

GrafView

Users Manual

Version 4.1

Table of contents

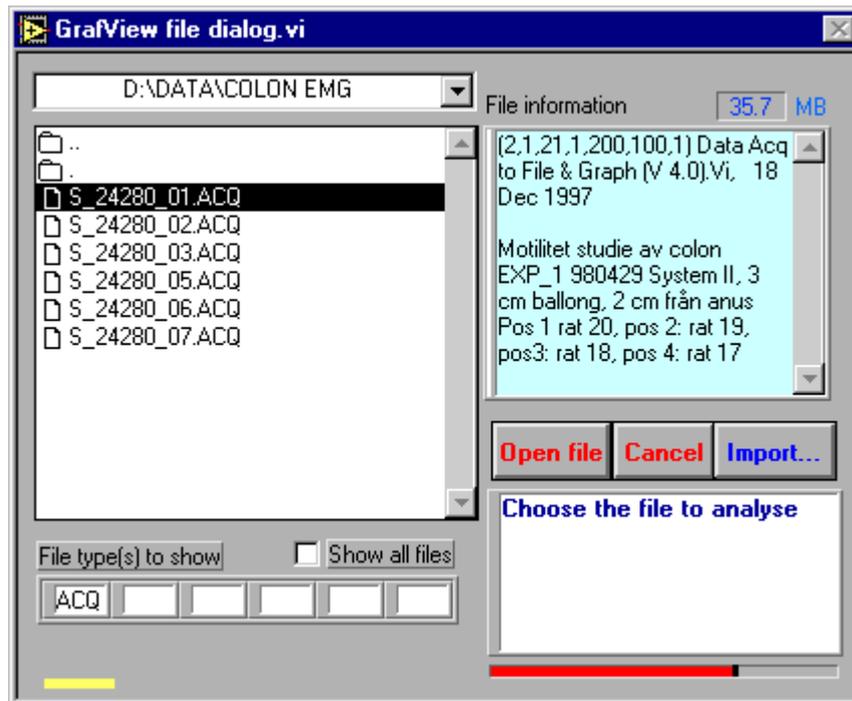
INTRODUCTION	3
CHOOSE FILE	4
HOW MANY CHANNELS TO SHOW	5
MAIN WINDOW	7
CURSOR CONTROL.....	8
FILE HEADER INFORMATION	8
STIMULATION WINDOW	8
TIME BETWEEN CURSORS	8
ACTUAL VALUES FOR RED & BLACK CURSORS	8
MAIN GRAPH WINDOW.....	9
COLUMN TITLES	9
FUNCTION BUTTONS.....	9
<i>NEXT PAGE</i>	10
<i>PREVIOUS PAGE</i>	10
<i>GO HOME</i>	10
<i>GO TO PAGE</i>	10
<i>SHOW</i>	10
<i>JUMP TO TIME</i>	10
<i>JUMP TO COMMENT</i>	11
<i>ZOOM IN/OUT</i>	11
<i>PRINT</i>	12
<i>SAVE</i>	13
ANALYSE FUNCTIONS	13
Statistics	13
Peak analyse	14
Filter	16
Area Under the Curve.....	17
Frequency	19
Power spectrum	20
Find base line	27
MMC	28
Analyse menu	30
CRD	32
PERIOD DETECTION	33
CALCULATIONS	34
CRD ANALYSE RESULTS	35
RESULTS GRAPH	37
COMPLIANCE GRAPH	38
VOLUME VS PRESSURE GRAPH	39
DIVIDE SIGNAL	39
SAVING CRD RESULTS	40
PRINTING CRD RESULTS	42
STOP	44
MOTILITY	45
SG IN RATS	48

INTRODUCTION

GrafView is an analyse program written in LabView graphical programming language version 5.0. The main aim of this program is to give the user the possibility of viewing and analysing large files which can not be kept in the memory as a whole. The program divides the file in pages of different size, chosen by the user, and can browse through the file. A number of analyse function are available both for parts of the file chosen by the user or automatic analyses of the whole file.

CHOOSE FILE

After loading the program the first thing to do is to choose the file to analyse. The following window is opened and the program waits for the user to choose the file to analyse.

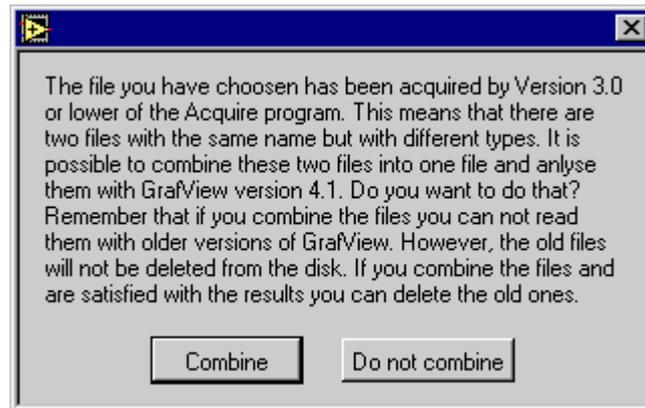


GrafView is designed to analyse files generated by an acquisition program named “Acquire” and a data logging system named “Multi Electrode System, MES”. The files from these two systems are binary files which can have different file type suffixes.

Files generated by Acquire (Version 4.0 or higher) has a suffix of “.ACQ” while files generated by MES can have any suffix chosen by the user. (Se manuals for Acquire and MES).

In older versions of Acquire each experiment generated two files: 1) a small text file (*.TXT) which contained the comments and file information and 2) a large binary file (*.BIN) containing the actual data. If files from version 3.0 or lower are going to be used the text file (*.TXT) **should be chosen**.

GrafView will then inform you that the file is acquired by an older version of Acquire program and will show the following window.

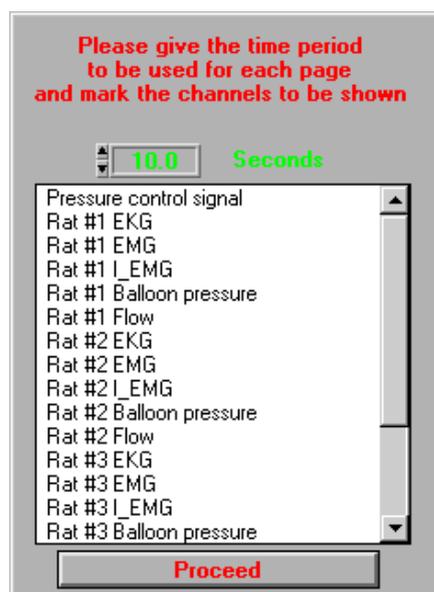


The user have then the choice of combining the two files changing them to version 4.1 or analysing the files as they are. If the combine function is chosen GrafView will generate a new file which is the combination of the two files with necessary changes to the version. This new file is located in the same directory as the old files, has the same name as the old files with a suffix of “.ACQ”. The old version of the file will not be deleted by the program. If needed it should be deleted by the user.

Choose the file named “C:\GrafView\Test data.ACQ” to analyse by marking the file and clicking on the “Open file” button or by double clicking on the file.

HOW MANY CHANNELS TO SHOW

After clicking on the “open file” button the “GrafView file dialog window” will be closed and a new window “Channels to show” will be opened as bellow.



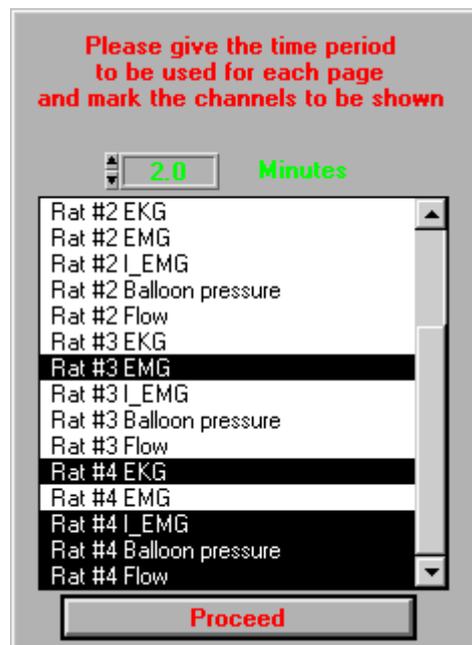
Here the user can choose the number of channels shown at the same time on the screen.

The window shows the names of all the channels available in the file and suggest a time length to be shown on the screen.

Clicking on a column name will marked that column. For selecting more than one channel hold down the “Shift” button and click on one of the column names. By this way two or more channels could be selected. If you want to deselect a chosen channel hold down the “shift” button and click on that column name, that channel will be deselected. Remember that you can chose the columns in any order.

The time length of data to be shown on the screen can be changed to any value higher than zero. A value of (-1) will tell Grafview to read the whole file. Clicking on the text “Seconds” will change the text to “Minutes” by this way you can chose different time periods to be shown on the screen. How long time period of the data you can maximally read in your computer is dependent on the sampling rate of the data, the number of channels chosen to be shown on the screen at the same time and the memory capacity of your computer. Experiment with these parameters until you find out the limits of your computer.

Select “Rat #3 EMG, Rat #4, I_EMG, Rat #4 EKG, Rat #4 Balloon pressure and Rat #4 Flow” from the column name list, and chose a time period of “2 minutes” to be shown on the screen. The screen should look like the figure bellow.

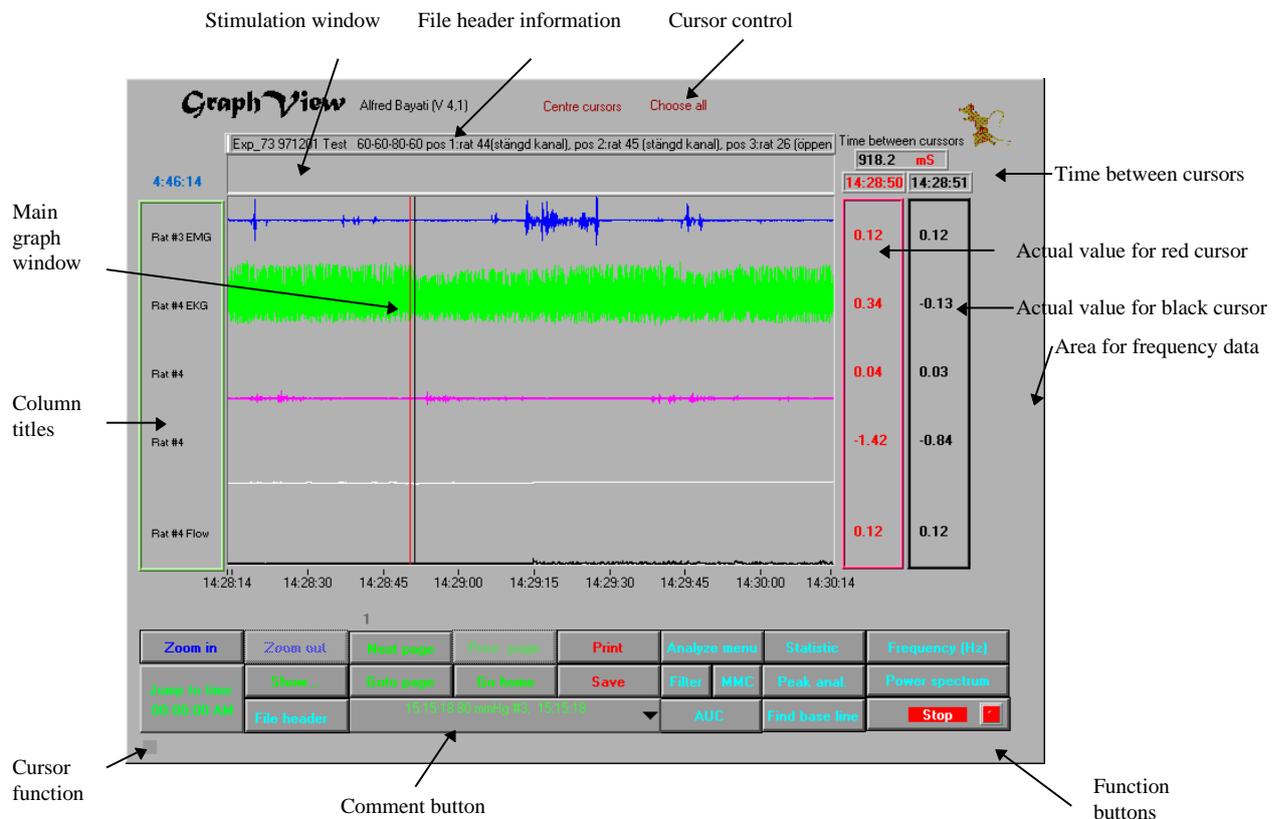


If you know press the “Proceed” button the first two minute of the five chosen channels will be shown on the screen.

Click on the “Proceed” button.

MAIN WINDOW

After a while, depending on the computer you use, the memory in your computer, the page width, total number of channels chosen and sampling rate, the main GrafView window will be presented to you.



Familiarise yourself with the main window.

Starting at the top of the window we will now go through all the functions available.

Cursor control

The cursors (red and black) can be moved by the mouse. Point at one of the cursors and click and hold down the left mouse button. Now you can move the cursor. In some cases if you loose one or both of the cursor, (the cursor/s are out of the printing screen) click on the “Centre cursor”. This will bring both the red and the black cursor to the middle of the screen.

Click on “Centre cursor” text.

If you want to analyse a whole page you have to put one of the cursors at the beginning of the page and the other at the end. You can do this by moving the cursors to the beginning and the end of the page or you can simply click on the “Chose all” text. This will put one of the cursors at the beginning of the page and the other at the end.

It has no significance which of the cursor is positioned at the beginning or at the end of the page. The cursor at the left side (independent of the colour) is the lower cursor.

File header information

File header information from the acquired file will be presented in this box. If no file information could be found in the file then the text “No file information” will be shown.

Stimulation window

The data shown in this window is either the data from a channel named “Pressure control signal” or data from a digital channel. Which of these data are shown or if the window is shown at all depends on the information in the acquired file. These parameters can be changed in the “Acquire” program.

Time between cursors

The time between the two cursors and the actual time of each cursor are shown here. The text in the box can be mS, S or Min. depending on the time between the cursors.

Actual values for RED & BLACK cursors

These two boxes contain the actual value from the raw data. These are the values at the junction of the cursors and the curves. In our case there are 5 values in each box. The first value in the red box is the actual value of the first curve at the point where cursor is standing. If you move the red cursor

the values in the red box will be changed. In the same way the black box shows the actual values of the graphs in the junction between the black cursor and the graph.

Move the black and the red cursors and see the effect of this on the results in these two boxes.

Main graph window

The graphs are presented in this window.

Column titles

The column titles, as given in the file, are presented in this box. Sometimes when the name of the column is long, just a part of the name will be presented. In our case the fourth channel name is “Rat #1 Balloon pressure”, however, only a small part of the name is presented. If no column titles are given in the file the “Column titles” box will be empty.

Function buttons

There are a total of 25 function buttons available (you can only see 22 of them). These buttons are grouped in 4 different groups by text colour.

The buttons with green text are the ones which will navigate you through the file .

The buttons with dark blue text are Zooming buttons.

The buttons with red text will send out data to either a printer or a disk.

The light blue buttons will analyse your data.

There is one button with red text (STOP) with a red blinking lamp. This button is the stop button. The lamp on this button should blink which means that the program is running. If this lamp stops blinking it could have two meanings.

- You have activated another window which has its own blinking lamp. In this case the lamp will start blinking when you go back to the main window.
- The program has stopped functioning. In this case you have to close down the program and restart it.



NEXT PAGE

Clicking on this button will read and present the next page in the file. The current page number is shown above this button. This button will be disabled when you reach the last page in the file

PREVIOUS PAGE

This button is disabled when you read the first page of the file. The button is activated from page 2 to the last page of the file. Clicking on this button will read and present the previous page in the file.

GO HOME

Clicking on this button will read and present the first page in the file.

GO TO PAGE...

Clicking this button will bring up a window where you can type the number of the page you want to go to. The given page will be read and presented.

SHOW...

Clicking on this button will bring up the “channels to show” window (see page 5) by which you can browse through the different channels and change the time length of each page shown on the screen.

JUMP TO TIME

By using this function you can jump to a specific time in the file. Triple click on the time (all the figures should be activated) or delete all the figures and type the time you want to jump to and then click the mouse once somewhere in the main window or press “Return”. GrafView will now read the data and present it.

Some rules about timing:

If you type 9 and press return GrafView will jump to 09:00:00

If you type 9:25 and press return GrafView will jump to 09:25:00

If you type 13 and press return GrafView will jump to 13:00:00 or 01:00:00 PM

If you type 1 and return GrafView will jump to 01:00:00 AM

If you type 9.25 and return GrafView will jump to 09:00:00

If you type 9 and any character except “.” and 25 followed by return GrafView will jump to 9:25:00

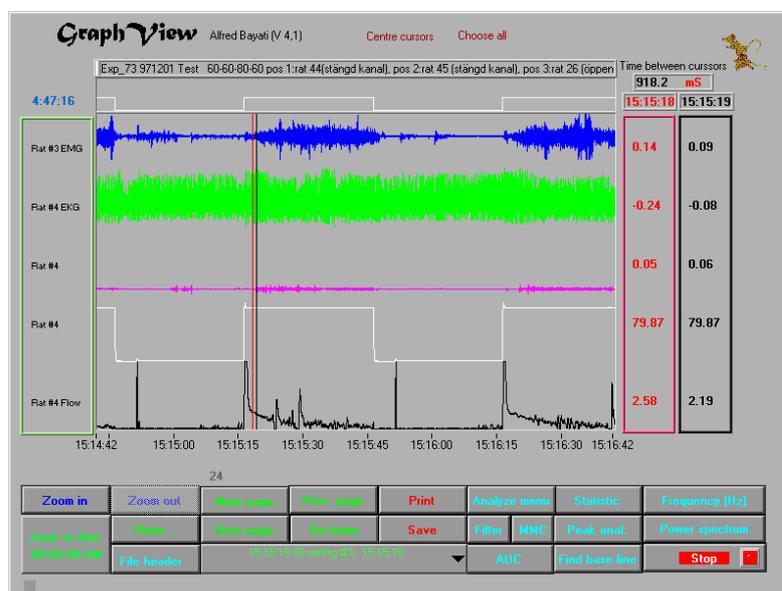
If you type “543” or “hgt” or any nonsense combination of characters and press return GrafView will jump to 00:00:00

When you give a time for GrafView to jump to the program will read and present the data in a way that the given time will be placed at the left 1/3 of the main graph window. This is done to be able to see some data before the time given.

JUMP TO COMMENT

If there are comments in the file, these will be available during the analyse of the file. Click on the comment button and hold down the left mouse button. Move the cursor to the comment you want to jump to and release the left button. GrafView will now jump to that comment, place the time corresponding to the comment at the left 1/3 of the main graph window and put the red cursor at that time.

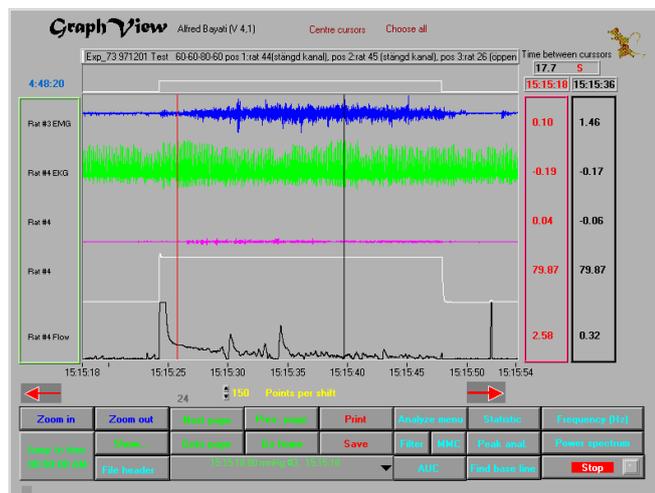
Click on the comment button and choose “80 mmHg #3, 15:15:18 ”. The following data should be shown.



ZOOM IN/OUT

Zooming is one way of looking on details of data. Zooming in GrafView is always between the cursors. Move the cursors surrounding the area of interest and click on the “Zoom” button. The chosen data will be shown on the whole area of the “Main graph window”. You can now either click on the “Zoom” button again to zoom the area between the two cursors or move the cursors and then click on the “Zoom” button. This process can be repeated as many times as you want.

During Zooming two arrows will be visible under the “Main graph window”. By clicking on these arrows the graph could be scrolled to the left or to the right. The speed of scrolling can be changed by changing the value between these two arrows called “Points per shift”.

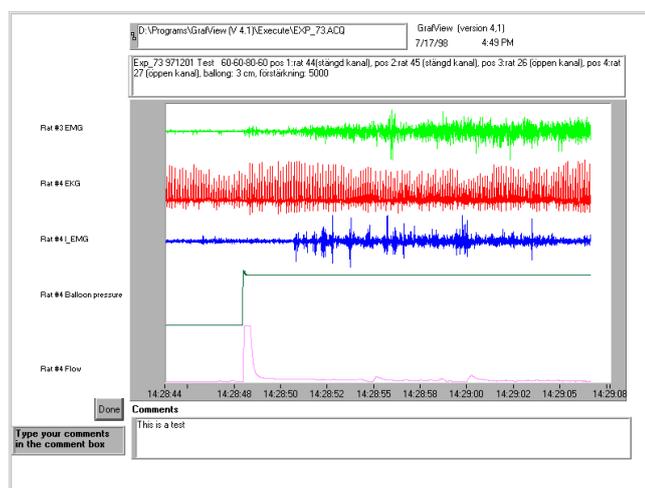


Clicking the “Zoom out” button will unzoom the data exactly the same number of steps that zooming has been used. That is, If you click on the “Zoom in” 5 times you have to click on the “Zoom out” 5 times in order to go back to the original graph. When you have reached the original graph the “Zoom out button” will be disabled.

PRINT

Data between the cursors can be printed on an A4 paper using a laser printer. GrafView uses the default printer in windows environment.

Move the cursors surrounding the area of interest. Click on the “Print” button. A new window will be opened.



Type comments in the “Comments” box and then click on the “Done” button

Clicking on the “print” text will send the page to the default printer installed in Windows.

Clicking on the “Proceed” button will bring up a new window asking if the results should be saved. If “YES” is chosen a file management window will be opened asking for the name of the file for the results. The calculated results will then be saved as an ASCII file which can be read in programs like Excell, Origin etc.

If an existing file is chosen the data in the file will be deleted and the new results will be saved in the file.

Peak analyse

This function will analyse pulse pattern and determines the best set of pulse parameters that describes the pulse.

If the pulse pattern does not contain a rising edge, plateau, and falling edge, then GrafView will analyse the data, assigns values to as many pulse parameters as it can identify, and sets parameters it cannot identify to NaN (Not A Number).

The parameters calculated are:

Slew rate:	is defined as	$(90\% \text{ of amplitude} - 10\% \text{ of amplitude}) / \mathbf{Risetime}$
Overshoot:	is defined as	(maximum value of the pulse - Topline)
Risetime:	is defined as	the time required to rise from 10% amplitude to 90% amplitude on the rising edge of the pulse
Top:	is defined as	the line that best represents the value when the pulse is active
Amplitude:	is defined as	difference between the Topline and Baseline
Base:	is defined as	the line that best represents the value when the pulse is inactive
Undershoot:	is defined as	(Baseline - minimum value of the pulse)
Falltime:	is defined as	the time required to fall from 90% amplitude to 10% amplitude of the falling edge of the pulse
Width:	is defined as	(falling edge time - rising edge time) at 50% amplitude
Delay:	is defined as	(time origin - time at which 50% amplitude occurs on the rising edge)

Surround one pulse by the cursors and click on the “Peak analyse” button. The following window will be shown.

The value “Channel to show” can be changed to browse through all available channels in the file. Clicking on the “print” text will send the page to the default printer installed in Windows.

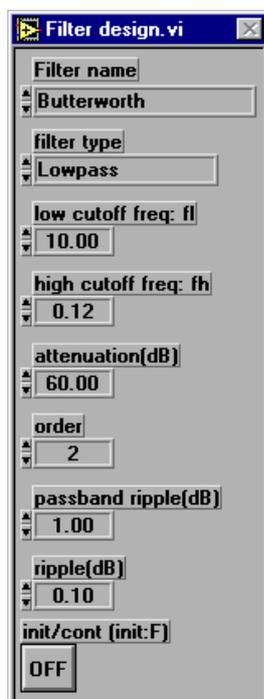
Clicking on the “Proceed” button will bring up a new window asking if the results should be saved. If “YES” is chosen a file management window will be opened asking for the name of the file for the results. The calculated results will then be saved as an ASCII file which can be read in programs like Excell, Origin etc.

If an existing file is chosen the data in the file will be deleted and the new results will be saved in the file.

Filter

Clicking this button will filter the data. The type and the parameters of the filter can be changed using the function button (F6). Pushing this button will open a new window as shown bellow. In order for the changes in this page to be affective the filter should be reactivated by clicking on the “Filter” button. The default values are: Lowpass Butterworth filter with a low cut-off frequency of 10 Hz and an order of 2. To deactivate this window push F7.

Use this function with care. In some cases the profile of data can be changed leading to false calculations. **Remember that when data is filtered by this function it will influence all the calculations performed on the data by main analyse functions.** However this function has no effect on the analysis from page two of analyse buttons (i.e. CRD, Motility etc. see page 28) i.e. original data will be used for these analyse.



Area Under the Curve

This is a special case of calculating Area Under the Curve (AUC) which is designed for signals with sinusoidal pattern. The process of calculating AUC is as follows:

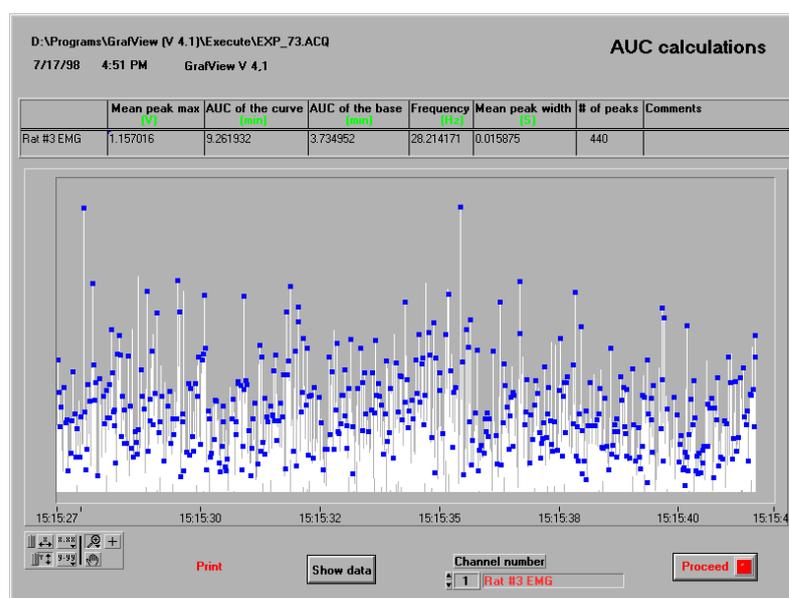
- 1) a mean value of the data is calculated.
- 2) this value is used as the base line
- 3) all data below the base line is discarded
- 4) all the peaks are detected (the detected peaks are shown on the screen by blue circles)
- 5) the number of peaks is calculated
- 6) the area under each peak to the base line is measured
- 7) the area under the base line corresponding to each peak is calculated
- 8) the following parameters are calculated

Mean peak Max: is the mean of the maximum values of peaks detected
 AUC of the curve: is the sum of the AUC of peaks detected down to the base line
 AUC of the base: is the sum of the AUC of peaks detected under the base line
 Frequency Hz: is the frequency of peaks
 Mean peak width: is the mean of the width of all peaks detected
 # of peaks: is the total number of peaks detected

This measurement should not be used for data which have no sinusoidal pattern like EKG.

Click on the "AUC" button

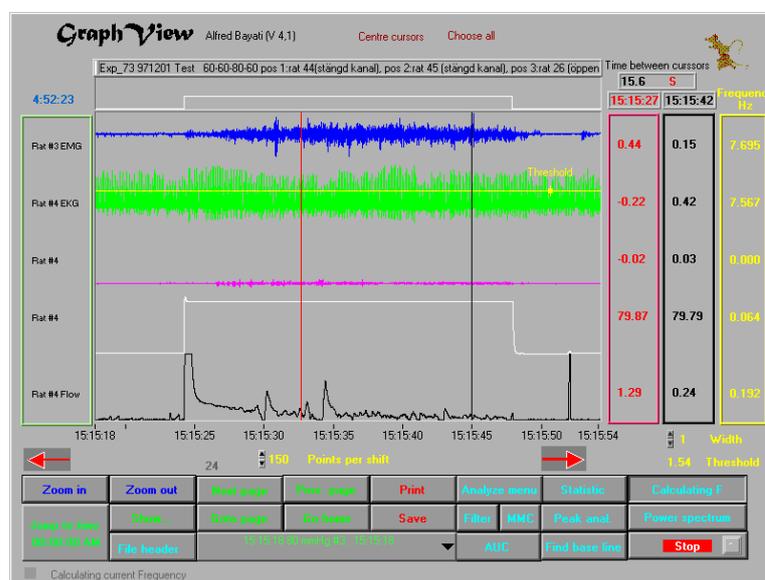
A new window will open as bellow.



Frequency

Frequency of the data presented on the screen can be measured continuously during browsing through the data. Click on “Frequency” button. The text will change to “calculating F”. A new yellow coloured box will be presented to the right of the screen. In our case there should be 5 values in this box. Each value corresponds to one channel presented in the “Main graph window”. Below this box two values will be visible, both in yellow colour. In the “Main graph window” a new horizontal yellow cursor will be visible.

This yellow cursor can be brought to the centre of the screen by clicking “Cursor control” “Centre cursors”, (se page 8).



The frequency is calculated as follows:

- 1) all the peaks in the data will be detected using a threshold value
- 2) all the peaks with a peak width less than “Width” will be discarded
- 3) the frequency is calculated

Both the width and the threshold can be changed on the run:

Width can be changed by either double clicking on the value and typing a new value, or by clicking on the up or down arrow heads placed close to the value.

Threshold can be changed by moving the yellow horizontal cursor. This cursor will calculate threshold for the channel the cursor is placed on. In the figure above threshold is set at 1.54 and is calculated for channel two. This means that the calculated frequency is correct for the channel the threshold is calculated for and not for the other channels. In our case the frequency is correct for channel two (7.567 Hz). The other frequencies could be wrong. If you want to calculate frequency for channel three then move the yellow cursor to channel three and place it at the threshold you want. The frequency calculated will be correct for channel three.

It must be mentioned that the frequency is calculated for the data between the red and black cursors. The closer the two cursors together i.e. the smaller the amount of data, the less the security in the calculated frequency.

Click on the “Calculating F” button. The button will change to “Frequency”. The frequency box, threshold, width and the yellow cursor will be invisible.

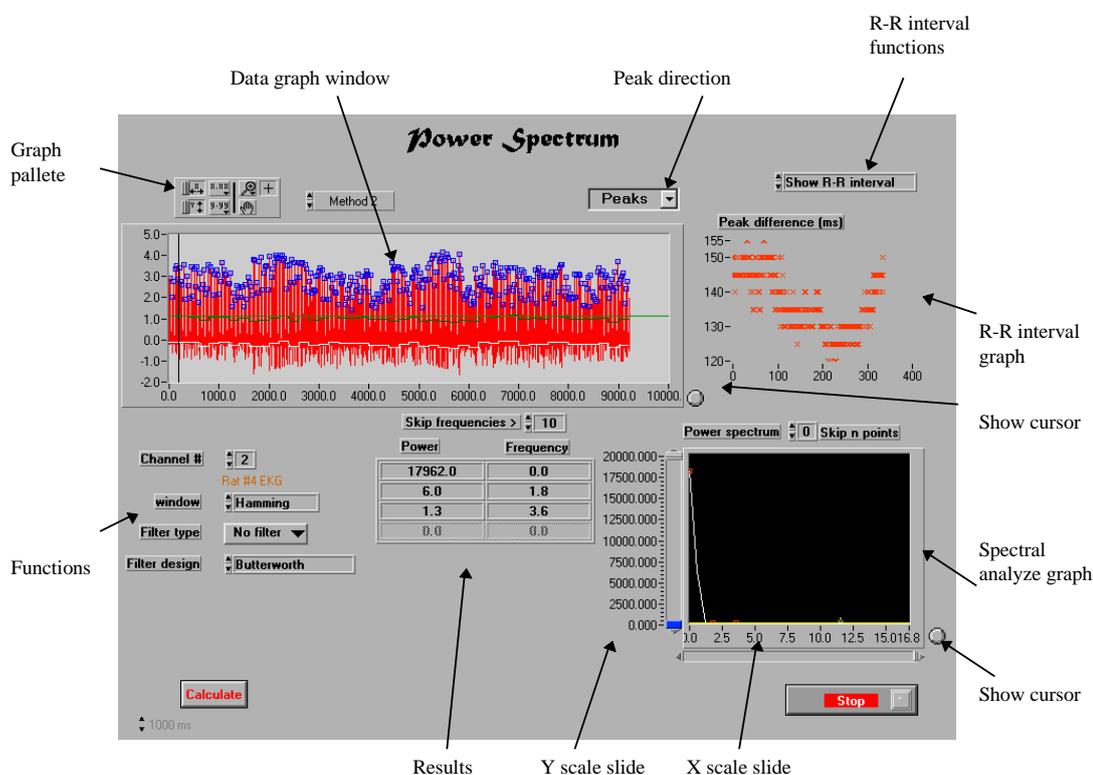
Power spectrum

This program is designed to analyse data between the cursors for their frequencies using Fast Fourier Transfer (FFT)

Click on the “Zoom out” button until it is disabled. Click on the “Cursor control”, “Chose all”. Click on “Power spectrum” button.

This process will chose two minutes of data for power spectrum analysis.

A new window “Power spectrum” will be opened. All the tools needed for calculating FFT of chosen data are available in this page. We will now go through an analyse session during which all the possible functions will be explained.



Step 1: Change the channel number to 2

The channel to be analysed can be selected by changing the “Channel #” function. In our case channel 2 is EKG data.

Step 2: Move the horizontal cursor in the “Data graph window” to the threshold level you want. If the cursor is not visible click on the “Show cursor” button close to the (Data graph window). This will bring the cursor to the middle of the window.

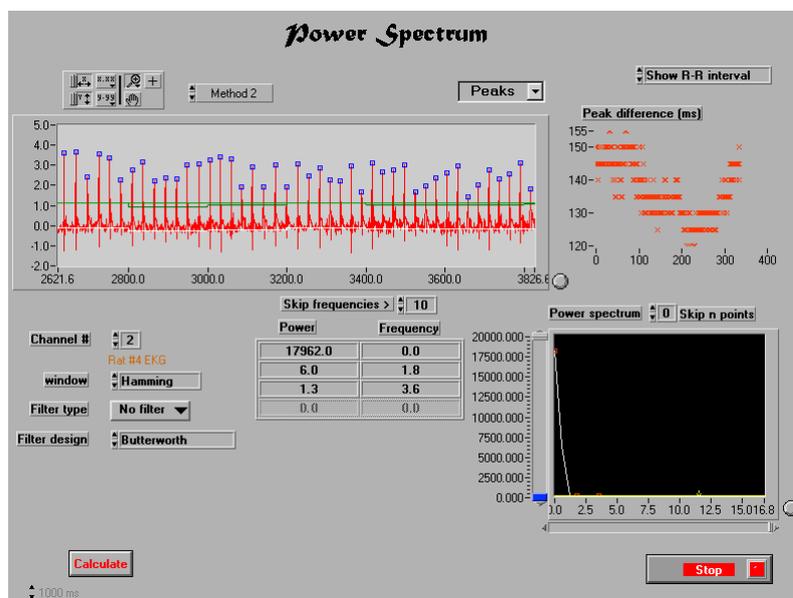
The peaks for this analyse will be detected using a threshold value.

Step 3: From the “Peak direction” button choose either Peaks or Valleys depending on how the data looks like. In our case chose Peaks. Click on the “Calculate” button.

The program will now find all the peaks in the data chosen and will place a blue square on each detected peak. It is very important to verify that the detected peaks are correct and that all peaks are detected. This will highly influence the calculated power spectrum.

Step 4: In the “Graph Pallette” click on the magnifying glass and choose the horizontal zooming icon. This icon have two vertical lines on the graph. Go to the “Data graph window” the cursor will be changed to a magnifying glass. Click and hold down the left mouse button on the graph. Move the cursor and release the left mouse button.

GrafView will now zoom in the area chosen. Check that all the peaks are detected and that no other blue squares are visible.



If some of the peaks are not detected or if extra blue squares are visible you should change the threshold value and recalculate the data. Do as follows:

In the “Graph pallette” click on the “+” sign. Move the cursor to the “Data graph window”. The cursor will be changed to a plus sign. Using the cursor move the threshold line to the new position and click on the “Calculate” button. Zoom in a part of data and control the detected peaks.

If all the peaks are detected and no extra blue squares are visible then go to next step.

Step 5: Click on the hand in the “Graph pallet” and move cursor to the “Data graph window”. The cursor will be changed to a hand.

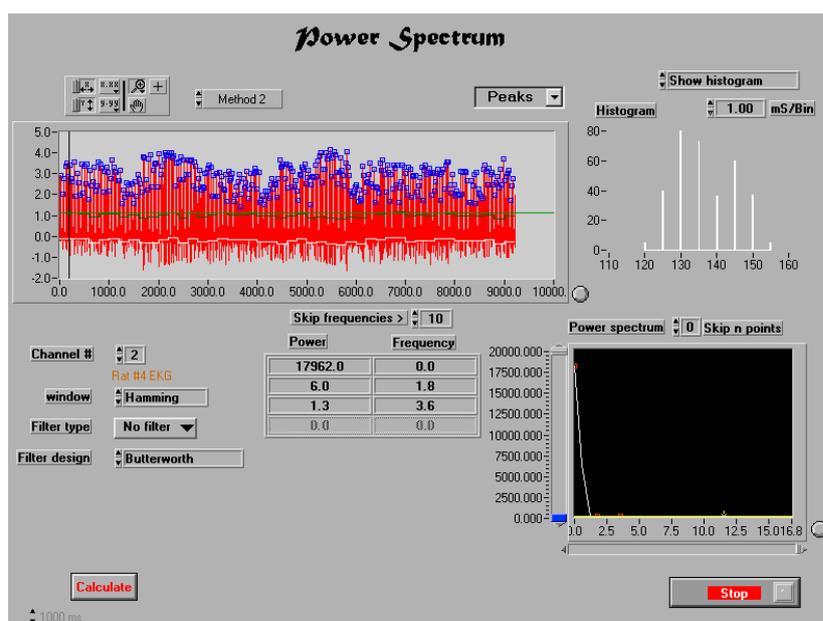
This function will help you to browse through all the data and check if all the peaks in different areas of the data are detected.

Click and hold down the left mouse button.

If you know move the cursor the data will be scrolled to the left, right, up or down. Use this function and check all the peaks in the data and see that all the peaks are detected and no extra blue boxes are visible. If this is true go to next step. If not, change the threshold (*Repeat steps 2-5*).

R-R interval graph shows the distribution of the R-R intervals. The “X” axis is the number of R-R intervals and the “Y” axis is the time distance between two consecutive R peaks in milliseconds. The graph in the figure above shows a distribution of R-R interval between 130-150 ms, with some peaks at 120 ms. This data can also be presented as a histogram.

Step 6: Click on the “R-R interval functions” and choose “Show histogram”. The graph will be changed and shows the histogram of the R-R intervals. In this case X axis represents the R-R interval in mS and Y axis represents the number of R-R intervals



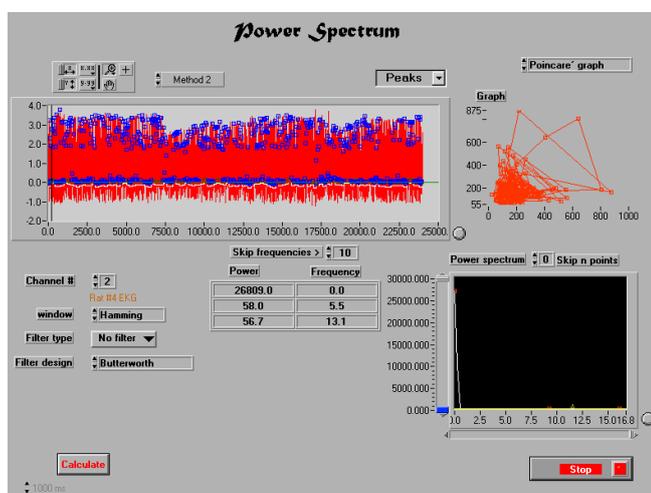
R-R intervals can also be presented as a Poincaré graph.

Step 7: Click on the “R-R interval functions” and choose “Poincaré”. The graph will be changed and shows the Poincaré presentation of the R-R intervals. In this case both X and Y axis represents the R-R interval in mS.

Poincaré graph is the relation between two consecutive points of data. In our case the first point on the graph has the value of the second R-R interval as X and the value of the first R-R interval as Y. The second point has the value of the third R-R interval as X and the value of the second R-R interval as Y and so on. By this way the relations between two consecutive points can be shown as a graph.



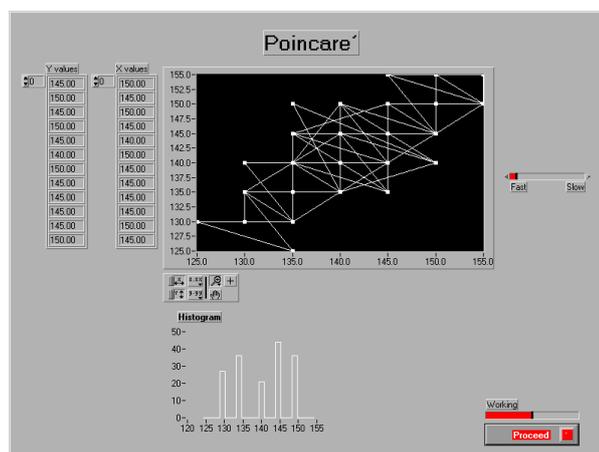
If the graph results in a symmetrical presentation of geometrical figures with no outliers, as in our case, then the data is fit to be used for spectral analysis. However if there are outliers the data should not be used for spectral analysis. As shown in the figure below



The movement of the Poincaré point can be followed in order to specify the approximate location of possible outliers.

Step 8: Click on the “R-R interval functions” and choose “Draw Poincaré”.

A new window will be opened and will show the movement of Poincaré point.

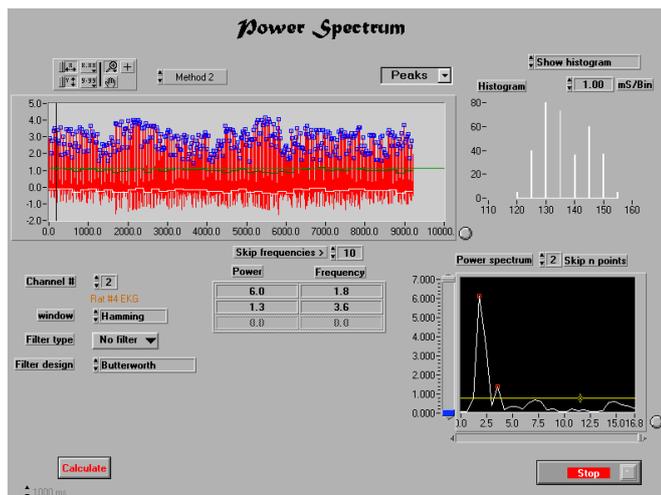


Experiment with different thresholds and study the distribution of R-R intervals.

Spectral analyse graph shows the spectral analyse results. The first peak in a spectral analyse is usually a zero and has a very high power compared to the rest of the peaks. In order to be able to see all the smaller peaks one or two first peaks in the spectrogram could be ignored during the graphical presentation. This process can be performed using the “Skip n points” function located above the “Spectral analyse graph”.

Step 9: Double click on the zero of the “Skip n points” and type 2. Or click two times on the up arrow head close to the zero value. Click on the “Calculate” button.

The screen should look like the figure bellow.



Step 10: Click on the “Show cursor” button close to the “Spectral analyse graph”. Move the horizontal cursor to the threshold level you want and click on the “Calculate” button.

The program will now find all the peaks available in the spectrogram and will put a blue circle on each detected peak. The program will also fill the “Result table” with the frequency and power of the detected peaks. The screen should look like the figure below.



In the figure above the power spectrum has found three frequency domains in the analysed data. First, a frequency of 1.2 Hz with a power of 6.0, second a frequency of 3.6 Hz with a power of 1.3 and third a frequency of 7.1 with a power of 0.6. These values could be somewhat different on your screen. This could be caused, among other, by a different threshold level.

Above the “result table” you can see a “Skip frequencies” function. This function defaults to 10. This tells GrafView to ignore all the peaks found with a higher frequency than 10 Hz. This value can be changed to any frequency desired.

GrafView, however will show one frequency above this threshold in the table as a sign of the start of peaks higher than the threshold.

The raw data can be filtered and windowed before FFT analyse. As default the data is Windowed using Hanning model and no filtering is performed. These parameters can be changed as desired.

The possible windowing models are:

Hanning, Hamming, Blackman-Harris, Exact Blackman, Blackman, Flat top, 4 Term B-Harris, 7 Term B-Harris.

The possible filters are:

Low pass, High pass, Bandpass and Bandstop.

For each of these filter types the following methods are available:

Butherworth, Chebyshev, Inverse Chebyshev, Elliptic, Bessel.

When a filter type is chosen new parameters relevant to the chosen filter will be visible and should be set to proper values for reliable filtering. These parameters will significantly influence the filtering results. The data will be analysed after filtering and windowing.

Power spectrum can also be performed on the raw data by choosing “Method 1” of the functions. When chosen the “R-R interval graph and functions” will be invisible. **The rest of the analyse is the same as in “Method 2”. Method 1 is not recommended for power spectrum analysis of EKG.**

The power spectrum analyse in GrafView is not meant to be used as a last point analyse tool. This program is designed for daily analyse of data and experimenting with data. The final analyse of the data should be performed in a macro written in SAS language. (Statistical Analyse System) which will analyse data in a much more sophisticated way. GrafView in this case is used for data reduction.

When using “Method 2” the R-R intervals can be saved in an ASCII file in a special way for SAS-macro.

Step 11: Click on the “R-R interval functions” and chose “Save R-R intervals”.

The following window will be shown.

Power Spectrum

Save data

In order to save the R-R intervals in a way that they can be analysed properly different parameters should be known as below

Animal number: This is the animal number you want to analyse

Position: This variable marks different parts of data with different numbers. This will give the possibility to compare special parts of data between experiments. Max value is 4.

Happening: This variable marks a happening, ex. Before and after a special treatment, before and after conditioning, Signal number etc.

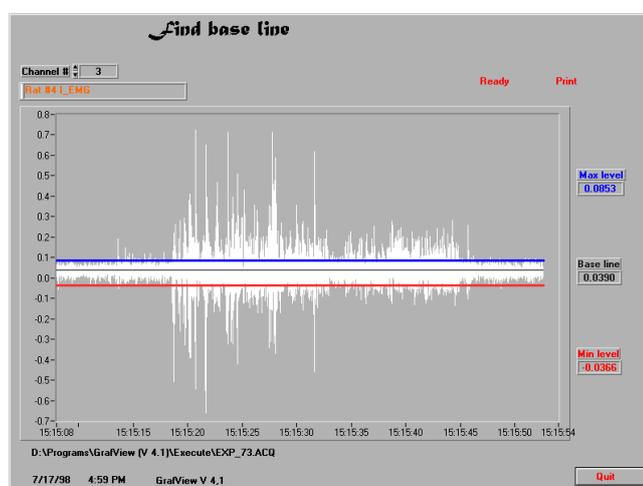
Change the variables and click on the “Save data” to save the results or click on the “Don’t save” to go back to power spectrum window.

Click on the “STOP” button and go back to the main window.

Find base line

This function is aimed to help the user to find the base line of different data. The baseline is calculated as the value which is found in the data the highest number of times.

Surround the area of interest with the cursors and click on the “Find baseline” . A new window will be opened as below.



Change the “Channel number” to the channel of interest. A graph will show the data in white and the base line in black. The base line value is also shown to the right of the graph.

Two other values are calculated namely Max. and Min. values. These two values represent the level of changes in the signal when no activity is present in the signal. In our case as the data used is abdominal EMG these values will represent the tonus of the muscle.

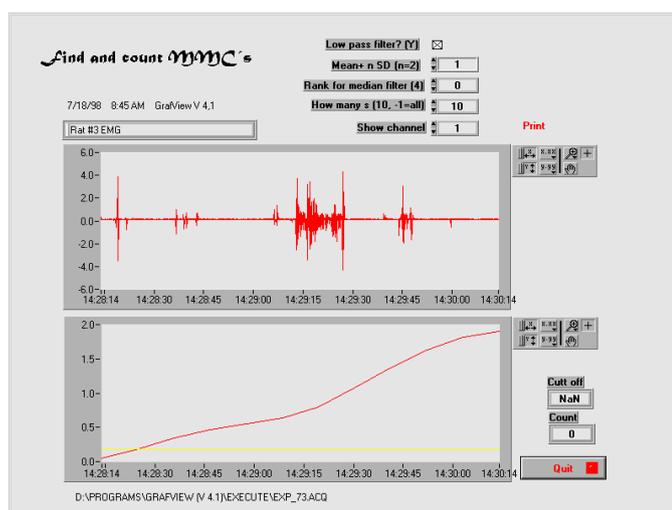
Click on the “STOP” button to go back to the main window

MMC

This function is designed to find and calculate the number of activity bursts in the analysed data. In an EMG data this could be called Migrating Myoelectrical Complex (MMC) with strain gage data from the gastrointestinal track this could be called Migrating Motor complex (MMC).

Click on the MMC button

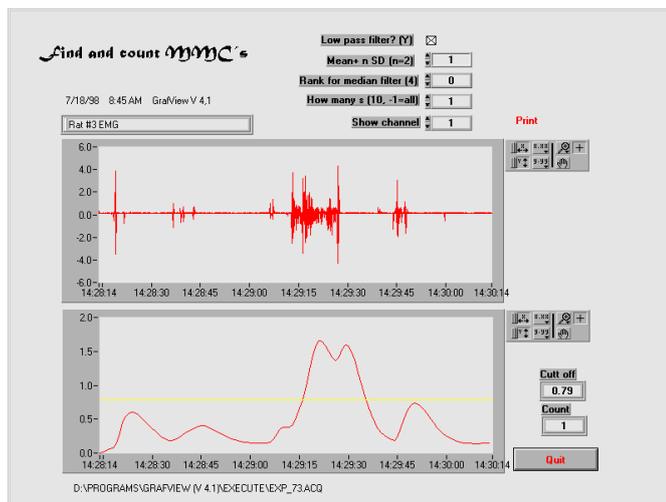
A new window will open as bellow



Different parameters can be changed to fit the analyses to different types of data.

Change the “How many s (10, -1=all)” to 1, this will tell Grafview to divide the data set into one second periods.

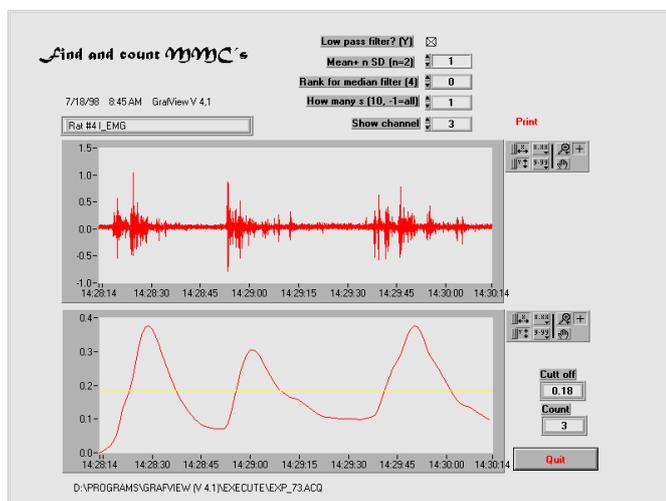
The graph should look like the figure bellow



The program has now found one activity burst or one MMC.

Change the channel number to 3

This is data from Intestinal EMG, the window should now look like the figure bellow and the program could be able to find 3 MMC's.



Experiment with different parameters and find the way they influence the results.
The recommended settings are:

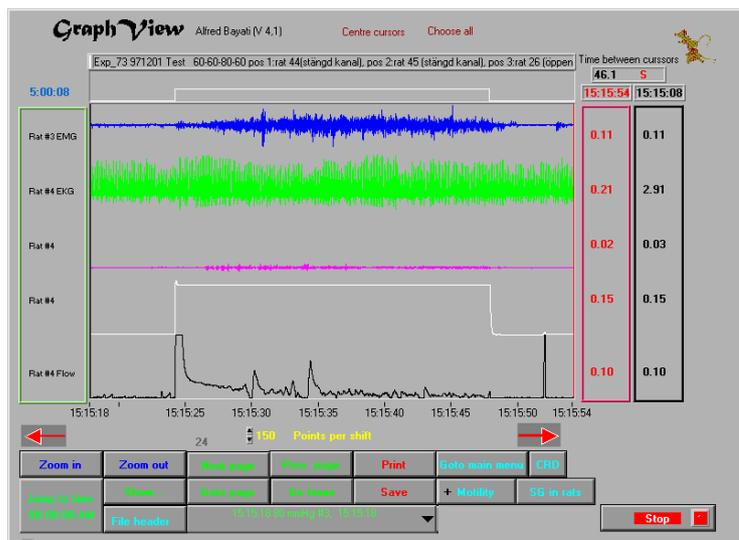
Data type	Function	setting
Colon EMG	Low pass filter	True
	Median filter	False=0
	Time	1s
	Mean +n SD*	1
Abdominal SG	Low pass filter	True
	Median filter	False=0
	Time	1s
	Mean +n SD	1
Colon SG	Low pass filter	True
	Median	True=2
	Time	10s
	Mean +n SD	1
Duodenum SG	Low pass filter	True
	Median filter	False=0
	Time	10s
	Mean +n SD	1
Stomach SG**	Low pass filter	True
	Median filter	False=0
	Time	10s
	Mean +n SD	1

* This is the threshold used to detect the peaks

**When data from stomach is used the experiment should be performed during fasting state. If the experiment is during postprandial state this function should not be used.

Analyse menu

Clicking on this button will bring up page two of the analyse menu.



The main difference between these two pages are that the analyse functions on the first page are performed on the data between the cursors. On the other hand analyse functions on page two are not affected by the cursors, page width, filtering and channels shown on the screen but they will analyse the raw data of the whole file.

Because of this way of working each function on this page is designed specially to analyse one type of file.

CRD

This function is designed to analyse files from the Colo_Rectal Distension (CRD) studies. The column names in these files are of extreme importance as GrafView will analyse different columns in different ways depending on the name of the column.

Column names in this file should be as follows:

Column name	Description
Pressure control signal	Signal used for controlling the pressure device
Rat #1 EKG	EKG data
Rat #1 EMG	Abdominal muscle EMG
Rat #1 I_EMG	Intestinal muscle EMG
Rat #1 Abdominal SG	Strain gauge data
Rat #1 Blood pressure	Blood pressure data
Rat #1 Balloon pressure	Balloon pressure data
Rat #1 Flow	Air flow in the balloon

For the next animal the only change will be “Rat #”. For animal 2 Rat #2, for animal 3 Rat #3 etc. “Pressure control signal” is common for all the animals and should be used only once in each file. All the channels need not to be present in the file.

The order of channels is not significant.

GrafView is case sensitive when looking for the column names.

No space should be typed before or after column names.

The function will not ask for the name of the file but it will analyse the current file opened by GrafView.

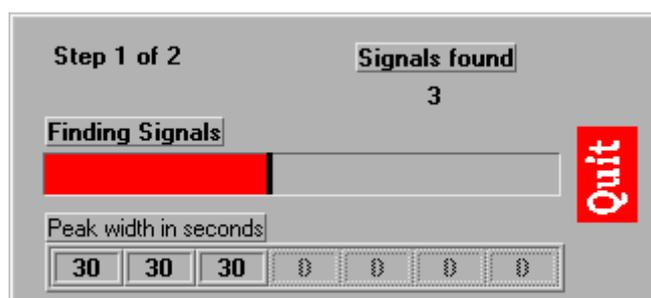
The analyse process for CRD is performed in 2 different steps.

First the program must find all the active signals in the “Pressure control signal”

Second the program will calculate all the parameters.

Click on “CRD” button.

A new window will be opened as shown bellow.



The program will now go through the “Pressure control signal” column and will find all the active signals showing the number of signals found and the width of each signal in seconds. It is advised to control this process to make sure that all the signals known in the file has been found and that the signal width calculated by the program is correct.

After finding all the signals the program will go to step 2 and analyse all the parameters.



PERIOD DETECTION

For each signal the program will read some data before and after the signal. The length of these are the same as the length of the signal, i.e. a signal with a width of 30 seconds will have 30 seconds of data before the signal and 30 seconds of data after the signal. This is true if the time difference between the current signal and the signal before or after it is longer than the signal length. Consider the following example:



For the “First signal” the program will try to read the same amount of data before the signal, however, as the length of data before this signal, “Period A”, is less than the signal width then the program is forced to use the available data i.e. “Period A” as data before the signal. Data after the signal, “Period B”, is longer than the width of the “First signal”. In this case the program will read enough data to match the length of the “First signal”.

For the “Second signal” The data before the signal will be “Period B”. The program will try to read enough data to match the length of the signal, however, it will not include the previous signal in this data. This will force the program to read only “Period B” and use it for the “Second signal” even though this period is shorter than the length of the signal.

In this example the following data will be used.

Time before “First signal”	“Period A
Signal time	“First signal”
Time after “First signal”	Part of “Period B” which has the same length as the “First signal” width
Time before “Second signal”	“Period B”
Signal time	“Second signal”
Time after “Second signal”	“Period C”

It must be mentioned that “Period B” is used both as the time after the “First signal” and the time before the “Second signal”.

CALCULATIONS

For each signal the calculations will be performed on the time before, during and after the signal. The program will read one second of the data at a time and perform the calculations needed. The results shown in the CRD analyse results window (se bellow) are the results from these one second periods.

The decision of which type of calculations should be performed on the data is based on the name of the column where the data is located as follows:

Column name	Calculations
Pressure control signal	Mean of data
Rat #n ¹ EMG	<ol style="list-style-type: none"> 1) Calculate baseline 1) find all peaks using base line as threshold 2) bring the base line to zero 3) find the max. amplitude of the detected peaks 4) calculate sum of the max. amplitude of the detected peaks 5) calculate frequency 6) calculate area under the absolute values of the curve (AUC) using trapezoidal rule
Rat #n I_EMG	<ol style="list-style-type: none"> 1) Find max. amplitude of data

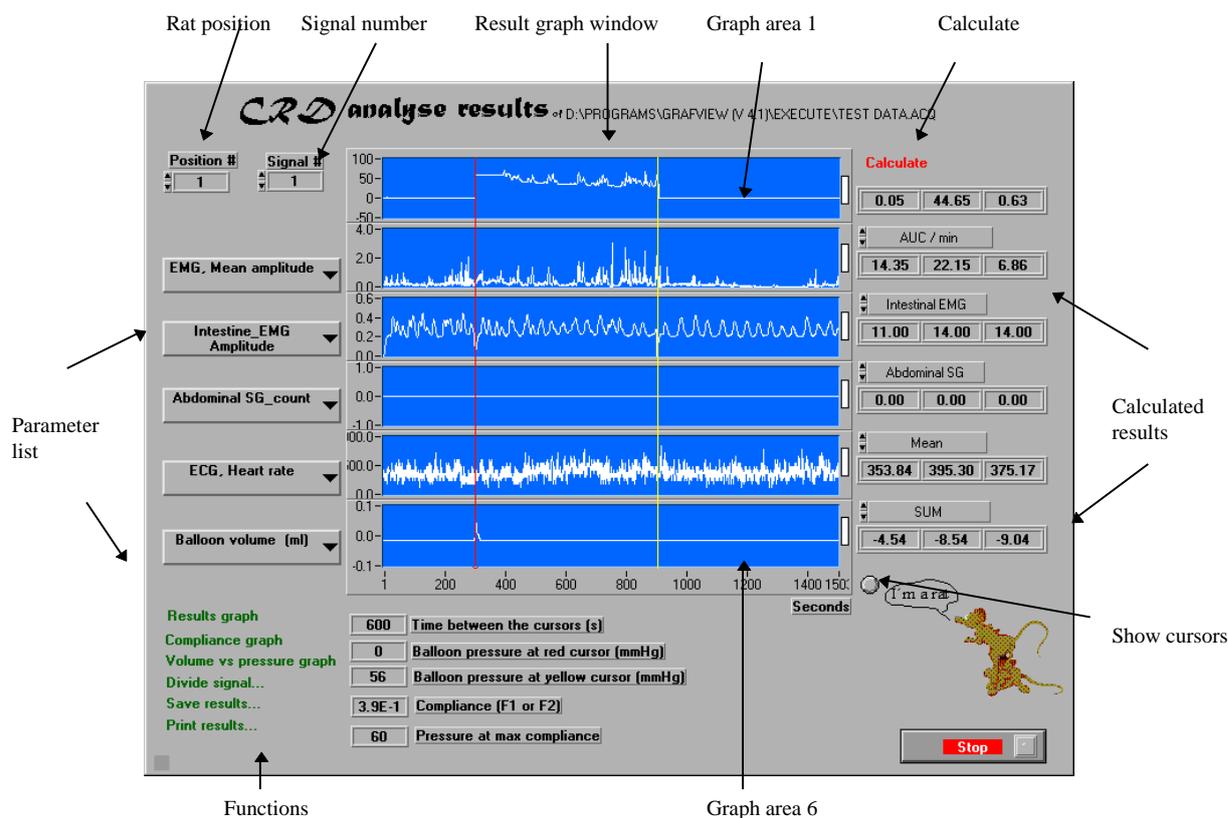
- Rat #n Blood pressure
- 1) Calculate threshold as (Max value + Min value)/2
 - 2) calculate Max, Min and mean values of the peaks above the threshold and use as Max, Min and mean systolic pressure
 - 3) calculate Max, Min and mean values of the valleys below the threshold and use as Max, Min and mean diastolic pressure
 - 4) find all peaks above the threshold
 - 5) calculate heart rate as number of peaks per minute
- Rat #n Flow
- 1) Skip the first 10% of each signal²
 - 2) calculate area under the absolute value of the curve using trapezoidal rule
 - 3) count number of peaks using a threshold equal to 5 ml/min or 0.5 volts and use as number of contractions
 - 4) calculate the total air flow in to the balloon (balloon volume) as $\sum Xi * \frac{1}{60}$, where Xi is the base line of the actual measured values per second. The air flow during contractions calculated in step 3 should not be included in the balloon volume
 - 5) calculate the sloop of a line drawn from volume as the X and pressure as the Y co-ordinates. Compliance is then the inverted value of the sloop.
- Rat #n EKG
- 1) Filter data using a Low pass Butterworth filter with a low cut-off equal to 10 Hz and an order of 2
 - 2) bring base line to zero
 - 3) count number of QRS complexes
 - 4) calculate heart rate as number of QRS complexes per minute
- Rat #n Abdominal SG
- 1) Find max. amplitude of data

1= n could be 1 to 4 corresponding to the rat position number

2= This process is only used for the calculation of the number of contractions. The first part of signal is influenced by a very fast flow change which will give false high contraction number if used.

CRD ANALYSE RESULTS

After calculating all the data a new window (CRD analyse results) will be opened showing the results of calculations.



The “Results graph window” is divided in 6 different graph areas. The data presented is the calculated values per second (see calculations).

Graph area number one shows always the results from calculations on the “Balloon pressure” column. This area can not be changed by the user. All other areas are open to be changed by the user.

An analyse session could be as follows:

Choose the rat position

This is the position of the animal in the experiment. A maximum of 4 animals can be tested at the same time in the CRD system. Remember that the “Animal number” and the “Position number” need not to be the same. In our case chose position #4.

Choose the signal of interest

In our case chose signal #1

Choose the parameters to analyse

Using the “Parameter list” you can choose any one of the calculated parameters.

In our case choose

EMG, Mean amplitude

for graph area #2

EMG, Mean peak sum

for graph area #3

EMG, Intestinal_EMG Amplitude

for graph area #4

ECG, Heart rate

for graph area #5

Contractions (n)

for graph area #6

Choose the function to use

The three different areas on the “Result graph window” i.e. before, during and after the signal can be analysed in different ways by choosing one of the functions available in the “Calculating function” buttons.

In our case choose:

AUC/min

for graph area #2

AUC/min

for graph area #3

Intestinal EMG

for graph area #4

Mean

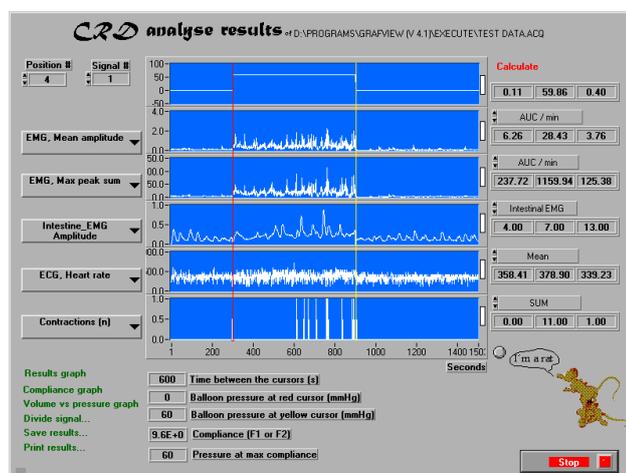
for graph area #5

Sum

for graph area #6

Click on the “Calculate” text

the screen should look like the figure bellow



The figures presented in the “Calculated results” are the calculations from the period before, during and after the signal respectively.

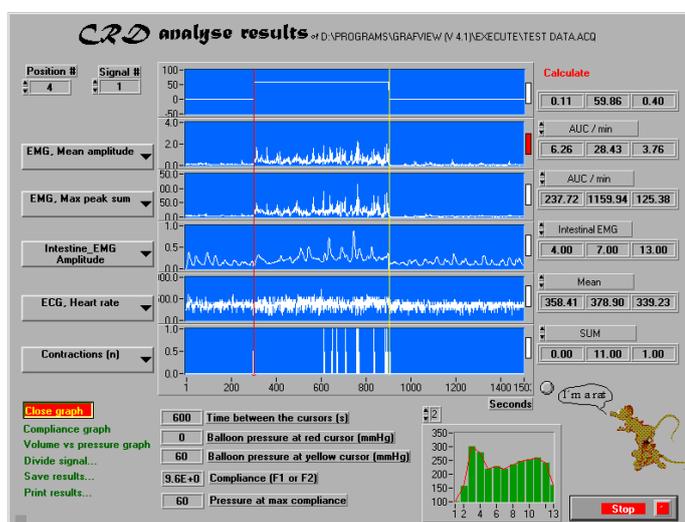
Change the position number and/or the signal number and familiarise yourself with this “Analyse results window”.

RESULTS GRAPH

Click on the “Results graph”

This will bring up a small window showing a bar graph as shown in the figure bellow. This graph is a simple way to see a trend in the data of the experiment. The results are calculated as the mean of the difference between the response during and before the signal of all positions in the actual experiment i.e. if there are 4 animals in the current experiment this graph is the mean value of all 4 animals. If there are only three animals then the graph is a mean value of three animals etc. All the signals in the experiment are then compared to the first signal and the results are presented as % change compared to the first signal in this way the first signal is always 100%.

The value shown above the “Results graph” represents the parameter that will be calculated. The default value for this parameter is 6. This means that the parameter and the calculations chosen for graph area 6 are used. Change this value to 2. This will show you the trend in data as corresponded to the “AUC/min of the EMG, Mean amplitude” of all four positions in the data set i.e. the data in graph area 2.



Click on the “Results graph” to close this graph

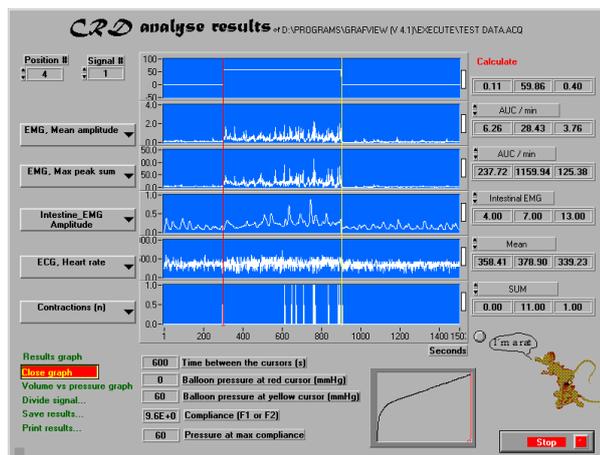
COMPLIANCE GRAPH

Click on the compliance graph

This will bring up a window as shown in figure bellow. This graph is the calculations of the compliance per second during the signal. The maximum value of this graph is the compliance of the system. Remember that in order for the balloon volume and the compliance calculations to be correct two conditions should be met.

- The signal should be at least two minutes
- The signal should be a ramp

This means that the balloon volume and the compliance calculated in this example are not exact.

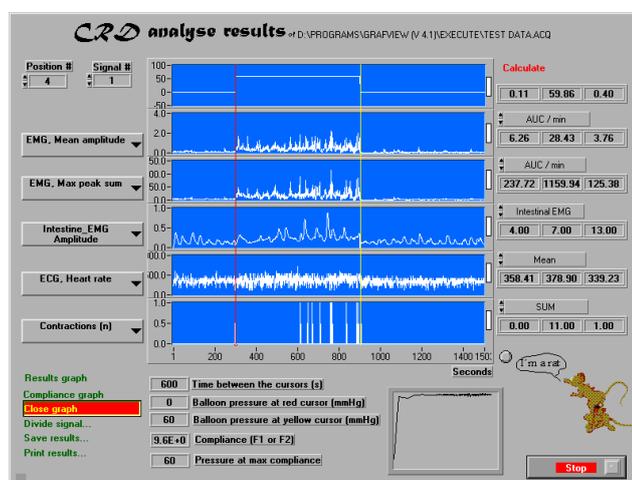


Click on the “Compliance graph” to close this graph

VOLUME VS PRESSURE GRAPH

Click on the volume vs pressure graph

A new window will be opened as shown bellow. As abvious from the name this graph represents the relationship between pressure and volume.



Click on the “Volume vs pressure graph” to close this graph

DIVIDE SIGNAL...

Using this function you can divide the signal in different parts and calculate the different parameters for each part. This function is of interest if the response to distension is different in different parts during the signal.

SAVING CRD RESULTS

The results calculated by GrafView can be analysed using special designed macros in SAS programming language. The results can be save in two different ways.

- Saving mean values: This will save the calculated values i.e. the values shown to the right of the screen one for before the signal one during the signal and one after the signal
- Saving raw data: This will save the calculated data per second i.e. the data you can see in the graph area. Be careful when using this function remember that in the current file there are two 10 minutes signals in the beginning followed by 10 pulses of 30 seconds each and at the end a signal of 10 minutes. This will give a total of 6300 seconds if one calculate the time before, during and after the signals. As each second produces one column in the saved file this will give 6300 columns for each parameter. As a comparison it can be mentioned that Excell can not read more than 255 columns.

Click on the “Save results” text

A new window named “Start information for CRD save” will be opened as bellow.

The screenshot shows a dialog box titled "Start Information for CRD save". It is organized into several sections:

- Signal number:** A dropdown menu showing "1".
- Signal form:** A dropdown menu showing "IV".
- Administration route:** A dropdown menu showing "PO".
- Date:** A text field showing "07/17/98".
- Position number:** A dropdown menu showing "1".
- Race:** A dropdown menu showing "SPD (Rat)".
- Fasted:** Radio buttons for "Yes" and "No", with "No" selected.
- Sex:** Radio buttons for "Male" and "Female", with "Female" selected.
- Animal number:** An empty text field.
- Comments:** A text area containing: "No comments", "Do not use this experiment", "Colon EMG placerade 5.5 cm fr. caecum", "Colon EMG placerade 3 cm fr. caecum", "Colon EMG placerade 2 cm fr. caecum".
- Treatment info:** A section with fields for "Substance name", "Substance ID", "Batch number", "Dose", "Administration volume", "Dose sort", and "Volume sort".

On the right side of the dialog, there is a cartoon character holding a green plant. Below it are several buttons: "Project number", "Series number", "Experiment number" (all empty text fields), "Empty all", "Undo last signal", "New signal", "Proceed", "Saving mean values", "Save settings", "Load settings", and "Quit".

Type in or choose the appropriate information for all the signals in the file, add new signals by clicking on the “New signal” button or delete all the signals except signal number one to start all over by clicking on the “Empty all” button. You can delete that last activated signal by clicking on the “Undo last signal” button.

All the settings in this window can be saved using “Save settings” button. Old settings can be recalled using “Load settings” button.

The “Proceed” button is inactive and will remain inactive until the first three parameters i.e. Project number, Series number and Experiment number are given.

When all the information for all the signals has been chosen click on the “Proceed” button. This will open a new window as bellow.

Here you can control that all the given settings for different positions and different signals are correct. If any thing is wrong you can go back to the previous window by clicking on the “Don’t save” button, correct the wrong information and use the “Proceed” button to go back to “Start information for CRD save” window.

The settings can be saved using “Save settings” button. This is the same function as in the previous window.

When ready click on the “Save results” button.

Control Start Information for CRD save

Saving mean values

	Signal #1	Signal #2	Signal #3	Signal #4	Signal #5	Signal #6	Signal #7	Signal #8
Date	07/17/98	07/17/98	07/17/98	07/17/98	07/17/98	07/17/98	07/17/98	07/17/98
Project number	1	1	1	1	1	1	1	1
Series number	1	1	1	1	1	1	1	1
Experiment number	1	1	1	1	1	1	1	1
Sex	Male							
Fasted?	Yes							
Substance name
Substance ID
Batch number
Dose
Dose sort
Administration volume
Volume sort
Race	SPD (Rat)							
Signal number	1	2	3	4	5	6	7	8
Position number	1	1	1	1	1	1	1	1
Animal number
Signal type	Puls							
Administration route
Comments	No comment							

A new window will be opened as bellow showing the progress of saving the results. At the end of this process a file management window will be opened asking for the name of the file for the results. If you give a new name the results will be saved in a new file. If you choose an existing file the results will be appended to the file.



If “Saving mean values” has been selected the following parameters will be saved together with the information supplied in the “Start information for CRD save” for periods before, during and after each signal.

Pressure control signal	Mean
EMG, Mean amplitude	AUC/min
EMG, Frequency	Mean
EMG, Max peak sum	AUC/min
EMG, AUC	SUM
Intestinal EMG, Amplitude	Number of MMC's
BP, Max systolic	Mean
BP, Min systolic	Mean
BP, Mean systolic	Mean
BP, Max diastolic	Mean
BP, Min diastolic	Mean
BP, Mean diastolic	Mean
BP, Heart rate	Mean
AUC of flow	SUM
Balloon volume (ml)	SUM
Contractions (n)	SUM
ECG, Heart rate	Mean
Abdominal SG Compliance	Number of contractions

If the “Saving raw data” has been chosen the data from the graph area will be saved.

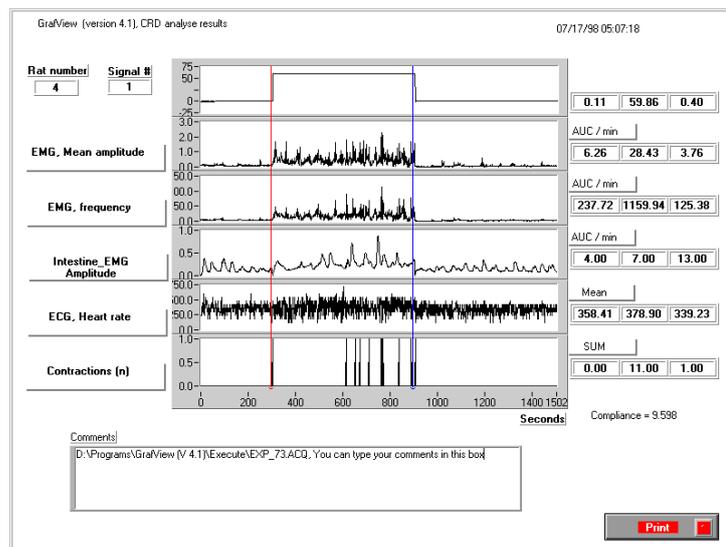
It must be mentioned that only the number of signals chosen will be saved i.e. if the original data file contains 12 signals and you only choose 8 signals in the “Start information for CRD save” window the results from the first 8 signals will be saved.

The file containing the results is an ASCII file and can be read in programs like Excel.

PRINTING CRD RESULTS

Click on the “Print results” button.

A new window will be opened. GrafView will put the name and address of the file analysed in the “Comments” box at the bottom of the window. Click in this box and type any more comments you want to add.

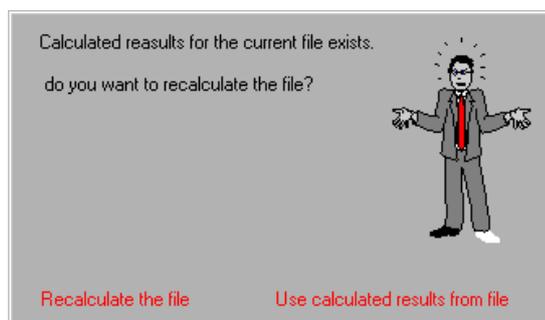


Click on the “Print” button

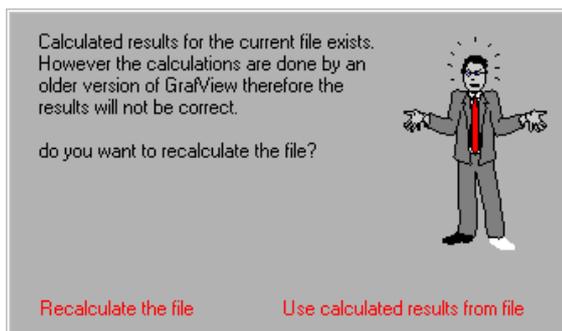
The page will be printed and the “Analyse results window” will be shown.

Click on the “Stop” button to go back to the main window

The results calculated by the “CRD” program will also be saved in the same directory and with the same name as the original file. The suffix of the file will, however, be changed to “RES”. The next time you choose “CRD” for this file a new window will appear informing you that you have already analysed the file.



If the results exists but are calculated by an older version of GrafView the following window will be shown.



Two choices are available:

If you want to recalculate the file Click on the “Recalculate the file”

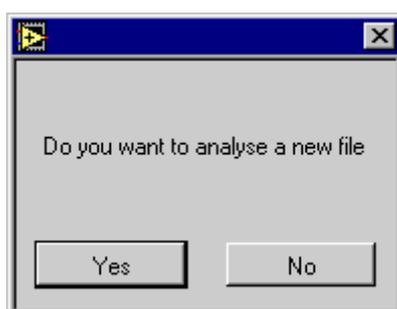
If you want to use the calculated results click on the “Use calculated results from file”

In this case GrafView will read the results from the file and get you directly to the results window.

STOP

Click on the “Stop” button

A new window will open and give you the opportunity to either close the program or to read a new file.



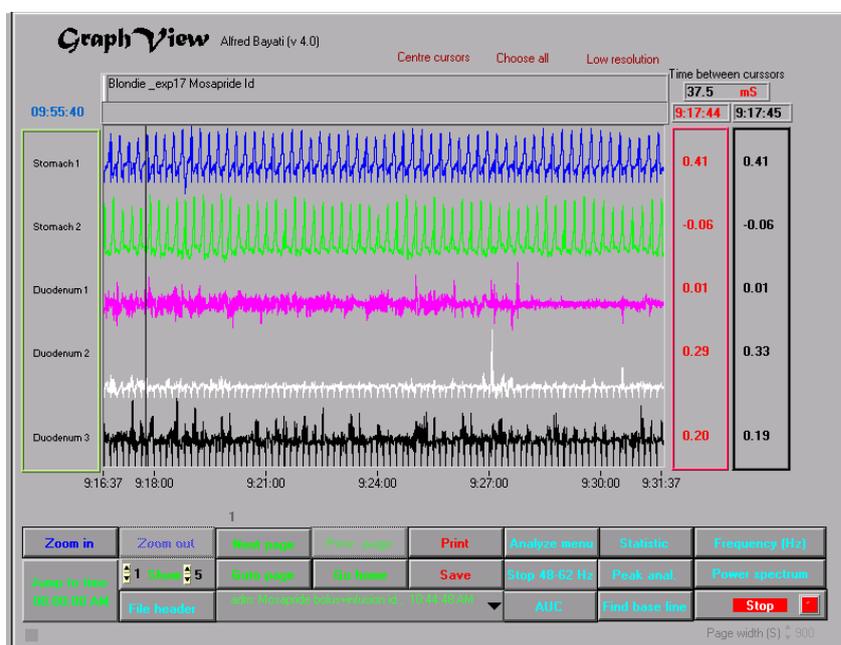
If you want to quit the program click on the “No” button.

If you want to analyse a new file click on the “Yes” button.

MOTILITY

Click on the “Yes” button
the “GrafView file manager” will be opened. Chose the file named
“C:\GrafView\Test_data2.ACQ” in the next window chose a few channels and click on the
“Proceed” button

After a while the “main window” will be opened showing the new data set as figure bellow. This
new data file is needed to explain the “Motility” analyse function.



Click on the “Analyse menu” button

The “Motility” button has a “+” sign on it. If you click on this sign it will be changed to “-“. This sign is equal to the function we used in the “Power spectrum” analyse when we choose between peaks or valleys. The “+” sign is equal to peaks and the (-) sign is equal to valleys.

Chose “+” and click on the “Motility” button

A “file management window” will open asking for the file containing the start information to analyse the data. GrafView will read predefined Start information, if they exists, from a file which usually has the same name as the file you are analysing but with “INI” as a prefix. This file contains all the information of different animals and their ID, different substances and their batch number and so on.

Type new information or chose information from the predefined data and fill all the appropriate boxes.

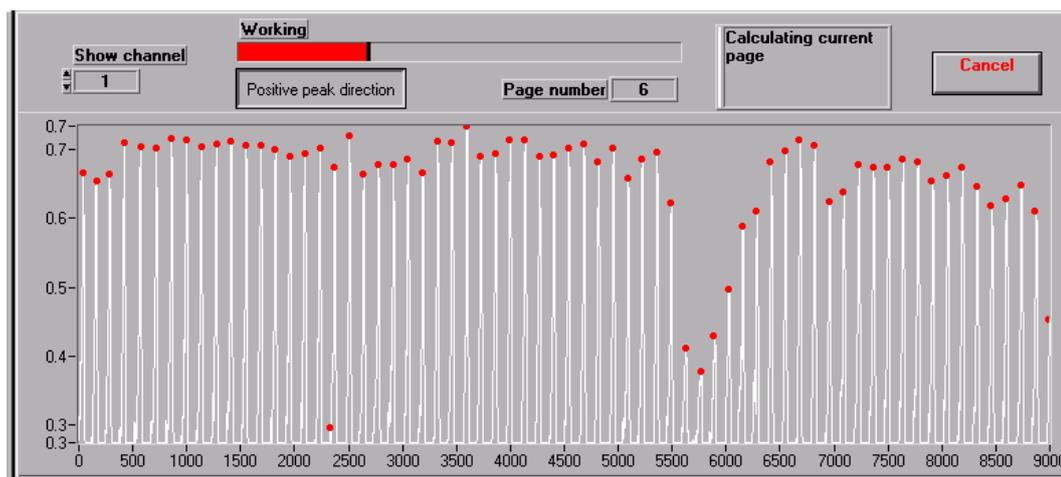
At the bottom of this window you can see three comment fields. You can chose the “Start of analyse”, the “Administration time” and the “End of the analyse” by choosing different comments. This will tell the program where in the file to start analysing the data “Start of analyse”, how long time should be used before the administration as the control period (Administration time) and where is the end of data for analyse “End of the analyse”.

“Period time (min)” and “Min. peak width (s)” are very important parameters and always should be answered. “Period time (min)” is the length of data the program will read each time and will analyse as one block i.e. a value of 15 means that the program will divide the whole file in 15 minute periods. This is true for the data after the administration comment. All the data before this will be read as one block and will be used as control period.

“Min. peak width (s)” tells the program which peaks should be accepted as contractions. A value of 1 means all the peaks having a width of more than 1 seconds should be accepted.

After filling all the parameters click on the “Proceed” button

A new window will be opened. GrafView will now read the control period analyse the data and will show you all the peaks detected. The program will then read the first block of data after the administration comment and will analyse while showing you the detected peaks. This process is important as it will give the user a chance to control that the program is working properly by finding the peaks that the user can accept.

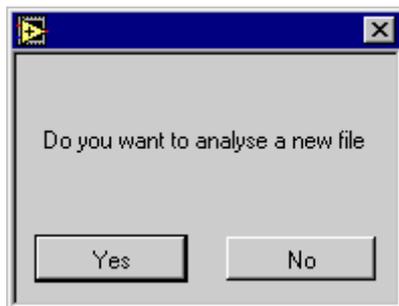


When all the data has been analysed the program will save the results in a file designed to be used by a SAS macro for further statistical analyse.

SG IN RATS

Click on the “Stop” button

A new window will open and give you the opportunity to either close the program or to read a new file.

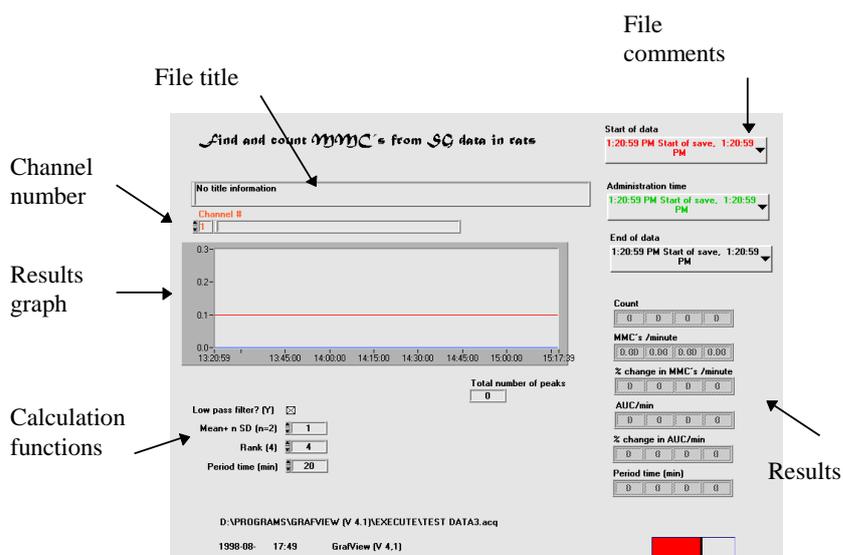


If you want to quit the program click on the “No” button.
If you want to analyse a new file click on the “Yes” button.

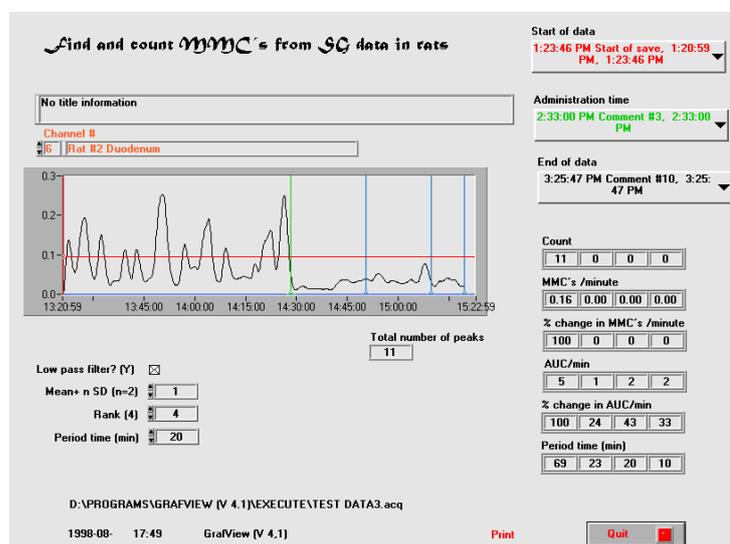
*Click on the “Yes” button
the “GrafView file manager” will be opened. Chose the file named
“C:\GrafView\Test_data3.ACQ” in the next window chose a few channels and click on the
“Proceed” button*

After a while the “main window” will be opened showing the new data. This new data file is needed to explain the “SG in rats” analyse function.

Click on the “Analyze menu” and then click “SG in rats” a new window will be opened as bellow.



After a while when calculations are completed the results will be shown on the screen. Click on the “File comment, Start of data” and chose “1:23:46 Start saving”, click on the “File comments, Administration time” and chose “2:23:00 Comment #3”, click on the “File comments, End of data” and chose “3:25:47 Comment #10”, chose channel number 6 the window should look like the figure below.



The red cursor is the position of the start of the data that will be calculated. All the data between this cursor and the green cursor will be handled as control period. The rest of the file up to the last comment chosen “End of data” will be divided into 20 minute periods and will be compared to the control period.

The values on the right side of the screen are the results of calculations and are as follows:

- | | |
|----------------------------|---|
| ■ Count | These are the number of MMC found in each period |
| ■ MMC's/min | These are number of MMS's per minute for each period |
| ■ % change in MMC's/minute | Each period is compared to the control period and presented as % change |
| ■ AUC/min | This is the area under the curve for each period normalised to one minute |
| ■ % change in AUC/min | Each period is compared to the control period and presented as % change |
| ■ Period time | The actual period time used |

Experiment with different channels and change the “calculation functions” and see the effects on the results. In the current version the results can not be saved. However the whole page can be printed by clicking on the “Print” text.

When ready click on the “Proceed” button. This will bring you back to the main menu of the GrafView program.

END