Values	The 1/4 to 1/2 of the actual detection peak width is the standard for the peak half value. Analysis using packed column: 5 to 10 sec Regular capillary analysis: 0.4 to 2 sec High-speed analysis using narrow bore column: 0.04 to 0.2 sec
--------------------	--

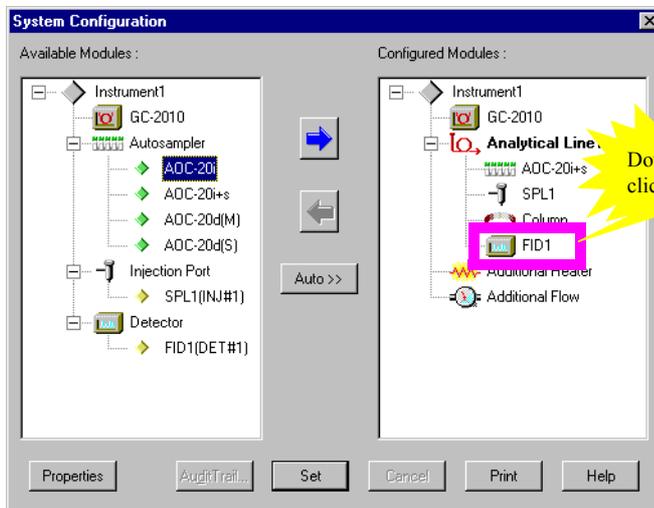


4.4.2 Setting the Detector Base Period

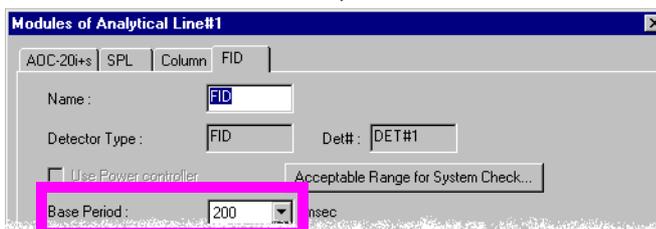
Base period can be set on <System Configuration>



Assistant Bar of
<GC Real Time
Analysis>



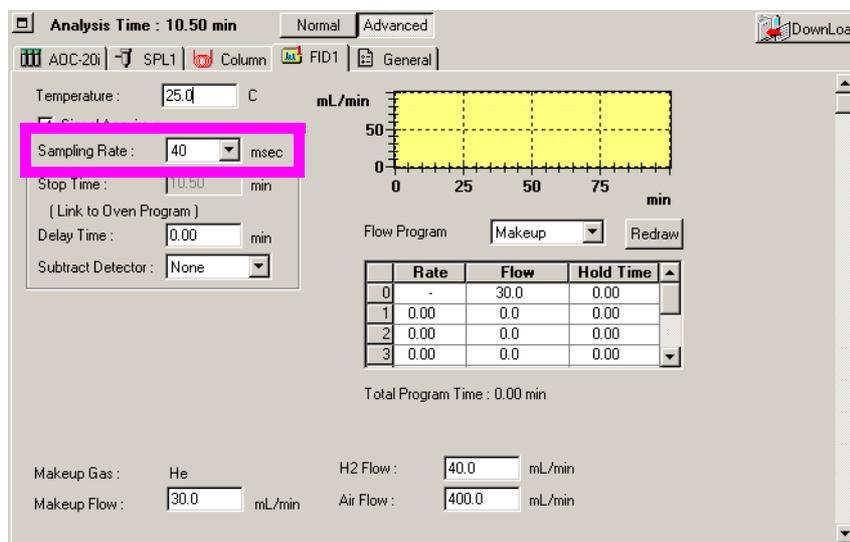
<System Configuration>



<Analytical Line> - [Detector] Tab

4.4.3 Setting the Detector [Sampling Rate]

[Sampling Rate] is a parameter of the GC instrument method.



<Instrument Parameters> - [Detector] Tab

4 Next Step - Data Acquisition

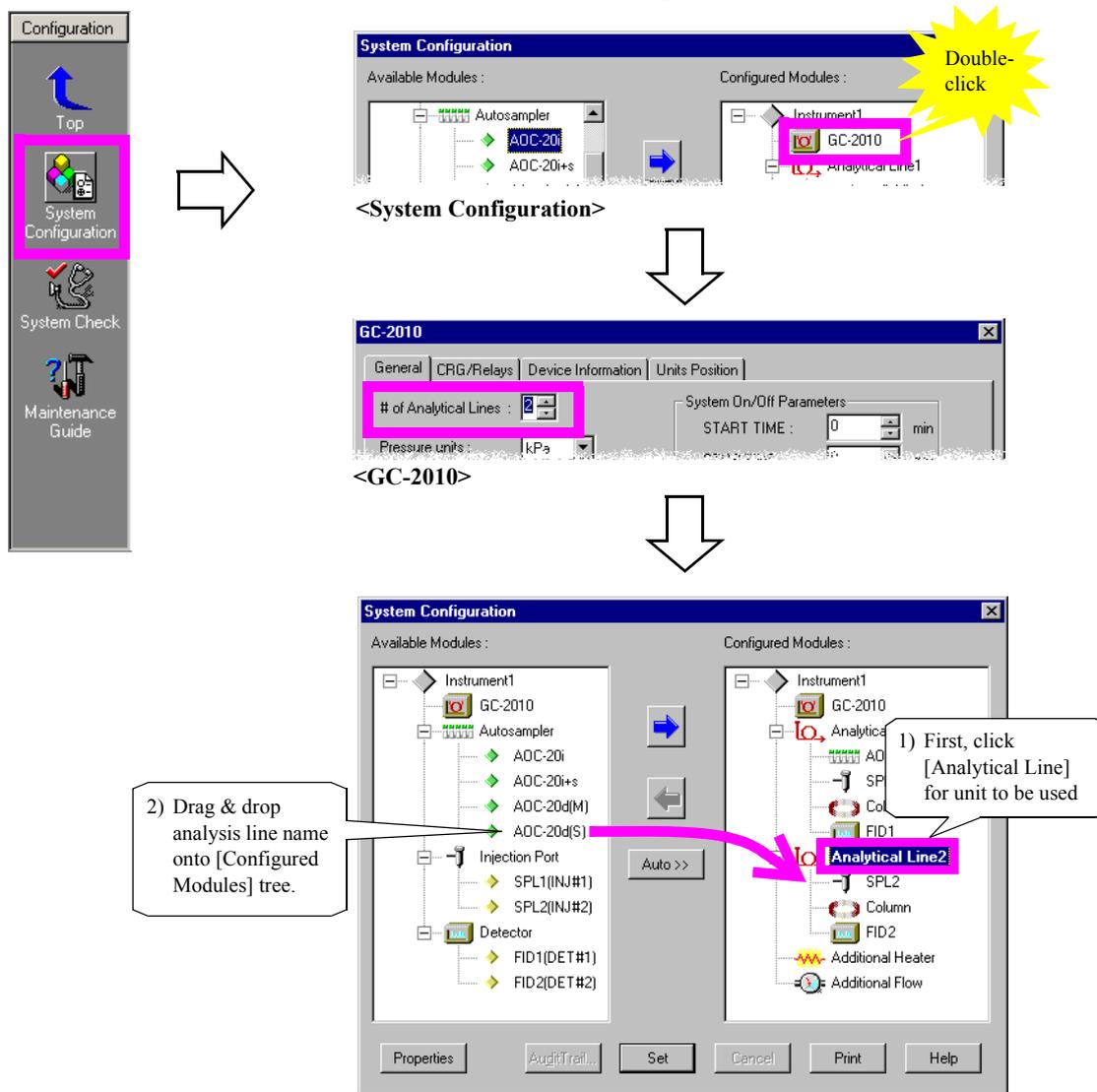
4.5 Performing Dual-Line Analysis

GCsolution supports dual-line analysis, where two system lines (injection unit -- column -- detector) are installed in one GC unit and synchronous analysis can be performed.

4.5.1 System Configuration for Dual-Line GC

Even when there are two or more sets of "injection unit -- column -- detector", selecting either single-line or dual-line configuration will depend on the physical GC gas piping. Therefore, system configuration cannot be performed automatically.

The number of analysis lines will be designated using the following procedure.





4.5.2 Instrument Parameter Settings for Each Line

<Data Acquisition>

Use right-click menu in <Chromatogram> view area to display [Display Settings] window.
<Display Settings> (Reference Manual page 82)
<Properties> (Reference Manual page 562)
Perform the settings based on the dual-line configuration.

Select a line and set instrument parameters for each displayed line unit. [Column] and [General] tabs are common for all lines.

Line 1 (FID1) Parameters:
Analysis Time: 10.50 min | Normal | Advanced | **Select Line** | Line1 | Line2
ADC-20d(M) | SPL1 | Column | FID1 | General
Injection Volume: 1.0 uL (10.0 uL syringe)

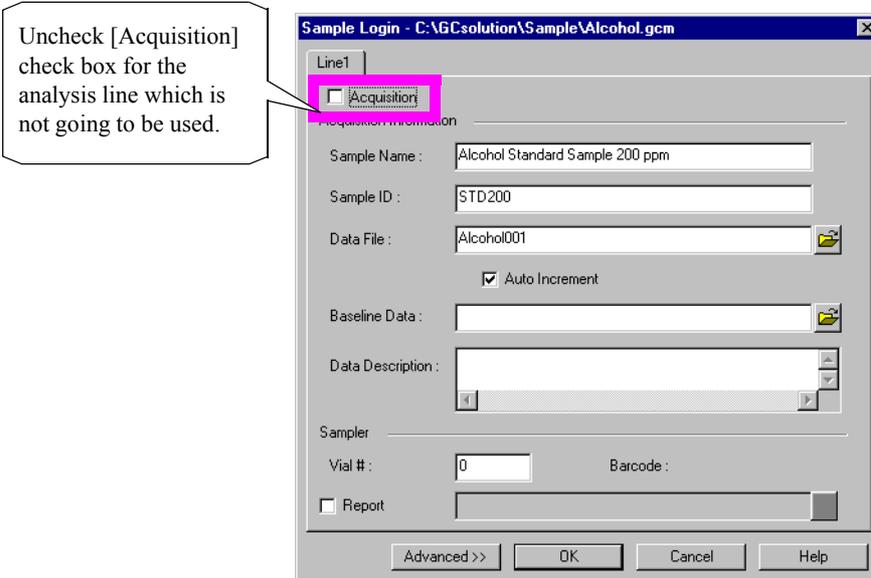
Line 2 (FID2) Parameters:
Analysis Time: 10.50 min | Normal | Advanced | **Select Line** | Line1 | Line2
ADC-20d(S) | SPL2 | Column | FID2 | General
Injection Volume: 1.0 uL (10.0 uL syringe)

Note: GCsolution can control up to 3 detectors (channels) for [Analytical Line1] and 1 channel for [Analytical Line2]. The channel 1 for [Analytical Line2] is called channel 4 in the <Data Acquisition> window for convenience.

4.5.3 Performing Single-Line Analysis with a Dual-Line Configuration

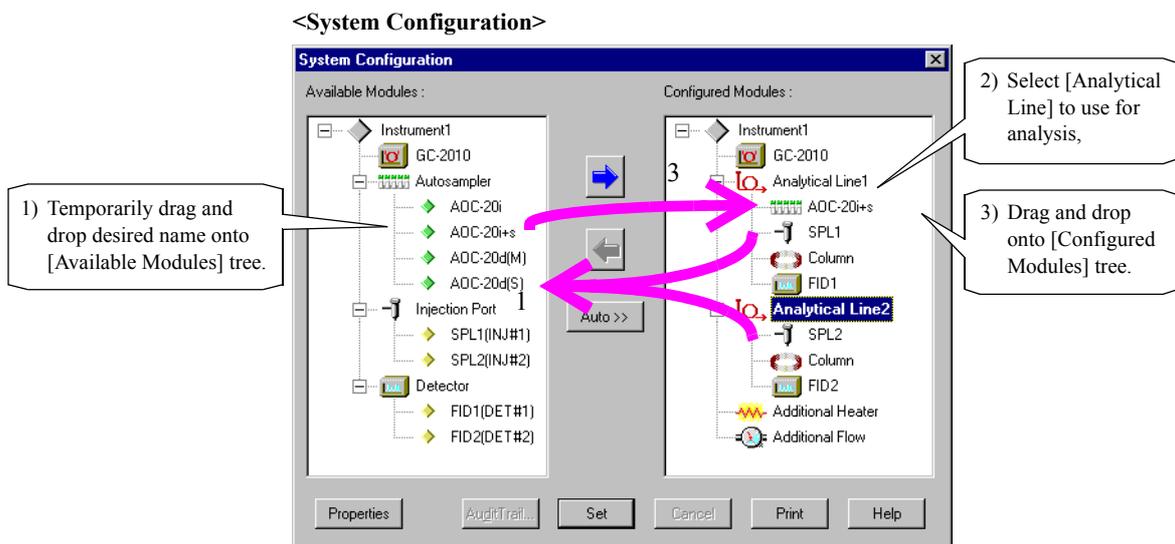
To perform analysis only on the analytical line 1 with a dual-line configuration, use the following procedure.

For the single run analysis, uncheck [Acquisition] in the <Sample login>.



In the case of the batch analysis, select batch <Settings> window - [Type] tab - [Line 1 only].

To use only one auto-sampler connected to the line on which analysis will be performed, connect it to the analytical line that uses the auto-sampler in the <System Configuration> window.



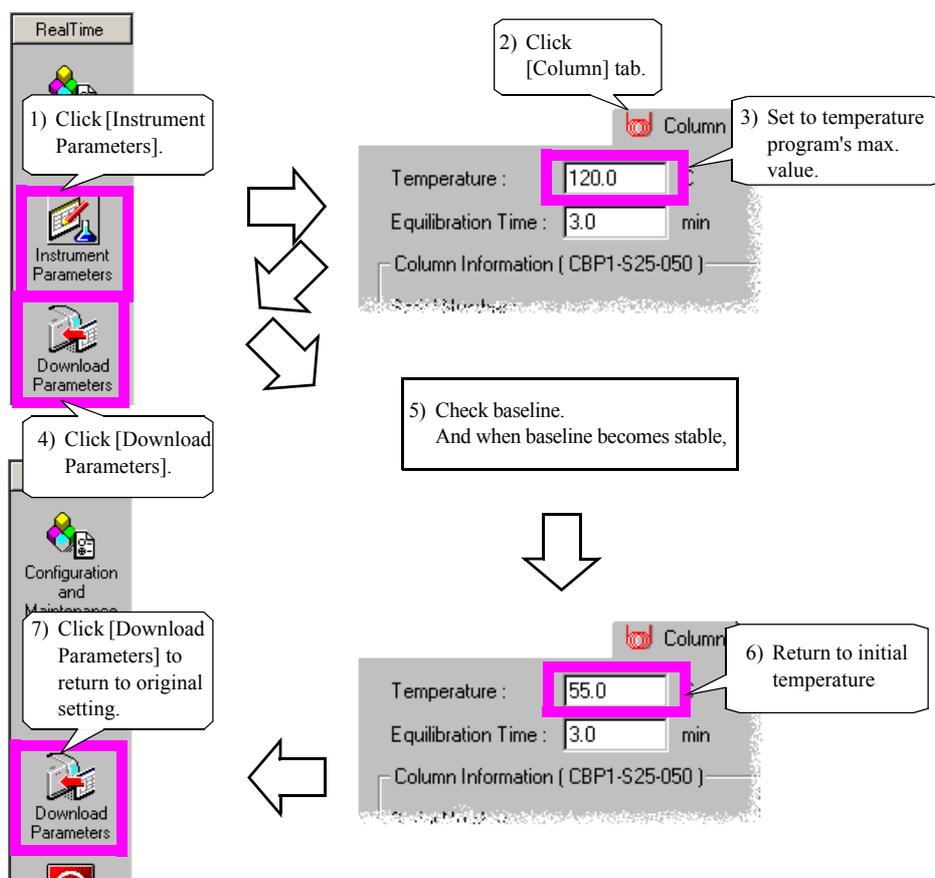
4 Next Step - Data Acquisition

4.6 When the Baseline is Unstable

Immediately after starting the GC, the previously used analysis samples could still remain in the injection unit and column(s). Because of this, the baseline may become unstable or ghost peaks may appear. In such a case, conditioning the GC or temporarily increasing the oven temperature are effective to solve the problems. This method can also be used to remove any samples in the column(s) when analysis fails due to incorrect sample injection, etc.

4.6.1 Changing Oven Temperature

For example, when the column temperature for analysis is set to 55°C (hold for 3 min.) --> 120°C (programming rate: 10°C/min.), change the column initial temperature to its maximum temperature, 120°C and perform conditioning.





4.6.2 Performing a Clean up

Clean up is performed using a column temperature program for an analysis. Without injecting sample, running the GC with the same condition as an analysis is effective to clean up flow line. Operation is the same as regular single-run analysis procedure. Use vial number 0, then the GC will start without a sample injection.

❖ Without data acquisition:

Remove the check from the [Acquisition] check box (see figure at right). In this state, perform the same operations as in normal single-run analysis without injecting a sample.

Sample Login - C:\GCsolution\Sample\Alcohol.gcm

Line1

Acquisition

Acquisition Information

Sample Name : Alcohol Standard Sample 200 ppm

Sample ID : STD200

Data File : Alcohol001

Auto Increment

Baseline Data :

Data Description :

Sampler

Vial # : 0 Barcode :

Report

Advanced >> OK Cancel

4.6.3 Performing a Blank Analysis

To check for ghost peaks and others, raise the column temperature by injecting solvent instead of actual samples. Operation is just the same as regular analysis procedure.

Note: In the case of the sample injection unit is dirty, increase the temperature of the sample injection unit and inject a large amount of solvent. Then replace the glass insert and septum, and take other appropriate measures. Then, perform conditioning.

4 Next Step - Data Acquisition

4.8 Usage count for septum and glass insert

The GC-2010, GC-2014 and GC-2025 are equipped with "Analysis Counter" that counts the times (sample injection times) of a septum and a glass insert usage to notify you of the time to replace them.

The message to notify you of the time to replace a septum and a glass insert is enabled by setting <Injection Port Maintenance> in <System Configuration>. If the sample injection times exceeded the times specified there, the message is displayed.

Note: This feature is not available in GC-14/GC-17A/GC-1700.

4.8.1 Setting <Injection Port Maintenance>

The image illustrates the process of setting the injection port maintenance counts. It begins with a 'Configuration' sidebar where 'System Configuration' is highlighted. An arrow points to the 'System Configuration' dialog box, which shows a tree view of the instrument components. Another arrow points to the 'Modules of Analytical Line#1' dialog box, where the 'SPL' tab is selected. A final arrow points to the 'Injection port Maintenance (SPL)' dialog box, where the 'Septum Used Counts' and 'Insert Used Counts' are both set to 100.

<System Configuration>

<Analytical Line> - [Injection Port] tab

The default value for the septum usage count and insert usage count are both 100.

Recommended time for replacing inserts differs depending on the analysis conditions and samples used. You need to estimate the replacement time by checking their level of filth in advance. Recommended time for replacing septa is around 100 times when the syringe for auto-injector (AOC-20i) is being used, though it depends on the thickness of the syringe needle.



4.8.2 Resetting usage counter

After replacing septa and glass inserts, be sure to reset the analysis times counter to 0.

1) Click [System Check] on the [Configuration] Assistant Bar.

2) Click [Advanced<>>] then [Reset...].

3) Click [Reset] to reset replaced consumables' counter.

System Check

Last Run Date : Check: Consumables

Consumables

<input checked="" type="checkbox"/> LCD Back Light	<input checked="" type="checkbox"/> Septum	<input checked="" type="checkbox"/> CRG Coolant
<input checked="" type="checkbox"/> Fan Motor	<input checked="" type="checkbox"/> Insert	

GC Check

<input checked="" type="checkbox"/> Heat Sensor	<input checked="" type="checkbox"/> CPU	<input checked="" type="checkbox"/> ECD Cell Frequency
<input checked="" type="checkbox"/> DC Voltage	<input checked="" type="checkbox"/> Detector ROM	<input checked="" type="checkbox"/> Flow Unit Board ROM
<input checked="" type="checkbox"/> Environment	<input checked="" type="checkbox"/> Detector ADC	<input checked="" type="checkbox"/> Flow Unit Board ADC
<input checked="" type="checkbox"/> Primary Pressure	<input checked="" type="checkbox"/> Detector High Voltage	<input checked="" type="checkbox"/> Flow Control
<input checked="" type="checkbox"/> Baseline Noise, Drift	<input checked="" type="checkbox"/> Detector Ignite	<input checked="" type="checkbox"/> Column Dimensions Check
		<input checked="" type="checkbox"/> Detector Gas Leak, Clog Test

Consumables Reset

SPL1(INJ#1)	Septum Used Counts : <input type="text" value="0"/>	<input type="button" value="Reset"/>
	Insert Used Counts : <input type="text" value="0"/>	<input type="button" value="Reset"/>
SPL2(INJ#2)	Septum Used Counts : <input type="text" value="0"/>	<input type="button" value="Reset"/>
	Insert Used Counts : <input type="text" value="0"/>	<input type="button" value="Reset"/>
(INJ#3)	Septum Used Counts : <input type="text" value="0"/>	<input type="button" value="Reset"/>
	Insert Used Counts : <input type="text" value="0"/>	<input type="button" value="Reset"/>
CRG Coolant Used Time	Column Oven : <input type="text" value="0"/> min	<input type="button" value="Reset"/>
	(INJ#2) : <input type="text" value="0"/> min	<input type="button" value="Reset"/>
<input type="button" value="Close"/>		

<System Check> (Reference Manual p184)

4 Next Step - Data Acquisition

4.9 Acquisition start from instrument

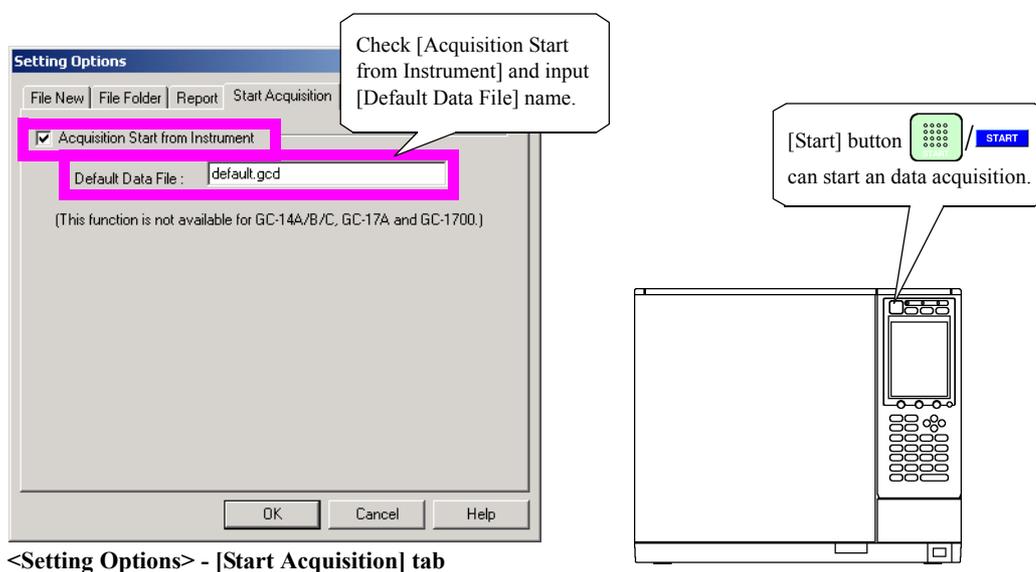
Usually, to run a single-run analysis, you need to do <Sample Login> first, then press the single-run analysis [Start] button, and then inject the sample while pressing the [Start] button of the GC (in the case of manual injection).

To start acquiring data by just pressing the [Start] button of the GC instrument without pressing the single analysis [Start] button, make the settings as follows:

Note: This feature is not available in systems which use GC-14/GC-17A/GC-1700.

Note: The method file to be used for analysis needs to be loaded into the <GC Real Time Analysis> in advance. When the method file has no name or the <GC Real Time Analysis> has been locked, the analysis cannot be started.

4.9.1 Setting <Start Acquisition>



With the settings shown above, press the [Start] button of the GC instrument to start analysis (data acquisition). Acquired data is saved in the same folder as the method file with a name specified in the [Default Data File]. As data files are auto-numbered at the end of their filenames, they are not overwritten even if you run an analysis several times.

The method settings have to be downloaded when <GC Real Time Analysis> is started, and when you want to change settings after that. Especially using "Other (CBM-102)" system, you have to download method, otherwise an analysis can not start.

For this function, GC instrument's program is necessary (other than "Other (CBM-102)" system). Setup the oven temperature program for the analysis. Even for the consistent oven temperature case, set the hold time in the program.

When the analysis starts, the GC parameters are uploaded from the GC instrument and saved into the method file currently active in the <GC Real Time Analysis> overwriting the existing ones. Because of this, even if the parameters have been changed in the GC instrument and the analysis is resumed, the values actually used in the analysis are saved in the method file and data file.



4 Next Step - Data Acquisition

4.9 Acquisition start from instrument

Note: Specify only the filename including file extension (gcd). Data files are stored in the same folder as the method file is stored, you cannot set the folder here.

Note: Even after making the above settings, you can still run a usual single-run analysis by pressing the single-run analysis [Stat] button of the <GC Real Time Analysis>. In addition, you need not make the settings above every time since the settings are stored in the system.

Note: When [Acquisition] check box is unchecked, a data file will not be created after analysis started by this function.

4 Next Step - Data Acquisition

4.10 Vial number 0

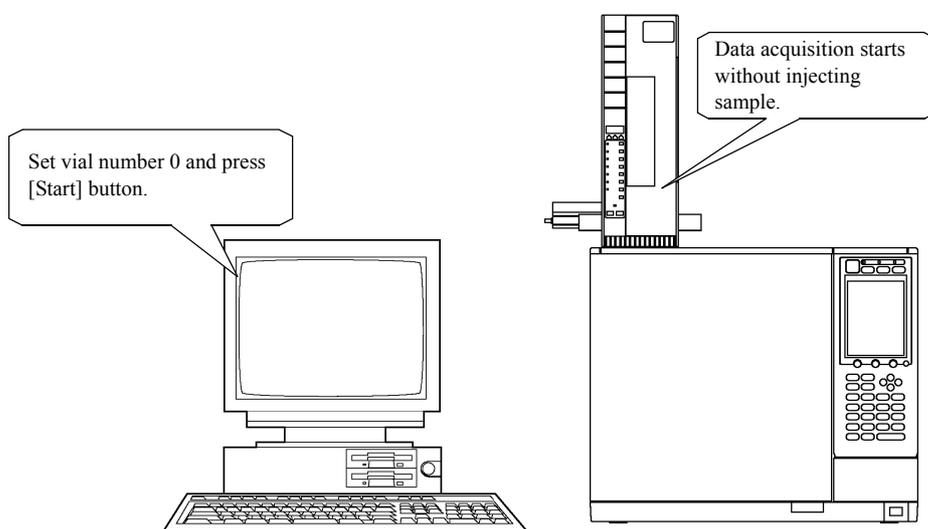
If you start an analysis with the vial number set to 0 in a single-run analysis or batch analysis, pressing the [Start] button starts the GC automatically and data acquisition starts. This feature is used when measuring baseline data during temperature-programmed analyses or aging the column, etc.

Note: This feature has the following limitations depending on the GC type being used.

GC-14A/GC-17A/GC-1700 : This feature is available only when the auto-injector (AOC-20i) is used.

GC-2010/GC-2014/GC-2025 : This feature is available only when the auto-injector (AOC-20i) is used or manual injection is used.

Note: In the previous versions (version 2.10SU2 or earlier), when the GC-2010 was used in the manual injection mode, pressing the [Start] button of the GC instrument started analysis even if the vial number had been set to 0. In this version, however, if the version number has been set to 0, pressing the [Start] button in the GCsolution automatically starts data acquisition. Be sure to take note of this change.



5 Next Step - Data Processing

5.1 About GCsolution data file

GCsolution records various information such as method and configuration setting in a data file.

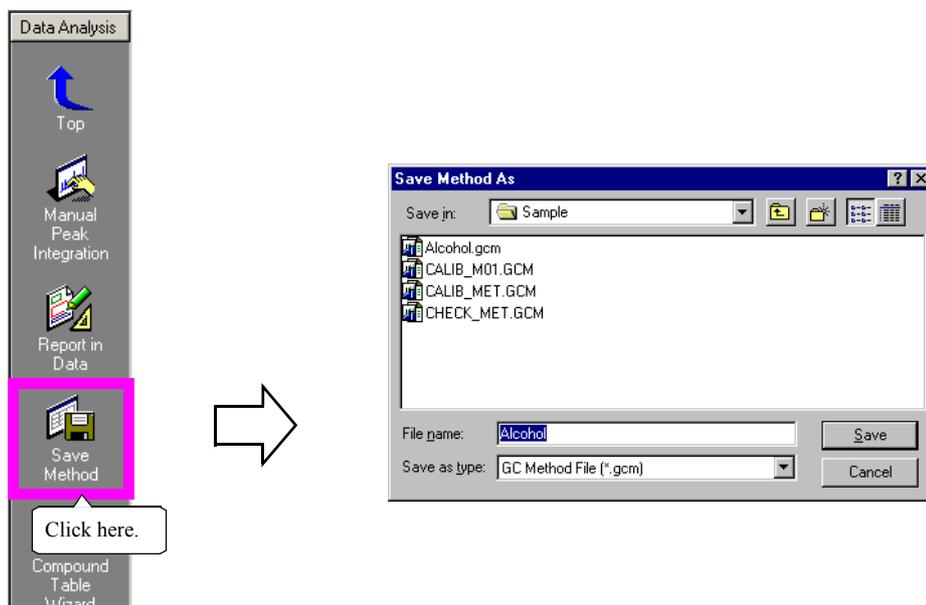
To allow you to analyze a data file using a method stored in another data file or analyze a data file using a method file separately stored, GCsolution allows you to import or export methods.

For more about the file structure, refer to Administration Manual "4.1 Important File Concepts for Operation".

5.1.1 Import/Export Method File

In the <Data Analysis> screen, a method recorded in a data file is edited and post-run analysis is run using it. To mirror the current method settings to another method file, you can export the method in the data file. By using this export feature, you can overwrite another method file by a method in a data file or save it as a standalone file.

To export a method, use the [Save Method] icon on the [Data Analysis] Assistant Bar.



Note: [File]-[Save Data and Method File] can save both data file and its method file at the same time (A confirmation message will be displayed before saving the method file).

Note: If you have exported a method to an existing method file overwriting the original, only the data processing method is overwritten leaving the device parameter section intact.

On the other hand, you can import the settings in a method file into the data file currently open in the <Data Analysis>. When a method is imported, only the data processing method section is imported by overwriting the corresponding section in the data file, i.e. no device parameter is imported.

To import a method, use [File] - [Load Method] menu.

In a batch post-run analysis, this method import command is consecutively executed for multiple files.



5.1.2 Import/Export Report Formats

A data file contains a report format.

You can import and export a report format to/from a data file using the [Open Format File] and [Save Format File As] commands in the [File] menu.

You can display the report format in a data file (data report) by clicking the [Report in Data] icon on the [Data Analysis] Assistant Bar. If you load a report file in that state by selecting [File] - [Open Format File], that report file is imported into the data file currently open. Also, you can export the report format in a data file as a report file by selecting [File] - [Save Format File As].

5.1.3 Using the same method file between <GC Real Time Analysis> and <GC Postrun>

In the case of performing a batch data processing on the <GC Postrun> using the method file which is currently loaded in <GC Real Time Analysis> or overwriting the method file from <Data Analysis> or <Calibration Curve>, to make the method file available to <GC Postrun>, it has to be closed and released from <GC Real Time Analysis>. As GCsolution has automatic closing and reloading function, usually the operation can be done without any extra steps.

But if the method file has changed and not saved yet, some confirmation messages are shown. Save the method file by following the message. On the other hand, when the method file is automatically re-loaded in <GC Real Time Analysis>, the icon might be blinking, but it is not an error.

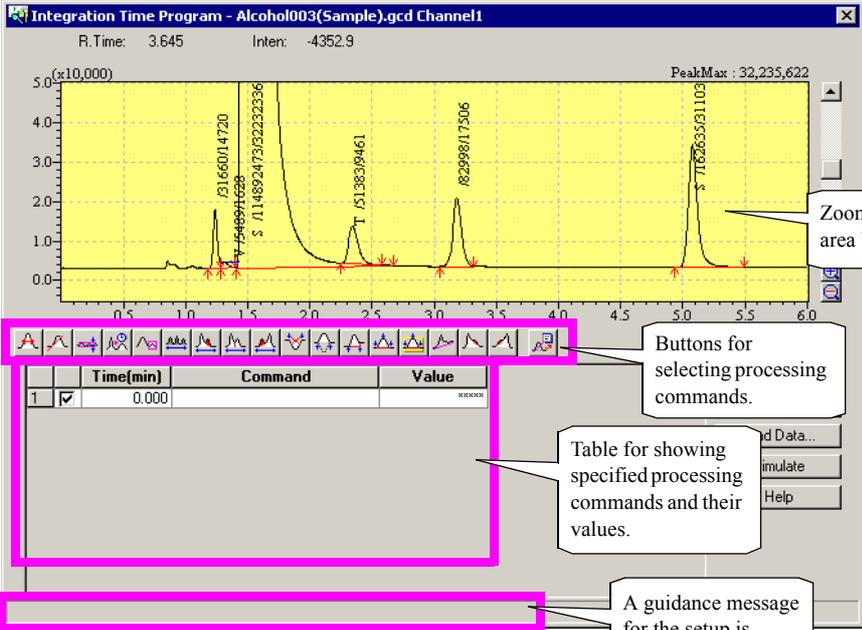
5.2 Next Step - Data Processing

5.2 Peak Integration Time Program

By using integration time programs, you can cater for the processing needs which integration parameters alone cannot fulfill.

5.2.1 Peak Integration Time Program

After setting the method view for <Data Analysis> or <Calibration Curve> to the [Edit] mode, click  button in the [Integration] tab page to open the <Integration Time Program> screen.



Zoom in on dragged area by the mouse

Buttons for selecting processing commands.

	Time[min]	Command	Value
1	<input checked="" type="checkbox"/>	0.000	*****

Table for showing specified processing commands and their values.

A guidance message for the setup is displayed here.

Click one of the processing command buttons and specify the time to execute it by clicking a point in the chromatogram. The selected command will be executed at the time of selection. Since some processing commands require you to specify the starting and ending points, follow the guidance message shown in the bottom-left corner of the screen.

The settings specified are shown in the program table. You can also edit this table directly.

You can check the program by clicking the [Simulate] button, which starts processing using the specified integration time program and show the resultant baseline and area values for the chromatogram.

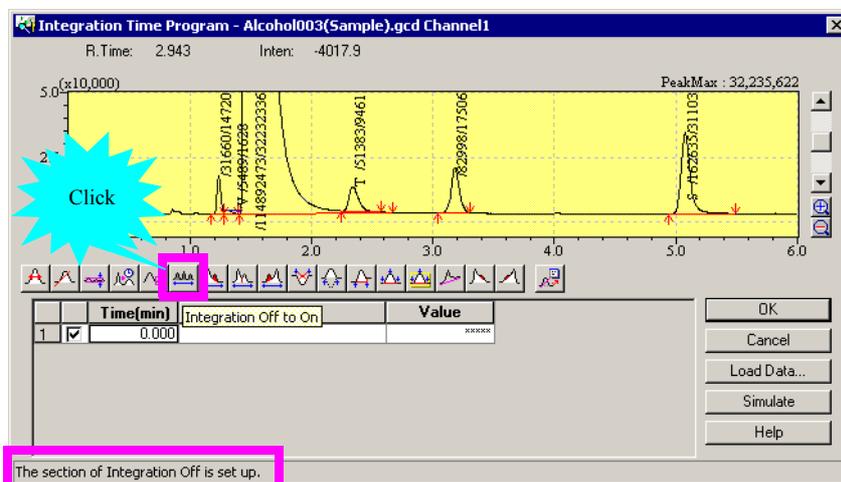
After completing all the settings, click the [OK] button to close the <Integration Time Program> screen. If you set the method view in the <Data Analysis> or <Calibration Curve> screen to the [View] mode, integration is performed and its result is displayed.

Note: An integration time program created in the <Calibration Curve> screen is saved in a method file. When you set up a method in the <Data Analysis> screen, you can save it as a method file by exporting it.

5.2.2 Setting Integration Time Program Examples

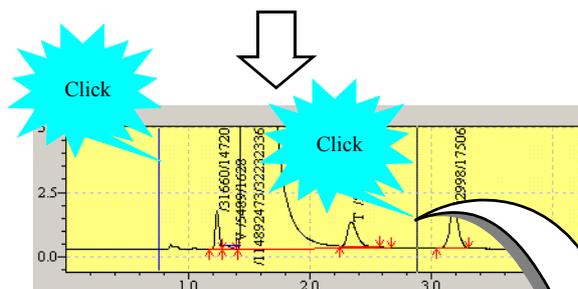
❖ Operational procedure for setting up integration time program (Peak Integration Off/On)

- 1) Click the [Integration Off to On] button.



A guidance message will appear.

- 2) Following the guidance, specify the starting and ending points of the section by clicking on the chromatogram.



- 3) When the ending point is clicked, a screen opens for your confirmation. After confirming the starting and ending times of the section, click the [Simulate] button.

Start Time: 0.757 min

End: 2.816 min

Simulate

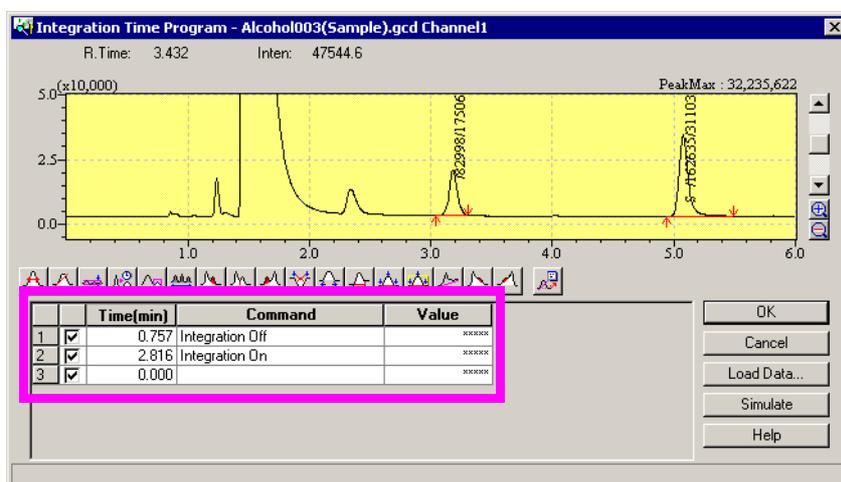
Cancel

Add Table

Help

- 4) The specified processing command is shown on the program table.

After checking the processing result, click the [OK] button.



5.3 Next Step - Data Processing

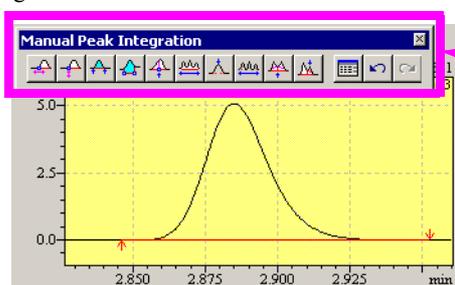
5.3 Manual Peak Integration (Manipulation)

By using the manual peak integration feature (manipulation), you can move the starting or ending point of a specific peak or remove unwanted peaks.

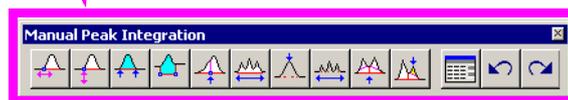
5.3.1 Manual peak integration feature (manipulation)

You can use the manual integration feature in the <Data Analysis> and <Calibration Curve> screens.

Click the  button on the Assistant Bar for <Data Analysis> or <Calibration Curve> to show the <Manual Peak Integration> toolbar.



You can change the toolbar size by using the [Large Icon] and [Small Icon] buttons on the right-click popup menu.



Click a processing command button and specify the time to execute it by clicking on a point in the chromatogram. Since some processing commands require you to specify the starting and ending points, follow the guidance message shown in the bottom-left corner of the screen.

If the [View Table] button is clicked, the settings specified are shown in the program table. You can also directly edit this table.

In the <Calibration Curve> screen, you can perform manual peak integration on the data used in the calibration curve. In the case of multi-level calibration curve, select your desired data in the calibration data file tree. The result of manual integration is immediately applied to the calibration curve.

	Time(min)	Command	Value
1	2.222	Move BL	2.266
2	3.170	Reject Peak	*****
3	0.000		*****

In the <Data Analysis> screen, you can perform manual integration on the data currently open.

Processing commands for manual integration are saved in the target data. Therefore, they will not be saved in a method file even if the method is exported in the <Data Analysis> screen. Also, manual integration processing commands will not be overwritten by any method file even if post-run analysis is run for the data using another method file in <Data Analysis> or <Batch Table>.

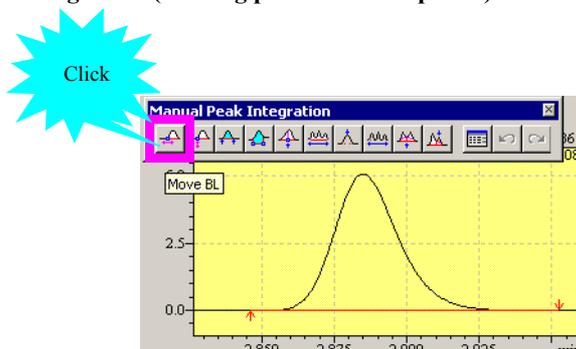


5.3.2 Setting Manual Peak Integration Examples

❖ Operational procedure for setting up manual peak integration (Shifting peak detection points)

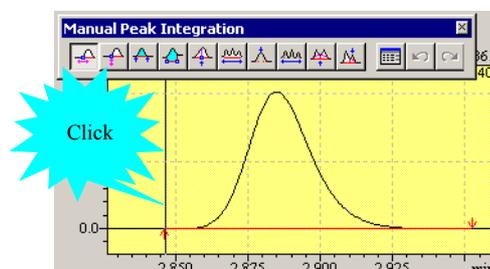
- 1) Click the [Move BL] button.

A guidance message will appear in the bottom-left corner area of the screen.

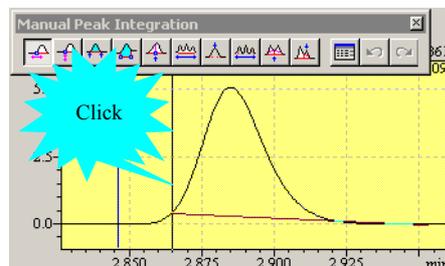


- 2) Click the detection point you wish to move.

The baseline for the peak starts moving along with the mouse movement.



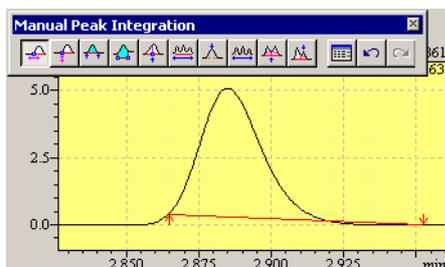
- 3) Checking the baseline, click at the point to which you wish to move the peak detection point.



- 4) The peak detection point moves to that point and the resultant baseline is displayed.

If you have mistakenly moved the point to an undesirable place, you can cancel the move by clicking

the  button.



5 Next Step - Data Processing

5.4 Setting up for Peak Identification and Quantitation

Peak identification is the processing to identify a detected peak with a compound in the sample. Usually, peak identification and quantitation are performed at the same time.

To perform identification and quantitation, you need to set up the parameters for defining the conditions and compound table. You will specify a peak identification method and quantitation method and such in the parameters and retention time, type, and concentration of each component to the compound table. All these settings are saved in a method file.

When a standard sample data is analyzed using a method file for which the settings for identification and quantitation have been defined, a calibration curve is created based on the data of peaks identified. Then an unknown sample data is analyzed, identified peaks are quantitated using the calibration curve.

5.4.1 Setting Peak Identification Parameters

You can set up the identification and quantitation parameters in the <Method> view of the <Calibration Curve> or <Data Analysis> screen.

[Quantitation] parameters

Select your desired quantitation method and calibration curve type, and set other items in accordance with your selected quantitation method.

Set the number of concentration levels of calibration curve to [# of Calib. Levels].

When the internal standard method is used, you are additionally required to specify the internal standard substance in the compound table. When the area normalization method is used, each compound is not quantitated, but each peak's percentage of area (height) to the entire peak area (height) is calculated instead.

[Identification] parameters

Select the identification method and set other items accordingly.

When the relative retention time method is selected, you are required to set the reference peak in the compound table.

When identification is performed with the [Peak Select] field set to [All Peaks], all the peaks fell into the window or band set for a target component are identified as that component. In that case, when no grouping has been used, concentration is evaluated for each of peaks and then the total of them is given. When grouping has been used, concentration is evaluated after adding up all the areas (heights) of peaks.

When you use grouping method, you additionally need to create a group table.

[Correction of RT]

Set this field to correct the retention times set in the compound table using the retention times of the identified peaks.

This correction is performed only in analyzing standard samples.

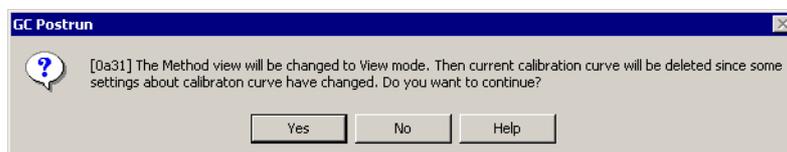
This feature is useful when peak retention times are shifted little by little because of the degraded column and such while a number of samples are analyzed in a batch.

Some of the parameters here are also settable in the compound table. For those parameters, priority is given to the settings in the compound table. When the setting in the compound table is left to [Default], the settings made here are used for computation.

When the setting is made in the <Calibration Curve> screen, a calibration curve is computed and shown when the [View] button is clicked.



When the setting is changed in the <Data Analysis> screen, it will conflict with the calibration curve stored in the data file. Therefore, the calibration curve in the data file may be deleted along with the quantitation result when the [View] button is clicked, depending on the parameters changed. In that case, a confirmation message is displayed.



In the case of [Ret. Time] for the compound table, however, it can be used for quantitation even if it has been changed, allowing you to quantitate and identify peaks in unknown samples located at a position different from the ones in the standard sample.

When the settings in a method is changed in the <Data Analysis> screen, only the data file currently open in the <Data Analysis> screen will be analyzed using the modified method.

To analyze another data file using the modified method or use the method for analyses thereafter, save (export) the method in the current data file as a method file. Click the [Save Method] icon on the Assistant Bar to export it or select [File] - [Save Data and Method File] to write it back to the original method file.



5.4.2 Setting up Compound Table

In Chapter 3, there introduced how to create a new compound table using the Compound Table wizard. Here, those are some features for editing the table directly.

❖ Editing features

To edit a compound table, enter desired values to cells directly. The popup menu shown by right-clicking the table offers useful commands for supporting to edit the table.

ID#	Name	Type	Ret.Time	Conc.1	Unit	Calc.by
1	n-PrOH	Reference	2.320	200		
2	isoBuOH	Target	3.170	200		
3	isoAmOH	Target	5.080	200		

Right-click [Compound] table to display pop-up menu.
Use to perform main editing operations for table.

If data processing is not done yet, can use [Cancel Edit] to undo edited data.

Use [Table Style] to display column display condition (displayed or hidden).

ID#	Name	Type	Ret.Time	Window/B	Band
1	Nonene	Reference	2.080	Band	0.20
2	Decane	Target	2.750	Band	0.20
3	Undecane	ISTD	3.680	Window	Default
4	Dodecane	Reference	4.830	Window	Default
5	Tridecane	ISTD&Ref	6.090	Window	Default

Enter values into cells for setting each compound individually.
If it is not necessary to specify setting values for each compound, set them to [Default]. You can set a cell to [default] by pressing the [Delete] key on your keyboard. The values specified by the identification and quantitation parameter are automatically set to these cells.

❖ Set the retention time using the mouse

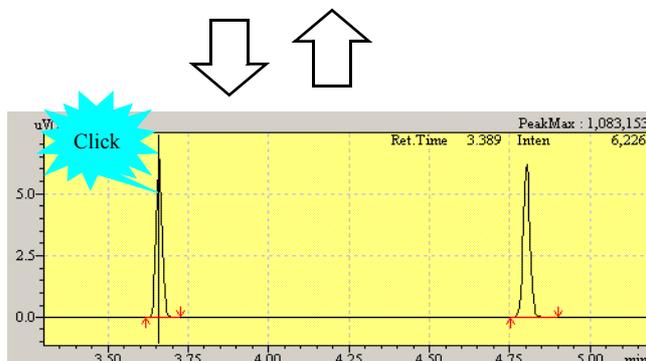
You can set retention times for compounds visually by clicking on the chromatogram.



ID#	Name	Type	Ret.Time	Conc.1	Unit	Calc.by
1	n-PrOH	Reference	2.320	200	%	Default
2	isoBuOH	Target	3.170	200	%	Default
3	isoAmOH	Target	5.080	200	%	Default

- 1) Set the method view to the [Edit] mode.
- 2) Click the [Ret. Time] cell on the compound table.
- 3) Click the peak of your selection. The retention time of the peak is set to the compound table.
- 4) Next, click the [Ret. Time] cell for another ID number. And then click your target peak and set the retention time.

Note: Be sure to set [Peak Position Line] to display when you edit the table.



You can use this feature in <Data Analysis> and <Calibration Curve>. This feature allows you to set a retention time in a easy and precise manner by just clicking the [Ret. Time] cell and a peak on the chromatogram.

5.5 Next Step - Data Processing

Operations in the <Data Comparison> Window

Drag and drop data file icon and add up to 8 data items to display.

To close display data, use right-click menu on data file name and click [Close].

Use right-click menu in <Chromatogram> view area to magnify, shift, or undo chromatogram display.

Use [Base Shift] to display entire chromatogram shifting an equal distance.

Focus a chromatogram by holding down its number.

Increases/Decreases display attenuation in intensity direction.

Use splitter to change display ratio. Upper area is <Chromatogram> view area, lower area is <Peak Table> view area.

Displays information on currently focused chromatogram peak.

Copy chromatograph data to Clipboard and paste into other files as an image.

Peak#	Ret. Time	Area	Height	Conc.	Compound	Compound	Gr	ID#	Group
1	1.302	3007155.7	1083158.4	0.00000	VE				
2	1.383	119332.0	102359.8	0.00000	SV				
3	2.072	8309.0	7805.3	77.53947					
4	2.732	8491.8	7127.8	77.58756		1 No			
5	3.659	8462.0	6345.3	77.66992		2 De			
6	4.803	9087.1	6160.0	77.70859		3 Ur			
7	6.065	8559.5	5261.1	77.73277		4 De			

<Data Comparison> (Reference Manual p311)

- Example of upper-lower shift (use the same procedure for left-right shift)

Click [Move Up/Down].

Drag mouse vertically.

Chromatogram will then shift for dragged distance.

- Example of upper-lower stretch/contraction (use the same procedure for left-right stretch/contraction)

Click [Base Point] to select base point. Click [Scale Up]/[Scale Down].

Drag mouse vertically.

Chromatogram will then stretch/contract for dragged distance (B/A times).

5 Next Step - Data Processing

5.6 Checking data with CLASS-Agent

If the option software for data management, "CLASS-Agent" is set up on the PC on which the analysis was carried out, the analytical results data be registered automatically in the Agent database.

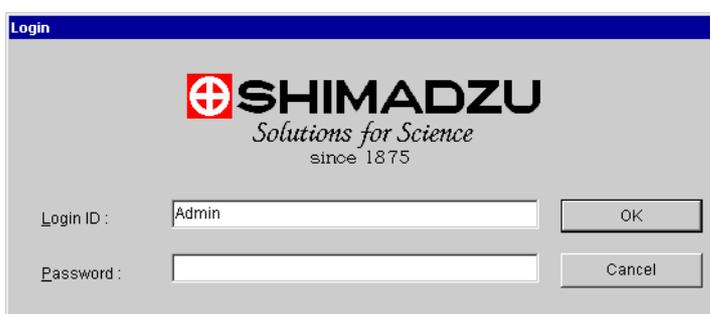
The following describes how to check the registered data with CLASS-Agent.

1. Start CLASS-Agent Manager.

Click on the [Database] icon  on the [Administration] tab.

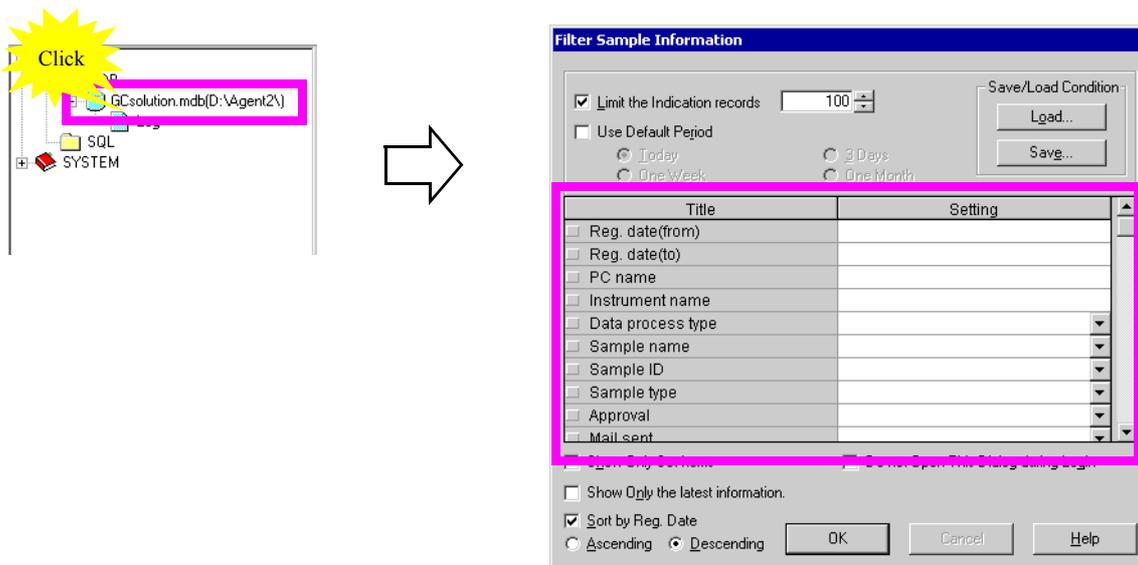
2. Login window will appear.

Enter your login ID and password.(The initial ID is "Admin" and no password is required.)



Note: The login ID and password for CLASS-Agent Manager must be specified using [Tools]-[User Administration] menu on "CLASS-Agent Manager".

3. In the Select Database window, click on the database where the GCsolution data is registered. The dialog box will open, prompting you to enter the conditions for more detailed search on the database.



Enter the conditions for the desired data and click on the [OK] button. If you specify an analysis date, a registration date, an analysis system, and other conditions, you will be able to extract only the desired data from the registered one.



To specify the database where the GCsolution data is registered, use [Data Reg. Settings] icon on the [Administration] tab - [Assign Database per Instrument] (If Agent registration is not set up, no data can be registered).

4. Search the list of data registered in the database for the desired analysis data, and click on the row for the data. The analysis results of the selected data will be displayed at the bottom of the window.

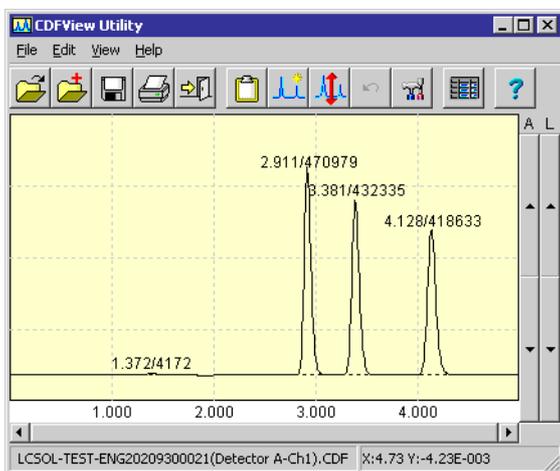
	Reg. date	Instrument name	Data process type	Sample name	Sample ID
1	2002/09/30 14:54:43(+0900)	Instrument2	GCsol	Unk3	12
2	2002/09/30 14:54:36(+0900)	Instrument2	GCsol	Unk2	11
3	2002/09/30 14:54:27(+0900)	Instrument2	GCsol	Unk1	10
4	2002/09/30 14:54:20(+0900)	Instrument2	GCsol	Lv3	9
5	2002/09/30 14:54:12(+0900)	Instrument2	GCsol	Lv3	8
6	2002/09/30 14:54:04(+0900)	Instrument2	GCsol	Lv3	7
7	2002/09/30 14:53:56(+0900)	Instrument2	GCsol	Lv2	6
8	2002/09/30 14:53:48(+0900)	Instrument2	GCsol	Lv2	5
9	2002/09/30 14:53:39(+0900)	Instrument2	GCsol	Lv2	4
10	2002/09/30 14:53:31(+0900)	Instrument2	GCsol	Lv1	3

GCSOL	Reg. date	PC name	Instrument name	Ch
1	2002/09/30 14:54:27(+0900)	GCSOL-TEST-ENG	Instrument2	1
2	2002/09/30 14:54:27(+0900)	GCSOL-TEST-ENG	Instrument2	1
3	2002/09/30 14:54:27(+0900)	GCSOL-TEST-ENG	Instrument2	1
4	2002/09/30 14:54:27(+0900)	GCSOL-TEST-ENG	Instrument2	1
5	2002/09/30 14:54:27(+0900)	GCSOL-TEST-ENG	Instrument2	1
6	2002/09/30 14:54:27(+0900)	GCSOL-TEST-ENG	Instrument2	1
7	2002/09/30 14:54:27(+0900)	GCSOL-TEST-ENG	Instrument2	1

To check the chromatogram for the analysis data, click on the [Chromato Preview] button  on the Toolbar.

This will allow you to check the integration results of the chromatogram for the selected analysis data.

To close the <Chromatogram> view, click on the [Chromato Preview] button  again.



Note: To preview the chromatogram, you must previously associate the *.cdf file (AIA ANDI format = common format in the industry for chromatographic analysis) with the application, "CDF Viewer" using the [Tool]-[Options] menu.

Refer to [Administration Manual] "6.4 Using CLASS-Agent".

6 Quantitation Parameter Settings

6.1 Setting Quantitation Parameters - Normalization Method

This section explains how to set the parameters required to perform quantitation using Area Normalization.

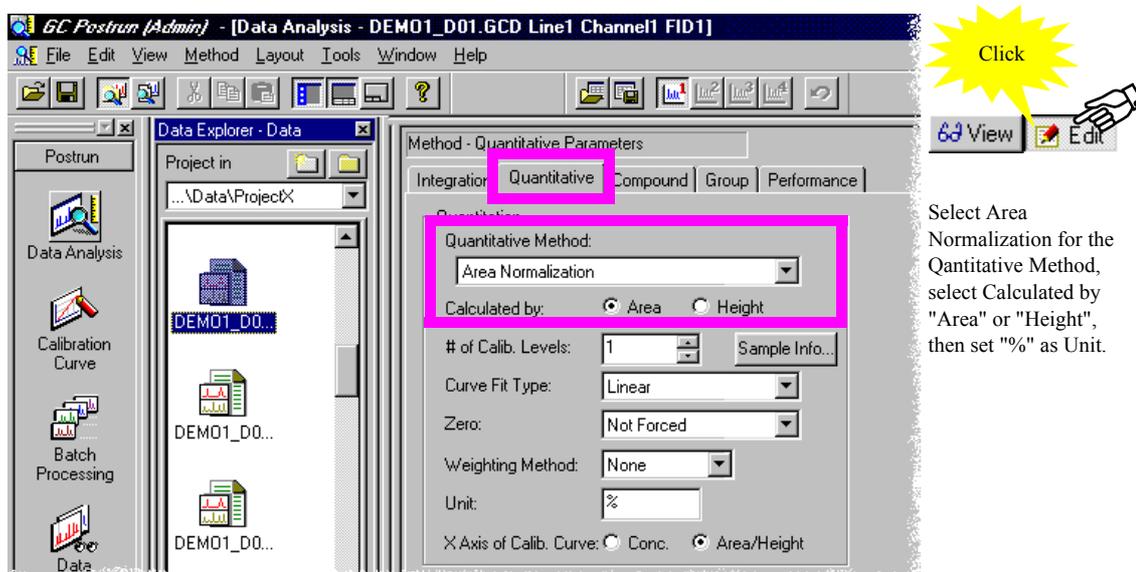
6.1.1 Area Normalization

The area normalization method is used to obtain the area (height) percentage of each peak to the area (height) of all the detected peaks.

As this method is not for finding concentration of target compounds like other methods do, it is not necessary to set up a compound table.

6.1.2 Setting Quantitation Parameters

Area Normalization method can calculate area or height percent of each peak.



The screenshot shows the 'Method - Quantitative Parameters' dialog box in the GC Postrun software. The 'Quantitative' tab is selected. The 'Quantitative Method' dropdown is set to 'Area Normalization'. The 'Calculated by' section has 'Area' selected with a radio button. The 'Unit' is set to '%'. The 'X Axis of Calib. Curve' has 'Area/Height' selected. A yellow starburst with the word 'Click' and a hand icon points to the 'View' button in the bottom right corner of the dialog box.

Select Area Normalization for the Quantitative Method, select Calculated by "Area" or "Height", then set "%" as Unit.

About quantitative methods, refer to Reference Manual "16.3 Quantitation Method".

Calculated values are shown in the peak table as conc. values.

6 Quantitation Parameter Settings

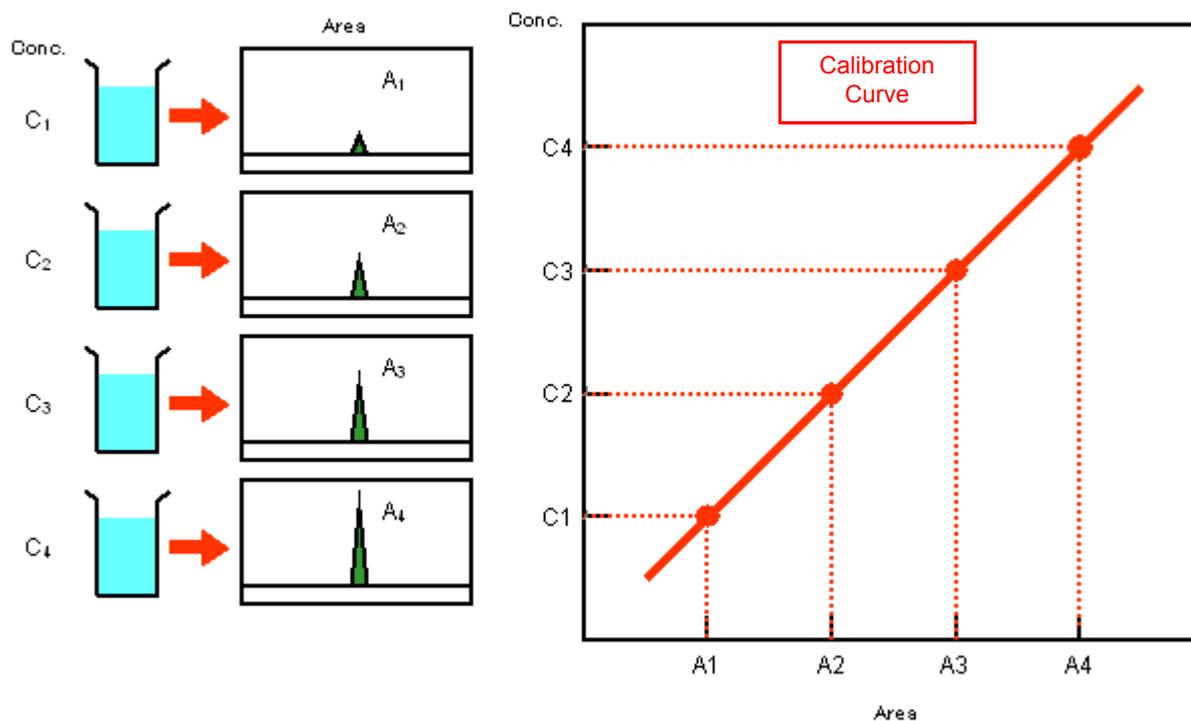
6.2 Setting Quantitation Parameters - External Standard Method, Corrected Area Normalization

This section explains how to set the parameters required to perform quantitation using one of these quantitative methods: External Standard, Corrected Area Normalization, or Correct Area Normalization with Scale Factor.

6.2.1 External Standard Method

The most commonly used quantitative methods is the external standard method.

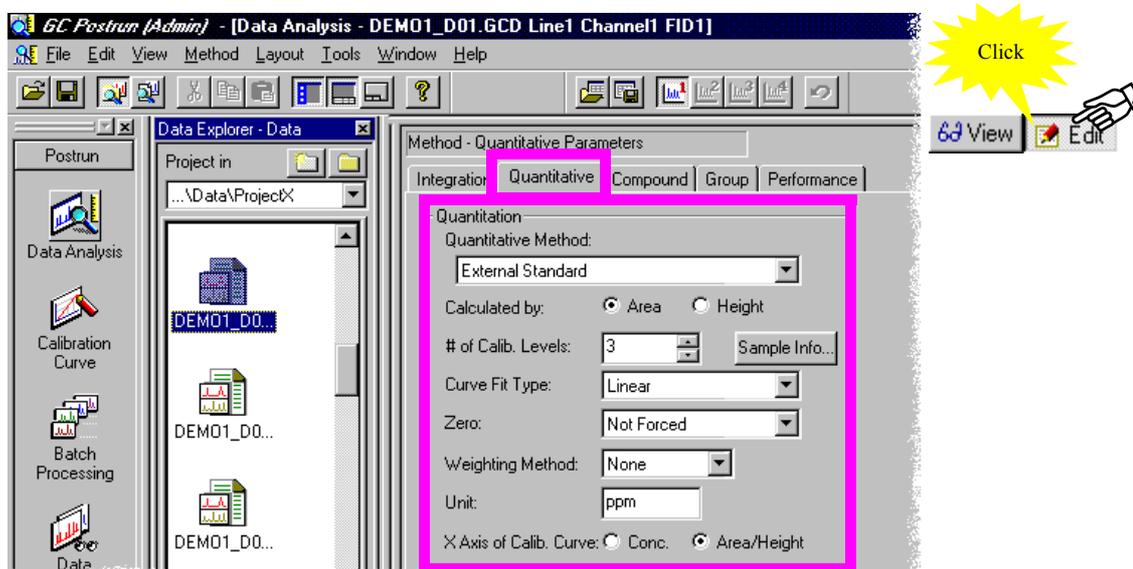
This method requires you to prepare solutions of your target substance's standard sample, each diluted to different levels of concentration, and inject a constant amount of them into the GC for analysis. Then, create a calibration curve setting the concentration (absolute amount) of the target substance in the injected sample solution to the vertical axis and the peak area (height) to the horizontal axis. (it is changeable the setting for the horizontal axis to [Conc.] or [Area/Height] by setting [X axis of Calib. Curve]. The vertical axis then changes accordingly.)



After creating a calibration curve, analyze the standard sample and an unknown sample by the same amount under the same conditions. The concentration of the target substance in the unknown sample is obtained by seeking the concentration (vertical axis) corresponding to the peak area detected in the sample (horizontal axis) using the calibration curve.

6.2.2 Setting Quantitation Parameters

After setting the [Quantitative] parameters such as [Quantitative Method] and [# of Calib. Levels], set up the compound table. Then create a compound table.



About quantitative methods, refer to Reference Manual "16.3 Quantitation Method" and "16.4 Calibration Curve".

6.2.3 Setting Compound Tables

Enter the standard (values) for each component that will be used to create the calibration curve. When using relative retention time method, set at least one reference peak in compound table.

ID#	Name	Type	Ret. Time	Window/B	Band
1	None	Reference	2.080	Band	0.20
2	Decane	Target	2.750	Band	0.20
3	Undecane	ISTD	3.680	Window	Default
4	Dodecane	Reference	4.830	Window	Default
5	Tridecane	ISTD&Ref	6.090	Window	Default

Quantitation can be performed using prepared standard samples for each compound. Here, perform the settings for the number of prepared standard samples. For the concentration values of compounds that are not included in samples to be quantitated, press the [Delete] key on the keyboard to enter [Not Used].

ID#	Name	Type	Ret. Time	Conc. 1	Conc. 2	Conc. 3
1	n-PrOH	Target	2.32	200	Not Used	Not Used
2	isoBuOH	Target	3.17	Not Used	200	Not Used
3	isoAmOH	Target	5.08	Not Used	Not Used	200

When preparing 3 standard samples to quantitate the 3 compounds, enter [Not Used] for concentration value of compounds not included among samples.

6 Quantitation Parameter Settings

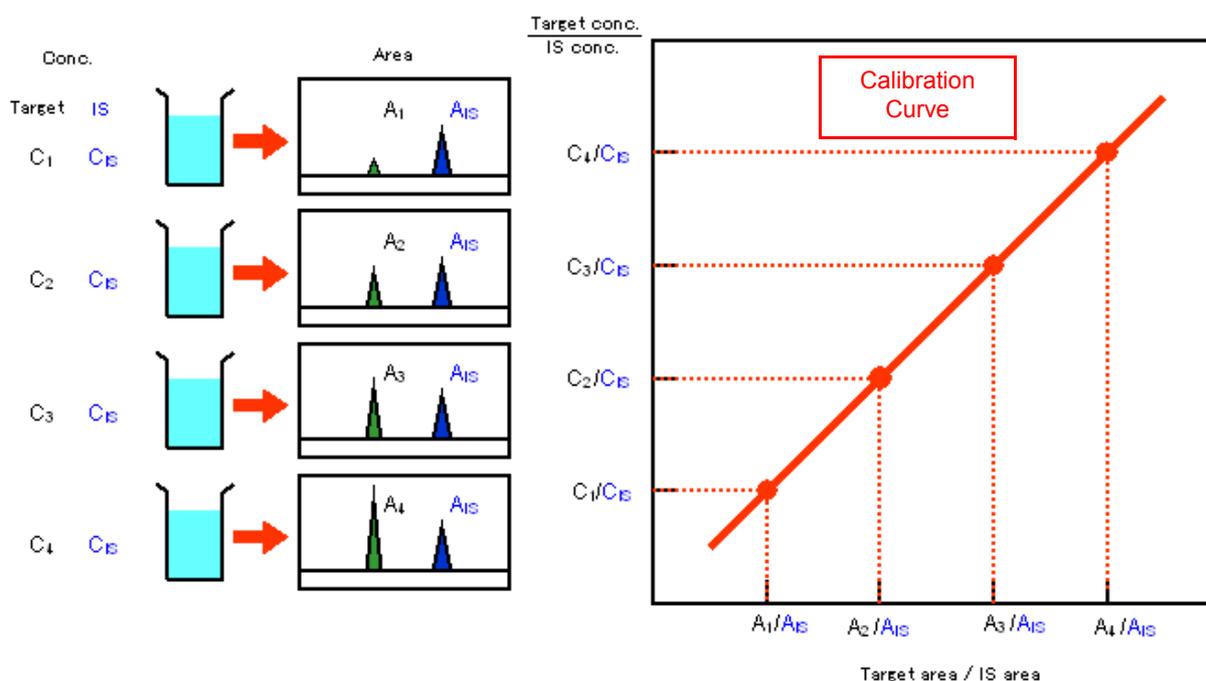
6.3 Setting Quantitation Parameters - Internal Standard Method

This section explains a method to set parameters required to perform quantitation using Internal Standard as a quantitative method.

6.3.1 Internal Standard Method

In the internal standard method, an internal standard (IS) substance different from the target substance is needed. An ideal internal substance would be a stable compound which is similar to the target substance in chemical property, eluted near the target substance, and completely separated from other components in the sample.

This method requires you to prepare solutions containing the constant amount of the internal standard substance (hereafter referred to as "IS") and your target substance (hereafter referred to as "X") each at a different concentration, and inject a constant amount of them into the GC for analysis. Create a calibration curve setting [X Conc. / IS Conc.] in the injected sample solution to the vertical axis and [X Area / IS Area] to the horizontal axis. (You can change the setting for the horizontal axis to [Conc.] or [Area/Height] by setting [X axis of Calib. Curve]. The vertical then axis changes accordingly.)

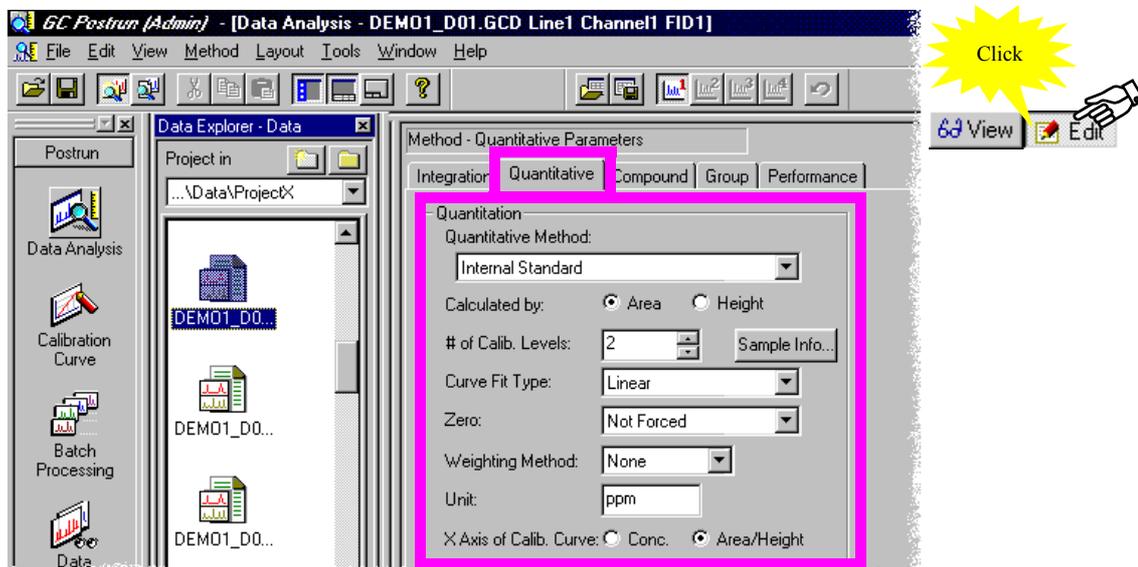


Next, prepare a solution from the unknown sample adding the IS so that the concentration of IS is about the same with the standard sample. Then, introduce it into the GC by the same amount with the standard solution to obtain its chromatogram for measuring the peak area. Now you can obtain the target substance concentration in the unknown sample by finding the ratio between the concentrations of X and IS (on the vertical axis) from the ratio between the peak areas of X and IS using the calibration curve, and multiplying it by the added IS's concentration.



6.3.2 Setting Quantitation Parameters

After setting the [Quantitative] parameters such as [Quantitative Method] and [# of Calib. Levels], set up the compound table. Then specify the internal standard substance in the compound table.



About quantitative methods, refer to Reference Manual "16.3 Quantitation Method" and "16.4 Calibration Curve".

6.3.3 Setting Compound Tables

Here, how to set compound table data is explained using quantitation of the following compounds using the Internal Standard method as an example.

- Comp.A: Internal standard component
- Comp.B: Quantitated using Comp. A
- Comp.C: Internal standard component
- Comp.D: Quantitated using Comp. C

An internal standard component must be there in a ISTD Group.

To analyze unknown samples, set ISTD amount (internal standard component amount) in the <Sample Login> or the <Batch Table>.

ID#	Name	Type	Ret. Time	Conc. 1	ISTD Group
1	Comp.A	ISTD	2.320	200	1
2	Comp.B	Reference	3.170	200	1
3	Comp.C	ISTD	5.080	200	2
4	Comp.D	Target	6.565	200	2

Set standard samples' internal standard concentration values for each internal standard component.

- ISTD: Internal Standard component.
- ISTD & Reference: Internal Standard & reference peak.

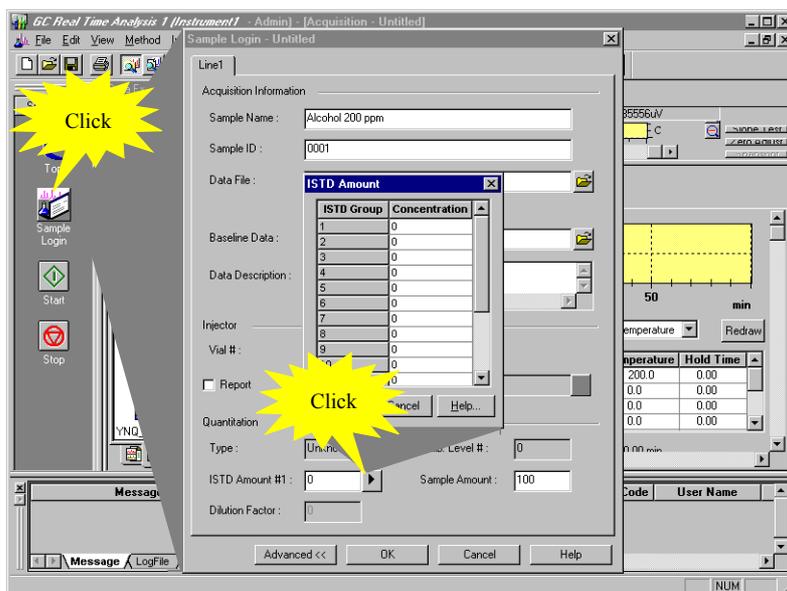
Set the same id number in [ISTD group] cells for compound to be quantitated and internal standard component to use for quantitation.

Note: If you use the grouping by [Group Calibration], you also need to make the similar setting in the group table.

- When performing a single-run analysis:

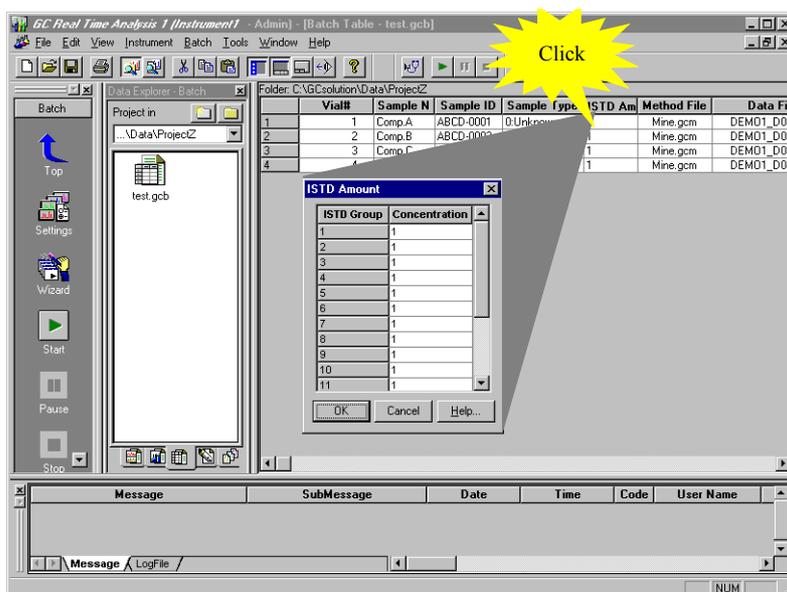
Set the unknown sample's ISTD amount in the <Sample Login> window's [ISTD Amount #1].

When using multiple internal standard components, click the button in the [ISTD Amount #1] field to display the <ISTD Amount> window. Then, set multiple internal standard component amounts in that window.



- When performing a batch analysis:

Set the ISTD amount in the <Batch Table> window's [ISTD Am.] column. (Only when the sample type is set to [Unknown], will the settings become effective. If the sample type is set to [Standard], the compound table's setting values will be used and the values entered here will be ignored.)



Note: For quantitative calculation, the ISTD amount of the same [ISTD Group] number as you set in the compound table or group table in method file is used. For example, if you set [ISTD Group] 2 for ISTD 'A', the amount you set for [ISTD Group] 2 in the <Sample Login> or <Batch Table> is used as the amount of 'A' for quantitative calculation of compounds in the ISTD group 2.

6 Quantitation Parameter Settings

6.4 Setting Quantitation Parameters - Standard Addition Method

This section describes how to set parameters required to perform quantitation using Standard Addition as the quantitative method.

6.4.1 Setting Quantitation Parameters

Click

Since an unspiked sample is also considered a calibration point, use 2 kinds of standard. spiked samples, e.g., as "1 unspiked sample + 2 different standard. samples = 3 calibration point".

About quantitative methods, refer to Reference Manual "16.3 Quantitation Method" and "16.4 Calibration Curve".

6.4.2 Setting Compound Tables

The Standard Addition requires to set the standard sample's [Conc. 1] to unspiked sample.

In the example below, set the parameters in the compound table shown in the right-side figure.

- Conc. 1: Unspiked sample
- Conc. 2: Spiked sample of 100 ppm
- Conc. 3: Spiked sample of 200 ppm

ID#	Name	Type	Ret.Time	Conc.1	Conc.2	Conc.3
1	n-PrOH	Target	2.320	0	100	200
2	isoBuOH	Target	3.170	0	100	200
3	isoAmOH	Target	5.080	0	100	200

To create a calibration curve, first, set all unspiked and spiked samples' [Type] to [Standard], and use the method file saved in the section above to perform data acquisition (to use existing data, perform post-run batch processing). After that, use the method file storing this calibration curve to change unspiked sample [Type] to [Unknown Sample] and perform post-run analysis. A quantitative calculation result can then be obtained.

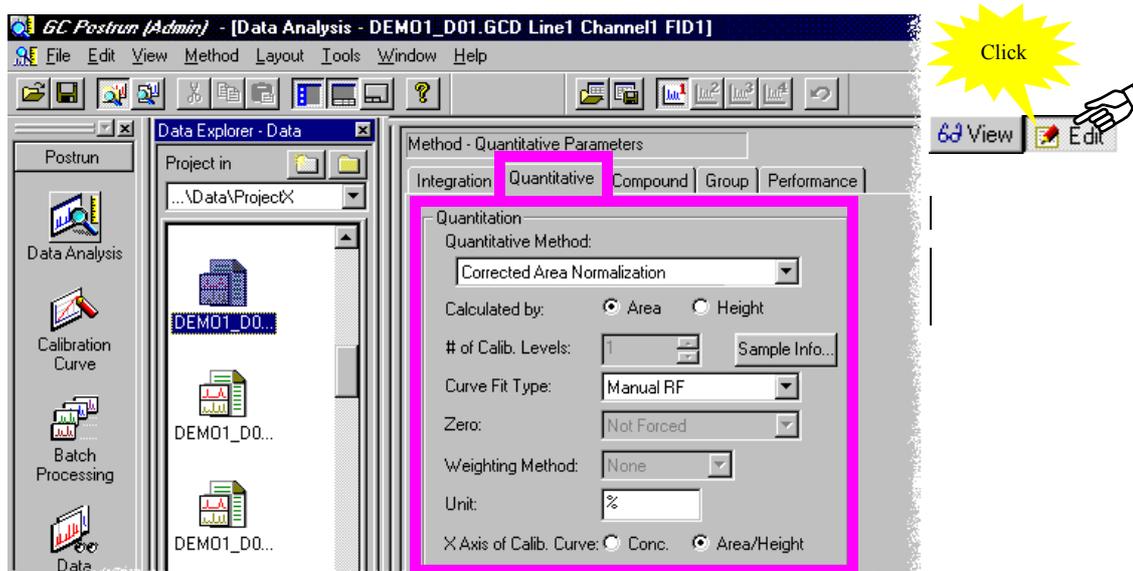
6 Quantitation Parameter Settings

6.5 Setting Quantitation Parameters - Manual RF Method

Here, a method is described to manually enter factors to perform quantitation. This method is used to perform quantitation using known sensitivity factors.

6.5.1 Setting Quantitation Parameters

Linear calibration curve coefficients can be used for [Manual RF] curve fit type.



About quantitative methods, refer to Reference Manual "16.3 Quantitation Method" and "16.4 Calibration Curve".

6.5.2 Setting Compound Tables

Enter factor in each compound's [RF] and [Y(0)] cells.

Method - Compound Table						
Integration	Quantitative	Compound	Group	Performance		
ID#	Name	Type	Ret. Time	RF	Y(0)	
1	n-PrOH	Target	2.320	0.012	3.45	
2	isoBuOH	Target	3.170	0.011	3.41	
3	isoAmOH	Target	5.080	0.01	3.37	

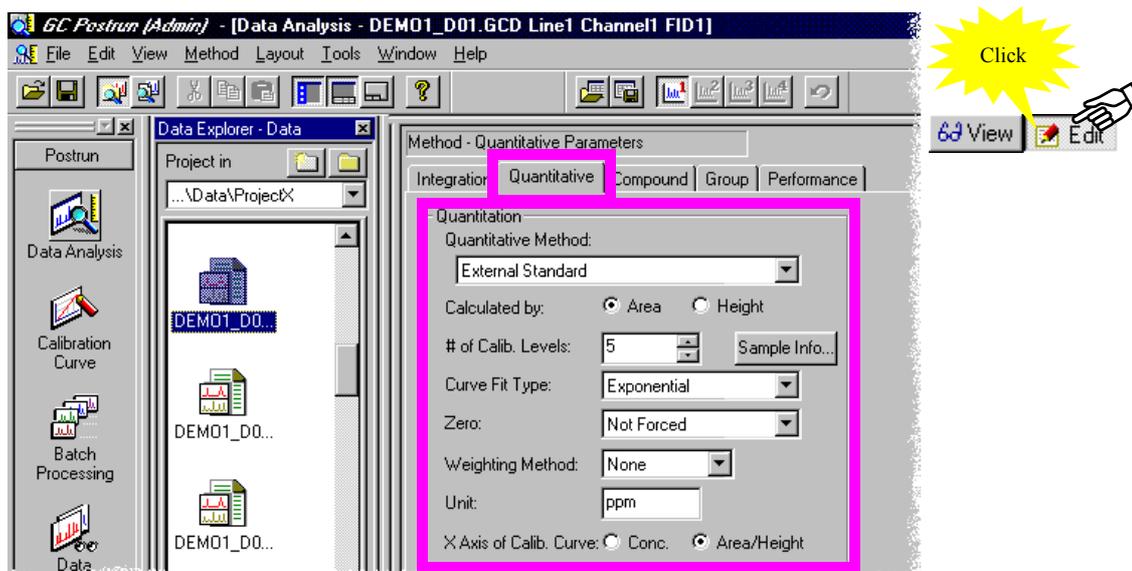
6 Quantitation Parameter Settings

6.6 Setting Quantitation Parameters - Exponential Method

This section explains the settings required when performing quantitation using the Exponential Function.

This method is used for quantitation where sample concentration and sensitivity values are not proportional, such as S-detection using a flame photometric detector (FPD).

6.6.1 Setting Quantitation Parameters



About quantitative methods, refer to Reference Manual "16.3 Quantitation Method" and "16.4 Calibration Curve".

6.6.2 Setting Compound Tables

For data settings required for the compound table's other items, use the same procedure as used for other quantitative methods.

Note: After creating a calibration curve with the [Curve Fit Type] designated as [Exponential], the graph display in the <Calibration Curve> window will change to natural logarithmic display.

Method - Compound Table						
ID#	Name	Type	Ret. Time	Conc. 1	Conc. 2	
1	Comp.A	Target	2.320	1	10	ppm
2	Comp.B	Target	3.170	1	10	ppm
3	Comp.C	Target	5.080	1	10	ppm

6 Quantitation Parameter Settings

6.7 Setting Quantitation Parameters When "Grouping"

Similar types of compounds, such as homologues and isomers, can be grouped, for which the contents can be obtained. This method is called "grouping".

Grouping is effective to use when you are classifying all the peaks to perform quantitative calculation for each group, or when collecting all impurities contained in a main component into one group to measure its total amount.

The section explains how to set the parameters required to perform quantitation using grouping.

Note: Identifying/quantitating a group of peaks that fall within a band width by setting it wider and [Peak Select] to [All Peaks] in the [Identification] parameter setting is another kind of grouping. This technique is useful for quantitating neighboring peaks as one group of peaks. In that case, however, you can identify and quantitate peaks using a compound table alone, so you have no need to set up a group table, so it is different from the grouping that this section describes.

6.7.1 Setting Quantitation Parameters When "Grouping"

The screenshot shows the 'Method - Quantitative Parameters' dialog box in the GC Postrun software. The 'Grouping' dropdown menu is highlighted in pink and set to 'Group Calibration'. A callout box points to it with the text: "Select either [Group Calibration] or [Conc. Summation].". A yellow starburst with the word "Click" and a hand icon points to the "Edit" button in the top right corner of the dialog box.

For more about quantitative methods, refer to Reference Manual "16.3 Quantitation Method".

Note: Two options are available for the "grouping" settings:

- **Group Calibration:**
Quantitation is performed creating a calibration curve for each group by totaling the grouped compounds' peak area or peak length values.
- **Concentration Summation:**
After creating a calibration curve and performing quantitation for each compound, the grouped compound's concentration values are totaled as the group's concentration value.



Note: When performing group calibration, the same correction factor is used for all grouped compounds. Therefore, if the compound correction factors are vastly different from each other, the group calibration method cannot be used.

6.7.2 Creating Compound Tables

When using grouping, enter the same [Group ID #] for all compounds to be grouped in the compound table.

In this example, Comp.A and Comp.B are grouped as Group ID #1, and Comp.C and Comp.D are grouped as Group ID #2.

Method - Compound Table

ID#	Name	Type	Ret.Time	Conc.1	Group ID#
1	Comp.A	Target	2.320	2	1
2	Comp.B	Target	3.170	2	1
3	Comp.C	Target	5.080	2	2
4	Comp.D	Target	6.565	2	2

Enter same number for [Group ID #] of all compounds to be grouped.

6.7.3 Creating Group Tables

Enter group name, ID and other in [Group] table for each [Group ID #]. Then, [Group Calibration] case, enter standard sample concentration value for each group.

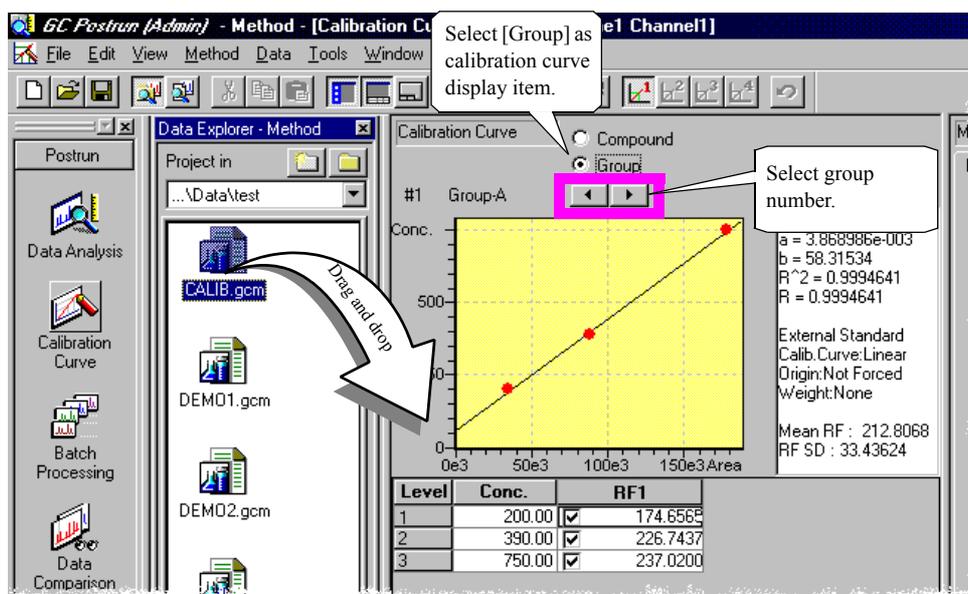
If you use group calibration using the internal standard method, you also need to set an internal standard substance (type ISTD) and ISTD group in the same way with the compound table.

Method - Group Table

Group ID#	Name	Conc.1	Conc.2	Conc.3
1	Group A	200	400	600
2	Group B	200	400	600

6.7.4 Checking Group Calibration Curves

Load the method file and select [Group] calibration curve on <Calibration Curve>.



Note: Clicking the [Group ID #] for the desired <Method> view area can also be used to designate a group number.

6.7.5 Checking Quantitation Results for Each Group

The result is shown on <Group Result> tab on <Data Analysis>.

The screenshot shows the GC Pestrun software interface. On the left, the 'Data Analysis' icon is highlighted with a yellow starburst and the word 'Click'. In the center, the 'Data Explorer' window shows a file named 'CALIB01.gcd' being dragged into the main workspace, with a white arrow and the text 'Drag and drop'. The main workspace displays two chromatograms. The top chromatogram has a peak at 0.345 minutes. The bottom chromatogram has a peak at 0.997 minutes. Below the chromatograms, the 'Results - Group Results' table is displayed, which is highlighted with a pink border. A callout box points to this table with the text 'Check results displayed in [Group Results] table.'.

Group#	Name	Conc.	Unit
1	Group-A	125.62062	ppm
2	Group-B	133.44790	ppm



7.1.2 Setting the Injection Volume and Multi-Injection Count

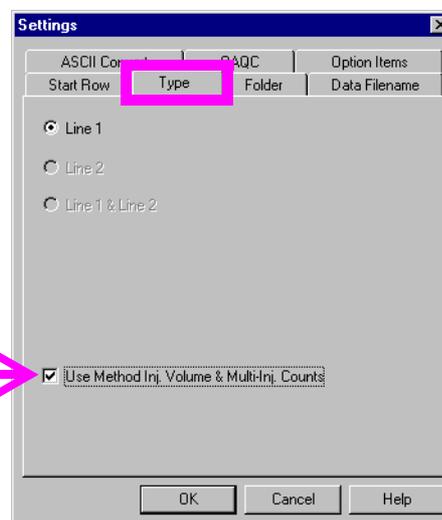
Set the sample injection volume and multi-injection count in a batch table using the following procedure.

The method file's sample injection volume and multi-injection count will be used as default values.

1. Click the [Settings] icon on the [Batch] Assistant Bar to call up the [Settings] window.
2. Select the [Type] tab.
3. Remove the check mark from the [Use Method Inj. Volume & Multi-Inj. Counts] check box.
4. Click [OK].
5. The display condition (displayed or hidden) for injection volume and multi-injection items can be selected using the batch table style settings.

Note: The settings designated in the <Settings> dialog box are stored per batch file.

<Settings>



7.1.3 Bracket Analysis

Select the type of bracket analysis.

❖ Overlap

Based on a calibration curve created from standard samples analyzed before and after a batch of unknown samples, each unknown sample is quantitated.

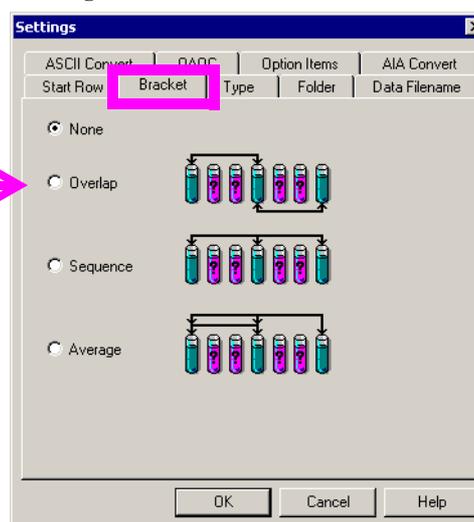
❖ Sequence

Based on a calibration curve created from all the standard samples regardless of their positions, each unknown sample is quantitated.

❖ Average

Based on a calibration curve determined by the average of the calibration curves created from the standard samples analyzed before and after a batch of unknown samples, each unknown sample is quantitated.

<Settings>



Note: In the bracket analysis, a calibration curve is redrawn before an unknown sample is quantitated regardless of whether or not it is sandwiched by standard samples.

Note: You can also open this setting screen from the <Standard Locations> screen of <Batch Table Wizard>.

Note: The setting is saved in each batch file.



7.1.4 Using Two Lines to Perform Batch Analysis

Perform real-time batch processing with two lines by selecting an analysis environment with two lines in the <System Configuration> window.

1. Click the [Settings] icon on the [Batch] Assistant Bar to call up the [Settings] window.
2. Select the [Type] tab.
3. Select [Line 1 & Line2].

Note: This option will appear dimmed if the two-line system configuration has not been set up, and indicates you cannot select it.

Note: The <Batch Table Wizard> can also set for this setting.

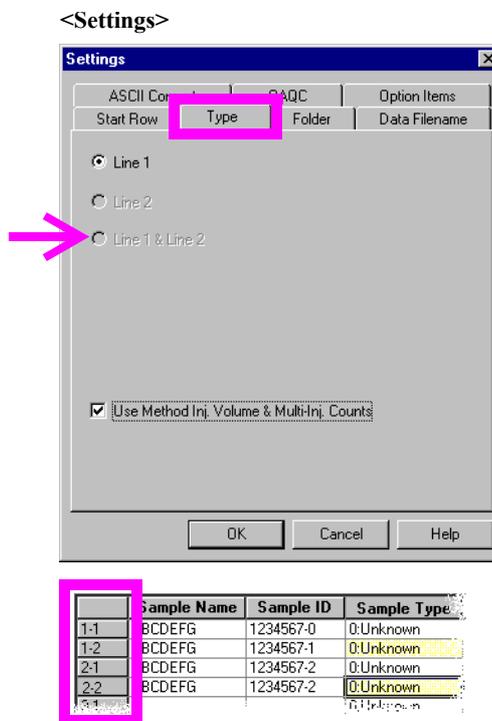
When selecting batch processing that uses two lines, the batch table row's number display will change to a [Row number + Line number] format, i.e. "1-1", "1-2", "2-1", "2-2", and data edit and processing will be performed two rows at a time (synchronous start).

Note: Since data edits will be performed two rows at a time, if you use the [Insert Row] function, two new rows will be inserted between a correct pair of rows. To use the [Delete Row] function, you must select two correct rows as a pair. To perform these operations smoothly, choose [Select Row] from a right-click menu to extend the current row range to include the new correct pair of rows.

Note: The following batch table items have setting limitations for both lines (for items set as two rows) or for Line 2.

- Limitation for both lines:
Sample type, method file, level, system check, user program, action.
- Limitation for Line 2 only:
Run mode (only [Process] - [Data Acquisition] and [Data Processing] can be used to set this mode).

Note: The settings designated in the <Settings> dialog box are stored per batch file.





7.1.5 Setting the Baseline Data File

A "baseline data file" is data called "background chromatogram". These chromatograms are subtracted from the targeted chromatogram during data processing. This is used to remove blank peaks as well as any components that deviate from the baseline in a particular pattern.

To process data with only one real-time batch processing run, set the parameters so that the baseline data will be acquired in a batch row above the row where the baseline data is being used.

Data must be acquired before using as baseline data.

	Vial#	Run Mode	Method File	Data File	Baseline Data File	Report
1	10	AQ	Test.gcm	BASELINE_D32.GCD		<input type="checkbox"/>
2	1	AQ DP	Test.gcm	DEMO1_D01.GCD	BASELINE_D32.GCD	<input checked="" type="checkbox"/>
3	2	AQ DP	Test.gcm	DEMO1_D02.GCD	BASELINE_D32.GCD	<input checked="" type="checkbox"/>
4	3	AQ DP	Test.gcm	DEMO1_D03.GCD	BASELINE_D32.GCD	<input checked="" type="checkbox"/>
5	4	AQ DP	Test.gcm	DEMO1_D04.GCD	BASELINE_D32.GCD	<input checked="" type="checkbox"/>

7 Batch Processing

7.2 Performing Post-run Analysis

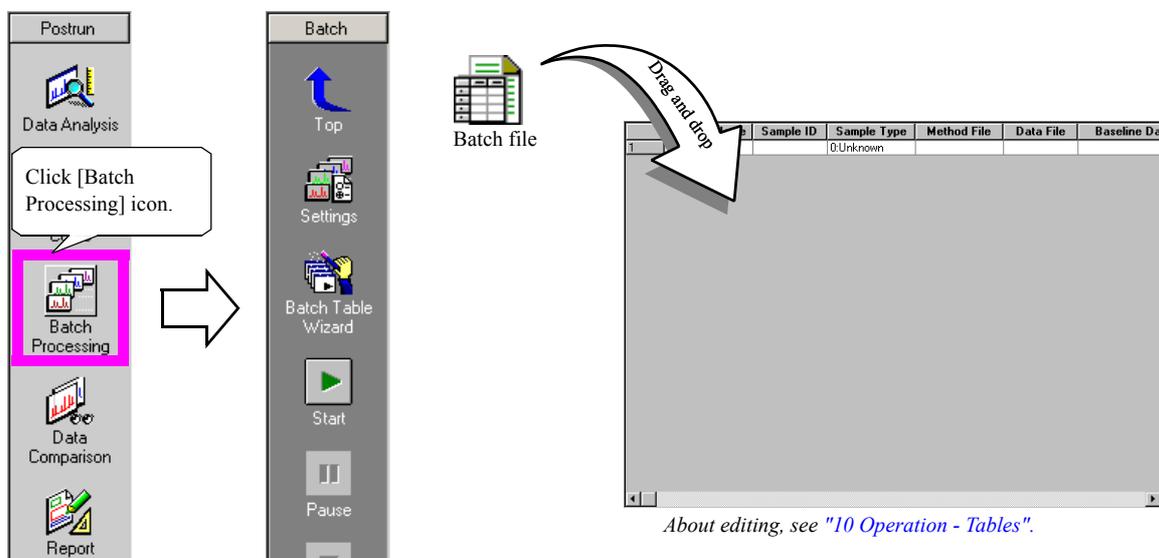
Continuous post-run analysis can be performed for the selected multiple data files where data acquisition has been completed.



GC Postrun

If the <GC Postrun> application has not started yet, click the [GC Postrun Analysis] icon on the [Operation] tab.

7.2.1 Displaying a <Batch Table> Window to Open Batch Files



You can perform a batch post-run analysis using not only batch files created in the <GC Postrun> screen but also ones used for a batch analysis.

To run a post-run analysis on a number of data files at once, the batch table is handy for the purpose, although it is still possible to do so one date by one data in the <Data Analysis> screen.

When an analysis batch file is loaded as a post-run batch file, GC-related items listed below are not shown. On the other hand, when a post-run batch file is loaded as an analysis batch file, the items below are allocated the default values or left blank. To remake it as an analysis batch file, you need to edit it in <Batch Table> of the <GC Real Time Analysis / Analysis Editor>.

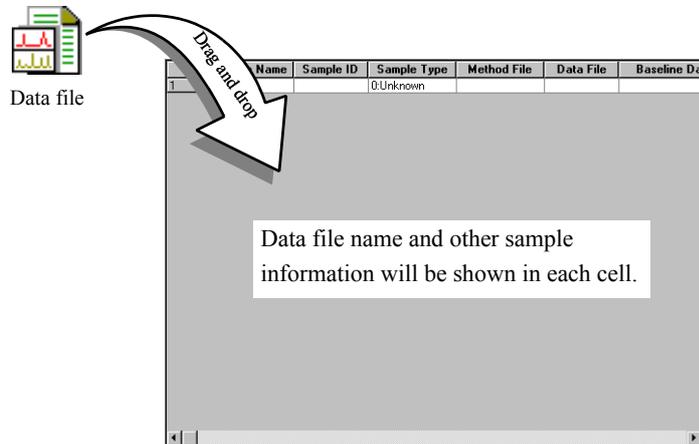
Items not shown in the batch table of <GC Postrun> are:

Vial#, Inj. Volume, Multi-Inj, System Check, User Prog. (before data acquisition)

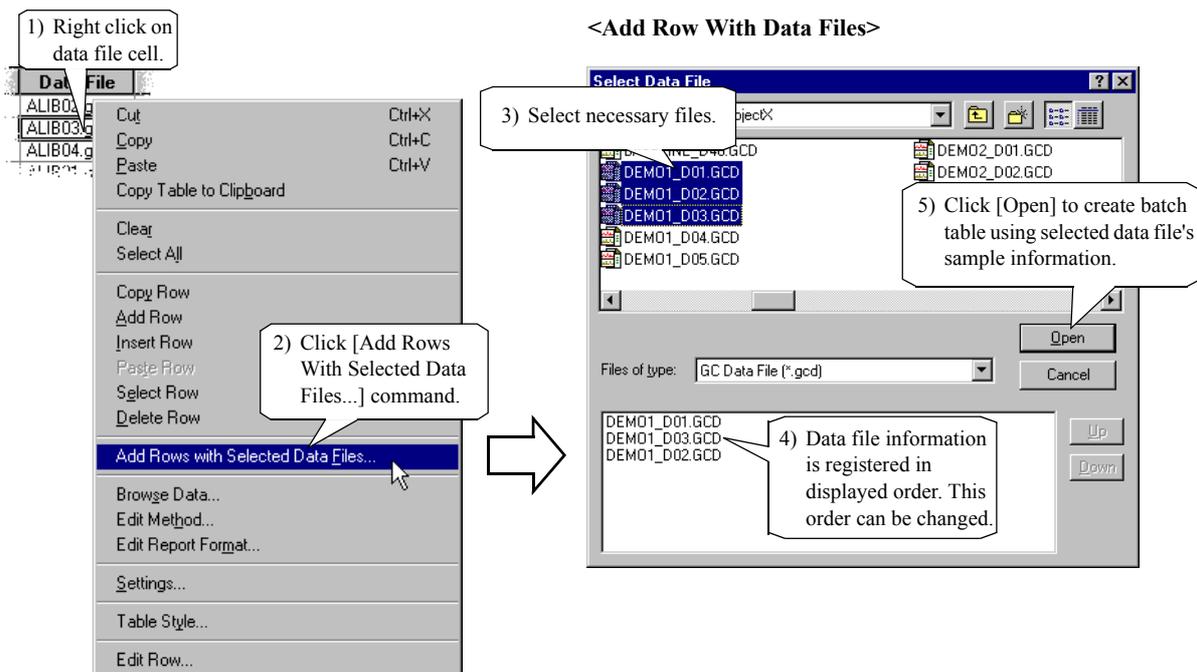
7.2.2 Selecting Data Files Used to Create a Batch Table

Drag and drop a data file onto the batch table, it will be added at the bottom row.

Click data files with [Ctrl] or [Shift] key pressed, multiple files can be selected and added by drag and drop at once.

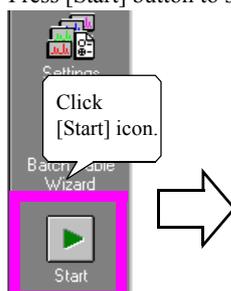


You can use [Add Rows with Selected Data Files] to add multiple data files in the order of your choice.



7.2.3 Performing Batch Processing

Press [Start] button to start a batch processing.



The row under data processing is shown in the reversed color.

	Sample Name	Sample ID	Sample Type	Method File	Data File	Baseline
1	Standard Sample	STD-0001	1:Standard(I)	Test.gcm	est001.gcd	
2*	Unknown Sample	UNK-0001	0:Unknown	Test.gcm	est002.gcd	
3	Unknown Sample	UNK-0002	0:Unknown	Test.gcm	est003.gcd	
4	Unknown Sample	UNK-0003	0:Unknown	Test.gcm	est004.gcd	

7 Batch Processing

7.3

Perform Additional Analysis During Real-time Batch Analysis

While a batch analysis is being run, you can pause the analysis and edit the batch table or add samples to analyze using the batch queue feature in <GC Real Time Analysis>.

7.3.1 Pause and Edit the Table

To add batch rows to the batch table currently running, click [Pause] on the Assistant Bar. In the batch table being paused, you can add, delete, and edit rows after the row where the analysis has been paused. After editing, click [Pause] on the Assistant Bar again to resume the analysis starting from the paused batch row.

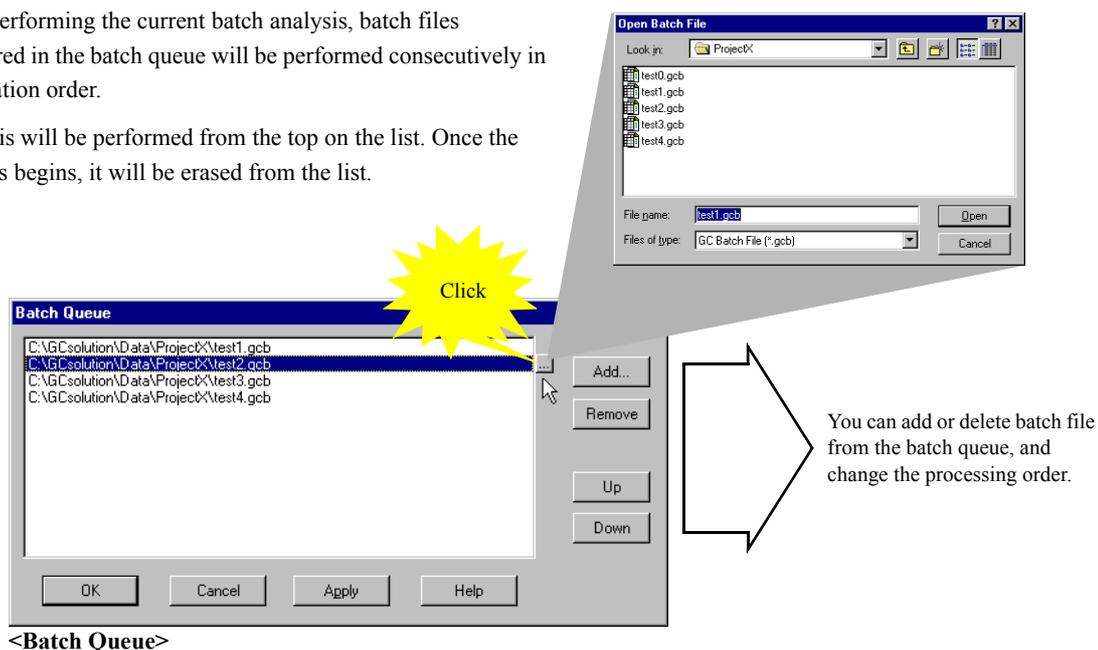
Note: If a batch is completely stopped using the [Stop] icon on the Assistant Bar and then resumed from the following batch row, some of the information will be cleared, such as the QA/QC function's criteria checking. Therefore, some actions may differ from those present when using [Pause].

7.3.2 Using Batch Queue

Another real-time batch processing task can be added to a batch queue during the current real-time batch analysis.

After performing the current batch analysis, batch files registered in the batch queue will be performed consecutively in registration order.

Analysis will be performed from the top on the list. Once the analysis begins, it will be erased from the list.



Note: For the Single Run analysis, the batch queue is not available.

Note: The setting of the batch queue will be deleted when <GC Real Time Analysis> is closed.

7 Batch Processing

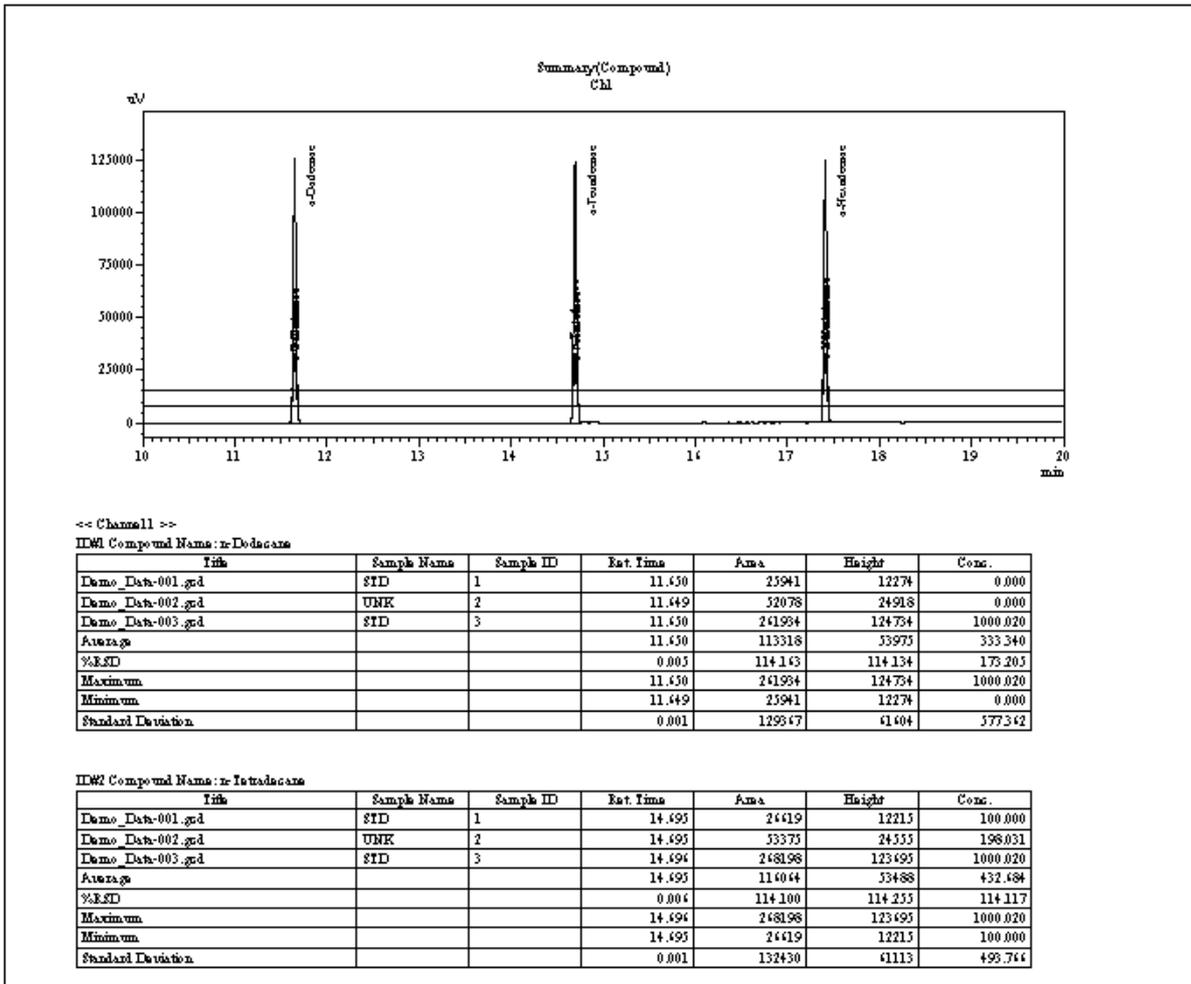
7.4 Summary Report

Summary report is a simple report format to report chromatograms and peak tables of two or more analyses.

The summary report comes in two variations:

[Conc.] : Shows concentration, area, and height of the result in one view.

[Compound] : Shows the peak information for each of the compound peaks, such as concentration and column performance.



7.4.1 Creating summary report

You can create a summary report using the procedure similar to the one described in "8 Report Functions". The following is the procedure for creating a summary report for post-run batch processing.

1. Select one of the [Summary] report items in <Report>, then create a report format.



Summary(Conc.) Summary(Compound)

2. Open the <Batch Table> screen and then a batch file.



3. Specify [Summary Type] and [Summary Report Format File] in the <Batch Table> screen.

Specify [Summary Start] to the data row at which you wish to start reporting in a summary report and select a predefined summary report format file. Set a report format file only to the starting row.

Next specify [Summary Run] to rows you wish to include in the summary report and [Summary End] to the last row to include in the report.

For example, if the setting is made as shown below, a summary report lumping the data of 01, 02, and 04 will be printed using the format in Summary.gcr when the batch is run.

	Sample ID	Method File	Data File	Summary Type	Summary Report Format File
1	01	External.gcm	Data-02.gcd	Summary Start	Summary.gcr
2	02	External.gcm	Data-03.gcd	Summary Run	
3	03	External.gcm	Data-04.gcd	None	
4	04	External.gcm	Data-05.gcd	Summary End	

4. Check the batch table setting, and click the [Start] icon on the Assistant Bar or the screen top to start the batch processing.

After the batch processing is completed, the summary report file set up here will be printed out.

Note: For bracket analysis, if there are both standard and unknown samples between "Summary Start" to "Summary End", some data cannot be printed out in a summary report.



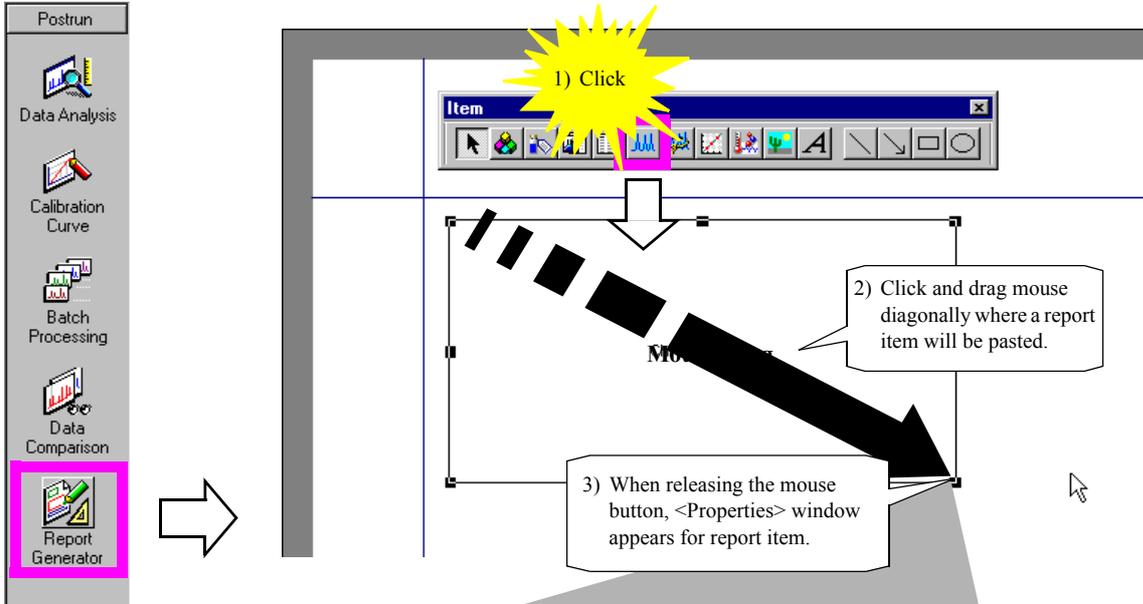
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8 Report Functions

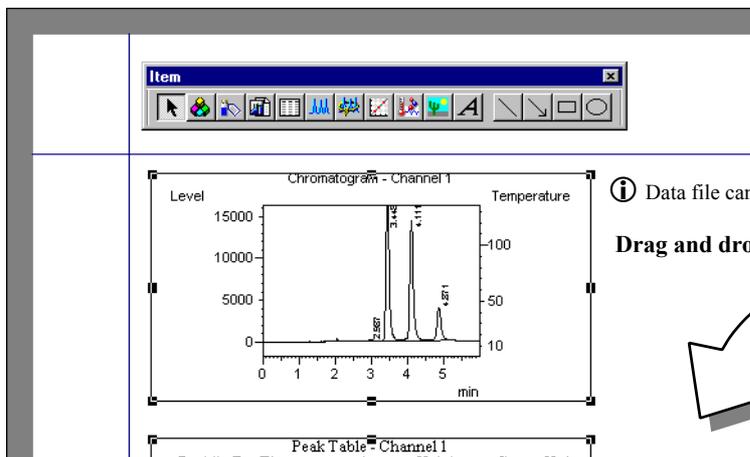
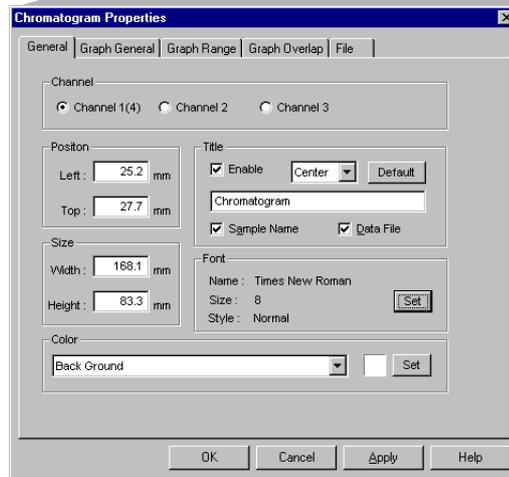
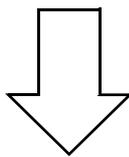
8.1 Creating Report Files

8.1.1 Adding report items

On the <Report> an existing report format can be loaded and edited, or new format can be created.

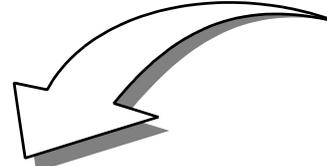


Note: The number of <Properties> screen tabs and settings are vary depending on the type of report items.



ⓘ Data file can be loaded to check the format.

Drag and drop file icon to read in.

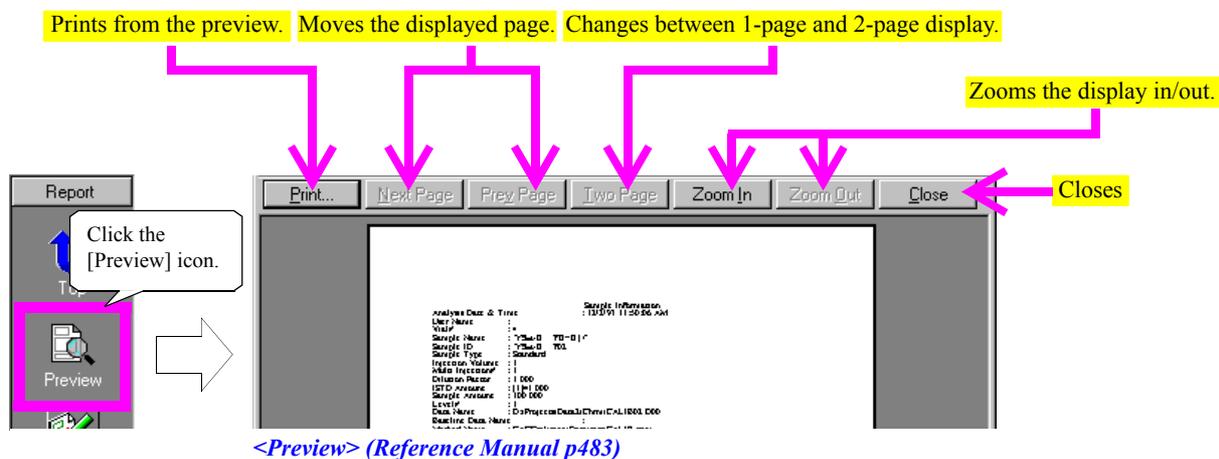


Data file



8.1.2 Checking the Print Image

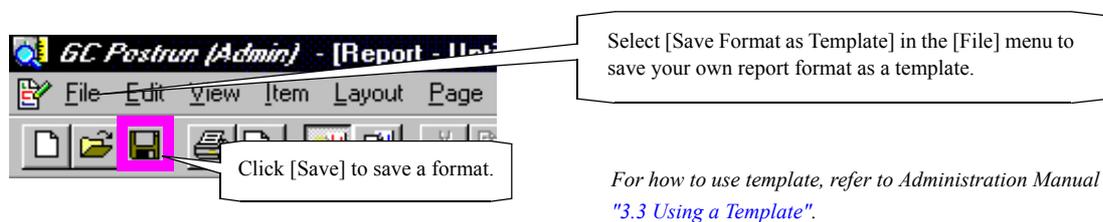
The printed result might be different from the format you created. You can check the printing image on the screen using the preview feature.



i This icon is also found on the toolbar 

8.1.3 Saving the Report Format File

Save the report file after editing.



8 Report Functions

8.2 Adjusting the Report Layout

This section explains how to edit and adjust a report layout using the report format created in the previous section.

8.2.1 Adjusting with Mouse or Properties

Clicking the mouse on a report item will select that item and enclose it with a solid lined square with eight ■ marks at its four corners and on the four sides.

The size of the report item can be altered with this status.

Double-click

With the mouse, drag the ■ mark to change the report item size.

Double-clicking the report item will display each item's <Properties>.

Here, you can edit format information, including the report item's correct size and position.

① The following area widths are required to print each data file's report items using the default font size (Times New Roman, 8 point).

Report Item	Standard print area width
System Configuration	Approx. 150 mm
Sample Information	Approx. 100 mm (depend on the string length like sample name)
Method	Approx. 170 mm (entire width of A4-size sheet)
Peak Table	Approx. 140 mm
Chromatogram	Approx. 60 mm (Width to draw Y axis and scale + α)
Group Results Table	Approx. 100 mm
Calibration Curve	Approx. 110 mm (minimum width is 50 mm but without Header Information.)
Status Information	Approx. 165 mm

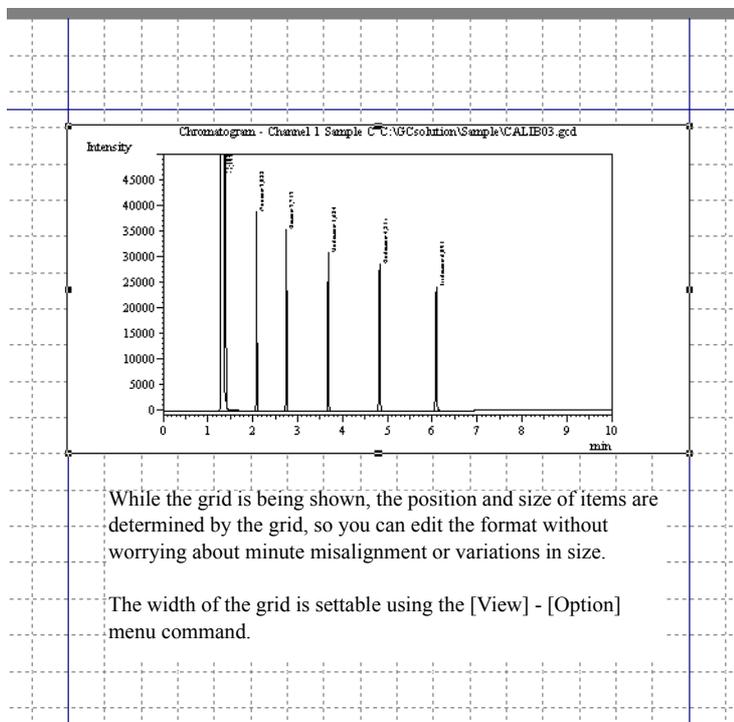


8.2.2 Using the Grid

By placing printing items using the grid, you can specify the position and size of items quickly.

- 1) Click [View] - [Grid] menu command.
(The grid appears on the screen.)
- 2) If an item is placed or resized when the grid is shown, its position or size is determined according to the grid.
- 3) Click [View] - [Grid] menu command once again to hide the grid.

This grid is just for editing, not printed even if it is shown on the screen.



8.2.3 Adjusting Multiple Report Item Sizes and Positions

If no report items have been selected, then drag the mouse to enclose multiple report items. Those report items will then be selected.

Clicking multiple report items while holding down the [Shift] key can be used to select multiple report items.

Once multiple report items are selected, they can be dragged and moved simultaneously, making it very easy to create a well-arranged report format using the following layout menus.

Also, report item display layers can be changed in the [Layout] menu.

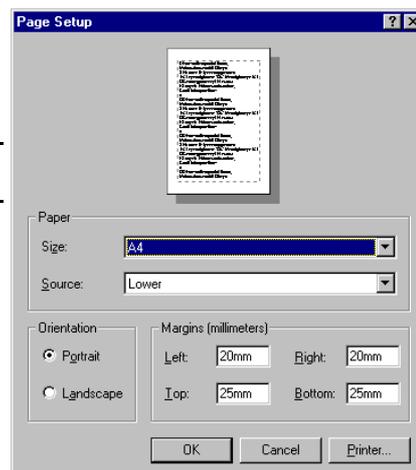
Layout Menu	Function
 Align/Left	Moves and aligns the left sides of selected report items with each other.
 Align/Right	Moves and aligns the right sides of selected report items with each other.
 Align/Top	Moves and aligns the tops of selected report items with each other.
 Align/Bottom	Moves and aligns the bottoms of selected report items with each other.
 Make Same Size/Width	Aligns the widths of selected report items with each other.
 Make Same Size/Height	Aligns the heights of selected report items with each other.
 Make Same Size/Both	Aligns both the widths and heights of selected report items with each other.
Order/Bring To Front	Moves the selected layer for a report item to the top.



Order/Send To Back	Moves the selected layer for a report item to the bottom.
Order/Bring Foreground	Moves the selected layer for a report item one level up.
Order/Send Background	Moves the selected layer for a report item one level down.

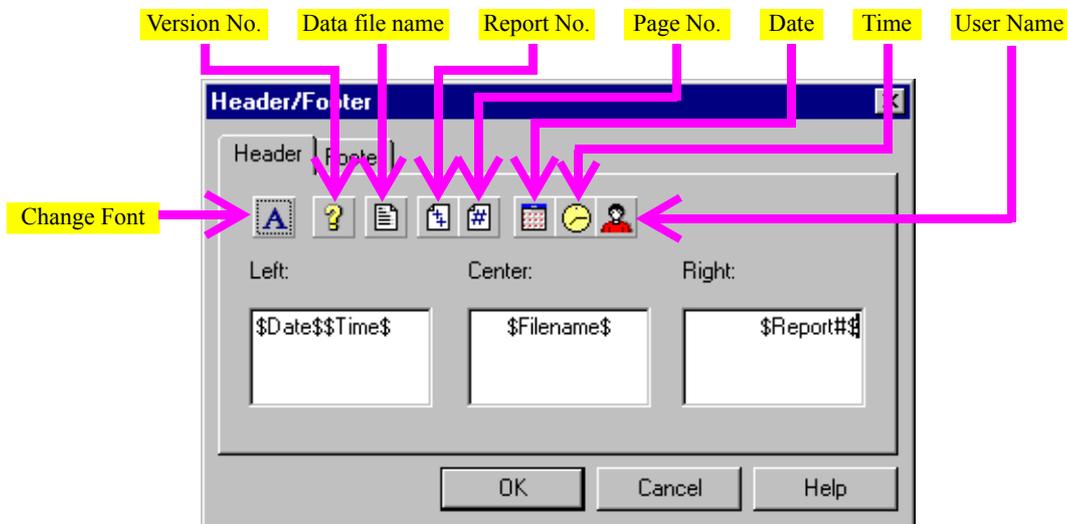
8.2.4 Setting the Page Size/Margin and Other Items

Use <Report>'s menu - [File] - [Page Setup] to call up the <Page Setup> window.



8.2.5 Setting the Header/Footer

1. Use <Report>'s menu - [Display] - [Header/Footer] to call up the <Header/Footer> window.
2. Select a position to add information from among [Left], [Center], and [Right].
3. Click the desired information button, and then a command to add the desired information will appear in the selected position field.
4. Click [OK].



<Header/Footer> (Reference Manual p400)

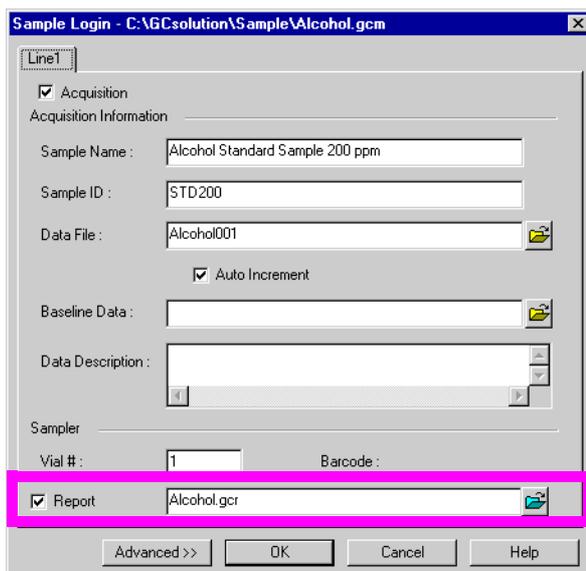
8 Report Functions

8.3 Printing Analysis Result

Report format file can be used for printing analysis result during the following data processing/operations.

8.3.1 Printing Reports in Single Run Analysis

If you have set <Sample Login> to print out the report and run the single-run analysis, a report will be printed at the end of the analysis.



8.3.2 Printing Reports in <Batch Table>

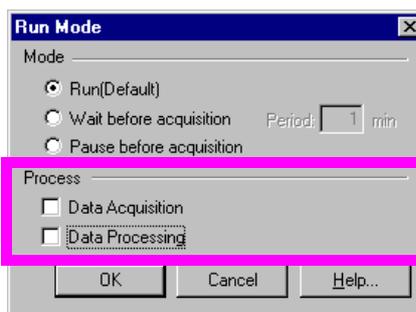
The batch table allows you to specify which rows to print report.

The rows for which a report format file has been specified and the [Report Output] check box has been check-marked are printed in the report.

Batch table

Report Output	Report File
<input checked="" type="checkbox"/> Print	test.gcr

In the case of the batch data reprocessing, if all [Process] item check marks in the <Run Mode> window are removed, even though no processing is performed during a batch run, all reports will be output at one time if the report output function is selected.



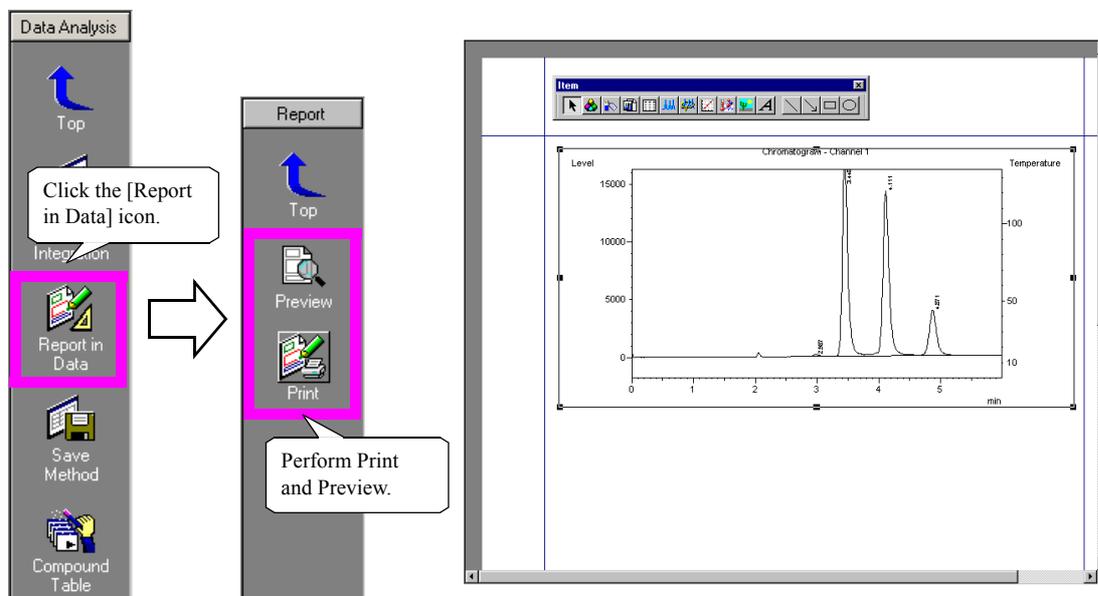
<Run Mode> (Reference Manual p364)



8.3.3 Printing Reports in <Data Analysis>

To call up the <Data Analysis> window, click the <GC Postrun> Assistant Bar's icon and drag-and-drop the desired data file from <Data Explorer> to open the file.

Print the reports for the data file using the following procedure after performing your desired processing on the file or as it is.



In <Data Analysis>, the report format stored in the data file is used for printing.

A report format is stored in data file at the time of data acquisition and retained within thereafter. Clicking the [Report in Data] icon opens the format stored in the current data file. You can edit this format and print the data using the edited format.

- ① You can drag-and-drop a report format file into the <Report> window from the Data Explorer to load the report format. As this report format is loaded into the report format area within the data file currently open, the data file itself is still active, which allows you to print the reports for it.

The report format is saved in the data file, which allows you to print the reports using the same format.



Note: The saved format will be reflected in a data file that has been read into memory. Save the format separately to save as a data file.

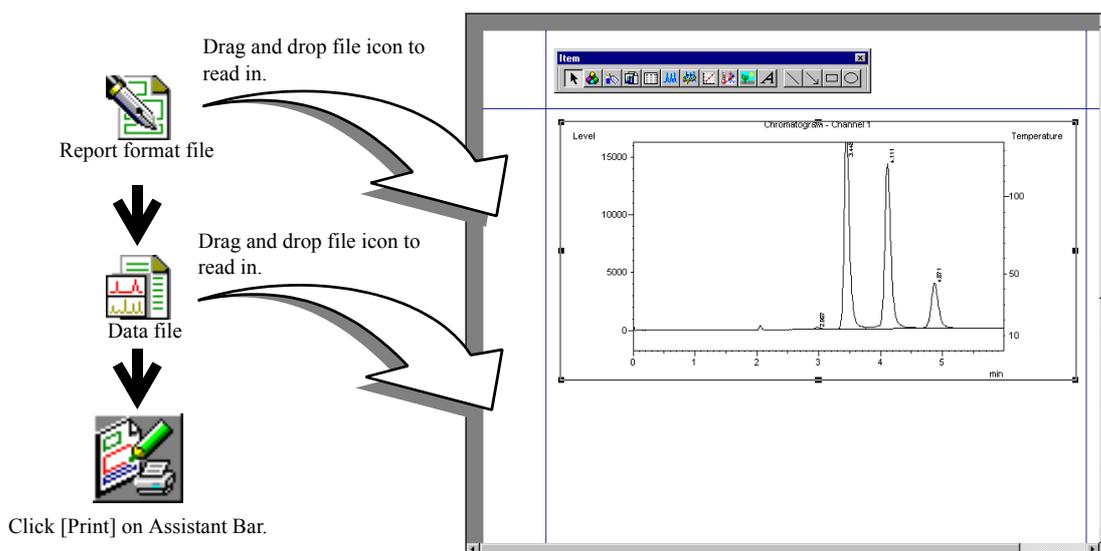


8.3.4 Printing Reports in <Report>

To print the report for a data file using a report format file, use the following procedure.

Using this procedure allows you to print the report independently from the report format retained in the data file. This feature is useful when you wish to print the report using the format different from the one retained in the data file without changing the data file itself.

You can also drag-and-drop data file icons into the <Report> window from the Data Explorer to view their report images.



In the above operations, one data file is displayed for all the items, however, you can set different data files to the printing items. To do so, specify a data file in the <File> tab sheet of the properties screen for the printing items. You can thus print multiple data items on a single report.

If you drag and drop an data file onto a summary (concentration/compound) item, different from the above, that data is added to the summary item, thus allowing you to create a summary report easily.

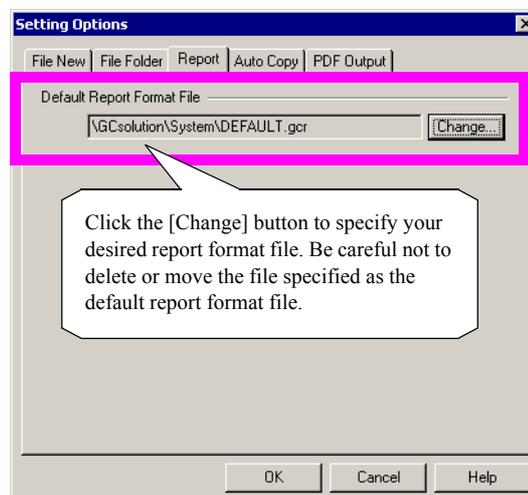
8.3.5 Default report format

If you print a report for single-run analysis or batch analysis without specifying a report format file, the default report format is used for printing.

You can specify the default report format by selecting the [Tools] - [Option] command from the <GC Real Time Analysis> screen.

The report format specified here will be used for printing when the items whose check box for reporting has been check-marked without format file specified in <Sample Login> or <Batch Table> of <GC Real Time Analysis>.

Note: When the format file field is left blank and printing is instructed in <Batch Table> of <GC Postrun>, the report formats stored in the respective data files are used for printing after the batch post-run analysis.



9 Operation - Windows

9.1 Displaying Windows and Bars

This software includes the two main programs: <GC Real Time Analysis>, used to set data acquisition parameters; and <GC Postrun>, used to perform analysis on the acquired data. Each program screen consists of multiple application and common windows that contain a variety of functions, as well as other types of windows called "bars" that provide a number of auxiliary functions.

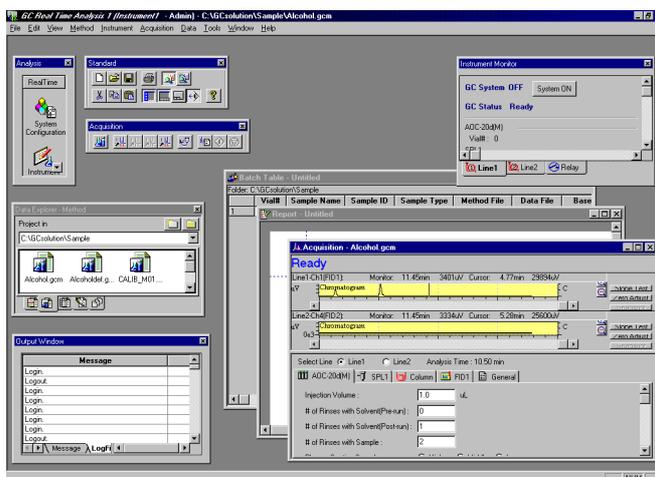
9.1.1 Window Types Appearing in Program Windows

Mainly, windows are classified into two types, application windows that provide main functions, and common windows that provide auxiliary functions.

You can call up common windows in an application window as part of the application window items. Toolbar icons are used to switch the common windows' display status between displayed and hidden.*

* However, the display status for the toolbar must be set using the [Toolbar] command in the [View] menu.

Note: Common windows are sometimes called "windows" and sometimes called "bars". This simply comes from these windows' visual impressions, since all windows (except for the Title Bar and Menu Bar themselves that frame the actual windows) can actually be displayed as windows (see figure on the right).



❖ Window Types (Toolbar icons)

	<GC Real Time Analysis>	<GC Postrun>
Application Windows	<Data Acquisition>	<Data Analysis> <Calibration Curve> <Data Comparison>
	<Batch Table> <Report>	
Common Windows/Bars	<Instrument Monitor> ()	
	<Data Explorer> () <Output Window> () "Assistant Bar" () "Toolbar" (Call up via the menu)	

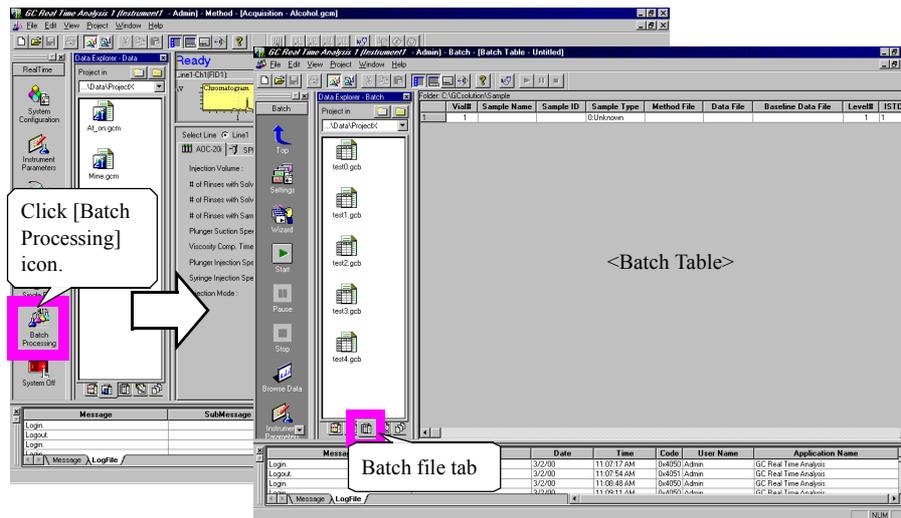
Note: Only application windows have their own toolbar and menu. A menu to be displayed will vary depending on which application window currently active.

9.1.2 Displaying Application Windows

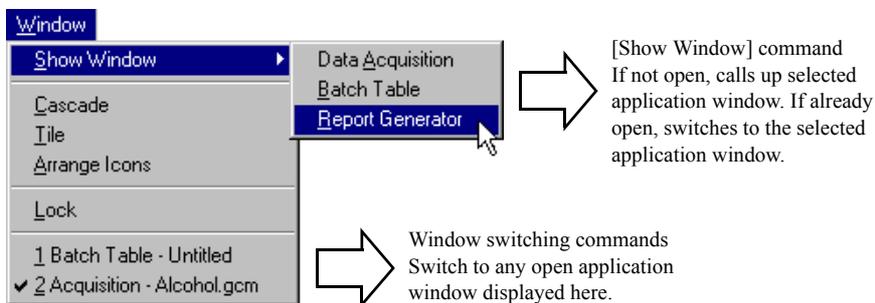
The following windows displayed in a program window can be open or closed using the operations described below:

❖ Using the Assistant Bar:

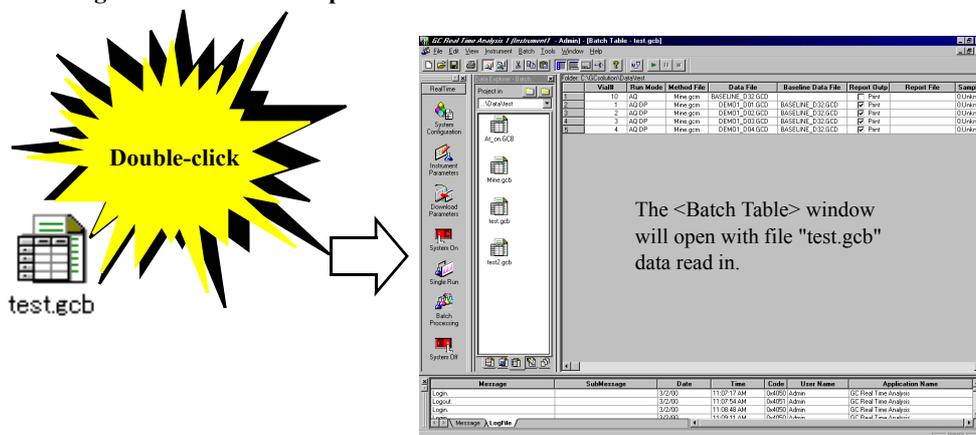
When you perform operations using the Assistant Bars, the start up and switching of application windows, as well as the switching of the Data Explorer file tabs will usually be performed automatically.



❖ Starting an application window using [Window] - [Show Window]



❖ Double-clicking a file in the Data Explorer



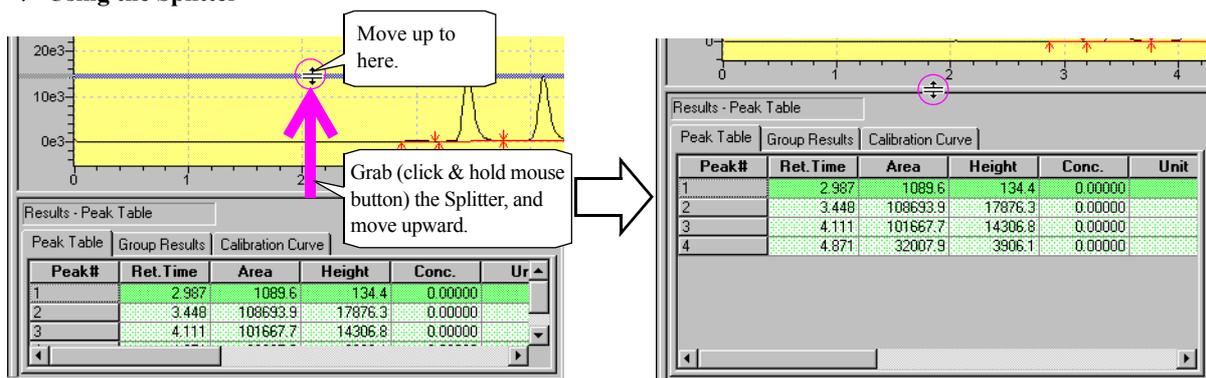
9 Operation - Windows

9.2 Customizing Windows

9.2.1 Changing the View Size

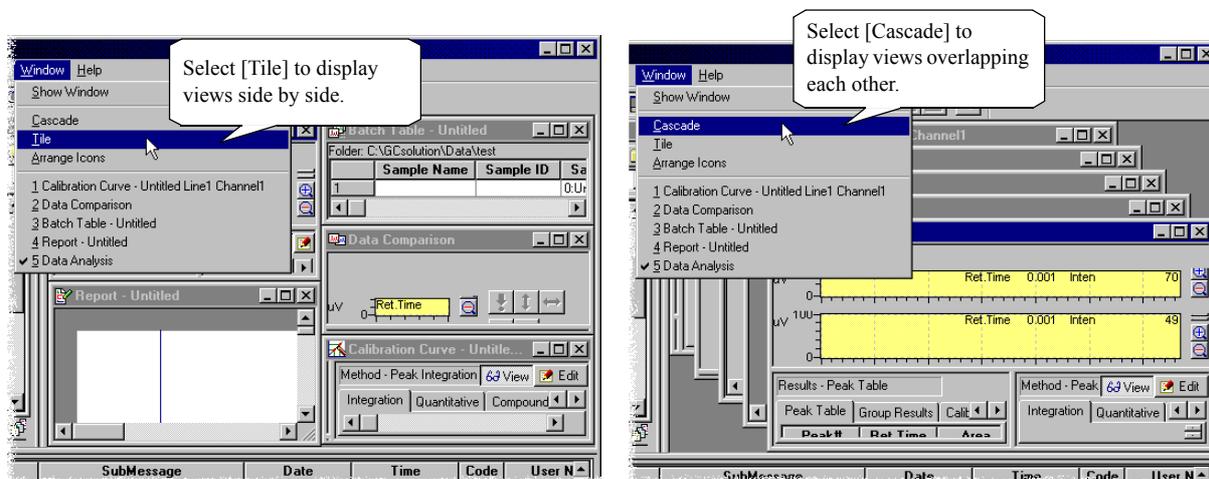
Some application windows consist of a number of "views" that can be displayed in several sections divided by the Splitter. The sizes of these views in each window can be modified using the operations below.

❖ Using the Splitter

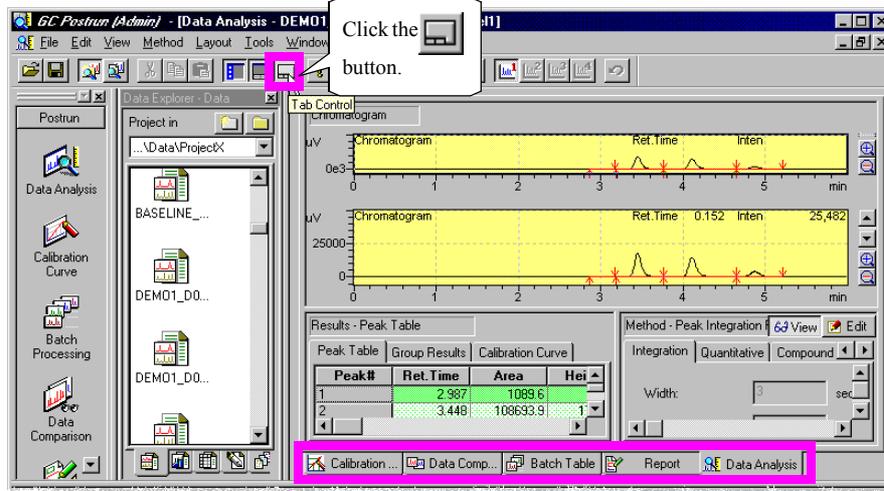


9.2.2 Changing the Application Window Display Format

❖ Displaying in window format



❖ Displaying in tab format

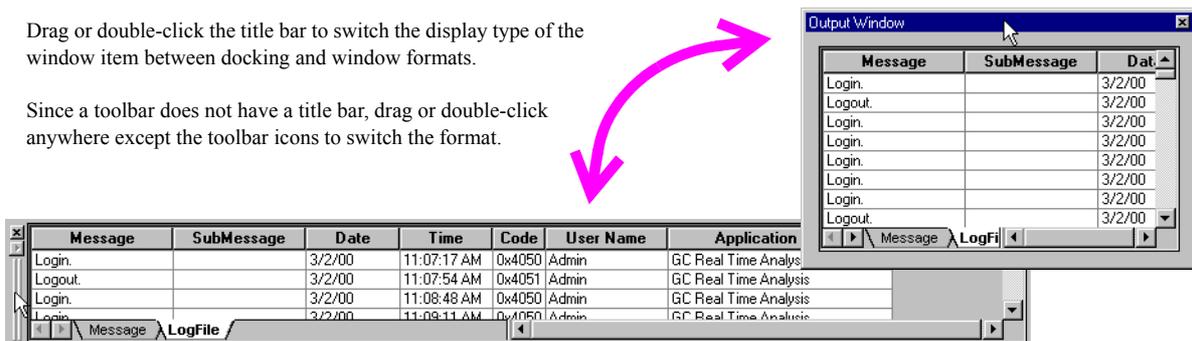


9.2.3 Changing the Common Window Display Format

❖ Displaying in window format

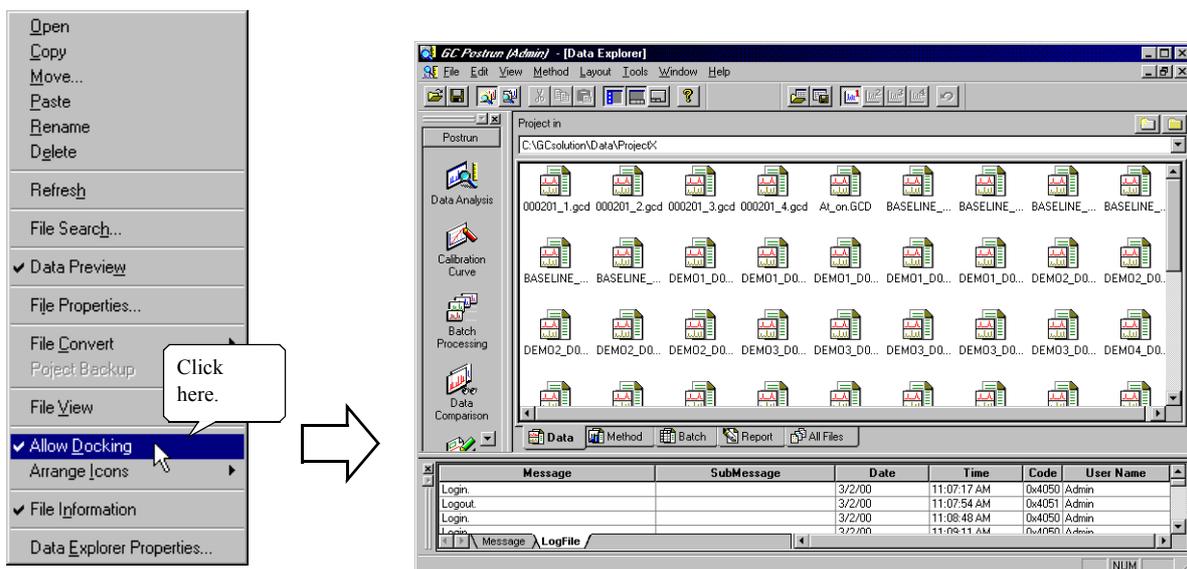
Drag or double-click the title bar to switch the display type of the window item between docking and window formats.

Since a toolbar does not have a title bar, drag or double-click anywhere except the toolbar icons to switch the format.



❖ Maximizing the Data Explorer

Deselect the [Allow Docking] command in the Data Explorer's right-click menu. Common windows will then be handled the same way as application windows, enabling you to display them maximized, side by side ([Tile]), or overlapping ([Cascade]).



10.1 Operation - Tables

10.1.1 Operating Table Columns

This section explains how to work with the columns in a table, using the <GC Postrun> program's <Data Analysis> window - <Method> view - [Compound Table] tab, as an example.

Leftmost gray-colored column is the "Row# column". Cannot delete or move.

A vertical group of cells is called a "table column".

A cell with an item's title displayed is called a "title cell".

Each input field of a table is called a "cell".

ID#	Name	Type	Ret. Time	Band
1	Nonene	Target	2.080	0.200
2	Decane	Target	2.750	0.200
3	Undecane	Target	3.680	0.200
4	Dodecane	Target	4.830	0.200
5	Tridecane	Target	6.090	0.200

10.1.1 Selecting a Table Column

Click [Row#] column's title cell to select entire table.

- Click a title cell to select an entire column.
- Drag multiple consecutive title cells to select all those columns simultaneously.
- While holding down the [Shift (Ctrl)] keys, click multiple consecutive (discrete) title cells to select only those columns.

ID#	Name	Type	Ret. Time	Band
1	Nonene	Target	2.080	0.200
2	Decane	Target	2.750	0.200
3	Undecane	Target	3.680	0.200
4	Dodecane	Target	4.830	0.200
5	Tridecane	Target	6.090	0.200

10.1.2 Changing the Width of a Table Column

Can also change [Row#] column width (but not delete or move.)

- Place cursor on title cell border, and cursor will change to this shape. Drag cursor to change column width.
- Perform while selecting multiple columns, and can change width of all those columns simultaneously.

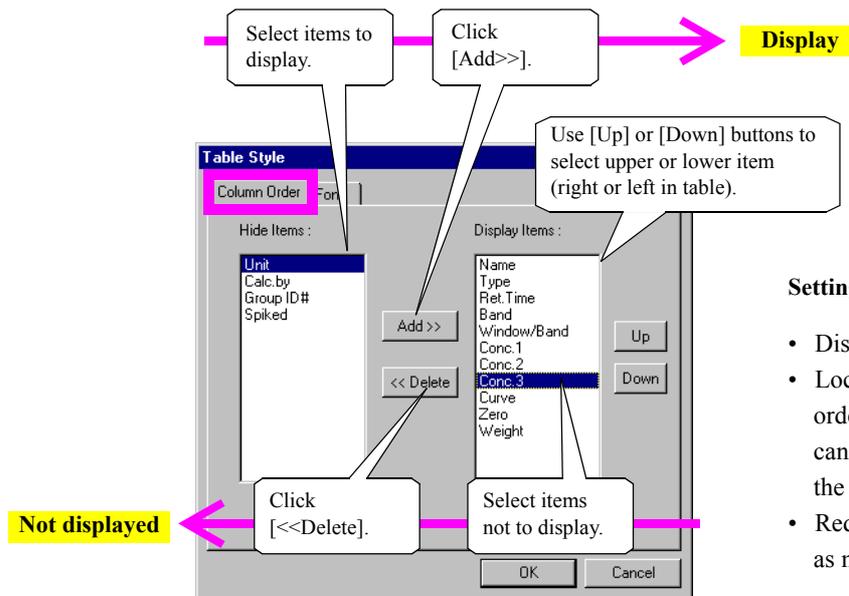
ID#	Name	Type	Ret. Time
1	Nonene	Target	2.080
2	Decane	Target	2.750
3	Undecane	Target	3.680
4	Dodecane	Target	4.830
5	Tridecane	Target	6.090



10.1.3 Changing the Table Column Display Condition (Table Style Settings (1))

Right-click the table to display a pop-up menu. The last (bottom) command in this menu is [Table Style]. Use this command to designate the table column display status (displayed or hidden) as well as the column display order.

Note: For some views displayed in table format, the <Table Style> window will not have a [Column Order] tab.



Setting Points:

- Display only necessary items.
- Locate items in higher frequency order, from the left. (That way, you can view those items without using the scroll bar.)
- Reduce the font size and cell width as much as possible.

<Table Style> - [Column Order] Tab (Reference Manual p567)

Note: In the [Hide Items:] and [Display Items:] lists, to select consecutive items simultaneously, click the first item and then the second one while holding down the [Shift] key. To select discrete items simultaneously, click the desired items while holding down the [Ctrl] key. The multiple selected items can be operated all at once using the [Add>>] or [<<Delete] button. However, to change the item display order with the [Up] or [Down] button, select only one item at a time.

Note: Double-clicking the desired item in either [Hide Items:] or [Display Items:] box moves the item to the other box (same effect as when using the [Add>>] or [<<Delete] button).

10.2 Operation - Tables

10.2 Operating Table Rows

This section explains how to work with the rows in a table, using the <GC Postrun> program's <Data Analysis> window - <Method> view - [Compound] tab, as an example.

Method - Compound Table

ID#	Name	Type	Ret. Time	Band
1	None	Target	2.080	0.200
2	Decane	Target	2.750	0.200
3	Undecane	Target	3.680	0.200
4	Dodecane	Target	4.830	0.200
5	Tridecane	Target	6.090	0.200

Topmost gray-colored row is the "title row". Cannot delete.

Lateral group of cells is called a "table row".

A cell in the [Row#] column is called a "row number cell".

Each input field of a table is called a "cell".

10.2.1 Selecting a Table Row

Method - Compound Table

ID#	Name	Type	Ret. Time	Band
1	None	Target	2.080	0.200
2	Decane	Target	2.750	0.200
3	Undecane	Target	3.680	0.200
4	Dodecane	Target	4.830	0.200
5	Tridecane	Target	6.090	0.200

Click [Row#] column's title cell to select entire table.

- Click a row number cell to select an entire row.
- Drag multiple consecutive row number cells to select all those rows simultaneously.
- While holding down the [Shift (Ctrl)] keys, click multiple consecutive (discrete) row number cells to select only those rows.

Note: As with a batch table used for 2-line continuous analysis, in a table where two rows compose one processing pair, selecting the correct two rows simultaneously is required for editing. In this case, right-click the table to display a pop-up menu and use the [Select Row] command to extend the selected range to include the correct two rows.

10.2.2 Adding/Deleting a Table Row

Method - Compound Table

ID#	Name	Type	Ret. Time	Band
1	None	Target	2.080	0.200
2	Decane	Target	2.750	0.200
3	Undecane	Target	3.680	0.200
4	Dodecane	Target	4.830	0.200
5	Tridecane	Target	6.090	0.200

Click here to enter [Edit] mode.

Right-click table to display pop-up menu.

- Adds a row to end of table.
- Inserts a row immediately above the row where cursor is positioned.
- Deletes the row where cursor is positioned and moves up the row beneath.

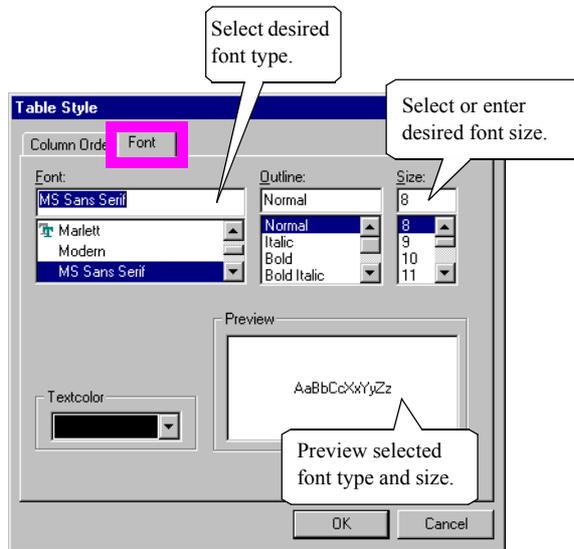
Context Menu:

- Cut
- Copy
- Paste
- Copy Table to Clipboard
- Clear
- Select All
- Add Row
- Insert Row
- Delete Row
- View Mode
- ✓ Edit Mode
- Cancel Edit
- Table Style...
- Wizard...



10.2.3 Changing the Table Row Display Quantity (Table Style Settings (2))

Although you cannot specify the exact number of rows that can be displayed in a table, this number can naturally be adjusted by changing the font type and size used in the table, using the [Font] tab in the <Table Style> window.



<Table Style> - [Font] Tab (Reference Manual p568)

Setting Points:

- Set the font size as large as possible.
- Select a font type that is easy to read even when set to a smaller size.

Note: The cell height will automatically change based on the selected font size. If the font size is set smaller, the number of displayed rows in the table will increase. However, since the cell width has been specified independently, this width will not change because of the font size. When necessary, use the procedure described in "10.1.2 Changing the Width of a Table Column" to change the cell width.

10.3 Operation - Tables

10.3.1 Editing Table Cells

10.3.1 Selecting Multiple Cells

Click [Row#] column's title cell to select entire table.

ID#	Name	Type	Ret. Time	Band
1	Nonene	Target	2.080	0.200
2	Decane	Target	2.750	0.200
3	Undecane	Target	3.680	0.200
4	Dodecane	Target	4.830	0.200
5	Tridecane	Target	6.090	0.200

Drag mouse diagonally to enclose all desired cells or hold down [Shift] key and click cells diagonally in desired area.

10.3.2 Copying/Cutting/Pasting/Clearing Cell Data

Copies and cuts selected cell data.

Copies selected cell data.

Pastes copied data into selected cell.

Copies entire table.

Deletes selected cell data.

Click here to enter [Edit] mode.

After selecting edit area, right-click table to display pop-up menu.

Note: If the data paste destination area is smaller than the data paste source area, the actual pasted area is determined by the source area. Also, if the destination area is larger than the source area, the source data will be pasted repeatedly until the destination area is filled.

Note: Data copied can also be pasted into commercial spreadsheet software such as Microsoft Excel.

10.3.3 Entering Values into Cells

Data can be entered directly into cells from the keyboard when the cells are editable. However, some cells have a special data entry format, and for those cells, a special function is supported to facilitate data entry in each format.

See below about how to enter data into batch table cells in the <Batch Table> window.

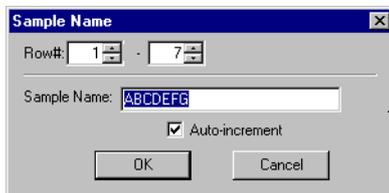


Type	Example	Description
Window pop-up type (For complicated settings)		After selecting a cell, click the arrow button at the right of the cell, and an appropriate pop-up data entry window for that cell appears. In this example, the file selection window will appear.
Drop-down list type (For selecting from many choices)		After selecting a cell, click the arrow button at the right of the cell, and a drop-down selection list appears. Click desired item in this list.
Spin box entry type (For entering specific data)		After selecting a cell, click either of the arrow buttons at the right of the cell to increase or decrease the cell's value the designated step value. To enter data with a different step value, use the keyboard to enter value directly into the cell.
Check box type (For ON/OFF entry)		Click the check box in the cell to attach or remove the check mark.

10.3.4 Cell Data Entry Auxiliary Functions (Batch Tables)

❖ For analysis batch tables

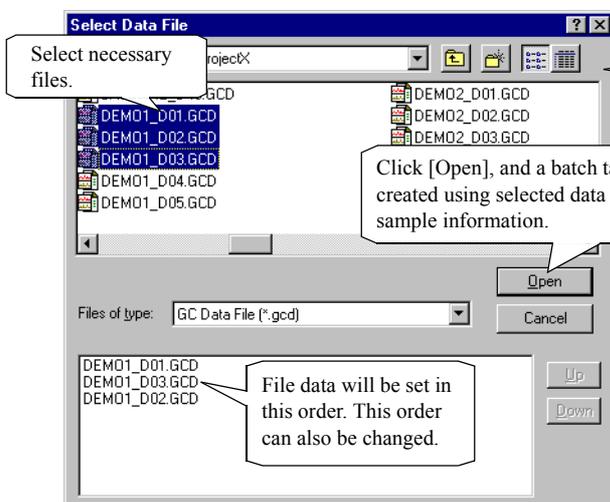
[Input Col. Data...] (Reference Manual p350)



Call up a right-click menu and select [Input Col. Data...]. A window to enter column information all at once will appear. This feature is available for [Vial#], [Sample Name], [Sample ID], and [Data File Name] items.

❖ For post-run analysis batch tables

<Add Rows with Data Files>



Select necessary files.

Call up a right-click menu and select [Add Rows with Data Files]. A window to automatically enter data file's appropriate sample information data in applicable cells will appear.

Click [Open], and a batch table is created using selected data file's sample information.

File data will be set in this order. This order can also be changed.

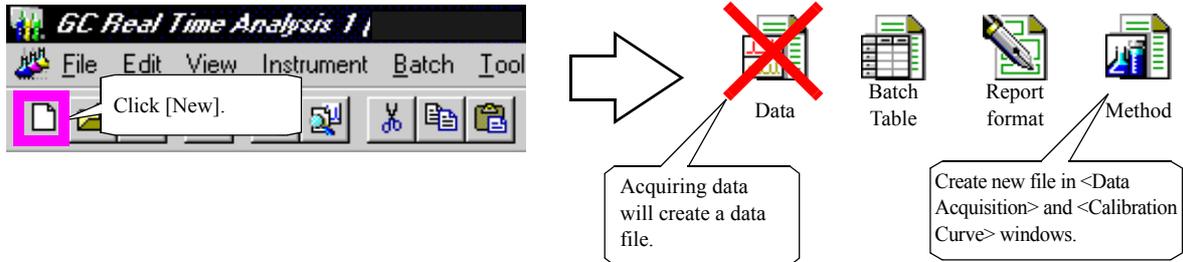
Note: Can also drag and drop desired data file onto batch table to add batch row to table end.

11.1 Operation - Files

11.1.1 Using Files (1)

This section describes the basic file operations that are common to all application windows.

11.1.1 Creating a New File



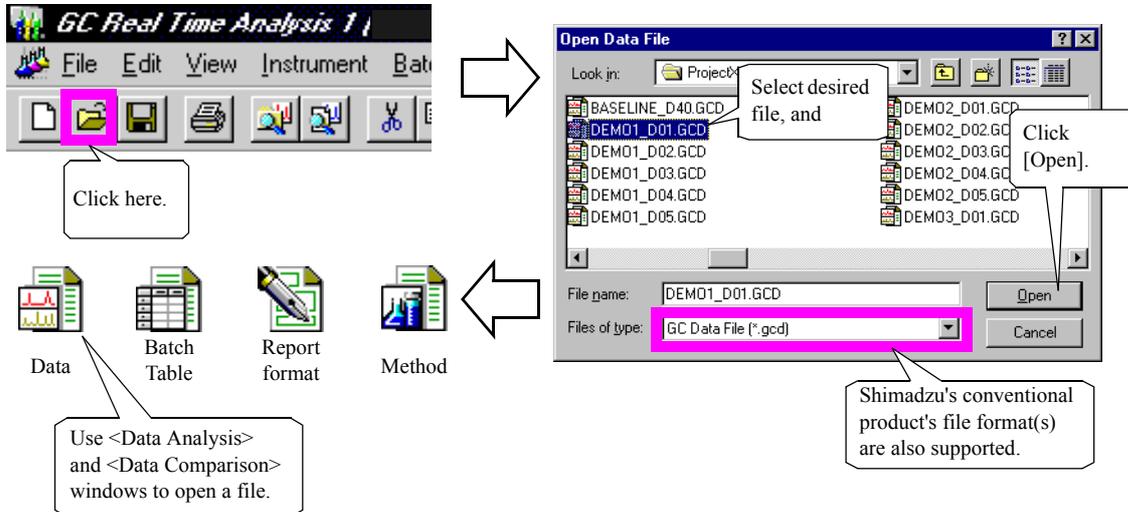
Note: New files cannot be created using the <Data Analysis> and <Data Comparison> windows in the <GC Postrun> program.

Note: When creating a new file in the <Data Explorer> window, the new file type will be determined based on the application window that is active at the time.

Note: You can select a template for creating a new file. Also, you can preselect a template used for creating a new file.

For more about using template, refer to Administration Manual "3.3 Using a Template".

11.1.2 Opening a File (1)



Note: The basic file types that can be opened in application windows are the same as the types available when creating a new file. However, since files with data that needs to be read in (e.g., data files for a report format) do not have any toolbar icons, drag and drop the file or use the program menus to read its data (see page 103).

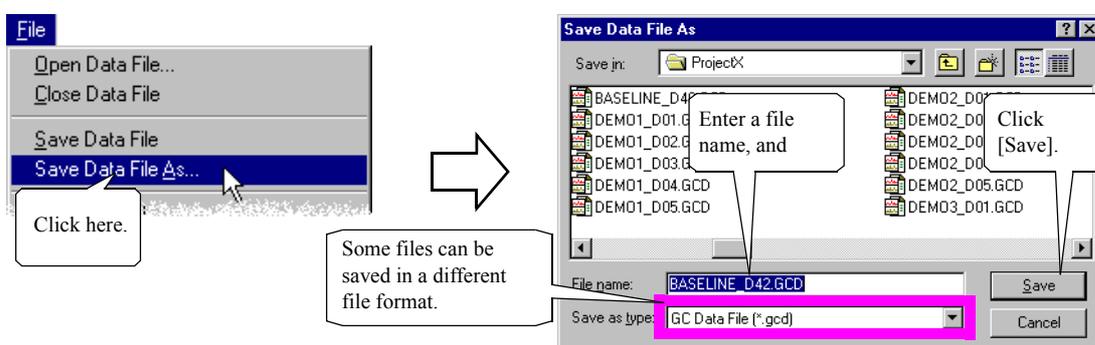
11.1.3 Saving a File



- With no file name (i.e., saving a new file)
-> Operation is the same as using [Save As].
- With a file name (i.e., saving an existing, previously saved file)
-> Data will be overwritten.

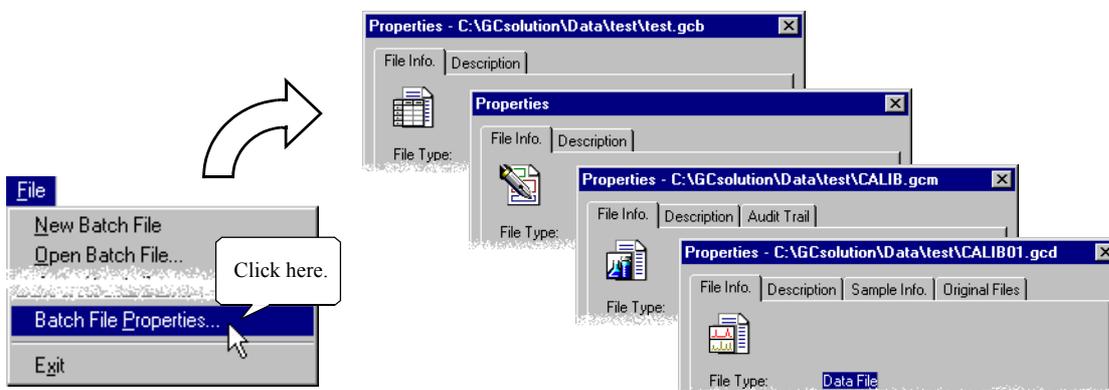
Note: When attempting to close a file or application window with a file data (including new file data) changed, a dialog box appears asking whether or not to save the file's data.

Name and save a file following the steps below.



11.1.4 Checking File History Information (1)

Check file creation and update dates using the following operations.



	Batch	Report	Method	Data	Description/Additions
File information	√	√	√	√	File type, creator, creation date, update data, etc.
Comment	√	√	√	√	Can be used as a file search keyword.
Audit trail			√		Designates if updated logs will be saved for each method recorded in the method file and data.
Sample information				√	Sample information used for data acquisition (sample name, sample ID, etc.)
Used file				√	List of method, batch, report format, baseline data file used for data acquisition.

11.2 Operation - Files

11.2 Managing Files Effectively

This software uses the <Data Explorer> window displayed in each program window to perform file management.

11.2.1 What is the Data Explorer?

File management is performed using the <Data Explorer> window that is commonly used for the <GC Real Time Analysis> and <GC Postrun> applications.

Click here to switch the <Data Explorer> window display status (displayed or hidden).

Data file (extension = 'gcd')

Method file (extension = 'gcm')

Batch file (extension = 'gcb')

Report format file (extension = 'gcr')

Drag and drop a file to read its data.

Peak	Time	Area	Height
1	2.988	1089.6	134.4
2	3.448	188693.9	17876.3
3	4.111	101667.7	14306.8
4	4.871	32007.9	3906.1

<Data Explorer> (Reference Manual p485)

11.2.2 What is a Project?

In the <Data Explorer> window, files are managed for each folder, which is called a "project". In GCsolution, all types of files are located in one project (folder) and are managed for each file tab using the [File] tab in the <Data Explorer>.

The project currently active is called reference project. For single-run analysis, it is the folder in which the currently-loaded method file is located; For batch analysis, it is the folder in which the currently-loaded batch file is located.

In other cases, the folder shown in the [Project in] list in the Data Explorer is the reference project. You can change the reference project shown in the [Project in] list by using the [Select Project (Folder)] button.

Note: When this software is first installed, an empty project (folder) with the name "Project1" will be created as a default.

Reference project

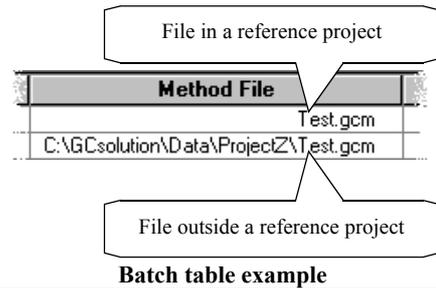
Click here to display list of reference projects.

Up to 10 projects recently used are recorded.



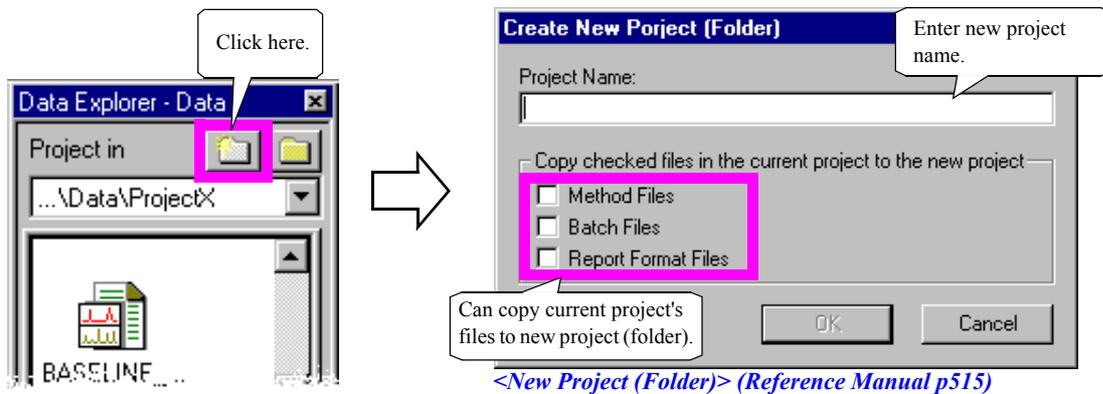
The reference project is effective in the entire range of each program's windows. For example, a folder initially displayed in the <Open File> window will always be listed as a reference project (folder).

Also, when designating a file name, that file is considered to belong to the reference project, not to any other specific folder. When the file is outside of a reference project, it is designated by a full path file name.



11.2.3 Creating a New Project (Folder)

Create a new project (folder) using the following steps.

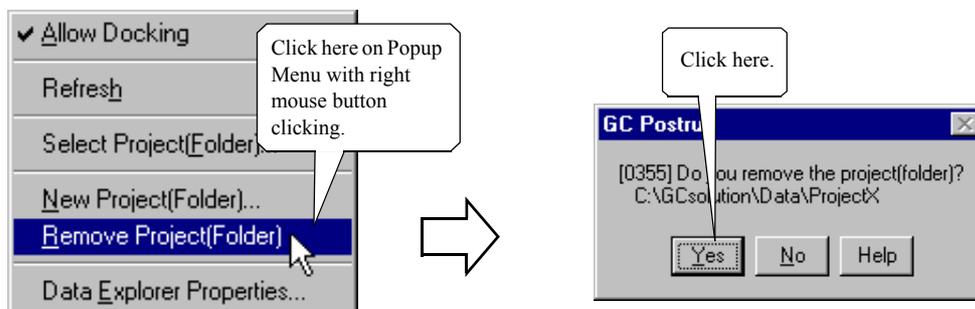


For example, when designating a method file for a batch table in a reference project, a closed reference project's file will be designated. Then, if the batch file and method file are copied to a newly created project, only the new project is necessary to refer to the combination of those two files.

Because of this, if a set of method, batch, and report file data are copied to a new project, even if the current project needs to be erased (e.g., due to insufficient hard disk space), no problems will occur (since the current project's file was not designated).

Also, if a backup project is created for each project before it is deleted, it is easy to restore the project's environment later since a complete file is stored in the backup project. Moreover, analysis conditions that were set in a reference project will not be influenced by any other projects' changes.

11.2.4 Deleting a Project (Folder)



Note: A folder must be empty to be deleted.

11.3 Using Files (2)

This section explains how to operate files using the <Data Explorer>.

11.3.1 Opening a File (2)

❖ Double-clicking the <Data Explorer>'s file.

An application window used to read the file data will become active and the file's data will be displayed.

File Type	Window Type	
Method file	<Data Acquisition>	Analysis program
	<Calibration Curve>	Post-run program
Data file	<Data Analysis>	Common
Batch file	<Batch Table>	
Report format file	<Report>	

❖ Dragging and dropping a file from the <Data Explorer>

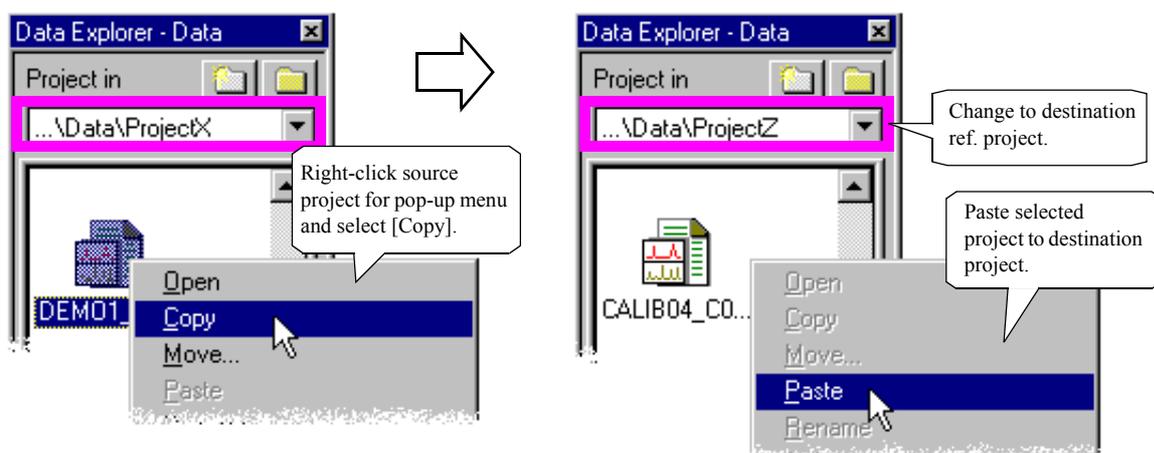
Drag and drop a file onto an application window.

When dragging and dropping a desired file onto the application window where the file's data is read in, functions equivalent to the following operations will become active and the file data will be displayed.

File Type	Drop Destination	Equivalent Operations
Method file	<Data Acquisition>	[File] - [Open Method File]
	<Calibration Curve>	[File] - [Open Method File]
	<Data Analysis>	[File] - [Load Method...]
Data file	<Data Analysis>	[File] - [Open Data File]
	<Calibration Curve>*	[Data] - [Add]
	<Data Comparison>	[File] - [Open Data File]
	<Batch Table>	[Edit] - [Add Rows with Data Files]
	<Report>	[File] - [Load Data File...]
Batch file	<Batch Table>	[File] - [Open Batch File]
Report format file	<Report>	[File] - [Open Report File]

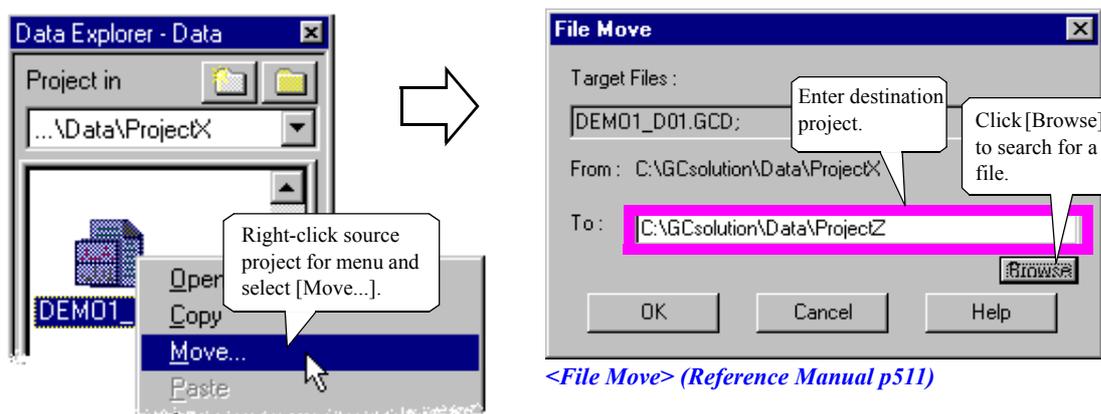
* Drop onto the <File Tree> view.

11.3.2 Copying a File



Note: Files can be copied between this software's <Data Explorer> window and the standard Windows File Explorer by dragging and dropping. (If the copy destination is on the same drive, perform the drag and drop while holding down the [Ctrl] key.)

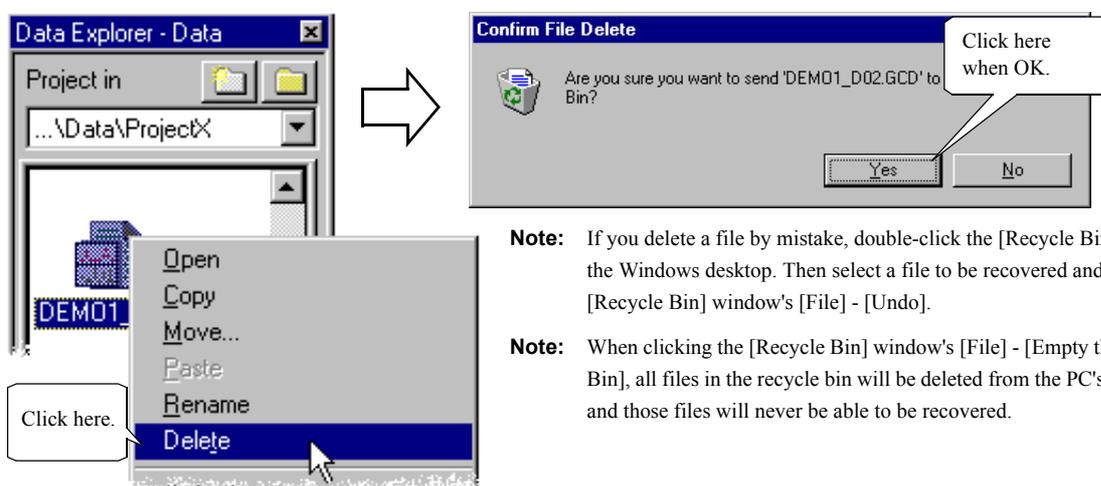
11.3.3 Moving a File



<File Move> (Reference Manual p511)

Note: Files can be moved between this software's <Data Explorer> window and the standard Windows File Explorer by dragging and dropping. (If the move destination is on a different drive, perform the drag and drop while holding down the [Shift] key.)

11.3.4 Deleting a File

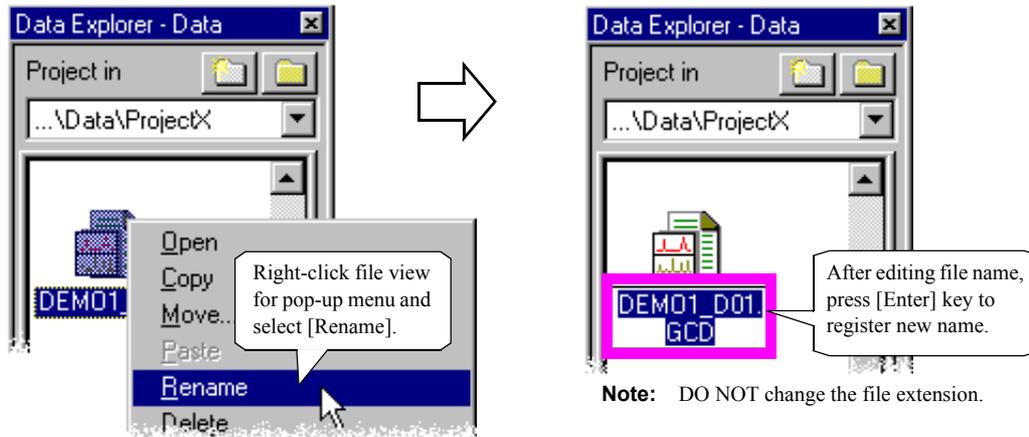


Note: If you delete a file by mistake, double-click the [Recycle Bin] icon on the Windows desktop. Then select a file to be recovered and click the [Recycle Bin] window's [File] - [Undo].

Note: When clicking the [Recycle Bin] window's [File] - [Empty the Recycle Bin], all files in the recycle bin will be deleted from the PC's hard disk, and those files will never be able to be recovered.

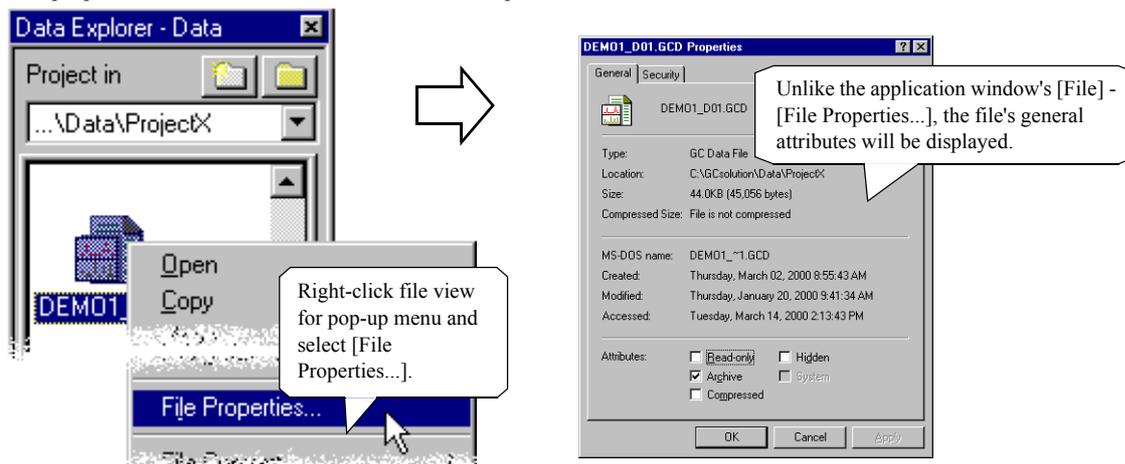


11.3.5 Changing File Names

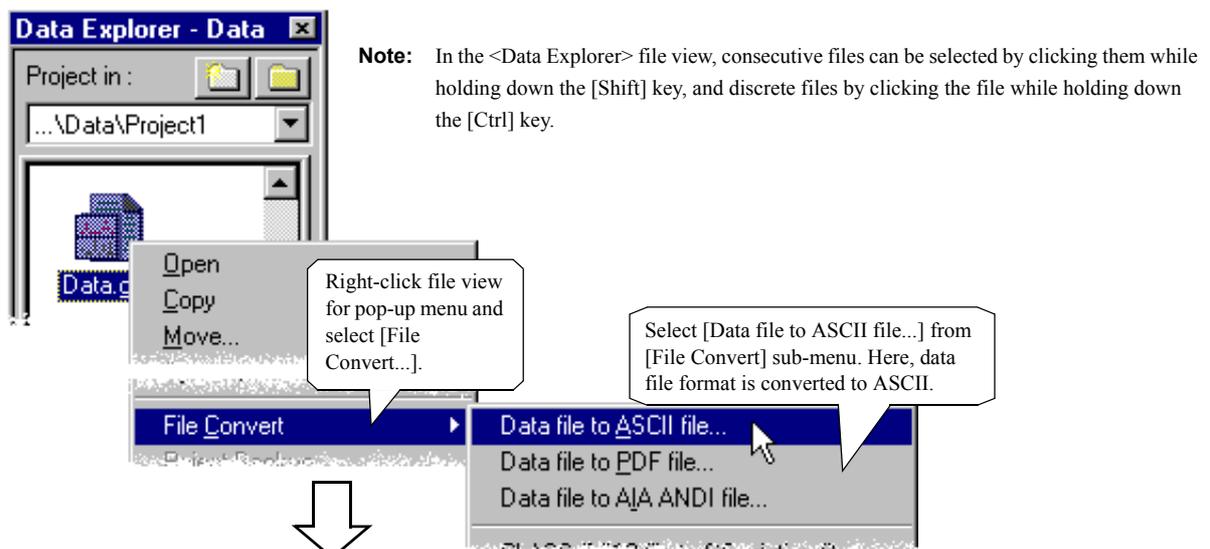


11.3.6 Checking File History Information (2)

File properties can also be checked in the <Data Explorer>.



11.3.7 Converting File Formats



Files selected using <Data Explorer>. (Multiple files can be selected.)

Select copy destination for converted file.

[Output Items] button appears only when converting to ASCII. Select which items will be output from data file.

Select output items to be converted.

Note: Extensions will automatically be changed.
 GCsolution data/method --> *.gcd/*.gcm
 ASCII file --> *.txt
 AIA ANDI file --> *.cdf
 Adobe® Acrobat® Format --> *.pdf

Click check boxes of items to be output.

Can select [Delimiter:] used between values in row direction.

<Convert Data file to ASCII file> (Reference Manual p505)

Note: When converting a file created via Shimadzu's CLASS-GC10/CLASS-VP4 to a GCsolution file, the following data will be reflected in the new file:

Convert Source Format	Convert Destination Format	Description
CLASS-GC10 data file	GCsolution data file	Converts the CLASS-GC10 data file and chromatogram referred to in this data file, to a GCsolution data file.
CLASS-GC10 chromatogram file	GCsolution data file	Converts a CLASS-GC10 chromatogram to a GCsolution data file. Note: Its peak table will have no data entered and method will be the default value.
CLASS-GC10 method file	GCsolution method file	Converts the CLASS-GC10 method file to a GCsolution method file.
CLASS-VP4 data file	GCsolution data file	Converts the CLASS-VP data file, which includes chromatogram, to a GCsolution data file.
CLASS-VP4 method file	GCsolution method file	Converts the CLASS-VP4 method file to a GCsolution method file.

12 Appendices

12.1 When Troubles Occur

12.1.1 Using Help

If you have any trouble:

Press the [F1] key

or

Click the [Help] button on the screen.

F1

Help

The online <Help> window will appear for the currently active window.

The <Results View -- [Peak Table] Tab> page displays (i) the results obtained by detecting peaks in accordance with the parameters set on the [Integration] tab page of the <Method> view, and (ii) the peak integration information and quantitative calculation results on each peak.

Peak#	Retention Time	Initial Time	Final Time	Area	Area%
1	1.123	1.123	1.123	1.123	1.123
2	2.234	2.234	2.234	2.234	2.234
3	3.345	3.345	3.345	3.345	3.345
4	4.456	4.456	4.456	4.456	4.456
5	5.567	5.567	5.567	5.567	5.567

The items displayed on the [Peak Table] tab page are listed below. Only the items that have been selected to display the corresponding columns on the <Table Style> window will be displayed within the view.

Item displayed	Description
Peak#	Shows the peak number that has been integrated.
Retention Time	Shows the retention time (minutes) of the peak.
Initial Time	Shows the initial time (minutes) of the peak.
Final Time	Shows the final time (minutes) of the peak.
Area	Shows the area of the peak.
Area%	Shows the percentage area of the peak.

(GC Help Window)

If you have questions about technical terms or parameters:

Select [Contents...] from the [Help] menu.

Help

Contents...

Online Manual

About GC PostRun...

Click the [Index] tab.

Select a term you want to find and click [Display].

Organization of GCsolution

<GC Real Time Analysis> screen

The <GC Real Time Analysis> screen is used to acquire data from single... It allows you to quickly prepare a report on the acquired data. This screen is connected to a personal computer.

Topics Found

Click a topic, then click Display.

Title

<Analytical Line> - [Injection Unit] Tab

<Instrument Parameter> View - [Injection Port] Tab

Display

Cancel

When the same term is mentioned in multiple topics, the <Topics Found> window will appear.

Select a term you want to check and click [Display].

Topics Found

Click a topic, then click Display.

Title

<Analytical Line> - [Injection Unit] Tab

<Instrument Parameter> View - [Injection Port] Tab

Display

Cancel

12.1.2 Using the Online Manual

Click [Online Manual] from the [Help] menu.

Use Adobe® Acrobat® or Adobe Acrobat® Reader™ to view the GCsolution's Instruction Manuals (Operations, Administration and Reference Manual).

You can search for terms using the index.

You can jump to a desired page using bookmarks (i.e., table of contents).

Reference and index items are displayed in blue and linked for quick reference of related items.

Each batch row relates to one data acquisition (single-run analysis). Enter necessary values in each batch row, such as [Method File] and [Data File] names to complete batch table.

Click [Batch Processing] icon.

After editing last row, a new row is added after last row.

Select necessary editing commands from right-click menu.

<Batch Table> (Reference Manual p23)

7 Batch Processing

7.1 Performing Continuous Data Acquisition

To perform continuous data acquisition for multiple samples, use the <Batch Table> on the <GC Real Time Analysis> screen.

When the <GC Real Time Analysis> screen has not started yet, double-click the desktop's [GC Real Time Analysis 1] icon.

72 of 215

8.26 x 11

Note: Viewing the Online Manuals requires installing "Adobe Acrobat® Reader™" or "Adobe® Acrobat®" (4.0 or later version). If you try the steps mentioned above without first installing it, a dialog box will appear prompting to install Acrobat® Reader™.

Note: Adobe Acrobat® Reader™ 5.0 is stored on CD-ROM. Follow the steps below to install it.

- Place the CD-ROM into your computer's CD drive.
- The GCsolution installation program will start up. Cancel and then exit it.
- Double-click the [My Computer] icon on the desktop. Next, right-click the CD-ROM icon to display a pop-up menu, and select [Open].
- Double-click the "\Acroread\rp500enu.exe" file icon on the CD and follow the instructions displayed on the screen to complete the installation.

Note: For more about Adobe Acrobat® Reader™ 5.0, refer to the Adobe Acrobat® Reader™ 5.0 software's Online User's Guide and the Adobe Corporation's Internet Homepage.

Note: Although data stored in the GCsolution Online Manual (Reference Manual) is the same as the Help data, we recommend that you use Adobe Acrobat® Reader™ 5.0 when printing for better quality.

12.2 Installing GCsolution

This section describes how to install the GCsolution software.

Note: Prior to reinstalling GCsolution when it starts malfunctioning for some reason, first, uninstall the current GCsolution software. To do so, refer to "12.2.3 Uninstalling GCsolution".

Note: The install disc is stored on CD-ROM.

When executing the GCsolution setup program, the install disc's compressed files will automatically be extracted with the install disc's special program and then copied to the computer's hard disk.

This software will not operate if you merely copy the CD-ROM data to the computer's hard disk without extracting it. Be sure to follow the correct installation procedure.

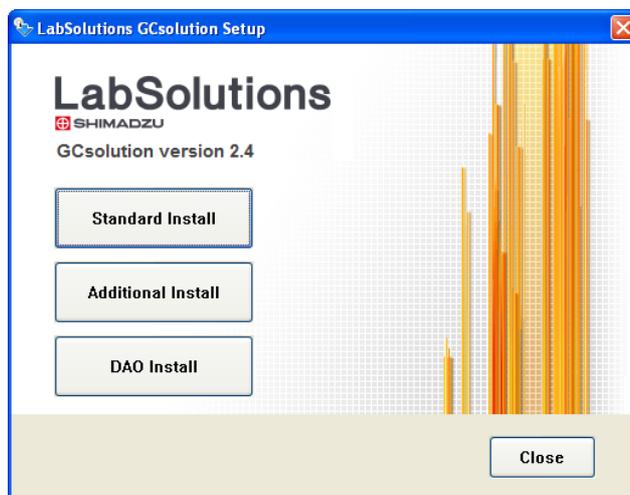
Note: To install this software, Windows2000 professional, WindowsXP professional, WindowsVista Business or Windows7 Professional system must already be installed as the computer's operating system (OS).

Note: To start the installation on WindowsVista or Windows7, a message pops up to ask your permission. In such case, click on the [Continue (C)] button.

12.2.1 Installing DAO

1. Turn on your computer's power. After Windows starts up, place the GCsolution install disc into the CD drive.

"GCsolution Setup" will automatically start up and the <LabSolutions GCsolution Setup> window will appear.



Note: If the <LabSolutions GCsolution Setup> window does not open automatically, select the Task Bar's [Start] menu - [Run...]. Then, enter "E:\Autorun.exe" in the displayed <Run...> window's [Open] text box, and click [OK].

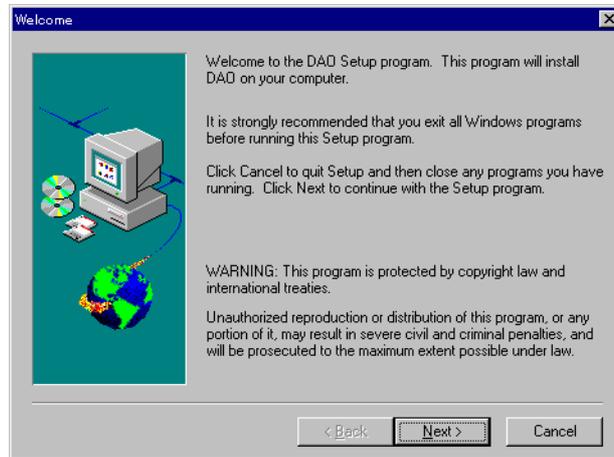
For WindowsVista or Windows7, click on [Run...] under the [Accessories] menu. Then, enter "E:\Autorun.exe".

(Here, the CD drive is designated as "E:").



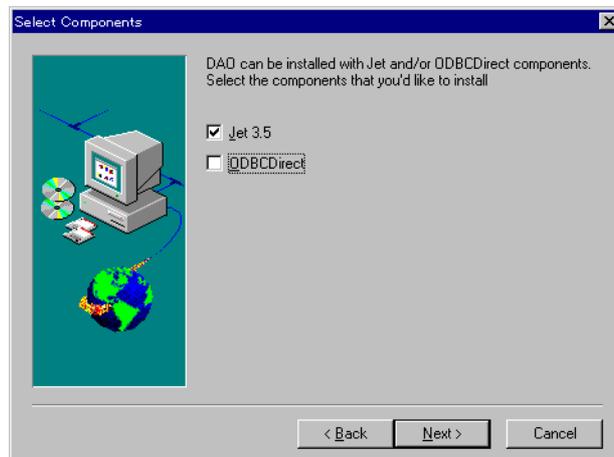
2. Click [DAO Install] in the <LabSolutions GCsolution Setup> window.

"Data Access Objects (DAO) Setup" will start up and the <Welcome> window will appear.



3. In the <Welcome> window, click [Next>].

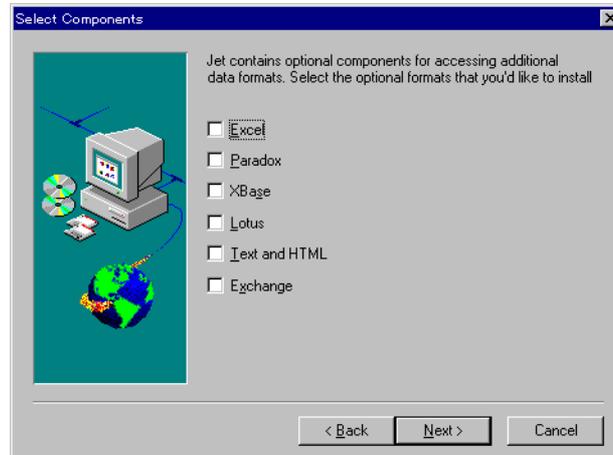
The window will then change to the <Select Components> window.



4. In the <Select Components> window, click only the [Jet 3.5] check box and then click [Next>].

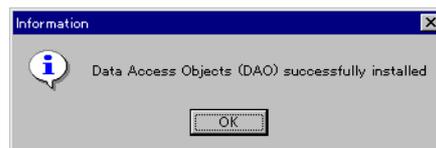


The window then changes to one where you can select the data formats to add.



5. Remove all check marks and click [Next>].

The DAO installation begins, and when finished, an <Information> message box will appear.



6. In the <Information> window, click [OK] to complete the Data Access Objects (DAO) Setup.

Note: Once the DAO installation is finished, install GCsolution.

If the DAO installation failed, the following message will be displayed:

"The OLE automation DLL, OLEAUT32.DLL, could not be found or is an older version that is incompatible with DAO3.5. If you continue, DAO will not register properly. Continue anyway?"

In such a case, simply continue the DAO installation.

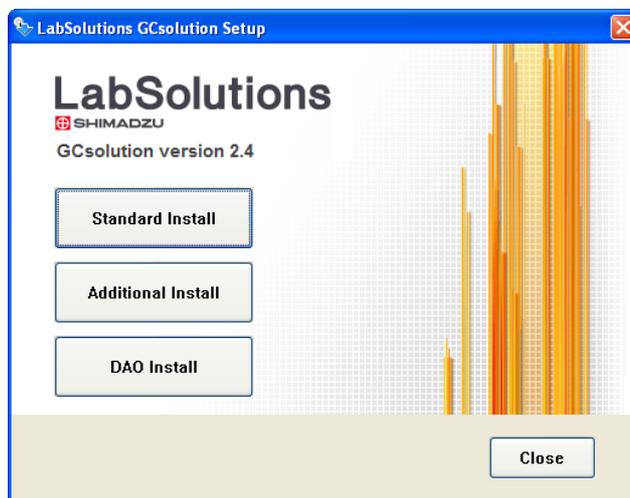
Then, install GCsolution. If GCsolution installation finishes normally, then the DAO installation also is finished. If the GCsolution installation failed, install DAO and then GCsolution once again.



12.2.2 Installing GCsolution

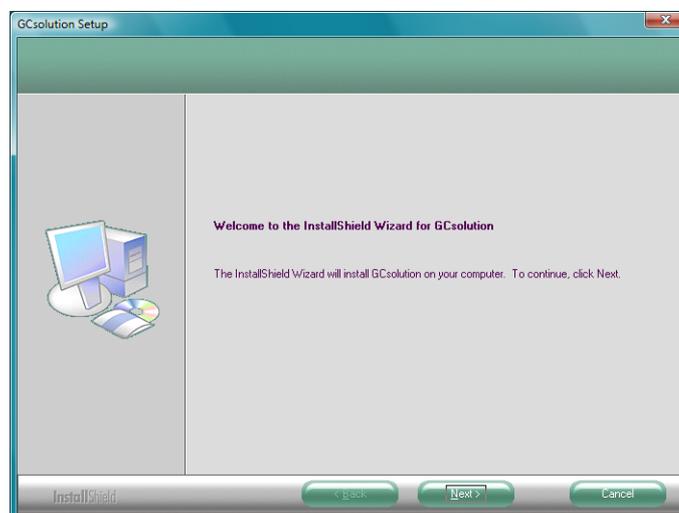
1. Turn on your computer's power. After Windows starts up, place the GCsolution install disc into the CD drive.

"GCsolution Setup" will automatically start up and the <LabSolutions GCsolution Setup> window will appear.



2. In the <LabSolutions GCsolution Setup> window, click [Standard Install].

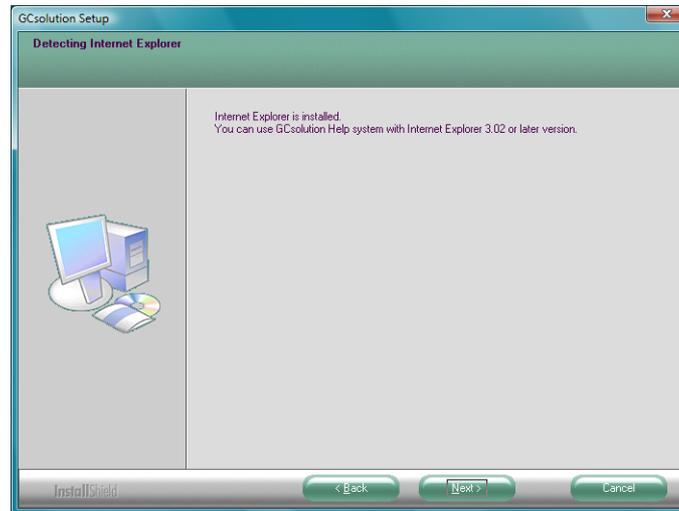
The <Welcome> window will appear.



3. In the <Welcome> window, click [Next>].

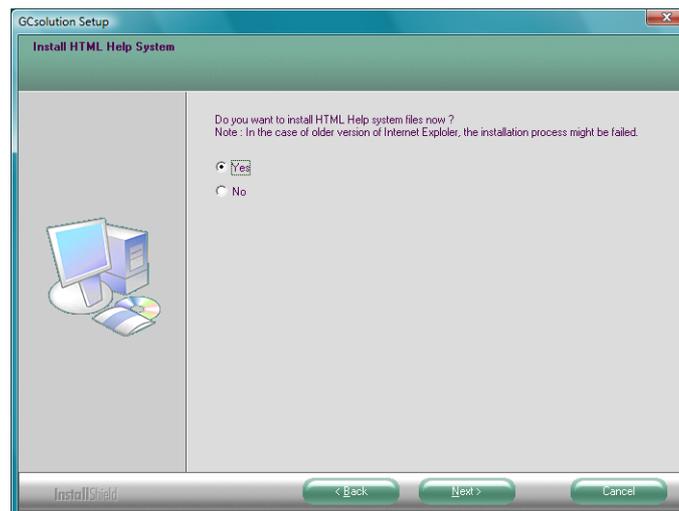


The window will then change to the <Detecting Internet Explorer> window.



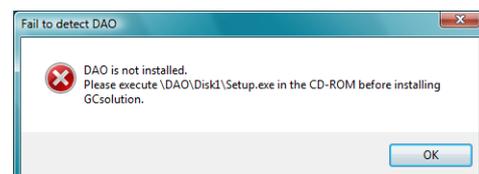
4. In the <Detecting Internet Explorer> window, click [Next>].

The <Install HTML Help System> window will then appear.



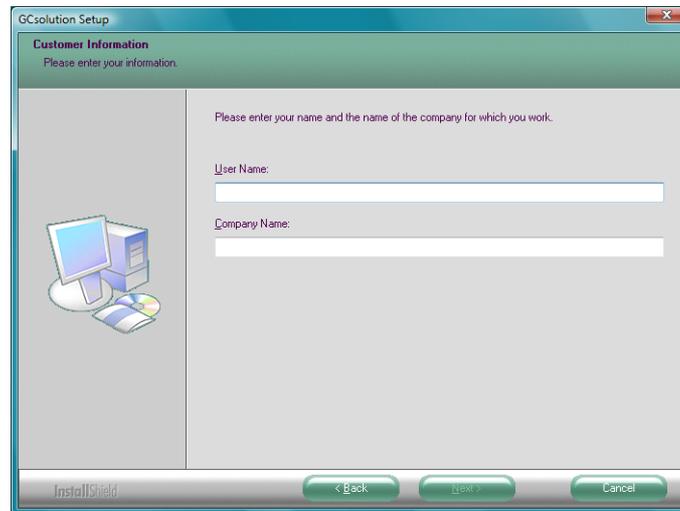
5. Usually, select [Yes] here. If you know you will never use the Help data, or if the version of Internet Explorer is not correct, select [No]. After selecting either one, click [Next>].

Note: If you click [Next>] in the <Install HTML Help System> window, and the <Fail to detect DAO> message box appears (see figure on the right), click [OK] to quit the installation. Then, referring to "[12.2.1 Installing DAO](#)" install the DAO (Data Access Objects) and begin the GCsolution installation again.



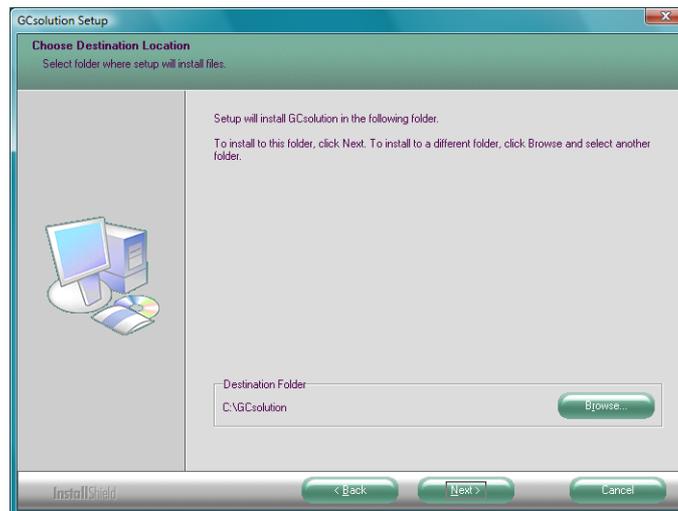


The <User Information> window will appear.



6. In the <User Information> window, enter the user name in the [Name] field and the user group in the [Company] field. Then click [Next>].

The <Choose Destination Location> window will appear.



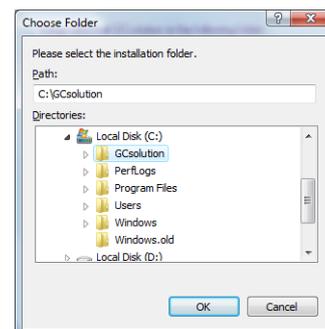
7. The GCsolution software will be installed into the folder shown in the [Destination Folder] field in the <Choose Destination Location> window. Usually, use this displayed folder as it is.

Note: To change the destination folder, click [Browse...] in the <Choose Destination Location> window.

The <Choose Folder> window will then open.

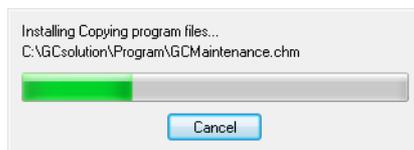
Select the destination folder either by entering the full path name in the [Path:] field, or by finding and double-clicking a folder in the [Directories:] list box.

To change the destination drive, click the [Drives:] drop-down list box and select the desired drive.

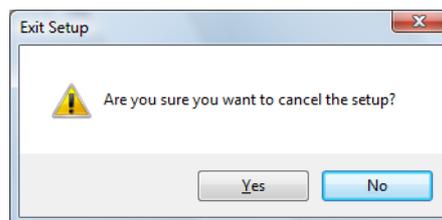




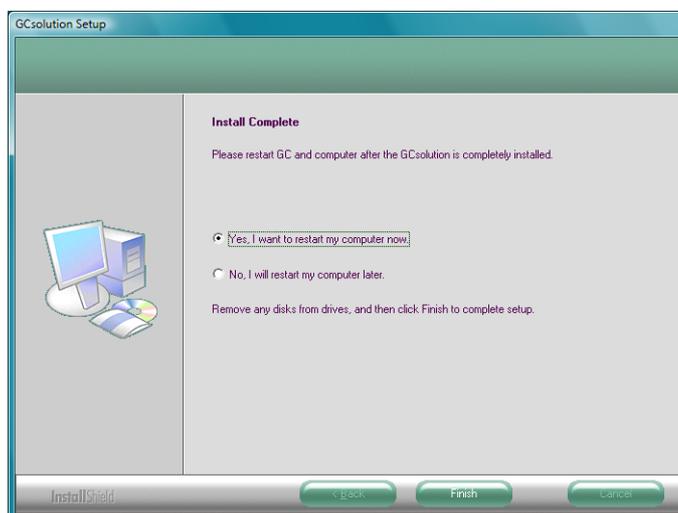
Click [Next>]. A message box will appear stating "Copying program files..." as program file installation begins.



- Note:** To cancel installation, click [Cancel].
The <Exit Setup> window will appear.
To continue the installation, click [Resume]. The <Exit Setup> window will then disappear and the installation will continue.
To completely stop the installation, click [Exit Setup]. The <Exit Setup> window will then close and the installation will stop.
The GCsolution setup then stops.



8. If the installation finishes normally, the <Install Complete> window will appear.

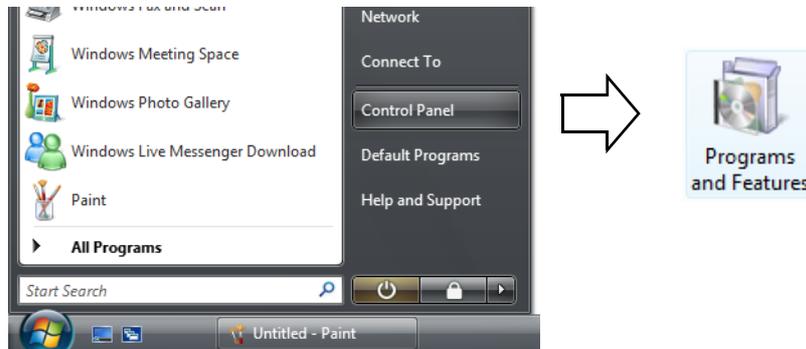


9. In the <Install Complete> window, click [Finish]. The <Install Complete> window will then close, completing the GCsolution setup. Selecting [Yes, I want to restart my computer now.] will automatically restart the Windows system. If you select [No, I will restart my computer later.], be sure to restart the Windows system before you first use the GCsolution software.

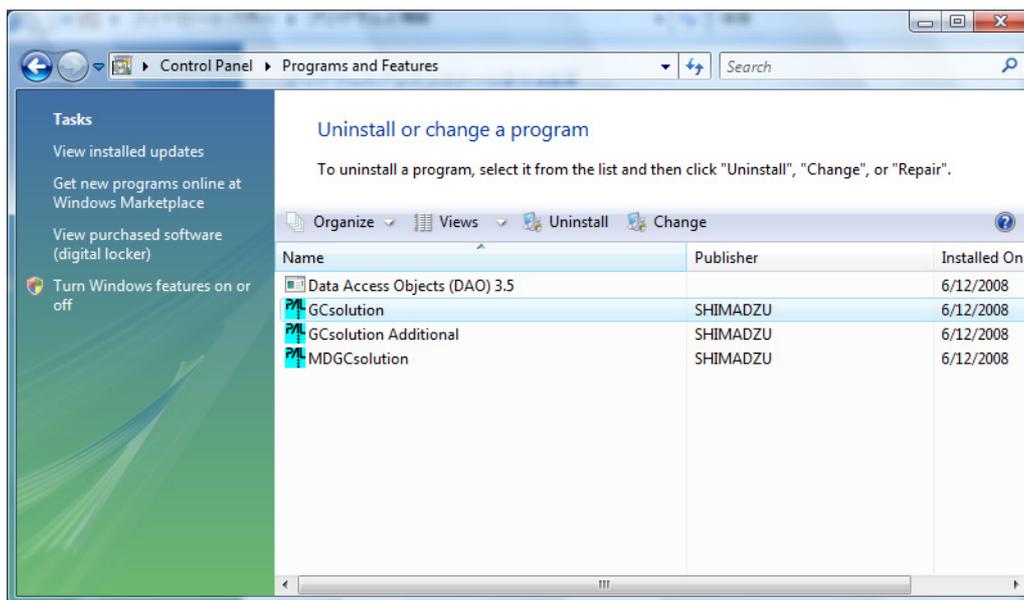


12.2.3 Uninstalling GCsolution

1. From the Start menu, point to [Settings] and select [Control Panel]. Double-click the [Add/Remove Programs] icon. For Windows Vista or Windows 7, click [Uninstall a Program]. (In the case of Classic View (Windows Vista) or Large/Small icons view (Windows 7) of the Control Panel, double-click [Programs and Features].)



The <Add/Remove Programs Properties> window will appear.



2. From the list box on the [Install/Uninstall] tab, select [GCsolution]. Then, click [Add/Remove...]. For Windows Vista and Windows 7, click [GCsolution] and then click [Uninstall].

Note: To delete the GC settings entered in "12.2.4 Installing Additional GC Units", select [GCsolution] - [Additional] and follow the same steps above to delete GCsolution.

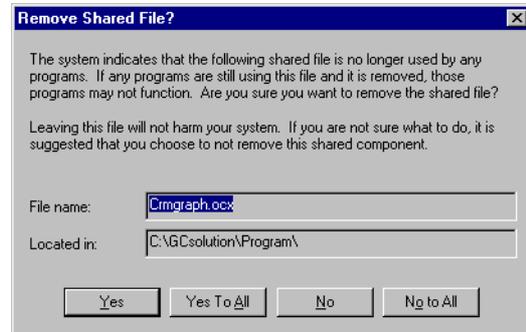


3. The <Confirm File Deletion> window will appear asking you if you want to delete the files. If you do not want to delete them, click [No].

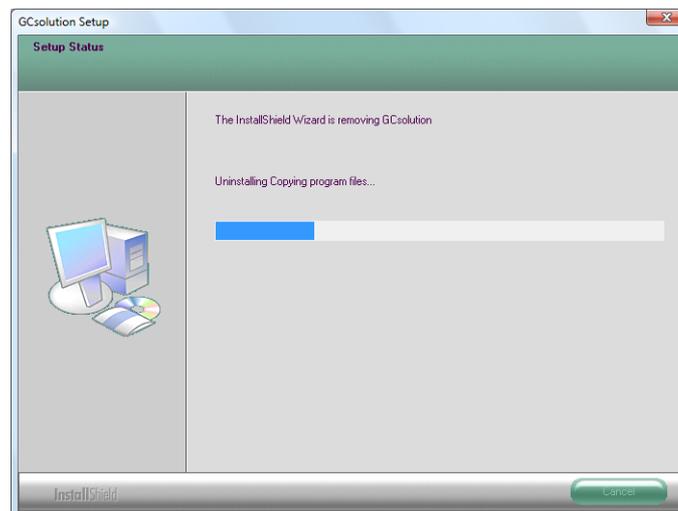
Note: At this time, the <Remove Shared File?> window may appear asking if you want to delete the shared files.

If other applications are installed on your computer besides GCsolution, those applications may be using the shared files. Therefore, it is recommended to click [No] to not delete them. If you click [Yes], the shared file whose name is displayed in the [File Name] field will be deleted. This operation will be repeated for each shared file. Each time this window appears, click the desired button.

If you click [Yes To All], the <Remove Shared File?> window data will change to a window asking if you want to delete all unused shared files.



4. The <Remove Programs From Your Computer> window appears and the GCsolution application is deleted.



5. Once the uninstall for the GCsolution application has completed, the [OK] button in the <Remove Programs From Your Computer> window becomes active. Click [OK].
When this window closes, the GCsolution uninstall is finished.



12.2.4 Installing Additional GC Units

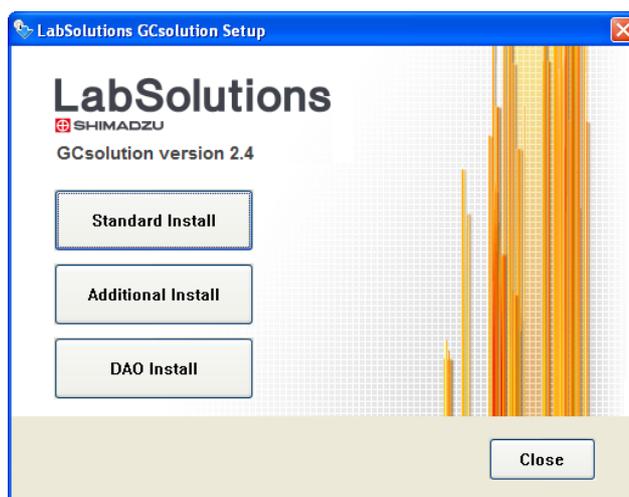
Note: Although multiple GC units can be connected to the GCsolution software, the Standard Installation will only install one GC unit.

Note: To install additional GC units, the following conditions are required:

- Installation for the first GC unit has completed.
- The GCsolution software is not running.

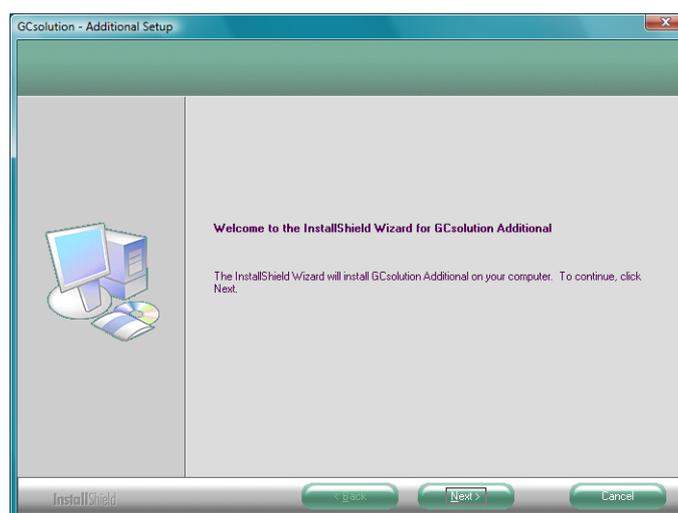
1. Turn on your computer's power. After Windows starts up, place the GCsolution install disc into the CD drive.

"GCsolution Setup" will automatically start up and the <LabSolutions GCsolution Setup> window will appear.



2. In the <LabSolutions GCsolution Setup> window, click [Additional Install].

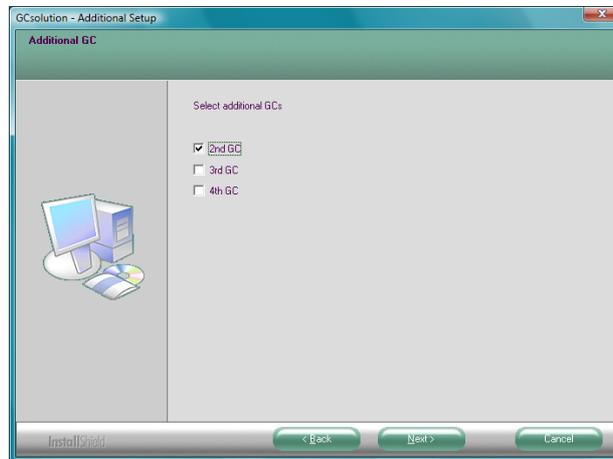
The <Welcome> window will appear.





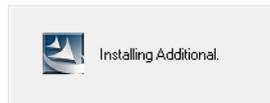
3. Click the [Next>] button in the <Welcome> window.

The <Additional GC> window will be opened.

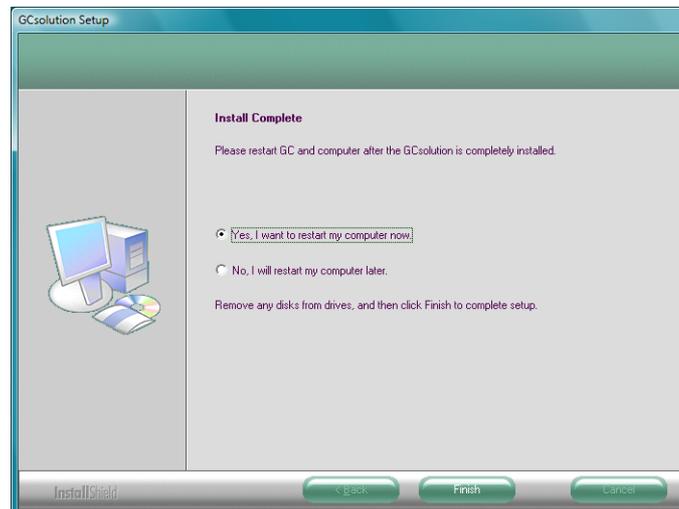


4. In the <Additional GC> window, click [Next>].

As program file installation begins, a message box will appear stating "Setup is searching for installed components...".



5. If the installation finishes normally, the <Install Complete> window will appear.



6. In the <Install Complete> window, click [Finish]. The <Install Complete> window will then close, completing the GCsolution setup. Selecting [Yes, I want to restart my computer now.] will automatically restart the Windows system. If you select [No, I will restart my computer later.], be sure to restart the Windows system before you first use the GCsolution software.



12.2.5 Connections to and settings on the GC

Note: The device names of communication ports (COM1, COM2, etc.) do not always match the actual port names on the rear of your personal computer (the symbol  and the port numbers of multiple standard ports, if any) because they can be changed using the OS settings. If a communication port is added using an optional board, the assigned device name varies depending on the specifications of that board.

After the communication port has been set, the connection to the GC may not be made properly. In this case, review the instruction manuals for the personal computer, OS, and added board.

Note: To connect the AOC-20 to the GC-17A, GC-1700, or GC-14B/C, a 3-channel optical link interface (PC-57N) must be provided on the CBM-102.

Connect connector 1 of the PC-57N to the connector marked "OPT LINK" on the rear panel of the AOC using the optical link cable.

❖ For the GC-2010, GC-2014, GC-2025:

1. Connect the connector marked "RS-232C" on the rear panel of the GC to the COM port on the personal computer using the provided transmission cable.
2. Turn ON the GC to display the LCD screen.
On the windows displayed by the following key sequences,

[FUNC]	
[6][ENTER]	(GC Configuration)
[3][ENTER]	(Transmission Parameter)

Then set* the	
Protocol	LEVEL3
Baud rate (bps)	115,200.

* The up and down cursor keys are used to toggle between items; the left and right cursor keys are used to select a value; and the ENTER key is used to establish the setting.

3. Once the settings are completed, turn OFF the GC momentarily and then turn it ON again. The settings of transmission parameters will be made valid.

❖ For the GC-17A V3, GC-1700:

1. Using the supplied transmission cable, connect the COM port on the personal computer to the connector marked "RS-232C" on the rear panel of the CBM-102.
2. Using the optical link cable, connect the connector marked "OPT LINK" on the rear panel of the CBM-102 to that marked "OPT LINK" on the rear panel of the GC.
3. Using the FUNCTION 15, set the transmission parameters for the GC as follows:

LINK PROTOCOL	EXTEND
BAUD RATE	2,400
COMMUNICATION	OPT.
PARITY	EVEN
STOP BITS	1
FILE FORMAT	14CH



4. Using FUNCTION 14, set the parameters for the purge APC and the APC for the detector on the GC.
5. After the settings have been completed, turn OFF the GC. Then turn it ON again. This will make the settings valid.

❖ **For the GC-17A V2:**

1. Using the supplied transmission cable, connect the COM port on the personal computer to the connector marked "RS-232C" on the rear panel of the CBM-102.
2. Using the optical link cable, connect the connector marked "OPT LINK" on the rear panel of the CBM-102 to that marked "OPT LINK" on the rear panel of the GC.
3. Using the FUNCTION 15, set the transmission parameters for the GC as follows:

LINK PROTOCOL	EXTEND
BAUD RATE	2,400
COMMUNICATION	OPT.
PARITY	EVEN
STOP BITS	1
GC-17A MODE	N

4. After the settings have been completed, turn OFF the GC. Then turn it ON again. This will make the transmission parameters valid.

❖ **For the GC-17A V1:**

1. Using the supplied transmission cable, connect the COM port on the personal computer to the connector marked "RS-232C" on the rear panel of the CBM-102.
2. A dedicated optical link interface is required for the GC. Using the optical link cable, connect the connector marked "OPT LINK" on the rear panel of the CBM-102 to the connector on the optical link interface.
3. Using the FUNCTION 15, set the transmission parameters for the GC as follows:

C.LOOP PROTOCOL	EXTEND
-----------------	--------

4. After the settings have been completed, turn OFF the GC. Then turn it ON again. This will make the transmission parameters valid.

❖ **For the GC-14B:**

1. Using the supplied transmission cable, connect the COM port on the personal computer to the connector marked "RS-232C" on the rear panel of the CBM-102.
2. A dedicated optical link interface is required for the GC. Using the optical link cable, connect the connector marked "OPT LINK" on the rear panel of the CBM-102 to the connector on the optical link interface.

❖ **For the GC-14C:**

1. Using the supplied transmission cable, connect the COM port on the personal computer to the connector marked "RS-232C" on the rear panel of the CBM-102.



2. Using the optical link cable, connect the connector marked "OPT LINK" on the rear panel of the CBM-102 to that marked "OPT LINK" on the rear panel of the GC.

3. Using the FUNCTION 15, set the transmission parameters for the GC as follows:

LINK PROTOCOL	EXTEND
BAUD RATE	2,400
COMMUNICATION	OPT.
PARITY	EVEN
STOP BITS	1
FILE FORMAT	14CH

4. After the settings have been completed, turn OFF the GC. Then turn it ON again. This will make the transmission parameters valid.



For other GC models:

1. Using the supplied transmission cable, connect the COM port on the personal computer to the connector marked "RS-232C" on the rear panel of the CBM-102.



12.2.6 System Configuration Settings

After the software is installed and wiring between your computer and the GC is completed, enter the initial (system configuration) settings:

Click [GC Analysis 1] icon.

Instrument1

<Login>

LabSolutions
GCsolution

User ID: Admin

Password:

Click [OK], with "Admin" still entered.

No password required.

<GC Real Time Analysis>

GC Real Time Analysis 1 (GC1 - Admin) - Method - [A...]

Configuration

System Configuration

Click [System Configuration] icon.

Select [Instrument Type:] of current connection.

Instrument

Instrument Name: Instrument1

Instrument Type: GC-2010

Communication: RS232C Po

LAN

IP Address: 192.168.1.100

COM2

COM3

COM4

Select port on GC of current connection.

To connect the AOC-20 to the GC-17A or the GC-14B/C, also open the <CBM-102 Settings> window.

CBM-102 Settings

Instrument Type: GC-17A V3

GC Connection

Optical Port #: 7

AOC Connection

Optical Port #: 1

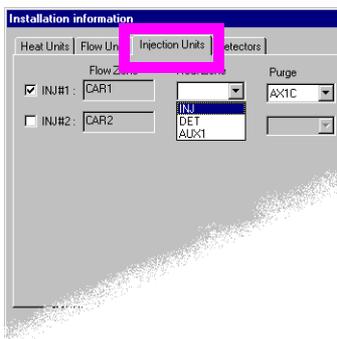
To use the AOC-20, put a check mark in the [AOC Connection] check box.

Set [Optional Port #] to 1.

For the GC-17A, GC-1700, or GC-14, enter settings for the heat unit port on the injection unit and that on the detector.
For the GC-14B, specify whether or not the heat unit port is available and then enter settings for the heat unit port on the injection unit and that on the detector.

For GC-2010, GC-2014 or GC-2025, this setting is not necessary as the units connected to the GC are automatically detected (if the communications ports have been properly set).

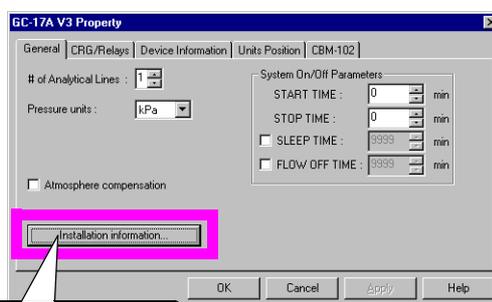
Setting the heat unit port on the injection unit



Setting the heat unit port on the detector

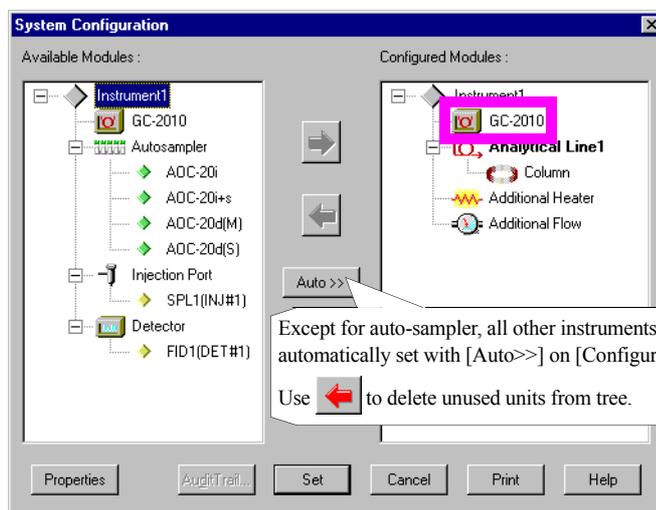
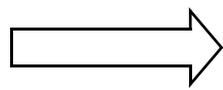


Specifying whether or not the heat unit port is available (GC-14B)



Click the [Installation Information ...] button.

Double-click on the instrument name.



Except for auto-sampler, all other instruments can be automatically set with [Auto>>] on [Configured Modules:] tree. Use [Left Arrow] to delete unused units from tree.

<System Configuration> (Reference Manual p17)

Clicking a unit name in [Available Modules] for selection and the right-arrow button after that specifies the device as one of the [Configured Modules]. Select devices needed to build your analysis system.

Double-clicking an device name allows you to set up the device. Make the settings such as the column information, carrier gas type and others necessary settings for your system configuration. The column information is the parameters required for automatic control of the pressure and flow rate, and the maximum temperature setting is required for protecting the column. Be sure to set the column information properly.



Note: When entering an additional GC (usually, instrument #)'s initial system configuration settings (#=2 to 4), first, start the GC analysis program with the [GCsolution Analysis #] icon, and then use the same procedure as used to set up the first GC settings.

At this time, be sure to select the correct communication ports for the GC units connected. If the same communication port is selected for multiple GC units that have been connected to the same computer, a conflict may occur, causing the units to malfunction.

- ① After all the settings, from software reinstallation to the above-mentioned settings, have been completed, it is recommended that you create a backup copy of all files in the "System" folder (located below the folder for this software). Specifically, since GCSysConfig#.cfg (for instrument #, where # is 1 through 4) files contain the system configuration information, you can easily restore the conditions obtained immediately after installation by writing these files back to the "System" folder after reinstalling the software.

12.3

12 Appendices

Network Mode

When using multiple PCs running GCsolution on your network, the use of the "Network" mode allows you to centrally manage the user information and the system policy settings on the server.

This section explains the procedure for setting up the networking mode, assuming that GCsolution is installed in the C:\GCsolution folder on each PC and the database file containing the user information and the system policy settings (hereafter referred to as "system administration database") is stored in the "GC_UserDB" folder on the server.

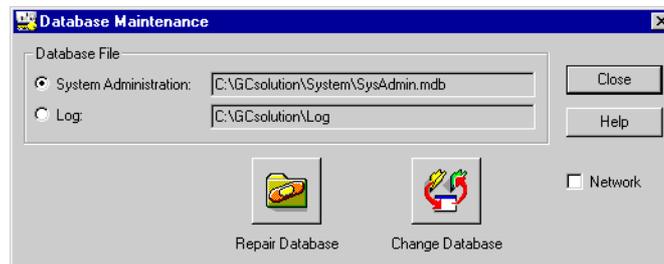
Note: Determine a folder in which you are storing the system administration database and then proceed to the following steps. The folder to store the system administration database must be shared on your network and accessible to all the users to read and write data.

12.3.1 Procedure for setting up the networking mode

1. Copy the system administration database to the "GC_UserDB" folder.
Copy the system administration database included in the System folder (C:\GCsolution\System\SysAdmin.mdb) on the first PC to be connected to the network to the "GC_UserDB" folder. This action is not required for the second and subsequent PCs.

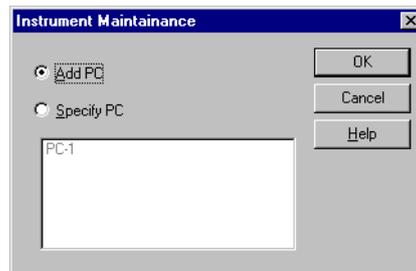
Note: If the first PC is a newly installed one and the user administration database file has not yet been created, open the <GC Real Time Analysis> window and then close it as it is. This will create the user administration database file in the System folder.

2. Set up the networking mode.
Start the database maintenance program (C:\GCsolution\Program\GCMntDB.exe).



Select [Network], press the [Change Database] button, and then select the system administration database included in the "GC_UserDB" folder. After completing the above settings, click the [Close] button to exit the <Database Maintenance>. This step must also be performed for the second and subsequent PCs. Perform the same step to bring all the PCs into the networking mode.

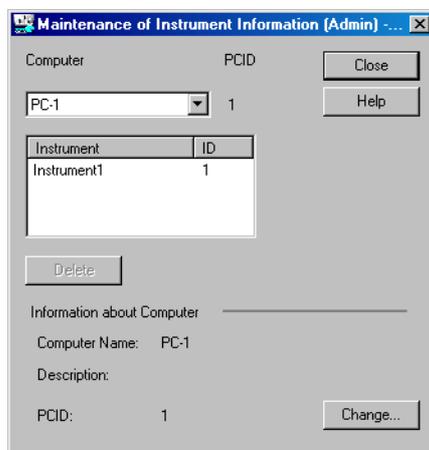
3. Register the PCs in the system administration database.
Start the <Instrument Maintenance> (C:\GCsolution\Program\GCMntPC.exe).



To register the PCs, select [Specify PC] for the first PC and [Add PC] for the second and subsequent PCs and then click the [OK] button.



The following <Instrument Maintenance> will be opened. This window allows you to perform maintenance-related operations such as changing a PC name. Click the [Close] button to exit the <Instrument Maintenance>.



Note: If the first dialog box (Specify/Add PC) of the <Instrument Maintenance> is not displayed, temporarily close the <Instrument Maintenance> and double-click the resetting file (C:\GCsolution\Regist\ResetPCID.reg), then reopen <Instrument Maintenance>.

4. Register the GC units to the system administration database.

For all the GC instruments connected to the PCs, start the <GC Real Time Analysis> and complete the <System Configuration> settings. Even if once the <System Configuration> window is already completed, open <System Configuration> and be sure to press the [Set] button to close it.

Note: Each GC unit name is used for its identification on the network. Be sure to assign unique names to all the GC units.

Note: For a newly registered instruments, specify the right of using that instruments for each user, as necessary. Otherwise, no one other than the users with the system administration right can use that new instruments.

Note: The system administration database should be backed up in case of emergency such as corruption of the system administration database. After completing the basic settings such as adding users, specifying their rights, and specifying policies, back up the system administration database when no one logs on.

If the setup for the networking mode must be aborted during setup and the setup procedure must be started over, perform the following operations and then enter into the setup procedure.

When this operation is performed, all of the already completed user information and system policy settings, if any, will be cleared. Prior to the operation, record all the necessary information.

1. Delete the system administration database file on the server and copy it again to the server.
2. Double-click the resetting file (C:\GCsolution\Regist\ResetPCID.reg) on each PC to run it.



12.3.2 Registering users

After you have finished setting up the networking mode, register users and set up the system policy. To do so, choose <User Administration> and <System Policy> from the administration menu of the <GCsolution Launcher>.

In the networking mode, the user information and the system policy settings are shared among the PCs. Therefore, once you complete this procedure on a single PC, you will not need to repeat the procedure on any other PC.

For further information on <User Administration> and <System Policy>, refer to the administration manual.

❖ Using the user authentication tool

If you use the CLASS-Agent software (optional), you can manage the user information by using the user authentication tool.

The use of the user authentication tool allows you to share the list of users with other software using the user authentication tools (e.g., CLASS-Agent and LCsolution).

The initial settings in the GCsolution assume that the user authentication tool is not used. To use the user authentication tool, change the initial settings before registering users.

Double-click the AttestServer_ON.reg file in the Regist folder (normally, C:\Gcsolution\Regist) to run it. GCsolution will be changed so that the user authentication tool can be used.

For the installation of the user authentication tool and the related system configuration, refer to the instruction manual for this tool.

Note: If the settings are changed to use the user authentication tool, review the settings for the user rights in the <User Administration> window. If any user having the same name is already included in the system administration database, the password specified with the user authentication tool will become effective. Any user that is not included in the user authentication tool among the users that were specified before the change will be handled as the deleted users (these users may be restored later).

12.3.3 Registering a PC again

To register a PC for the networking environment, e.g., because of replacement of an existing PC, perform the steps described in "[12.3.1 Procedure for setting up the networking mode](#)". In step 4, select the computer name used on the former PC before the replacement, from the list of computer names in the <Instrument Maintenance> window, select [Specify PC], and then click the [OK] button.

Note: If you select a wrong computer name, temporarily close the <Instrument Maintenance>, double-click the resetting file (C:\Gcsolution\Regist\ResetPCID.reg) to run it, and then open the <Instrument Maintenance> again to select the correct computer name.

12 Appendices

12.4 About Windows user account

This note is applied in the either of the following cases:

- If you use GCsolution on WindowsXP professional with more than two users including "User" and/or "Power User".
- If you use WindowsVista or Windows7 with more than two users.

❖ Precautions for security on folders in Windows

In the condition above, in some cases, data files and folders can not be accessed by other users, because Windows default security settings of newly created folders and files are more strict or because of WindowsVista or Windows7's user account control (UAC) function.

In Windows XP-pro, access to folders created directly under the root directory (C:\) is prohibited for user accounts other than Administrators group accounts.

In order to avoid this problem, GCsolution changes the security rights for the "GCsolution" folder and its subfolders when installing it, thereby sharing data files and method files.

If a new data folder is created in any location other than the GCsolution installation folder (or its subfolders), you may become unable to perform some operations such as creating a subfolder and saving a file. It is therefore necessary to change the security settings for the folder by using the related capability of Windows.

Note: For how to change the security setting In Windows, refer to the user's manual for Windows.

Note: The access permission setting is a feature available only in the NTFS file system.

Note: WindowsXP, WindowsVista or Windows7 is equipped with the multi-user feature which enables you to change the login user without quitting the active programs on a PC shared by multiple users. If a user starts up the GCsolution when another user is using it, an error occurs and you may need to reboot the GC and PC. Therefore, do not use the multi-user feature while the GCsolution is active.

12.5 GCsolution specifications

Equipment connectable:

- When the GC-2010, GC-2014, GC-2025, GC-17A V3/V2/V1, GC-1700, GC-14B, or GC-14C* and up to two AOC-20i/20s/20d units are controlled, a maximum of 4 detectors each (3 detectors each when the sampling time is 4 msec) may be used. When the GC and up to four AOC-20i/20s/20d are controlled, 2 detectors/GC (1 detector for each line when 2 lines are used) may be used.

Note: For GC-2025, 1 line and 1 detector only .

Note: The GC-14C is destined for the Chinese market only.

Note: For any GC model other than the GC-2010 or GC-2014, the CMB-102 is required (for up to 2 channels per unit when the 2-channel board is added). Even an "Other GC model" allows you to acquire data by inputting analog signals from the detector to the CBM-102.

Note: Connection between GCsolution and GC Instruments via Ethernet is supported by GC-LAN Connect Option (optionally available).

Data acquisition:

- Min. sampling period: 4 msec (min. integration sensitivity: 0.004 $\mu\text{V}/\text{sec}.$) ... GC-2010, GC-2014, GC-2025
- Dual injection
 - compatible with high throughput analysis
- Single/Batch analysis
- Additional/Interruptive analysis
- Analysis time extension
- Snapshot
- Bracket Analysis

Data processing:

- Identification methods (window/band method, absolute/relative/multi-relative retention time method, and grouping)
 - can be feed back to the retention time in the compound table and then corrected automatically.
- 6 quantitative calculation methods (based on area/height)
 - area normalization method, corrected area normalization method, corrected area normalization with scale factor, internal standard method, external standard method, and standard addition method
- Manual peak integration
 - can be done on the chromatogram graph, stored as a time table.
- Data comparison
- Calibration
- 7 kinds of calibration curves (whether or not they pass through the origin; and weighting ($1/C$, $1/C^2$, $1/A$, $1/A^2$) are selectable)
 - linear, point to point, quadratic, cubic, mean RF, exponential, manual RF(linear, exponential)
- Number of calibration curves (16 levels x 10 points)
 - calibration curves can be created manually.
- Concentration or area/height can be selected for the X-axis of the calibration curve.
- Creation of report format:
- 18 reported items
 - System Configuration, Sample Information, Status Information, Batch Table, Method, Chromatogram, Peak Table, Quantitative Results, Grouping Result, Calibration Curve, Summary(Conc.), Summary(Compound), Picture, Text, and graphic object (line/rectangle/ellipse)



- A layout across multiple pages is supported, and 22 kinds of standard templates are attached.
- Preview

File:

- Method file, report format file, and batch file
→ SOP is supported with the template file.
- Data file (the following information is stored in the compound structure system)
→ chromatograms, data processing results, method, report format, batch, system configuration, and status information
- File conversion (AIA ANDI format [input/output], CLASS-GC10/VP4 format [input], ASCII format [output], and PDF(Portable Document Format) format* [output])

* You need to install Adobe® Acrobat® additionally.

GLP/GMP support:

- Password security
- Operational restrictions related to system administration and authorized group settings
- Locking function
- System check (GC self-diagnosis) ... GC-2010, GC-2014, GC-2025
- Status information log ... GC-2010, GC-2014, GC-2025
- Software corruption check
- Raw data integrity check
- Audit trail
- Data rollback
- All-in-one system data file structure
- Column performance calculation (USP, JP, JP2, EMG, EMG50%, Area/Height)
- QA/QC (statistical calculation)

Operational support:

- Assistant bar
- Data explorer
- File search
- Simple Instrument Parameter Setting mode (Normal mode)
- Batch table wizard
- Compound Table Wizard
- On-line manual

Automatic support:

- Automatic creation of data file names
- Automatic start/stop of the GC ... The GC-14B only provides automatic startup.
- Queuing of batch processing
- Automatic stop of batch processing
- User program startup by Pre/Postrun or criteria triggered run program function in each batch line.



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