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DEMED

Bvba Demed Hollebeek 145 B-9140 Temse
Tel/Fax ++32 (0) 3 711 26 09

Labgrab© User manual

Revision history

Rev.		Description	ORG	CHK	APP	Date (dd/mm/yy)
0.9x		Release	TDS			26/3/02
1.0		Extension with FAQ list	TDS			25/9/03

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2 Introduction

Labgrab© is a universal software package for post-processing & sampling of your captured research data:

- Labgrab© can visualize, chart & print captured data of a single or multiple cases. Graphical export into tiff, jpeg or bitmap are available.
- simple drag-and-drop interface: drag the file data onto the chart that you want to add it to the chart.
- Labgrab© can synchronize, subsample & combine sample data of single or multiple cases into other output files - see our [Labgrab© Sample wizard](#) page.
- Labgrab© output data is generated in a standard ASCII text data format allowing further processing in statistical, database or charting programs.
- import filters are being developed for different textual input files. Send us your monitor-generated data file layout; we can provide an input filter for it.

Labgrab© is designed to run on a Microsoft 32-bit Windows operating system: Win98, Win2K, WinNT, WinXP, WinMe.

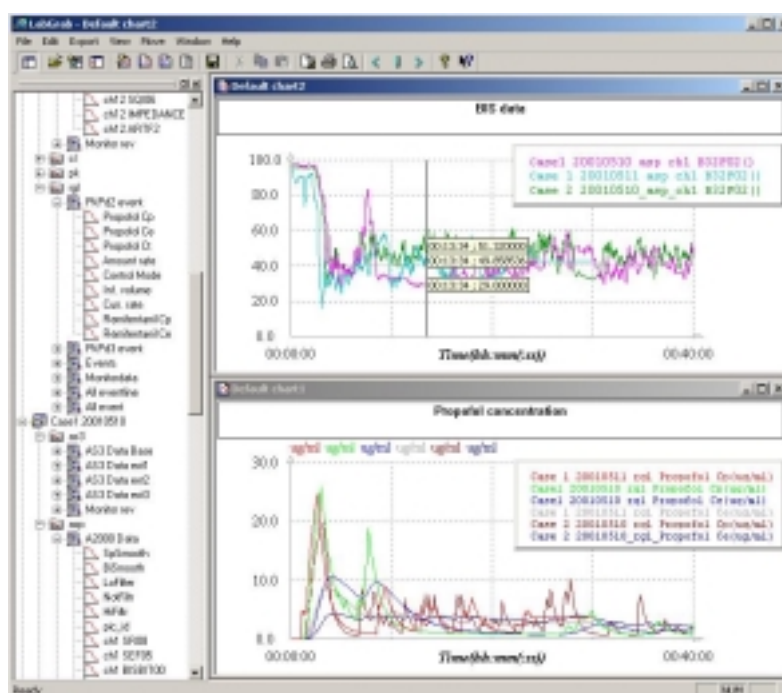


Figure 1

3 Software installation guide & registration procedure

Labgrab© comes as a self-contained installation package. The package will install the Labgrab© program, the help file and this manual.

Since the program is licensed, you will need a license key to operate it.

1. Run the 'setup.exe' program.
2. after successful installation, click the 'Labgrab©' icon on the desktop to start the program. The first time you start the program, it will calculate a key on your hardware, present you the key, and ask for an activation code corresponding to the key.
3. Contact DEMED to obtain a license code for the key code. You can cut & paste the key code into an e-mail, there are no hidden characters.
4. if you restart the program, it will again present you the key (it should be the same ;)) and you can enter the activation code. From then on, you are able to use the program.
5. Labgrab© has now been set up and is ready for use.

For license information, or if you'd have any questions, please contact:

Tom De Smet
Demed bvba
Hollebeek 145
B-9140 Temse, Belgium
Tel/fax ++ 32 3 711 26 09
Mobile ++32 475 55 24 70
e-mail: tom.desmet@demed.be
url: www.demed.be

4 User manual

4.1 Overview

The Labgrab© application is based around a dockable tree window that presents the cases currently loaded.

For charting of data, 2 chart types are available:

- the default time-chart
- the Hill-curve chart (not present in all releases)

Text data can be shown using the events viewer..

Last but not least, the sampling wizard procedure allows to sub-sample or combine-sample on large datasets.

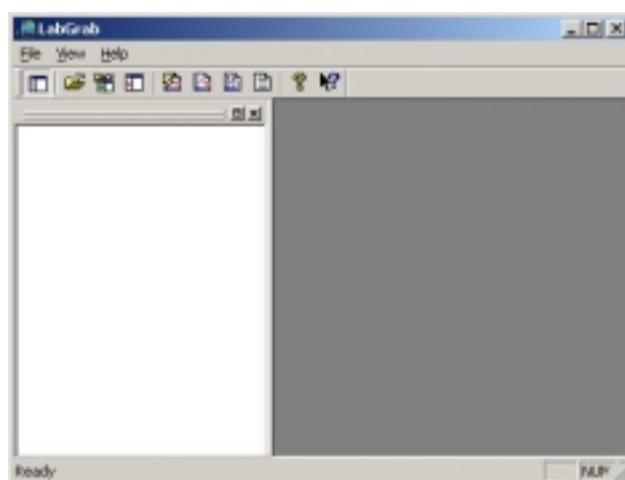


Figure 2 Labgrab start window

4.2 Menu & Toolbar

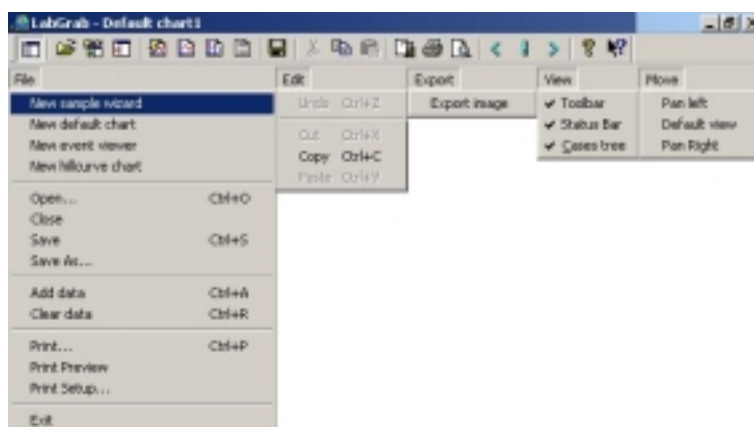


Figure 3 Menu & toolbar

Depending on the currently active document, the toolbar and the menu may vary.

4.2.1 Permanent menu-items



“New sample wizard” button starts a new instance of the sample wizard



“New default chart” opens a new chart window to drag trends into from the cases tree window.



“New Hill chart” opens a new Hill-chart window to drag trends into from the cases tree window. This button is not available in all releases, since it requires a specific data structure internally.



Use “New event viewer” to open a list window in which you can drag non-numerical data from the cases



The “Cases tree” button hides or shows the Cases tree window.



Use “Open” to open Labgrab©-generated documents. Default charts (.lgh), Hill-charts (.lgh) and event windows (.lge) can be opened. Any opened document will be appended to the cases tree window. A new window of the corresponding type is created, and the data is drawn into it with the correct colors. The chart legend is opened as well, and is moved to the location it had when the document was saved.



“Add data” will prompt you with a file dialog. Choose the files to add in the file dialog, and they will be parsed & their variables will be appended to the cases tree window. The file dialog opens with .rgl-cases by default. If you select a .rgl-file, all files with the same name but other extensions will be opened & parsed as files from the same case.



“Clear data” will clear the cases tree window



Use “About Labgrab©” to get more information on this program & the current release



“What’s this” gives direct information about a specific topic using a popup window. In case you’d need detailed information on a subject, you can also set the focus to it, and press ‘F1’ to get more detailed information.

4.2.2 Non-permanent menu-items



Use “save” to save the currently active document. Saving is only available on default chart, Hill-chart, and events view list. The chart will be saved, with the colors selected for the trends, and the legend position. Default extensions will be applied: .lgh for default chart, .lgh for Hill charts, and .lge for events view lists.



“Copy” is available on both charts and on the events view list. “Copy” will create a graphical copy of the chart to the clipboard. When you use “copy” on an events list, the events are copied to the clipboard as text lines.



“Print” will... print the chart or events view!



“Print preview” allows you to inspect the charts before really printing them.



“Export” can be used on both default chart and Hill-curve chart. This function creates a .bmp, .tif or jpg image of the chart as a separate file.



“Pan left” is available on charts. Use it to scroll to the left.



“Default” can be used to center a chart to its default position.



“Pan right” is used to scroll to the right.

4.2.3 Keyboard accelerators

Use the following keys for quick access to specific program functionality:

Ctrl + 'A'	Add data to cases tree window
Ctrl + 'C'	copy
Ctrl + 'O'	open
Ctrl + 'P'	print
Ctrl + 'R'	clear cases tree window
Ctrl + 'S'	save
Shift + 'F1'	“What’s this” - help

4.2.4 Shutdown progress window

Shutting down Labgrab© may take some time. To indicate the shutdown progress, a progress bar is shown. Shutting down Labgrab© improperly may invalidate file data or render it useless otherwise.

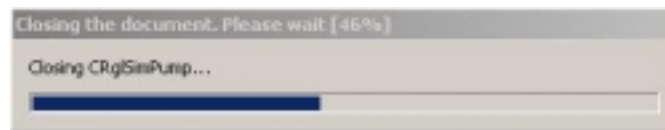


Figure 4 shutdown progress bar

4.3 Document types

4.3.1 Cases tree window



4.3.1.1 Cases tree window



This dockable window shows the data currently loaded in the application. Data is grouped in branches per case. For a detailed overview on how data is arranged in branches, see 4.3.1.3. Data in a leaf can be numerical or text data. This is indicated by a trend or text icon.

You can drag variables from the cases tree window into the charts & events windows to open them as trend or to display the contained text data.

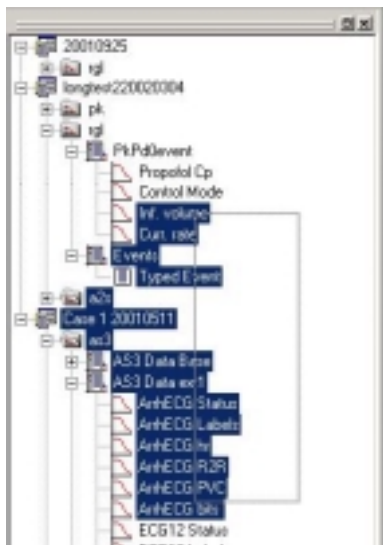


To add new data to the cases tree window, select the menu item 'File'-'>'Add data'.



Clear the list using 'File'-'>'Clear data'.

Figure 5 Case tree window



The cases tree window allows multiple selection of variables. This greatly simplifies creating charts from a large set of variables.

Multiple files selection is possible

- using 'rubber banding' method (drag the mouse over the variables to select)
- by clicking multiple variables while keeping the 'Ctrl'-button pressed to select / unselect a specific variable
- or by clicking 2 variables and holding the 'Shift'-button pressed while clicking the second one, to select all variables in between.

REMARK: only the VISIBLE lowest-level variables will be selected when using any method. In the example on the left, the variables in the "a2s" or "AS3 data base" branch will NOT be selected. This approach is taken to avoid overloading the charts with a single mouse click.

Figure 6 Selecting data in the case tree window

4.3.1.2 Add data dialog

“Add data” will bring up a file dialog that allows you to select files to add to the cases tree window. The files you select here will behave as explained in 4.3.1.3.

Rugloop© cases are the default cases that show in the file dialog. Whenever you select such case(s) to open, Labgrab© will open the specified file AND all other files with the same name but a different extension.

If you select ‘all files’, you can select a set of files with the same extension, or a set of files with the same file name. You should NOT select files with the same filename in case a .rgl-file is included (in that case, only select the .rgl-file) or select multiple files with multiple file names AND multiple extensions. (since Labgrab© won’t know then what files belong to one case).

4.3.1.3 File types & cases

Labgrab© was originally designed to process Rugloop© data files. Rugloop©-recorded cases consist of a set of files with the same name and different extensions. Also in general, Labgrab© defines a case as a set of files with the same name but different file extensions.

Files belonging to the same case will be arranged as branches in a tree of which the root is the common filename. Each file extension is a different branch in the tree.

Labgrab© will open all data files for which it knows the data layout. Normally, starting from the file extension, Labgrab will open & process the data file. In case the file format includes the names of the variables and possibly the units, Labgrab will extract & show these variables automatically in the cases tree window. This simplifies importing & processing data files.

RugloopII© files may internally contain multiple data lines per file, with each line having its own set of variables. When encountering such files, Labgrab© will start a branch per linetype, and will arrange all variables that occur in such line within that branch to get a more structured variables display.

In case you select a .rgl-file, Labgrab© knows this file is part of a Rugloop© case and will automatically open all companion files. Therefore, you don’t need to select multiple files if a .rgl-file is involved as well.

For other files, you can open either a set of files with the same name, which Labgrab© will arrange in the same case, or you can open a set of files with the same extension, which Labgrab© will arrange in a different case each.

Concerning the internal file data layout: Rugloop© files have a specific internal layout that Labgrab© will recognize automatically. Other text files can be recognized in case the file structure was added to Labgrab© as an import filters. Import filters for several file layouts are under development; if you have a specific file generated by a specific monitor, you can always request us to integrate the format into Labgrab©. We will regard each request for its potential, and implement the format if it is popular.

The file format of the Labgrab©-generated files (e.G. the wizard output files) equals the RugloopII© - format. These files can be read automatically in order to create charts from wizard output files.

4.3.1.4 File data

Labgrab© will generate output file data, e.g. when processing files with the sample wizard. The data format is equal to the format used in RugloopII© files.

All lines written in a Labgrab© output file have a checksum at their end, which allows reading them back in afterwards.

An output file can contain one or multiple different output data lines. All lines are identified by their identification string, unique for the type of line. This allows sorting the lines afterwards. Each file starts with a fixed file header, containing Labgrab© and file format revision numbers, and a set of line type headers.

A line type header has 3 lines that uniquely identify all lines appearing in the file:

(item separator, or LINE_ITEM_SEPARATOR, is assumed pipe character here)

```
L1: "LineType"|"RAppTime"|"RCaseTime"|"SystemTime"          |longname D0 ... DN
L2:  Gener. type|          |          |          |shortname D0..DN
L3:  LINE ID   |"25ms"    | d hh:mm:ss|mm/dd/yyyy hh:mm:ss.d |units D0..DN
```

The longname, shortname & units are repeated for the number of variables written in the line.

Each output data line then looks as:

```
LINE ID|APPTIME|CASETIME|SYSTEMTIME|data0|data1....|dataN
```

In practice:

- file header line:

```
RGL checked files|version|2.01|RugloopII v. |5.0|Date |21 november 2000|||ü
```

- line header:

```
LineType   |RAppTime|SystemTime          |BIS|EMG|SQI|Suppression|SEF95|Tot. Pow. |†
3          |        |                    |BIS|EMG|SQI|Supp      |SEF95|TP        |$
A2000 Data|1/25s   |mm/dd/yyyy hh:mm:ss.d|    |dB |%  |%          |Hz   |dB        |š
```

- data line: just starts with the line name, followed by the time & the values for the variables, depending on the linetype as described above:

```
A2000 Data|12468|01/06/2001 17:12:05.0|||55.4400|-
A2000 Data|12473|01/06/2001 17:12:05.0|||55.4400|@
```

REMARK: when the data to be written to file is invalid, an INVALID_DATA_STRING (currently xxx) is written to file. This allows clear distinction between valid & invalid data.

At file level, a checksum preceded by an item separator is added to the lines. All lines in the output (input) file have the same number of line_item_separators. This simplifies importing them into spreadsheets etc.

4.3.2 Loading RugloopII® and Labgrab® data in a spreadsheet – Microsoft Excel®

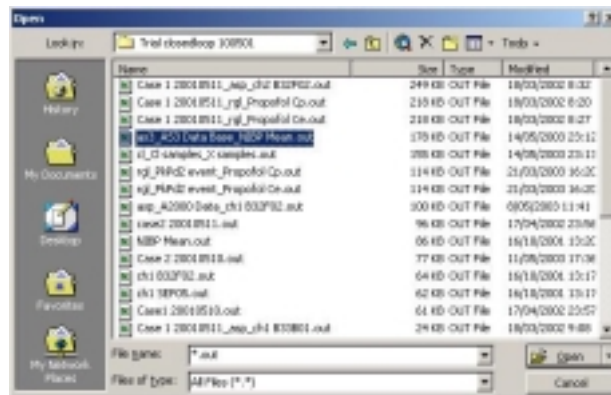
The file data format layout described in 4.3.1.4 is used by both RugloopII® generated files as by the Labgrab® program. (obviously the data in these will be different). The files are ASCII text files that can be read using any spreadsheet program. They may need to be slightly tuned before they can be used in a statistical package as well. Opening either RugloopII® generated or Labgrab® generated files (the .out-files) in Excel is straightforward:

IMPORTANT REMARK: BEFORE opening any RugloopII® / Labgrab® file in Excel, you need to set the international number settings correct: RugloopII® / Labgrab® files use the ‘.’ as a decimal separator. You need to do this in Windows from the Control panel:

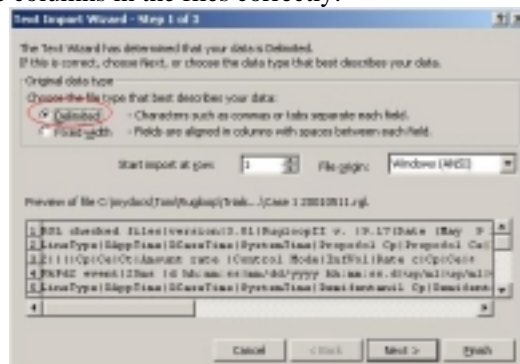
Windows 2000: ‘Start’->‘Settings’->‘Control panel’->‘Regional options’; in the displayed dialog, select the ‘numbers’ tab. Make sure the ‘Decimal symbol’ is set to the dot (‘.’), and set the ‘digit grouping symbol’ to space ‘ ’)

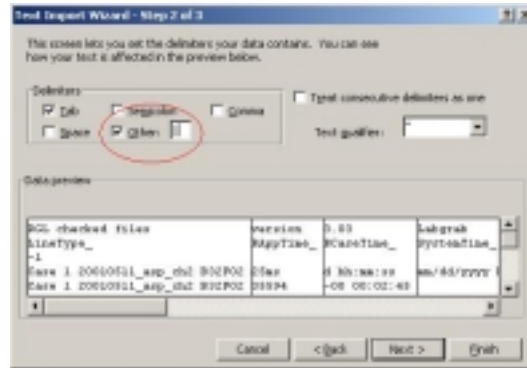
Windows XP: ‘Start’->‘Settings’->‘Control panel’->‘Regional options’; TBD

- open Microsoft Excel®
- From within Excel, choose ‘File’->‘Open’.
- In the ‘open’ dialog, set the ‘Files of type’ to ‘All files (*.*)’ or literally type ‘*.out’/‘*.rgl’/... or any extension you’d like to open. Next, select the file(s) to open

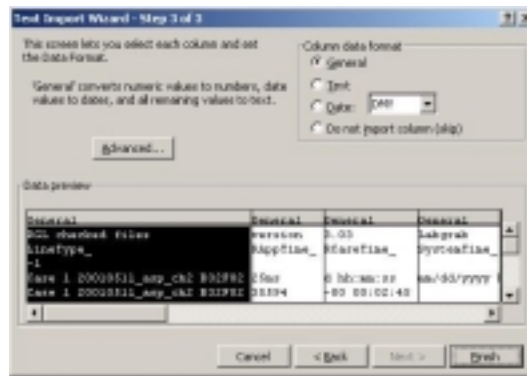


- Since the RugloopII® / Labgrab® sample wizard generated files are not native Excel files, the ‘Text import wizard’ is presented automatically. RugloopII® and all Labgrab® generated files are ASCII text files using the ‘pipe’ character (|) as delimiter. Selecting the pipe character enables Excel to distinguish the columns in the files correctly.





- the next page in the Microsoft Excel © text import wizard does not require modifications.



- the opened Labgrab © or Rugloop © files in Excel show as below. Some general comments:
 - column A has the line type (see also 4.3.1.4)
 - column B has the relative application time: this is the time, in 25msec units, since the RugloopII© application was started. This column is only valid for original RugloopII©-generated files, NOT for Labgrab©-generated files.
 - column C carries the relative case time: the time since you've pressed the 'start' button in RugloopII©. THIS TIMING IS USED TO SYNCHRONISE MULTIPLE CASES. In RugloopII©-generated files, the relative case time in this column is zero until you press the start button, in Labgrab©-generated files, the relative case time actually counts down in negative numbers, until time zero is reached.
 - Column D has the system time: this is the absolute PC time on which Rugloop© was running, in the format specified at row 4.
 - Row 1 is a general RugloopII ©/ Labgrab© file identifier
 - Row 2 carries the long variable name for all data
 - Row 3 has the short names for the variables
 - Row 4 contains the data units (since the displayed data is BIS data, which is unit less, no units are displayed).

Microsoft Excel - Case 1 20010511_esp_ch2 B3CF02.wk

File Edit View Insert Format Tools Data Window Help

HI A B C D E F G H I J K L M N O P Q R S T U V W X Y Z

1 BOL checked files version 3.03 Logbook 1.9 Date Mar 14 2002 Code 0

2 LastType_ RAppTime_ RCaseTime_ SystemTime_ ch2 B3CF02_case2 20010511 ch2 B3CF02_case1 can200 ch2 B3CF02_Case 2 20010511

3 BSch2 BSch2 BSch2

4 Case 1 20010511_1 2584 d 00:00:00 new/td/yyyy 00:00:00 d

5 Case 1 20010511_1 37994 00:00:01:50 97 430002 97 430002

6 Case 1 20010511_1 37994 00:00:01:50 97 300003 97 300003

7 Case 1 20010511_1 37994 00:00:01:45 97 430002 97 430002

8 Case 1 20010511_1 38194 00:00:01:40 97 599998 97 599998

9 Case 1 20010511_1 38394 00:00:01:35 97 599998 97 599998

10 Case 1 20010511_1 38594 00:00:01:30 96 599998 97 900002

11 Case 1 20010511_1 38794 00:00:01:25 96 900002 97 900002

12 Case 1 20010511_1 38994 00:00:01:20 96 900002 97 900002

13 Case 1 20010511_1 38194 00:00:01:15 96 599998 97 900002

14 Case 1 20010511_1 38394 00:00:01:10 97 430002 58 799999 97 900002

15 Case 1 20010511_1 38594 00:00:01:05 97 5 61 599998 97 900002

16 Case 1 20010511_1 38794 00:00:01:00 97 5 58 5 97 800003

17 Case 1 20010511_1 38994 00:00:00:55 97 5 61 599998 97 900002

18 Case 1 20010511_1 40194 00:00:00:50 97 599998 61 599998 96

19 Case 1 20010511_1 40394 00:00:00:45 97 599998 62 599998 96

20 Case 1 20010511_1 40594 00:00:00:40 97 599998 52 430002 96 599998

21 Case 1 20010511_1 40794 00:00:00:35 97 5 58 700001 96 599998

22 Case 1 20010511_1 40994 00:00:00:30 97 5 58 96

23 Case 1 20010511_1 41194 00:00:00:25 97 599998 68 96

24 Case 1 20010511_1 41394 00:00:00:20 97 599998 71 430002 96

25 Case 1 20010511_1 41594 00:00:00:15 97 599998 74 300003 96

26 Case 1 20010511_1 41794 00:00:00:10 97 599998 79 430002 96

27 Case 1 20010511_1 41994 00:00:00:05 97 599998 79 5 96 599998

28 Case 1 20010511_1 42194 00:00:00:00 97 599998 79 300003 96

29 Case 1 20010511_1 42394 00:00:00:35 97 599998 79 599998 96

30 Case 1 20010511_1 42594 00:00:00:30 97 430002 90 96

31 Case 1 20010511_1 42794 00:00:00:25 97 430002 79 599998 96

32 Case 1 20010511_1 42994 00:00:00:20 97 300003 79 599998 97 900002

33 Case 1 20010511_1 43194 00:00:00:15 97 300003 81 900002 97 900002

34 Case 1 20010511_1 43394 00:00:00:10 97 300003 79 599998 96

Microsoft Excel - Case 1 20010511_esp_ch2 B3CF02.wk

Ready Sum=0

Further remarks:


- for Labgrab©-generated files, the interval between opening Rugloop© and pressing ‘Start’ is not the same for all patients, so not all columns will start at row 5: empty datapoints will exist for those patients where the delay between opening the case and pressing start was shorter.
- To allow processing Labgrab© data in a statistical package that derives variable names from column headers, you first need to open the file in Excel, strip all yellow-colored information, and save the file again to allow subsequently opening it in SPSS for example.
- When opening a RugloopII© / Labgrab© - generated file from the Windows explorer, specifying Excel to open the file, the text import wizard is not shown. Instead, the data is all grouped in the first column:

[illegible]

This can be corrected by selecting the first column ONLY, and by selecting ‘Data’ -> ‘Text to columns’, which will bring up again a wizard similar to the ‘Text import wizard’ described earlier in this chapter.

- More frequently asked questions about importing data can be found in chapter 4.5.

4.3.3 Default chart window

 The default view window has a chart, a legend rectangle and a title rectangle. The window can be used for showing numerical trend data. You can tune your chart of choice by dragging trends into it from the cases tree window. Trends from the same or different cases can be combined in a chart (e.g. the drug concentration trend for multiple cases): the cases will be synchronized automatically.

4.3.3.1 chart

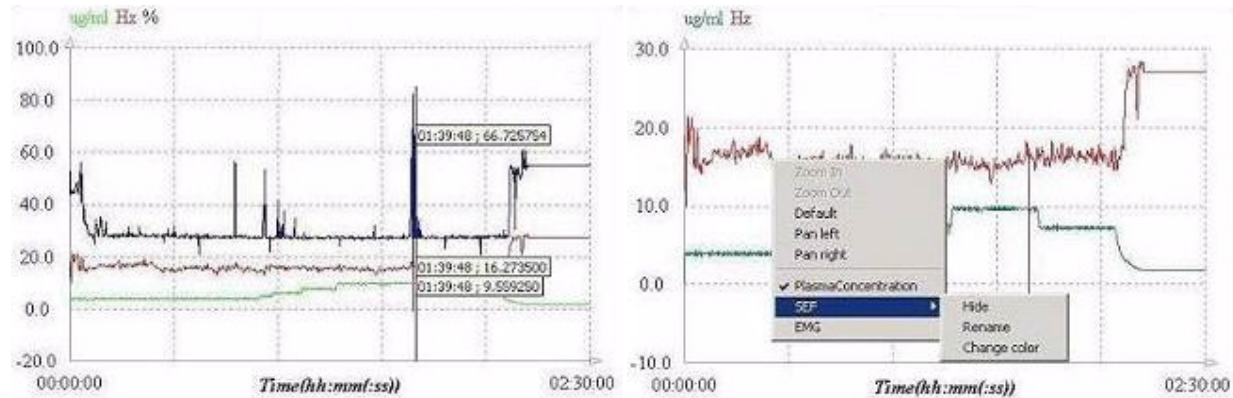


Figure 7 default chart

4.3.3.1.1 Context menu & zoom

Use the context menu of the chart (right-click the mouse) to tune trends. If the context menu is called while the mouse is ON a trend, a submenu is available for that trend allowing you to (temporarily) hide, rename or change the color of a trend.

The other trends will be available in the context menu as well: visible trends will be checked, hidden trends unchecked. To show a currently hidden trend, just click it.

The context menu will always allow you to pan left/right the trend display, or to go back to the original trend layout.

To zoom in or out the chart, drag the mouse while holding down the right mouse button. The context menu appearing afterwards will allow you to zoom in or out the chart (only the time axis can be zoomed; the values axis is auto-scaling).

The context menu also allows to hide or show all trends at the same time.

Panning the chart can also be done using the dedicated pan buttons:



4.3.3.1.2 Trend values display

to show the actual values of the trends in the chart, click & hold the left mouse button. Tooltips will appear that show the trend values at the currently set time. The tooltips will be updated as you move the mouse. Tooltips are only available if a limited number of trends is present in the chart window.

4.3.3.2 legend

```
PlasmaConcentration (ug/ml)
SEF (Hz)
EMG (%)
```

The chart legend will automatically update when a trend is added to the chart, shown or hidden. The trends' names & units are shown in the trends' color. You can freely move the legend. Sizing the legend vertically will also size the applied font; size the legend horizontally to fit the text.

4.3.3.3 title

Update this field with your desired chart name, for printing purposes.

4.3.3.4 save / open



You can save a created chart for future use. If you press the 'save' button, you can select the file name to store the chart into. The default extension for default charts is ".lgd". The chart data is stored, as well as the trend colors and the legend location.

REMARK: this method is preferred if you want to make changes to the chart data afterwards, or if you'd like to use the tooltip/current value functionality on the loaded chart afterwards.

If you'd like to store the current chart in its zoomed state, with exactly the current chart position, it is preferred to use the export method which will export the chart graphically.



To open a chart, press the 'open' button, and select your stored files with the .lgd extension. The chart will open, and display all trends. The legend is sized as well.

REMARK: when opening a chart this way, the chart file data is added to the cases tree dialog as well.

4.3.3.5 export



If you want to make the current chart data available as an image for other applications, you can select 'export' to create an image file. A dialog will open to ask you where you want to put the graphical data. 3 export formats are supported: bitmap, JPEG and TIFF format. Select your desired format, and click OK.

REMARK: since the chart data exported this way is graphical, it cannot be reloaded afterwards for further manipulations in Labgrab©. (e.g. for a different zooming level). If you want to manipulate the chart data afterwards, you need to save it. (see 4.3.3.4).

4.3.3.6 Copy



The 'copy' operation will create a graphical image of the current chart on the clipboard. You can paste this image in other Windows applications.

4.3.3.7 printing / print preview



A created chart can be printed directly. Use 'Print' or 'print preview' for the printing functionality.

4.3.4 EventView

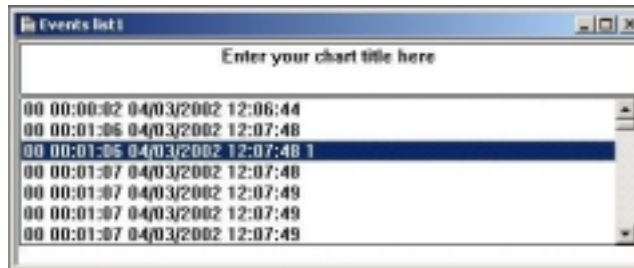


Figure 8 Event viewer window

This window is created to show non-numerical data in a text format. If you drag a text variable into this window, all entries of the variable will be opened in this list. This will allow you to get a quick overview of, for example, the typed events that you've entered.

4.3.4.1 title

Update this field with your desired events list name, for printing purposes.

4.3.4.2 save / open



You can save a created events list for future use. If you press the 'save' button, you can select the file name to store the data into. The default extension for event lists is ".lge".



To open an events list, press the 'open' button, and select your stored files with the .lge extension.

4.3.4.3 Copy



The 'copy' operation will create a copy of the events in the list as text. You can paste this text in other Windows applications.

4.3.4.4 printing / print preview



An events list can be printed directly. Use 'Print' or 'print preview' for the printing functionality.

4.3.5 Sample wizard



The Labgrab© sample wizard will help you to create extracted data files from large datasets that you've captured using RugloopII© or other data capture programs.

Data sampling is provided within cases (to create a sub-sampled file from the cases' multiple files) or over cases (to create a file that contains, for example, the synchronized & sub-sampled blood pressure values for all your 48 cases).

The sample wizard can operate on multiple cases with the same layout. For the definition of cases & files in Labgrab©, see 4.3.1.3. According to this definition, a 'case' is a set of files with the same name and a different extension. Since such a 'set' of files can also be a single file, the sample wizard can be applied to virtually any combination of datasets.

The output of the file wizard is one or multiple files. These files are added to the cases tree window of the current Labgrab© instance, to simplify creating charts from the processed data.

Since the sample wizard has a lot of settings, it is built as a wizard consisting of 4 pages. Data processing is an off-line process: once all parameters are set in the wizard, processing starts & will generate the output files as specified.

4.3.5.1 Page 1: select example case page

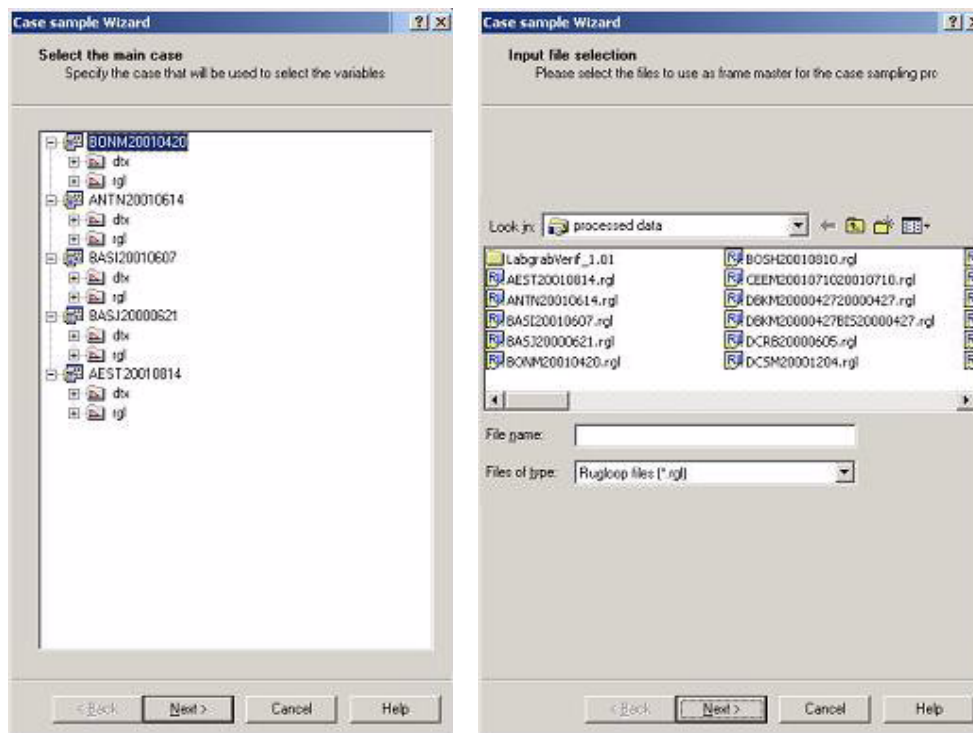


Figure 9 Sample wizard: select example case

This is page 1 out of 4 of the Labgrab© sample wizard.

The Labgrab© sample wizard will operate on a set of cases with the same data layout. To allow you selecting variables to process, the sample wizard needs a case with a representative layout.

In case you have loaded cases already into the cases tree window, the first page of the wizard will present you the cases that have been loaded. Otherwise, you will be shown a file dialog in the wizard. Remember that, according to 4.3.1.3, a Labgrab© case can be:

- a .rgl-file with all other files bearing the same name and other extensions
- or a combination of multiple (or even just one) non-rgl files having the same name and a different extension.

In the file dialog, you should, therefore, select either the representative rgl-file or a set of files with the same filename, that Labgrab© will then regard as a single case.

IMPORTANT REMARKS:

- only those files that Labgrab© has an import filter for will be validly processed. If you are unsure whether this is the case for a specific file, you can always try to load the file in the cases tree dialog before opening the sample wizard. If your file layout is not supported, you can contact us to obtain support for it.
- Labgrab© expects that all cases to process have been captured with the same structure (number of files & file extension, type of data, number of variables, sequence of variables) as the case you select as representative here.

4.3.5.2 Page2: specify sampling options

Page 2 of the sample wizard is used to gather information about:

- the type of sampling you want to perform on the data
- the sample interval & sample offset to use for data creation in the output files.
- the default data extraction method: this selection indicates the default extraction method for sampling. The next page will allow to correct this default method for each variable selected for processing.
- what you want to write in the output file when the sampling methods generate no data for specific datapoints in the output file.

The screenshot shows the 'Case sample Wizard' dialog box, specifically the 'Case Sample Type' page. The title bar reads 'Case sample Wizard'. Below the title bar, the text 'Case Sample Type' is followed by the instruction 'Please select the sampling algorithm type & specifications:'. The dialog is divided into several sections:

- Please select the output of the case sampler:** This section contains two radio buttons. The first is 'CaseSubSample: extract multiple variables from a specific case and combine them into a new file'. The second is 'CaseCombineSample: extract the same variable from multiple cases and combine them into one file'. To the right of these options is a text field labeled 'Output file extension' containing the text 'out'.
- Case sampling interval:** This section features a horizontal slider with a vertical marker. Below the slider, the value '5s' is displayed.
- Case sampling offset (case time):** This section features a horizontal slider with a vertical marker. Below the slider, the value '0s' is displayed.
- Default data sampling algorithm:** This section contains a list of radio buttons for different sampling methods:
 - Average values over sampletime-centered interval [,]
 - Average values over interval before sample point [,]
 - Last value before sample point [,]
 - Last value before sample point, exclusive in interval [,]
 - Last value in sample point-centered interval [,]** (This option is selected)
 - Last value in samplepoint-centered interval, exclusive in interval [,]
- Unavailable datapoints:** This section contains three radio buttons:
 - Leave empty** (This option is selected)
 - write value: []
 - write text: []

At the bottom of the dialog, there are four buttons: '< Back', 'Next >', 'Cancel', and 'Help'.

Figure 10 Sample wizard: sampling options page

4.3.5.2.1 Sampling output type

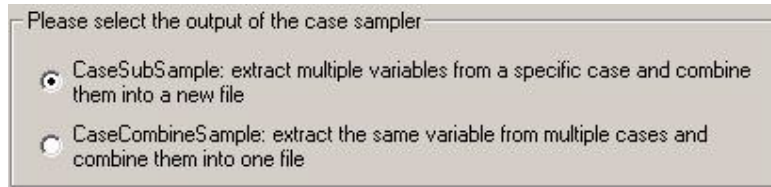


Figure 11 Sample wizard: sampling output type

The Labgrab© sample wizard performs 2 kinds of sampling. Each sampling method can be applied on multiple cases in one run.

- *the CaseSubSample method* is useful if you want to create new output files for a set of cases, e.g. if 2 data files exist per case that actually contain data on the same case, the subsample method allows to create one output file on such case that contains a combination of variables in either file. For each case specified in page 4 (Input file page), an output file will be created that contains the combined sampled variables for the concerning case, as specified in page 3. This sampling method may be interesting as well if you have large files that are actually over-sampled: it allows to create sampled data files that are easier to handle.
- *the CaseCombineSample method* is useful to combine variables from multiple cases into an output file per variable. For each variable selected in page 3 (Variables select page) an output file is created that contains the variable's value taken from all cases specified in page 4 (Input file page).

4.3.5.2.2 Data sampling algorithms

Sampling data means that we define output sample moments that are equidistant in time. The distance between the sample moments is the sampling interval. To calculate the output value at a sample moment, we define an interval around or before the sample moment. All input samples that occur within this interval are gathered to calculate a representative output value upon. The calculated value is then written into the output file as the sample value at the considered sample moment.

Since the sample moments are equidistant in time, the intervals applied on the input data for calculation will all be the same length as well.

For Labgrab© applications, we apply the following rules to the input data sampling intervals:

- sampling intervals are successive; and all have the same length.
- intervals can be located completely BEFORE an output sample time, or centered around it.
- Intervals are OPEN at the beginning and CLOSED at the end: if an input sample point occurs exactly at the edge between 2 intervals, it will be allocated to the FIRST interval, NOT to the second one.

An optimal sampling method depends on the nature of the variable. For lifesign data, an average of the input samples in the sampling interval would probably be most suitable as sampled output value. On the other hand, the most accurate way to sub-sample an infused volume variable is to take the last available sample before the output data time. A wrong sampling method may forge the results of your statistical data package results on the data as well..

To accommodate for all these requirements, the Labgrab© sample wizard provides 6 different sample methods. The appropriate sample method can be selected per variable to be processed. To visualize the sampling method, we will explain each one of them based on the timeline below.

The timeline shows 3 input data values I1..I3, and 3 equidistant sample moments S1..S3. For educational purpose, I2 is located exactly in the middle of S1..S2, and I3 is located exactly at S3.

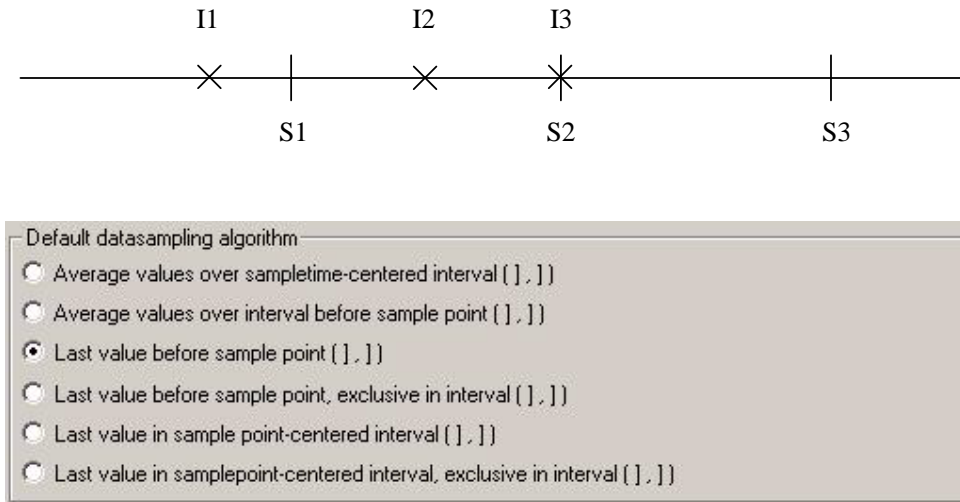
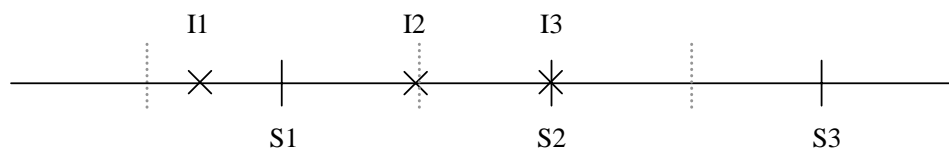


Figure 12 Sample wizard: averaging methods

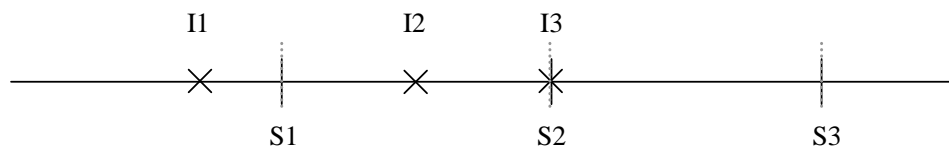
Available sample methods are:

- average values over sampletime-centered interval: each sample moment result is the average of the datapoints in the interval centered around the output sampletime. If no data is available, no output datapoint is calculated.

Applied on the example, we define the sampling intervals as shown below. In each interval, we calculate the average value of the data values. At sample 1, we get the average of I1 and I2 (since the interval is closed at the end), at S2 we get I3, and S3 has no output value.

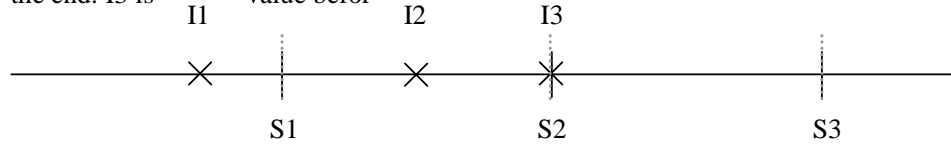


- average values over interval before samplepoint: each output datapoint is the average of the data points in the interval before the output sampletime. If no data is available, no output datapoint is calculated. We now define the sampling interval as ending at the sample time. Sample moment 1 now has I1, S2 equals the average of I2 and I3 (again, because the interval is closed at the end) and S3 again has no output value.

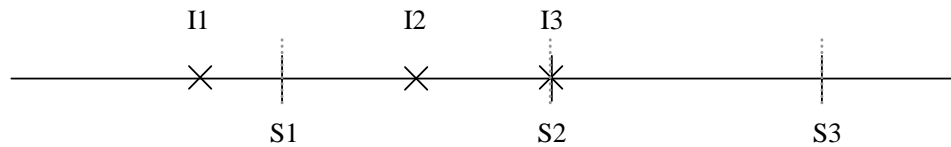


- last value before sample point: each output datapoint is the last available data point before the output sampletime. REMARK: this is not interval-limited: if no data is available in the interval, the value from the previous interval is repeated. Output starts from the first available sample and continues, repeating the last available input sample, until the output file ends.

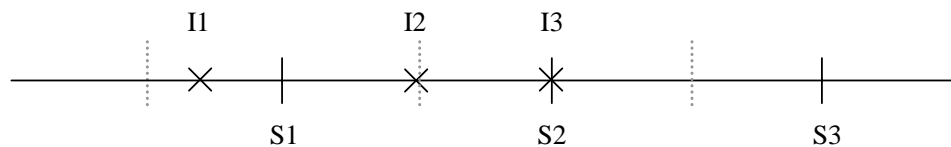
Applied on the example, S1 gets I1, S2 gets I3, and S3 ALSO gets I3. Since we only take into account the last value, I2 is ignored. I3 is assigned to S2, again, since the interval is closed at the end: I3 is the last value before S2.



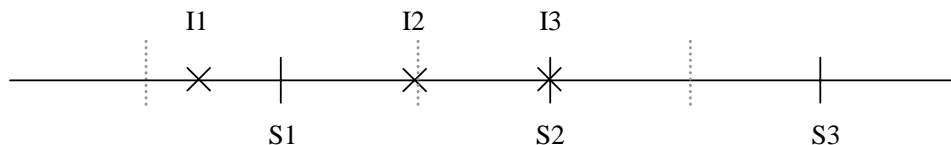
- last value before sample point, exclusive in interval: each output datapoint is the last available data point before the output sampletime, IF sample data is available in the interval. If no data is available, no output datapoint is calculated. In our example, S1 still gets I1, S2 still gets I3, but S3 is now empty since there is no data point in the interval before it.



- last value in sample-point centered interval: each output datapoint is the last available data point in the interval centered around the output sampletime. This may be beneficiary if you want to capture data samples coming in at time $(K \cdot \text{interval} + 1)$ for an output at $K \cdot \text{interval}$. REMARK: this is not interval-limited: if no data is available in the interval, the value from the previous interval is repeated. Output starts from the first available sample and continues, repeating the last available input sample, until the output file ends. In the example, S1 now gets I2, S2 gets I3, and S3 ALSO gets I3.



- last value in sample-point centered interval, exclusive in interval: each output datapoint is the last available data point in the interval centered around the output sampletime, IF sample data is available in the interval. If no data is available, no output datapoint is calculated. Again, S1 gets I2, S2 gets I3, and S3 now is empty again.



IMPORTANT WARNING: the sample method is a direct sampling method: you are **STRONGLY** advised to verify the calculation of the average methods in case your monitor sends status codes as well. (otherwise your status code may tweak the average calculations to nonsense values). We will be providing 'illegal values' filtering soon, allowing you to indicate what values are illegal.

4.3.5.2.3 Sampling interval /sampling offset



Figure 13 Sample wizard: interval sliders

Use these sliders to select the Labgrab© sample Wizard output data interval and sampling time offset. The output data sample time is calculated as $(K \cdot \text{interval} + \text{offset})$. This allows to generate output data at 5s, 15s, 25s, ... instead of 0s, 10s, 20s, ...

4.3.5.2.4 Unavailable data

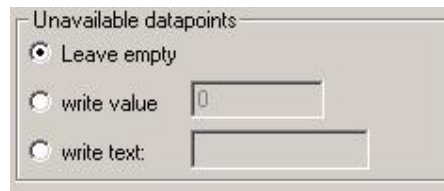


Figure 14 Sample wizard: unavailable data options

The sample methods described in 4.3.5.2.2 may produce empty datapoints for some sample methods. In the 'unavailable data' control you can indicate what data is written instead of empty output datapoints. The space can be left empty, a fixed value (e.g. -32535) or a fixed text (e.g. XXX) can be written. Your selection will depend on what is required for further processing of the data.

4.3.5.3 Page3: select variables

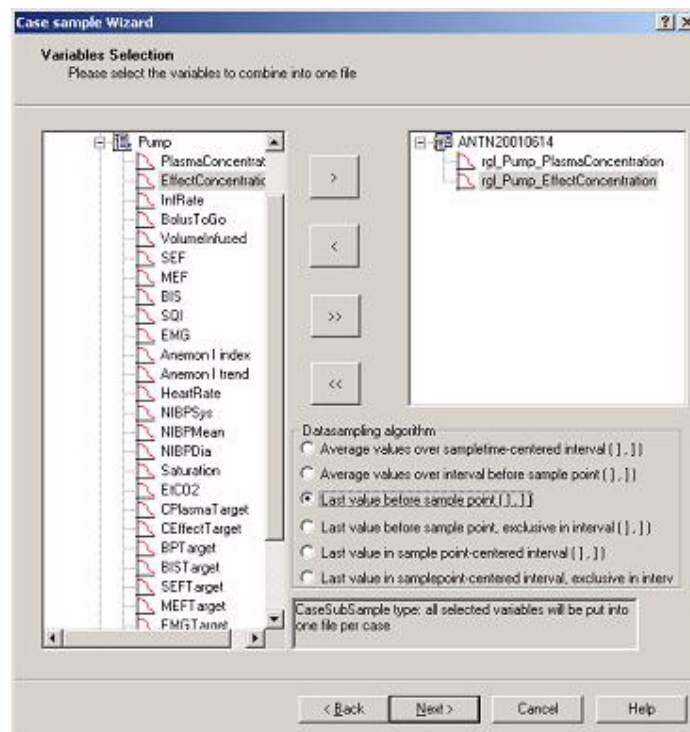




Figure 15 Sample wizard: select variables

This is page 3 of 4 of the sample wizard. This page allows you to select from the representative case the variables to be processed. The leftmost tree window shows all variables found in the input case file(s), sorted by the input file and per line; the rightmost list shows what variables will be processed. The icons indicate the data type of the variable. Possible icons are  and , indicating the variable is trend (numerical) data or text data. The sample wizard will only work correctly on numerical data.

Select any variable in the leftmost list, and press the [>] button to add it to the output list. The output variable name is compound from the filename, line name & variable name of the input variable. To remove a selected variable, highlight it in the rightmost list and press the [<] button. Adding/removing all variables to/from the output list is done using the [>>] resp. [<<] buttons.

For each variable in the rightmost list, the sampling method is set to the default method specified in page 2. To correct the sample algorithm for a specific variable, highlight the variable in the rightmost list, and set to the measure type of your choice for each variable.

Both sample output types CaseCombineSample and CaseSubSample allow selecting multiple variables to output. For CaseSubSample, an output file containing the indicated variables will be created per case; caseCombineSample will create an output file per variable, containing the variable from all selected cases.

As a mnemonic, the selected sample output type is indicated on the page as well.

4.3.5.4 Page4: select files to process

This is the last page of the sample wizard. Here, you can select what cases the wizard should act upon.

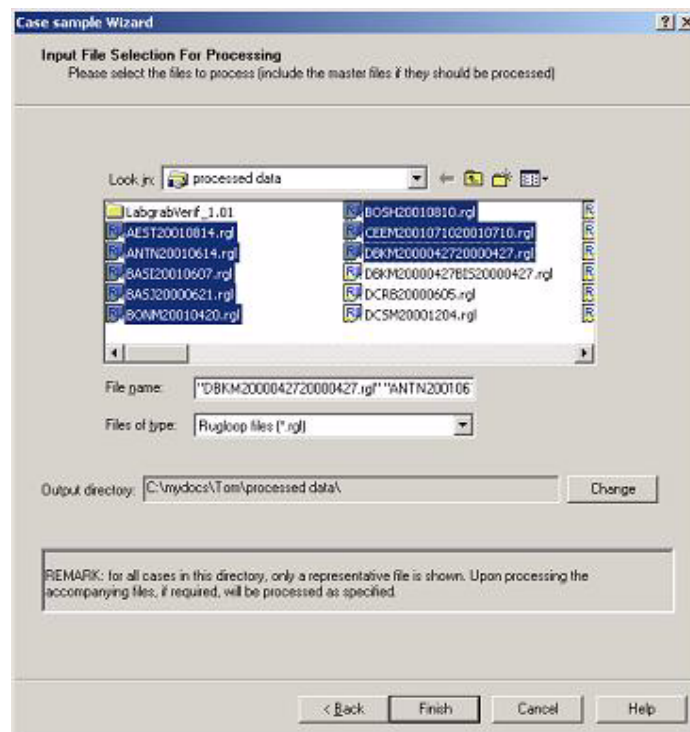


Figure 16 Sample wizard: select cases to process

For all cases that are eligible for processing according to your settings, a representative file is shown. You only need to select these files for the cases you want to process. All related case files will be opened during the processing.

DO NOT FORGET: if the case that you've selected as representative case needs to be processed as well, you have to select the representative file for that case as well.

Select all cases to process, and change the output directory to put the output files into, and press 'Finish' to start processing.

Processing will create the output files and add them to the cases tree view. Since this is a very complex operation, a detailed log file is created that enables you to verify what cases have been processed, and whether any error occurred in the process.

4.3.5.5 After processing

When the sample wizard has finished, the processed files are stored on your hard disk in your selected output directory, with the selected extension. You can open the generated files in three ways:

- In the cases tree window, the generated files are automatically added (Figure 28 Sample wizard tutorial: viewing the generated data) You can use the appearance here to drag any processed variable from the generated files into the charts, as you would do with original RugloopII© files.
- After closing Labgrab©, and re-opening, you can add the processed files to the case tree view again, using the 'add data' button. To add a specific processed file, you need to alter the displayed files extension to 'all files' or, better, to the file extension you've selected for your processed files.



IMPORTANT REMARK: see 4.3.1.3 File types & cases for a detailed explanation about the difference between a file and a case in Labgrab©. Most processed data will have file names different from the original case and, therefore, will be considered as a single file.

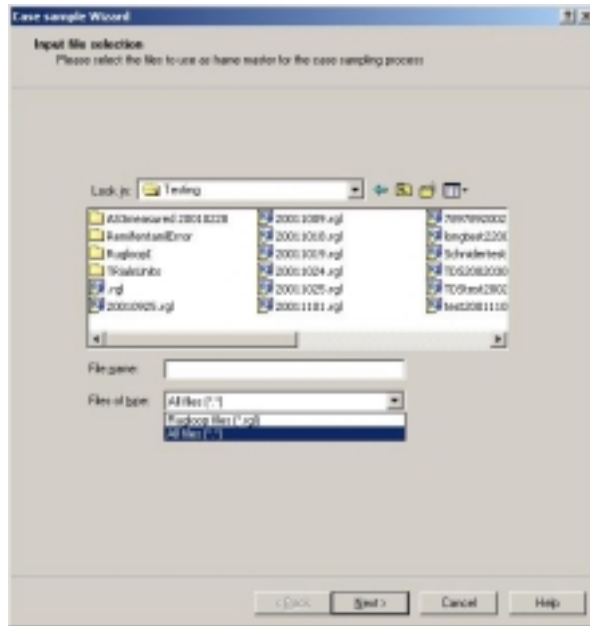
- you can open the processed files from your hard disk using a spreadsheet, for example, Microsoft Excel©, as ASCII data files containing your processed data. (see 4.3.2)

If you have retained the default file extension “out”, the generated data files will not overwrite the original RugloopII© files.

4.4 Sample wizard tutorial

4.4.1 Generic part: page 1

This tutorial will handle 2 examples to show you how easy large sets of data can be processed using the sample wizard.

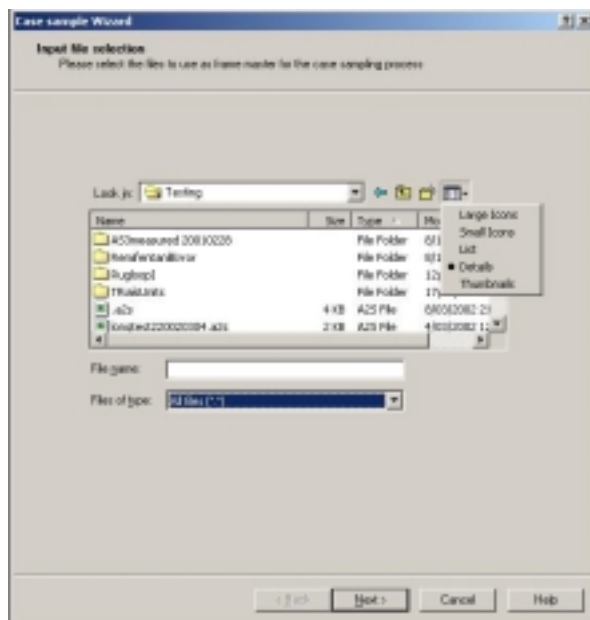


We start the wizard from the assumption that no cases have been loaded before. The first page of the wizard shows us the default file dialog page. In the file dialog page, we will search for the directory that contains our captured cases (they all have to be in the same directory).

If we'd be dealing with Rugloop©-captured cases, we can select any of the .rgl-files displayed by default in the file dialog, and use this file as representative case. For educational purpose, we will NOT do this, but combine our own case using a set of files.

In the file dialog page, we select the 'All files' section.

Figure 17 Sample wizard tutorial: select example case



To allow an easy selection of the files making up one case, we sort the files: show the details on the files, and click on the "Name" column in the file dialog.

Figure 18 Sample wizard tutorial: select example case (b)

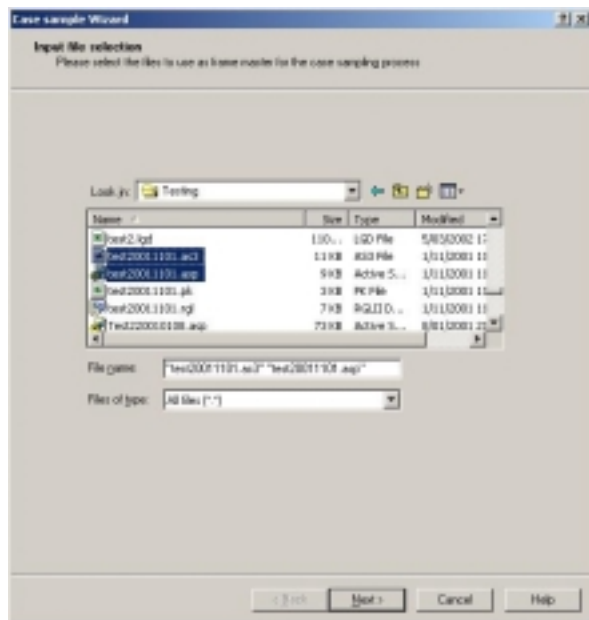


Figure 19 Sample wizard tutorial: select example case (c)

We search the files composing the case we want to process, and select the files with the extension .as3, .asp from a single case, since we only want the NIBP and BIS values.

Now, we press the 'next' button, to go to the next page.

While going to the next page, the selected files are opened, and a case is built in the cases tree window.

We will split the tutorial here. If you're interested in a CaseCombineSample example, you should continue at 4.4.3. For a CaseSubSample example, you can continue in 4.4.2

4.4.2 CaseSubSample

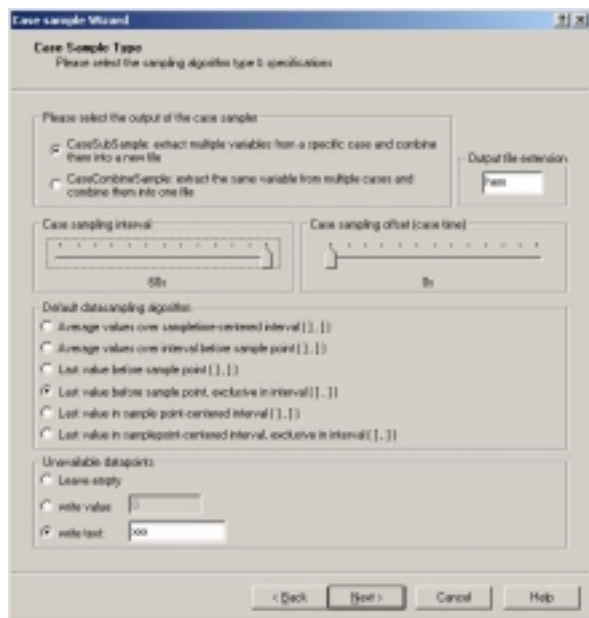


Figure 20 Sample wizard tutorial: case sample type page

Suppose we want to combine the NIBP hemodynamic parameters with the BIS values into one output file for a set of cases. Both variables have been captured with a different frequency: the NIBP parameters are usually set to a frequency of +/- 1 minute, whereas the BIS data is entering at least once per 10 seconds.

To combine such different datasets in a case, we need the sampling wizard. We select the CaseCombineSample option, and change the file extension to .hem: since the output file will bear the case name, we need to create a new extension to indicate they are the processed files. Since the NIBP data was captured at an interval of 60s, we set the sampling interval to 60s as well. The default sample method is set to

‘Last value before sample point, exclusive in interval’: since we will be processing the NIBP values captured at 60s interval: we don’t want the sample wizard to create sample points where it is not necessary. When no data is available, we want ‘xxx’ in the output file.

Press ‘next’ to goto the next page.

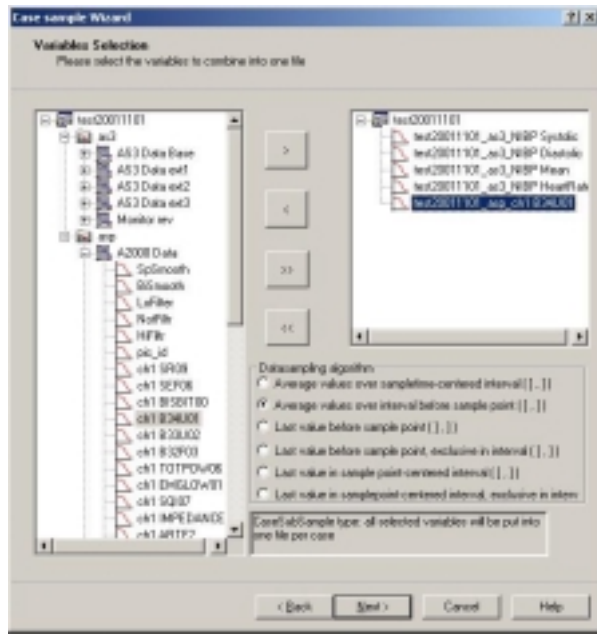


Figure 21 Sample wizard tutorial: variables selection page

Page 3 shows the case that we’ve built: the case root is the file name of the case, and the 2 selected files .asp & .as3 both constitute the branches. Since both selected files are RugloopII© - generated files, an additional level exists in the hierarchy to indicate the lines that are present.

Unfolding the AS3 -> AS3 data base line, we will come across the variables NIBP mean, NIBP diastolic, NIBP systolic, NIBP heartrate. After selecting each of these variables separately, we click the “>” button to add them to the variables to process.

The output variable name will be a combination of the case name, file extension, and variable name.

We fold back the .as3-branch, select the .asp->A2000 data, and select the Ch1 B34U01 variable from the line as well. Pressing “>” again adds the variable to the list of variables to process as well.

The NIBP variables can use the default sampling method as specified in the previous page. The BIS variable, though, needs another sampling method: since multiple samples may exist within a 60s interval, we want the average of the values occurring in the interval before the output sample time. We select the ch1B34u01 variable in the right list box, and correct the sample algorithm to the required one.

Now, we are ready to select the cases for which we want to create an additional output file. Press 'next' to open the case select page.

Figure 22 Sample wizard tutorial: files to process



In this case, the sampling wizard has selected the .as3-files as representative for the cases. We want to process all cases that are present in the directory, and therefore, we select all .as3-files.

Optionally, we set the output directory to the directory where we want the generated files to be put. This can be useful in case the input data is located on a readonly medium like a CD-rom.

Pressing 'Finish' will create the output files.

The sample wizard will now process the selected cases: 5 output files will be created (each file gets the case name with the extension .hem), as well as the log file.

In the example, we have selected DIFFERENT data for the cases to process than in the case we selected as representative. The encountered errors are logged in the log file, and are shown on the screen as well.

The Sample wizard will try to create the output files as close as possible to the requested processing. 5 output files have been created, and conform to the encountered errors, we find that the BIS data was not added to the output files, since it could not be found: the output files only contain the hemodynamic data, subsampled as requested.

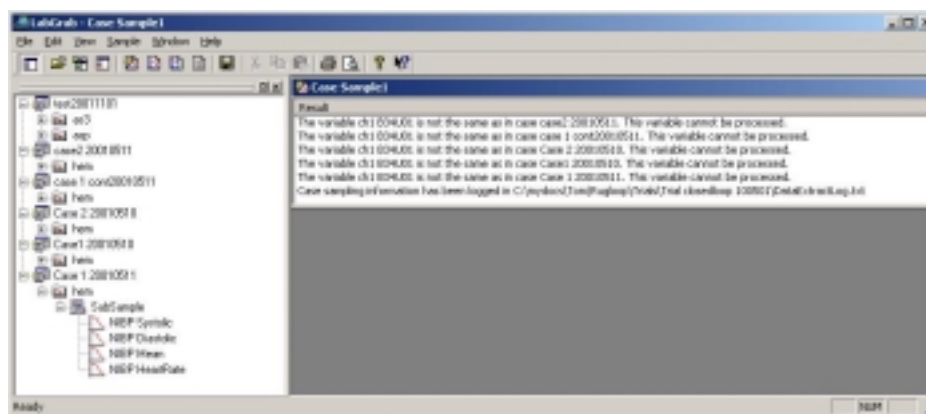
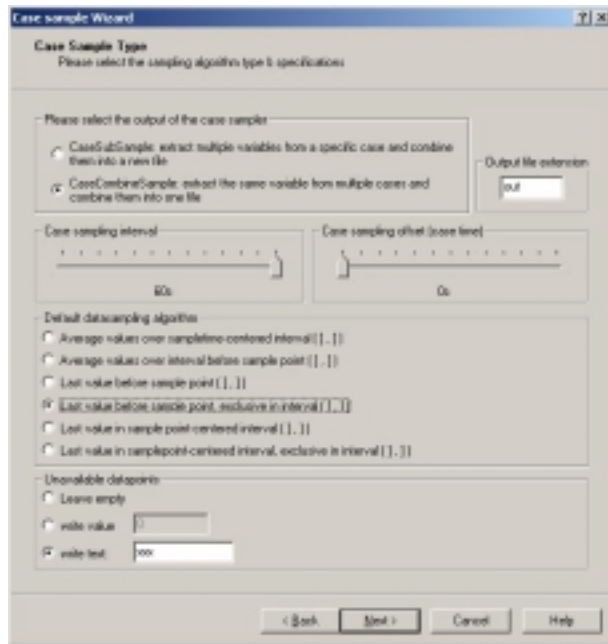


Figure 23 Sample wizard tutorial: error log

4.4.3 CaseCombineSample

Figure 24 Sample wizard tutorial: sample case type



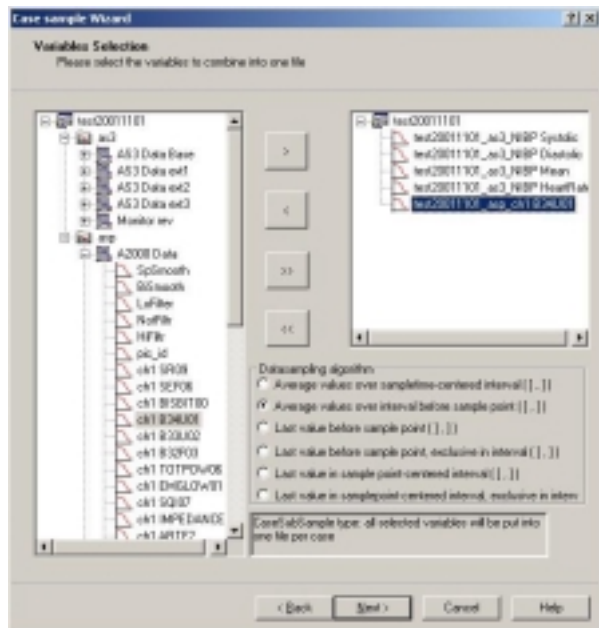
Suppose we want to compare the NIBP hemodynamic parameters and the BIS values over multiple cases. Both variables have been captured with a different frequency: the NIBP parameters are usually set to a frequency of ± 1 minute, whereas the BIS data is entering at least once per 10 seconds. Since the comparison does not have to be too detailed, we allow the same sampling frequency for all variables.

We select the CaseCombineSample option, and accept the default file extension .out. The output files will get the filename of the variable that is stored into it. Since the NIBP data was captured at an interval of 60s, we set the sampling interval to 60s as well. The default sample method is set to 'Last value before sample point, exclusive in interval': since we will be processing the NIBP values

captured at 60s interval: we don't want the sample wizard to create sample points where it is not necessary. When no data is available, we want 'xxx' in the output file.

Press 'next' to goto the next page.

Figure 25 Sample wizard tutorial: variables selection



Page 3 shows the case that we've built: the case root is the file name of the case, and the 2 selected files .asp & .as3 both constitute the branches. Since both selected files are RugloopII© - generated files, an additional level exists in the hierarchy to indicate the lines that are present.

Unfolding the AS3 -> AS3 data base line, we will come across the variables NIBP mean, NIBP diastolic, NIBP systolic, NIBP heart rate. After selecting each of these variables separately, we click the ">" button to add them to the variables to process.

The output variable name will be a combination of the case name, file extension, and variable name.

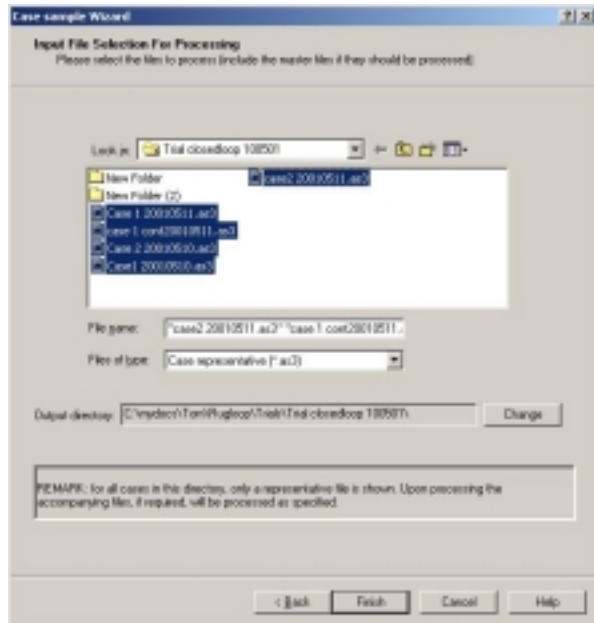
We fold back the .as3-branch, select the .asp->A2000 data, and select the Ch1 B34U01

variable from the line as well. Pressing ">" again adds the variable to the list of variables to process as well.

The NIBP variables can use the default sampling method as specified in the previous page. The BIS variable, though, needs another sampling method: since multiple samples may exist within a 60s interval, we want the average of the values occurring in the interval before the output sample time. We select the ch1B34u01 variable in the right list box, and correct the sample algorithm to the required one.

Figure 26 Sample wizard tutorial: file selection for processing

Now, we are ready to select the cases that we want to combine variables from. Press 'next' to open the case select page.



In this case, the sampling wizard has selected the .as3-files as representative for the cases. We want to process all cases that are present in the directory, and therefore, we select all .as3-files.

Optionally, we set the output directory to the directory where we want the generated files to be put. This can be useful in case the input data is located on a readonly medium like a CD-rom.

Pressing 'Finish' will create the output files.

The sample wizard will now process the selected cases: 5 output files will be created (each file gets the name of the variable that is combined in it, and the extension .out), as well as the log file. No specific errors have occurred, and we now have the processed sample data, added to the case tree window as well.

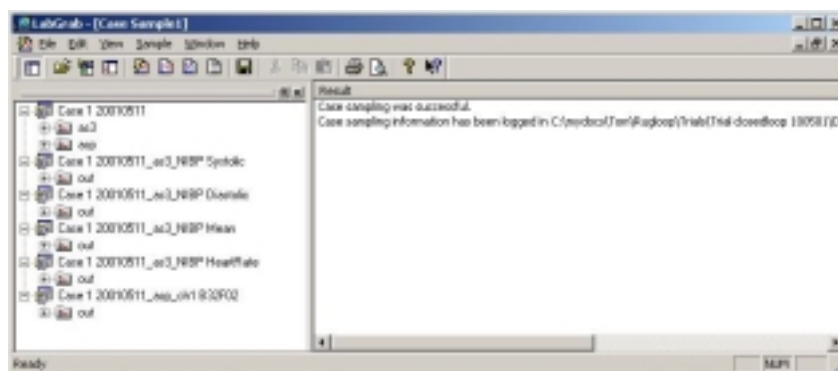


Figure 27 Sample wizard tutorial: error log

The data can be used directly to create charts from: unfold the branch for the B32F02 data, and select all variables. Drag them into a default chart window to view them right away.

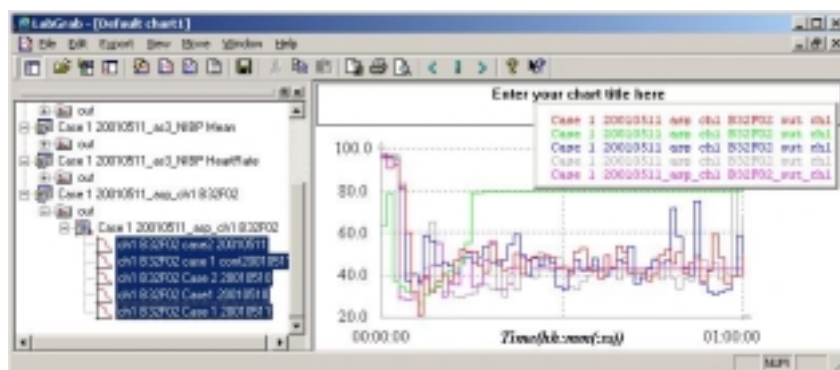


Figure 28 Sample wizard tutorial: viewing the generated data

The generated .out-file can now be opened in a spreadsheet or a statistical package for further processing. See 4.3.2.

4.5 Frequently asked questions

Q 1 when opening Rugloop © or Labgrab © files in Excel, the numbers are not presented correctly

Q 2: I forgot to press the 'start' button during my RugloopII© case. Can I still display the files in Labgrab© charts ?

Q 3: I forgot to press the 'start' button during my RugloopII© case. Can I still process the files using the Labgrab© wizard ?

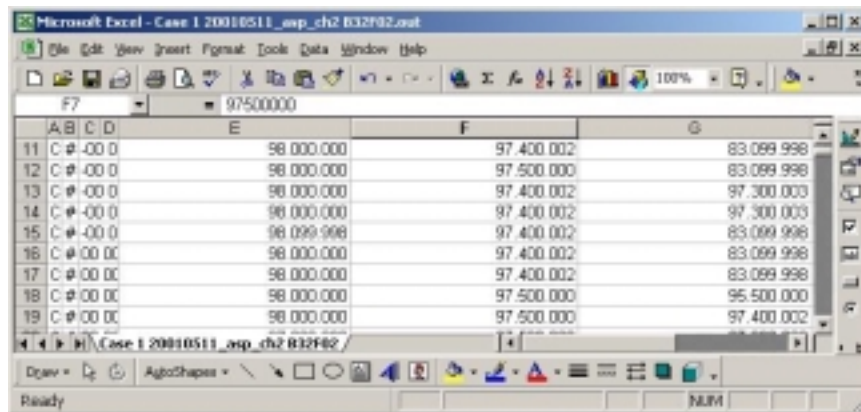
Q 4: I pressed the 'start' button during my RugloopII© case at the wrong moment. Can I still display the files in Labgrab© charts ?

Q 5: I pressed the 'start' button during my RugloopII© case at the wrong moment. Can I still process the files using the Labgrab © wizard?

Q 6: For the BIS, I do not know what data line to sample.

Q 7: For the A2000 data, I sometimes get the message "The variable ch1 DB11U02 is not the same as in casexxx. This variable cannot be processed." when sampling multiple files.

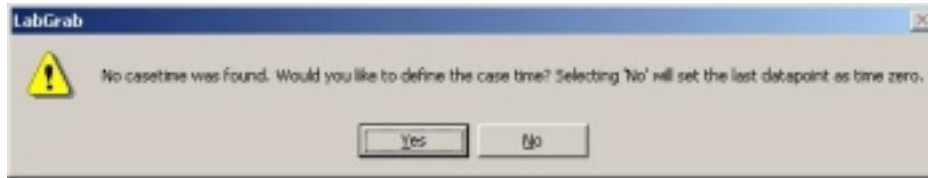
Q 1 when opening Rugloop © or Labgrab © files in Excel, the numbers are not presented correctly



A 1: your international settings are not set correctly. Both Rugloop© and Labgrab© use the '.' as decimal separator. In some countries, regional settings apply the ',' as digit grouping symbol, causing the input data to be interpreted incorrectly. To correct this, please refer to 4.3.2

Q 2: I forgot to press the 'start' button during my RugloopII© case. Can I still display the files in Labgrab© charts ?

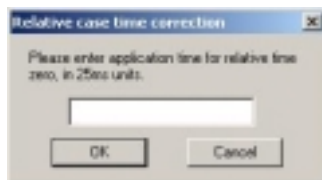
A 2: Yes you can. When dragging a variable from the case tree window onto the chart, Labgrab © will notice a lack of relevant case time, and will ask you whether you want to specify when you pressed start.



The information you need for this can be captured in case you've written down an event in RugloopII© allowing you to refer properly to the start of the case. Since the information you need is not regularly presented in Labgrab © currently, you need to open the 'yourcase.rgl' file in a text program, or more easily, in a spreadsheet. Open 'yourcase.rgl' according to the instructions in 4.3.2. The case below is a representative example. Your file may contain other lines in-between the 'event' lines. If you did not type anything during the RugloopII© case, you won't have any 'Events' lines.

LineType	RGL checked files	version	RAppTime	RCaseTime	SystemTime	string
Events	25000	d hh:mm:ss mm/dd/yyyy hh:mm:ss d	6978	00 00 00 00	53:39.6	00 00 00 00 12/09/2003 13:53:33 start prop infu
Events	18496	00 00 00 00			58:27.3	00 00 00 00 12/09/2003 13:58:24 Katarest
Events	27115	00 00 00 00			02:03.0	00 00 00 00 12/09/2003 14:02:01 R00
Events	45630	00 00 00 00			09:45.8	00 00 00 00 12/09/2003 14:09:40 start operative
Events	68188	00 00 00 00			19:09.8	00 00 00 00 12/09/2003 14:19:01 TESC 0.7
Events	112937	00 00 00 00			37:46.6	00 00 00 00 12/09/2003 14:37:44 TESC 0.8
Events	250357	00 00 00 00			51:44.0	00 00 00 00 12/09/2003 15:00:47 LOC, TESC 1
Events	295200	00 00 00 00			53:45.1	00 00 00 00 12/09/2003 15:53:39 Shark
Events	295966	00 00 00 00			54:04.2	00 00 00 00 12/09/2003 15:53:58 Geen response
Events	304894	00 00 00 00			57:47.4	00 00 00 00 12/09/2003 15:57:43 gain respons
Events	308955	00 00 00 00			59:29.0	00 00 00 00 12/09/2003 15:59:23 Stop prog infu
Events	311953	00 00 00 00			00:43.9	00 00 00 00 12/09/2003 16:00:41 RGR

To restore your *relative casetime*, you need to know at what *Relative application time* your case was actually started. In the example here, we can see that the 'start propofol infusion', which is to be considered as the actual case start, was typed at a *relative application time* of 6978. This is the number we need: if we pressed 'yes' to the message asking us whether we wanted to define the relative case time, the following message is this:



where we can enter our value of 6978. This does the correction, and will cause your case to load correctly. Obviously, this approach expects you have at some time entered a certain comment that allows you to refer to or count back to.

Now, suppose we only had the row 8 in the Excel sheet, and that we KNEW somehow that the start of the operation occurred 16 minutes 7seconds after the start of the case (e.g. because we'd written that down in our notes).

We can calculate the relative application time for start of case as follows:

16 minutes 7 seconds expressed in 25ms units eq. $(16*60+7)*40 = 38680$, since there are 40 times 25ms in a second.

The 'start operation' occurs at a relative application time of 45630; so the start of the case was at $(45630-38680) = 6950$. Even though this calculation generates a minor error compared to the exact 6978, the difference is less than a second.

Q 3: I forgot to press the 'start' button during my RugloopII© case. Can I still process the files using the Labgrab© wizard ?

A 3: Yes you can. Likewise to **Q 2**, Labgrab© will invite you to indicate the relative application time when you actually started the case, for each file that does NOT contain this data. The easiest way is, while Labgrab© sample wizard is running, to write down the cases where this information is required. Afterwards, you can then open the *yourcase.rgl* file to get the relative application time as described in **A 2**. for all cases where no casetime was found. You can then re-run the whole sample wizard again, or process only those files where the casetime was not found during the first iteration.

REMARK: it is important to realise that, if you don't enter a casetime specification when asked for it, Labgrab© will still generate (invalid) output data for that case, and that you should ignore the generated data.

Q 4: I pressed the 'start' button during my RugloopII© case at the wrong moment. Can I still display the files in Labgrab© charts ?

A 4: You can still display the files, but the case time will be wrong in the chart. You cannot actually correct the casetime for this issue currently, and present other cases in the same chart, expecting them to still be synchronised.

Q 5: I pressed the 'start' button during my RugloopII© case at the wrong moment. Can I still process the files using the Labgrab © wizard?

A 5: You can still process the files, but the data for the cases where you pressed the 'start' button at the wrong time will have been shifted compared to the other cases. This situation currently cannot be corrected using Labgrab© or the Labgrab© wizard.

Still, if you know when you exactly pressed the start button relative to the real case start, you can correct the column of data using Microsoft Excel©: after running the Labgrab© wizard, you can open the generated *yourprocesseddata.out*-file in Excel. (cfr. 4.3.2). The result will typically look as in the figure below (the Labgrab© sampling was done with 60s interval for clarity here).

Obviously, the start case button for case6 was pressed too late, since we have 15 minutes of data before case time zero.

If we know when the case time was pressed exactly, we can correct the data: we can shift the column of data downwards, since the Labgrab© wizard extracts data at fixed intervals!

A	B	C	D	E	F	G	H
1	asp_A2000Data	id	id	id	id	id	id
2	asp_A2000Data	id	id	id	id	id	id
3	asp_A2000Data	id	id	id	id	id	id
4	asp_A2000Data	id	id	id	id	id	id
5	asp_A2000Data	id	id	id	id	id	id
6	asp_A2000Data	id	id	id	id	id	id
7	asp_A2000Data	id	id	id	id	id	id
8	asp_A2000Data	id	id	id	id	id	id
9	asp_A2000Data	id	id	id	id	id	id
10	asp_A2000Data	id	id	id	id	id	id
11	asp_A2000Data	id	id	id	id	id	id
12	asp_A2000Data	id	id	id	id	id	id
13	asp_A2000Data	id	id	id	id	id	id
14	asp_A2000Data	id	id	id	id	id	id
15	asp_A2000Data	id	id	id	id	id	id
16	asp_A2000Data	id	id	id	id	id	id
17	asp_A2000Data	id	id	id	id	id	id
18	asp_A2000Data	id	id	id	id	id	id
19	asp_A2000Data	id	id	id	id	id	id
20	asp_A2000Data	id	id	id	id	id	id
21	asp_A2000Data	id	id	id	id	id	id
22	asp_A2000Data	id	id	id	id	id	id

Information about when the start case button was pressed can be found in your notes (if you had written it down) or from the Rugloop© events list (if you typed an event in Rugloop© allowing you to determine the exact case time).

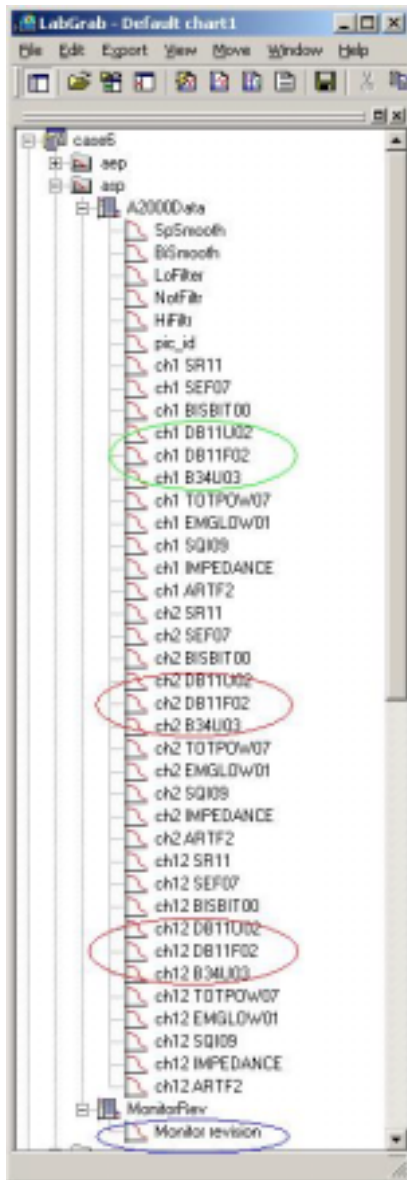
Suppose that you had a comment written down, allowing you to decide that the start case button was pressed 9 minutes after start of first pump. You can then just shift downwards the column for that case in Excel, and save the file as a different name for future processing. The file would then typically look as follows:

A	B	C	D	E	F	G	H
1	asp_A2000Data	id	id	id	id	id	id
2	asp_A2000Data	id	id	id	id	id	id
3	asp_A2000Data	id	id	id	id	id	id
4	asp_A2000Data	id	id	id	id	id	id
5	asp_A2000Data	id	id	id	id	id	id
6	asp_A2000Data	id	id	id	id	id	id
7	asp_A2000Data	id	id	id	id	id	id
8	asp_A2000Data	id	id	id	id	id	id
9	asp_A2000Data	id	id	id	id	id	id
10	asp_A2000Data	id	id	id	id	id	id
11	asp_A2000Data	id	id	id	id	id	id
12	asp_A2000Data	id	id	id	id	id	id
13	asp_A2000Data	id	id	id	id	id	id
14	asp_A2000Data	id	id	id	id	id	id
15	asp_A2000Data	id	id	id	id	id	id
16	asp_A2000Data	id	id	id	id	id	id
17	asp_A2000Data	id	id	id	id	id	id
18	asp_A2000Data	id	id	id	id	id	id
19	asp_A2000Data	id	id	id	id	id	id
20	asp_A2000Data	id	id	id	id	id	id
21	asp_A2000Data	id	id	id	id	id	id
22	asp_A2000Data	id	id	id	id	id	id

REMARK: a file modified in Microsoft Excel © cannot be opened in Labgrab© any more.

Q 6: For the BIS, I do not know what data line to sample.

A 6:



If you open a RugloopII©-created *yourcase.asp* in the Labgrab© case tree, you get the view to the left.

The binary data captured from the A-2000 by RugloopII© contains channel 1 (ch1), channel2 (ch2) and channel 12 (ch12) data. Per channel, 3 BIS values are output, each calculated with a different algorithm. (the excess values were originally included for research by Aspect Medical). The BIS values are represented by Labgrab© using the algorithm ID (e.g. DB11U02, DB11F02, B34U03)

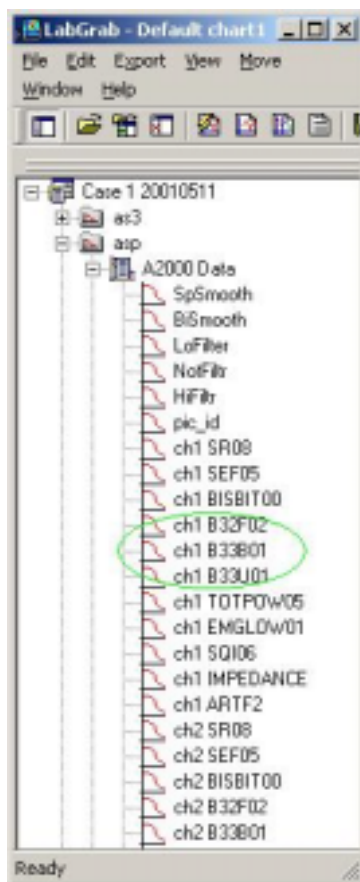
You can recognize the BIS data as 3 algorithm ID's subsequent to the BISBIT00 variable.

You need the monitor revision number to determine the actual BIS data channel. The monitor revision is indicated with the blue circle. It can be translated into the A-2000 FPGA revision as follows:

'MonitorRev'	FPGA rev.	A2000 system rev.
0	1.04	1.7
		1.8
		1.10
		2.0
1	1.06	2.10
2	1.07	3.00
		3.12

For all MonitorRev numbers larger than 0 (corresponding to FPGA revisions equal to or larger than 1.06 and A2000 system revisions from 2.10 on), you need the first BIS algorithm on channel1. (in the picture on the left, it would be ch1 DB11U02)

For earlier revisions, (MonitorRev. 0) it is recommended to use the third BIS algorithm on channel 1. (it would be ch1 B33U01 in the picture below.)



Q 7: For the A2000 data, I sometimes get the message “The variable ch1 DB11U02 is not the same as in casexxx. This variable cannot be processed.” when sampling multiple files.

A 7: Please also refer to

Q 6; starting with A-2000 software Rev. 2.10 (RugloopII© MonitorRev variable 1), the monitor transmits only one BIS index, in the bispectral_index variable. (The other two variables are set to - 32768.) This was done to eliminate confusion about which index to use, since 3 different algorithms were calculated AND transmitted by earlier A2000 versions. The monitor transmits either BIS 3.4U or DBIS 1.1U in the first BIS variable, depending on the type of sensor in use. RugloopII© properly swaps the labels depending on the type of sensor.

The problem is that the Labgrab© wizard compares BOTH the column index AND the column label to be equal to the values in your selected master case before processing a variable. If you've been using different sensors, you could end up with cases where the first BIS column is labeled either BIS 3.4U or DBIS 1.1U. If some of the cases are different than in your master case, these data columns are not processed.

The solution is to write down from the case sampling logging information ALL cases for which you get this error, and to re-run the case sampling wizard on those cases alone, making sure the master case is one of those cases as well. (You can select the master case by pressing the 'clear data' button (see 4.2.1) before starting the sampling wizard) Please also remember to save the results of your earlier sample wizard runs (*yoursamplingvar.out* files) under a different name, as they will be overwritten otherwise.