# SCIENTIFIC AND ENGINEERING FIRM "BACS"

# ANALYZER Control software for chromatographic gas analyzers

02.02 version.

# **OPERATOR'S GUIDE**

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### 1. Starting PC Software ANALYZER.

Make double-click on the ANALYZER icon in Desktop.

✓ If the Access System is activated, the dialog box «Access code» will appear (see Fig. 1.1). Enter the password and *click* the button or press <*Enter*>.

If you entered wrong password and did not change it within 30 seconds, ANALYZER will start *«Unregistered user»* mode (the time left before start this mode is shown at the bottom of the dialog box).

If you have forgotten the password, contact the Program Administrator.

If Access System is switched off, the Program automatically enters *«the Anonymous user»* mode with the *Chromatographer* right of access.

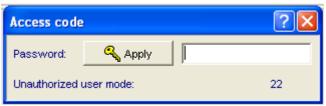


Figure 1.1.

### 2. Operating ANALYZER in Active Mode.

Access to <u>Active Mode</u> is allowed to any registered User. Main program window for this mode is shown on Figure 2.1 and includes:

- The main menu with sets of commands to control the work of the program;
- The main and additional toolboxes with shortcut keys of some commands from the main menu;
- Status panel of the device, showing the current parameters of the chosen chromatograph, settings of its discrete channels and the process of carrying out the analyses in the sampling mode;
- *Program status panel and line with* brief information on the current operating mode of the Program.

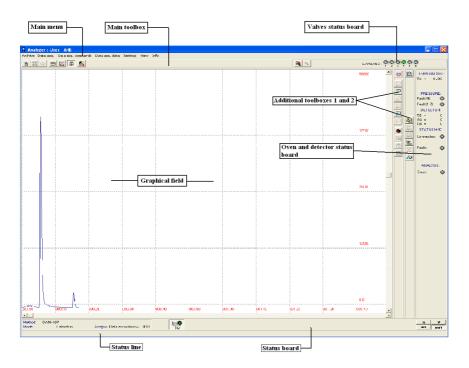


Figure 2.1.

### 2.1. Starting Active Mode.

Initial start or change of active mode could be done with dialog box *Select data acq. method* (see Fig. 2.2) which can be activated in two ways:

- by means of shortcut button in the Main toolbox;
- by Main menu: Data acq. / Select data acq. method

🕒 Anal	yzer : Us	er - And				
Archive	Data acq.	Data acq.	. commands	Data a	acq. data	
	Select d	ata acq. m	ethod	1		
	Data ao	q. settings				-
	1. 187		F1			1
L		9,	····· • • •	ਸ.ਜ		1
i i	1	<u> </u>		9		i
-	1	8	8:	88		ļ
1	1		-			ł

If necessary, you can view and change the mode of carrying out the analysis on the device by choosing from the list in *Chromatographs* of complex board.

Select data acq. method	?
Chromatographs of Complex: ※ 및 Dani -187 ※ 및 Dani-105	Detectors 187 DANI-187 (mode 02:Calibration)
	Work mode:
	🖉 Cancel 🖌 Apply 🏌 Exit

Figure 2.2.

If necessary, you can view and edit current lists of analysis methods (single analysis or series of analyses under the specified schedule). You can do that in the board *Detectors*.

To activate the mode of analysis, press the Apply button.

After that, buttons for the analyzers, will have appeared on *the Status board* (see Fig. 2.1). Every button is named in accordance with corresponding analyzer and equipped with a lamp, indicating the sate of analysis:

- red there is no analysis now;
- green the analysis is in process now;
- yellow there is a maintenance pause now:

- during th current analysis (the lamp has continuous yellow light);

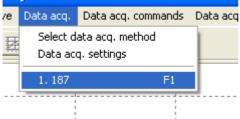
- between analyses in automatic mode (the lamp is flickering with yellow light).

### 2.2. Specifying chromatograph for work.

You can switch to work with an active analyzer in two ways

- by pressing a detector shortcut button <a href="Det\_N">Det\_N</a>, placed on the State Board (see Figure 2.1);
- by Main Menu: Data acq. / N. Det-N :..

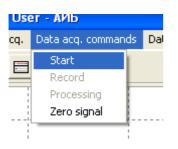
#### nanyzer : User - APID



# 2.3. Starting analysis.

You can start selected analysis process from activated window of this analyzer only:

- by pressing the button, placed on *the Additional toolbox 1*;
- by Main Menu: Data acq. Commands / Start



# 2.4. Process of analysis.

User can control the process of analysis:

- 1. In the *Analysis* line on *the Status board* the current state of analysis is reflected in one of the following forms:
  - Delay (in minutes, seconds) time since the analysis start is reflected;
  - Data acquisition (in minutes, seconds) time since the data acquisition start is reflected;
  - Delay (in minutes, seconds) time till the end of analysis is reflected;
  - *Collected (in minutes, seconds)* time of collecting the chromatogram is reflected.
- 2. During the analysis, *the Graphical field* of the Program shows current chromatogram.

During the data acquisition you can activate the Archive mode and perform any any operations with the chromatograms from the archive. You can also work with dialog box *Setting data acquisition parameters*. Regardless of the mode is being active, the analysis will be performed up to the end or user's intrusion.

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### 2.5. Ending analysis.

If **manual** mode of analysis has been chosen in current method settings, the analysis is automatically finished after ending of analysis cycle.

If **semi-automatic** mode of analysis has been chosen in current method settings, the analysis is automatically finished after ending of a certain (specified) number of analysis cycles.

If **automatic** mode of analysis has been chosen in current method settings, the analysis is automatically finished after logical end of sequence of analyses, that was programmed for this analytical mode.

Immediate stop of analysis can be fulfiled in two ways:

• by pressing the shortcut button placed on the Additional toolbox 1;

• by Main Menu: Data acq. commands / stop.

In case you want the analysys to stop automatically after finish of current data acquisition cycle, you can give a soft stop command to PC Software in two ways:

- by means of the button, placed on the Additional toolbox 2;
- by Main Menu: Data acquisition data / Soft stop.

#### 2.6. Saving analysis results.

If it is specified in the **Analysis mode** settings, the analysis is automatically stored after the end of data acquisition:

- chromatograms of unknown gas are stored to the archive folders Unknown gas analyses;
- chromatograms of calibration gas are stored to the archive folder **Calibration analyses**.
- maintenance or contingency chromatograms are stored to the archive folder **Maintenance analyses**.

When creating a new analysis the Program gives it the next serial number in the list of analyses of the current month (year).

#### Manual saving.

If the mode of carrying out analyses is stopped, you can manually save the results of this measurement into any analysis from the database. To do so, you should activate the *«Save chromatogram»* dialogue (see a Fig. 2.3):

- by means of the button on the Additional toolbox 1;
- by Main Menu: Data acq. commands / Record.

*«List of Databases»* board includes the list of:

- working analyses monthly archives,
- annual archive databases of calibration or supernumerary analyses.

✓ *«List of analyses»* board includes the list of already collected analyses for selected database.

*«Chromatograms of analysis»* board includes the table with the information on chromatograms saved within selected analysis. It is possible to save up to 10 chromatograms in one analysis. These chromatograms are calculated with averaging.

Icon is situated to the left of sample number means that the chromatogram is still kept on the hard disk;

Icon is situated to the right of sample number means that the chromatogram is processed and results of processing are still kept on the hard disk.

Button Add is for adding a new analysis into the list.

If any analyses database is selected, new analysis is created in the current month database of the current year. Otherwise, the new analysis is created in the corresponding current year database of calibration or supernumerary analyses.

To save results of last measurement:

- Choose the database in which you wish to place the collected chromatogram;
- Choose the required analysis from the database;
- Place the cursor on the needed sample field of the analysis table and make double click on it.

🚘 Save chromatogram		
Method: DANI-187, record on the analyzer 1	I	Analyzer 1:
List of databases : Analyses of 2006 years Analyses of 2008 years Analyses of April Analyses of Septembe Analyses of December Analyses of 2009 years Maintenance analyses Calibration analyses	List of analyses : N 1 of 03 (03:03)	sample 1
<>	<b>⊅</b> §Add	

#### Figure 2.3.

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### 2.7. Viewing zero line (no-load detector signal).

If analysis is stopped, you can watch current detector's signal in two wavs:

- by means of the button, placed on *the Additional toolbox 1*;
- by Main Menu: Data acq. commands / Zero.

To stop this mode, repeat one of these two actions.

### 2.8. Chromatogram superposition mode (overlaying).

To overlay any chromatogram onto current chromatogram, you

should press button, placed on the Additional toolbox 2.

Then the «Overlaying chromatograms» dialog box will open (see section 3.8).

# 2.9. Statistic protocols of analyses.

To view statistical protocols of analyses, use the «Final measurement protocol» expanded dialog box (see section 3.7):

- by Main Menu: Data acq. data / Protocols review;
- by means of the estimate the shortcut button on the Additional toolbox 2.

#### 3. Operating ANALYZER in Archive Mode.

Access to work in the <u>Archive</u> mode is given to any authorized User. The basic Program window in this mode looks the same as in the **Sampling** mode, and consists of (see a Fig. 3.1):

- The main menu with sets of commands to control the work of the program;
- The main and additional toolboxes with shortcut keys of some commands from the main menu;
- Status panel of the device, showing the current parameters of the last chromatograph, the User worked with before in the sampling mode;
- *Program status panel and line with* brief information on the current operating mode of the Program.

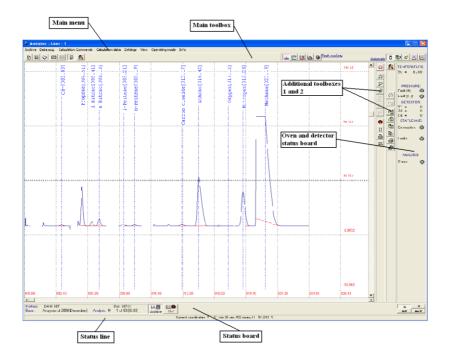


Figure 3.1.

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### 3.1. Starting Archive Mode.

Initial load of new analysis from the archive could be fulfiled by dialog box *«Select analysis»* (see Fig. 3.2) which can be activated in two ways:

- by means of the button on the Main toolbox;
- by Main Menu: Archive / Open analysis

*«List of databases»* board includes the list of:

- monthly archives of analyses of an unknown gas,
- annual archive databases of calibration and maintenance analyses.

*«List of analyses»* board includes list of analyses for selected database.

*«Chromatograms of analysis»* board includes the table with the information on chromatograms saved within selected analysis. It is possible to save up to 10 chromatograms in one analysis. These chromatograms are calculated with averaging.

E Select analysis	X
List of methods(F5): 🕅 DANI-187	Analyzer 1:
List of databases (F6): Analyses of 2006 years Analyses of 2008 years Analyses of 2008 years Analyses of April Analyses of December Analyses of December Analyses of December Calibration analyses	Sample 1
🛨 Delete 🖌 🛨 🗐 勉 🏝 🖻	Autoscaling mode:
Заказчик: Исполнитель: Анализируемая проба:	

Figure 3.2. 13

Icon is situated to the left of sample number means that the chromatogram is still kept on the hard disk;

Icon is situated to the right of sample number means that the chromatogram is processed and results of processing are still kept on the hard disk.

To activate the archive mode:

- select database with required analyses;
- select required analysis inside of the database;
- open required chromatogram inside of the analysis by double-clicking its icon. Usually one analysis has one chromatogram only, but it is possible to place up to 10 chromatograms in it. In this case all these chromatograms are processed with averaging.

After that,

- call button to operate the Archive mode and
- the information on the chromatogram, loaded from the archive.

on the Status board will appear (see Fig.3.1).

# 3.2. Switching to Archive Mode.

You can switch over from *the Active mode* to *the Archive mode* in two ways:



- by means of the Archive button on the Status board;
- by Main Menu: Archive / Open archive.

### 3.3. Marking of peaks.

If it was specified in the **Analysis mode** settings, the Software calculates chromatograms automatically and stores the results after the end of each analysis.

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#### 3.3.1. Automatic peak marking.

This mode is to calculate or re-calculate current chromatogram in accordance with previously defined parameters of peak marking. You can activate it by:

- Main Menu: Operating mode / Peak marking / Automatic;
  - - and buttons on *the Main toolbox*.

The Additional toolbox 2 in this case contains following shortcut keys:

Settings of automatic chromatogram marking;



- -
- Restoring previous calculation Settings;
- Saving current calculation Settings;

### Settings.

Parameters of automatic processing of chromatograms are specified in « Settings of automatic control mode » dialog window (see Fig.

3.3 ), which could be activated by pressing button on the Additional toolbox 2.

☑ <u>Identification.</u> If there are reference peaks in substance list, User can choose the mode of peak identification:

By retention time;

•

- By Linear Retention Index (LRI);
- By Kovats Retention Index (KRI).

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😽 Settings of automstic control mode 🛛 🛛 🔀						
The inquiry wheth Identification: The inquiry wheth	Time: (	• LRI: O				
	The whole chromatogram analysis:     •       The analysis of the chromatogram chosen area:     •					
Switch the error m	essages off whe	n calculating ✓ Apply	<b>v</b>			

Figure 3.3.

In this case User can activate control mode of reference peaks' identification.

Inquiry whether the reference peaks are marked properly. In this option User can activate control mode of peak identification.

Field of analysis. In these options User should specify field of chromatogram processing.

Off calculation errors messages. In this option User can give a command not to inform about errors appearing during processing the chromatograms.

### Processing of chromatograms .

To activate the mode of automatic peak marking, you should:

- Press button on the Additional Toolbox 1 or
- Choose <u>Calculation commands</u> / <u>Processing</u> in Main Menu.

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✓ If it is specified that calculation must be performed over selected field of chromatogram only, processing button will remain depressed, informing that the mode has been started. Otherwise, whole chromatogram will be calculated.

To select the field of chromatogram to be processed, you should go through the following steps:

- Put the cursor to one of the bounds of the field;
- After the vertical bound marker will appear by the left mouse button, *drag* it to the opposite end of the area.
- Withdraw your finger from the left mouse button.

After you finish calculation within selected field, repeat the same procedure, if necessary, to select another field of chromatogram.

### Reference peak identification.

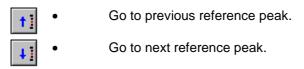
✓ if identification control of reference peaks is activated, the Software calculates whole chromatogram automatically in accordance with the previously specified algorithms of reference peak marking. After that, peaks marking will be corrected.

Otherwise, the *"Control of reference peaks auto-search"* dialog box will appear (see Fig. 3.4), in which you are able to:

- view all the reference peaks that were marked in accordance with previously specified algorithms;
- confirm that peak identification is correct.

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You can move within the group of marked reference peaks by using of following buttons:



When changing the reviewed peak:

- The enlarged picture of a chromatogram area between the previous and the next reference peaks is given in the graphic field of a dialog box and position of peak is marked by a special marker;
- Marked reference peak number is given in the data line of the dialog box;
- The chromatogram is scrolled with time-base scale on the main graphic field of the program, it is centered and marked with color .

The button is used for switching on/off the manual correction of reference peak position in case it was identified incorrectly.

To correct the reference peak position, you should to:

1. activate the adjustment mode. After that, on the graphic field of dialog box you will find markers, that show the expected elution time for peaks.

2. place the *cursor* onto the central reference peak.

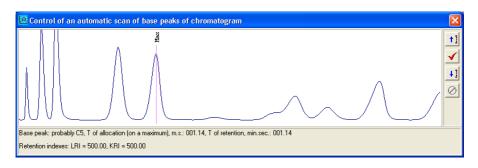


Figure 3.4.

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- 3. Drug and drop this peak marker to a new position on the chromatogram.
- 4. After you do that, the expected elution time will be re-calculated, so the corresponding markers on the graphic field of dialog box will change their positions.
- 5. Shut off the adjustment mode.

The button being activated when the adjustment mode is switched on, also helps you to leave this mode, restoring the previous position of reference peak.

### Peak identification of the analyzed compounds.

✓ If control of peak identification is switched off in the mode settings, the Software will process the whole chromatogram automatically or one of its areas in accordance with the previously specified algorithms of reference peak marking.

(see Fig. 3.5 ), in which you can:

- scroll through the chromatogram peak groups that are cut off and marked in accordance with previously specified algorithms;
- confirm that peak identification is correct.

You can move within the group of marked peaks by means of following buttons:

- Go to previous peak of the group.
  - Go to next peak in the group.

When you go to an other peak:

• The enlarged picture of marked peak appears in the left side of the dialog box (1);

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- The peak number in group is shown in data line of the dialog box (2);
- The information on marked peak is shown in data line of the dialog box (3);
- List of compounds corresponding to the peak on the chromatogram, is shown on right board of dialog box (4). You can select compound from the list for this peak.

The button is to confirm the peak identification. If you do that, a cross appears at the name of compound in the list.

In the group of marked peaks there can appear additional peaks, marked by the Software during automatic processing of the chromatogram. In this case, you should discard these peaks manually. If the peak identification was wrong (the peak was identified with incorrect compound).

you should select right compound in the list and press the <u>button for</u> confirmation.

Setting auto-search mode				×
		008.31 i 009.30 n 013.25 C 014.58 E 017.21 0	6+ ropane -Butane -Butane -Pentane -Pentane arbon dioxide thane	
Substance: probably Carbon dioxide, S of peak, r.u.*sec: 2.8871e+06 (3.4417e+0	1 % "sec), T of elution, min.sec.: 013.17			
Sorting:	Time: C LRI: C KRI: C			
1	3	2	4	

Figure 3.5.

# Saving the calculation results.

After finish working with the chromatogram, you can save calculation results. To do that, use the button on the Additional toolbox 2.

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# Discarding the calculation results.

If you decide to discard results of the measurements and to restore

previous calculation results, use the button on the *Additional toolbox* 2.

# 3.3.2. Semi-automatic peak marking.

This mode is to calculate or re-calculate current chromatogram in accordance with the specified algorithm. You can activate it by means of:

# • Main Menu: Operating mode / Peak marking / Semi-Automatic;

• and 🕑 on the Main toolbox.

In this case Additional toolbox 2 consists of the following shortcut buttons:



Setting the current algorithm of peak marking;



- Restoration of the previous stage of chromatogram calculation;
- Saving the current stage of chromatogram calculation.

### The Settings.

To specify the algorithm of peak cutting out and marking, you should activate the *«Parameters of peaks cutting out»* dialog box (see Fig. 3.6) by pressing the button on the *Additional toolbox 2*.

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😽 Parameters	of peaks cutting out	× ×
	Method of cutting out: Method of dividing: Limits of dividing: Within specified limits: Method of filtration:	Intersection  Divided peaks  Limits auto-definition  Position of peak is taker  Linear smoothing
⊘ Cancel	Smoothing half-interval, ms: Minimum peak height ( % ): Minimum width of peak (ms):	400 0.01 10000



Method of cutting out. Choose one of peak or group cutting out methods on the chromatogram from the list:

Intersection (recommended in most of cases)

- <u>Zero</u> (recommended in case of incomplete separation of two neighboring peaks)
- <u>Slopes I III</u> (Slope I is recommended in case of a peak on steep <u>slope)</u>,
- <u>Chromatogram zone.</u>

If you choose the first variant, the chromatogram peaks are cut out by line segments that connect the boundary lines of each separate peak.

If you choose the second variant, there will be an attempt to cut out whole group of peaks by one straight line that connect the boundaries of two peaks in the group – the first and the last ones.

Method of dividing. Choose one of the methods of dividing of an isolated group of peaks from the list.

For peaks cut out by  $\underline{\text{intersection}}$  method, there are two possible variants in the list:

- No division,
- Separate peaks (recommended).

For peaks that were cut out by  $\underline{\text{Zero}}$  method, there are following options:

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- No division,
- Normal, (recommended in case of incomplete separation of two neighboring peaks)
- Triangle,
- Gaussian peaks.

For the first option, total area of all marked peaks is equated to one of compounds from the list.

The rest of the options give a possibility to equate each separate peak of the group to one of compounds from the list.

Limits of dividing. Choose one of the methods of definition of the limits of the peaks:

- Limits auto-definition (recommended),
- Manual limits definition.

For first option, the Software automatically defines the limits of separated peaks.

Method of filtration. Choose the temporal filtering method for peak cutting out algorithm:

- Linear smoothing (recommended),
- Low frequencies filter,
- Non-linear smoothing,

And also you should specify the <u>Smoothing half-interval</u>. This value describes the ability of the Software to omit minute details of the chromatogram like noise or sudden change of the signal. The higher the <u>Smoothing half-interval</u>, the more large details are omitted. For the compounds with the concentration >100 ppm this value should be about 800-900 ms up to 1000 ppm. For the compounds with the concentration 100-1000 ppm, the <u>Smoothing half-interval</u> should be about 600-800 ms. For the compounds with the concentration 1000-5000 ppm, the <u>Smoothing half-interval</u> should be about 600-800 ms. For the compounds with the concentration 1000-5000 ppm, the <u>Smoothing half-interval</u> should be about 600-800 ms. For the compounds with the concentration 1000-5000 ppm, the <u>Smoothing half-interval</u> should be about 600-800 ms. For the compounds with the concentration 1000-5000 ppm, the <u>Smoothing half-interval</u> should be <400 ms. However, it is necessary to take into consideration that even for small peaks the value of <u>Smoothing half-interval</u> can be about 300 ms. Finally, you should find the proper values empirically so that the peak would cut out properly, i.e. from fold to fold without any superfluous areas.

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Further, by means of following options:

- <u>Minimum peak height</u> and
- Minimum peak width,

you can specify the screening criteria for peaks – if the peak does not meet one of these conditions, it will be omitted.

# Processing of chromatogram

Before you start working, enlarge required part of chromatogram so that the peak you want to process would be seen well and specify parameters of peak searching and processing. To activate the semi-automatic mode of peak processing in accordance with the chosen algorithm, you should use:

- the button on the Additional Toolbox 1 or
- Main Menu: Calculation commands / Processing.

During this the process, the button will remain pressed, meaning that the mode has been activated.

To process the chromatogram part, you should:

- place cursor to one of the bounds of required area.
- After you create the vertical boundary marker by the left mouse button, *drag* it to the opposite end of the area.

After this, the area will be processed.

✓ If the Software finds peaks in the specified area, the «*Marking* of peaks (semi-automatic)» dialog box automatically appears. By means of this dialog, you identify the peaks with compounds from the list. Peak identification is performed in the same way with Automatic peak identification dialog box.

After you finish calculation, repeat the same procedure, if necessary, for another part of the chromatogram.

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### Saving or discarding the calculation results.

After you finish your working with the chromatogram, you can save

the calculation results or discard it. To do so, you should use the in or

U buttons on the Additional toolbox 2.

# 3.3.3. Manual peak marking.

✓ In this mode, you can mark peaks manually by means of continuous chain line, specified by yourself. You can activate it by means of:

- Main Menu: Operating mode / Peak marking / Manual or
- by and we buttons on the Main toolbox.

In this case, the Additional Toolbox 2 includes following shortcut buttons:



Restoration of previous state of marking chain line;

- End of making chain line;



Restoration of previous state of chromatogram calculation;



Saving the current state of chromatogram calculation.

# Marking chain line building.

 $\mathbf{\nabla}$ Before you start working, enlarge the part of chromatogram you would like to process.

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You can activate the manual peaks marking by means of:

- button on the Additional toolbox 1;
- Main Menu: Calculation commands / Processing.



To build the marking chain line:

- place the cursor to one of the bounds of the peak on chromatogram.
- Press left button of the mouse, drug and drop it to the other bound of • the peak. That will be the first part of the marking line.
- Repeat these actions to form other parts of the marking chain line.

 If you made a mistake, you can discard any part of the marking line (you can even discard the initial point) by means of step-by-step pushing of

backtrack button

Finish building of marking chain line by means of the way button.

After that the <u>Marking of peaks (manual)</u> dialog box appears automatically. By means of this dialog box, you should identify the peak with compound from the list.

After you finish working with this peak, repeat the same procedure, if necessary, for another peaks.

#### Storing or discarding the calculation results.

After you finish working with the chromatogram, you can save its calculation results in the analysis or restore the previous state of calculation. To do so, you should use the im or im button on the *Additional toolbox 2*.

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#### 3.3.4. Settings of peak automatic search.

This mode is to adjust the algorithm of automatic cutting out and marking of peaks for each analyte. You can activate this mode by means of:

- Main Menu: Operating mode / Peak marking / Setting of peaks autosearch;
- the is and is buttons on the Main toolbox.

In this case, the Additional toolbox 2 consists of the one button:

Settings of current algorithm of peak cutting out and marking;

### Settings.

To specify the parameters of peak marking algorithm for each analyte for automatic cutting out and marking of peaks, you should activate the *«Parameters of peak cutting out» dialog box* (see Fig. 3.7) by pressing

the sutton on the Additional toolbox 2.

Reparameters of peaks cutting out	
Method of cutting out:       Intersection         Method of dividing:       No division         Limits of dividing:       Limits auto-definition         Within specified limits:          Wethod of filtration:       Linear smoothing         Method of filtration:       Linear smoothing         Method of filtration:       Linear smoothing         Method of filtration:       0         Method of filtration:       0         Method of filtration:       0         Minimum peak height (%):       0.0         Minimum width of peak (ms):       0	✓         000.00 nec-C5H12           ✓         003.08 C6+           ✓         004.56 Propane           ✓         005.47 iButane           ✓         000.25 nButane           ✓         000.31 iPentane           ✓         003.25 Catbon dioxide           ✓         013.25 Catbon dioxide           ✓         014.26 Ethane           ✓         017.21 0xygen           ✓         019.43 Methane
C Settings         Peaks review;           Times, m. s:         000.00         000.00         000.00           Fixation of limits, m. s:         Image: Comparison of limits, m. s:         Image: Comparison of limits, m. s:         Image: Comparison of limits, m. s:	Remove autosearch flag from the full list Change Settings for all peaks of the list

Figure 3.7.

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The <u>Settings</u> mode (it is activated when you open the dialog box) is to set the parameters of the algorithm of the current analyte peak cutting out. These parameters were described detailly before (See section 3.3.2).

The <u>Peak review</u> mode is to view and edit the parameters of the algorithm of automatic peak cutting out for each analyte. You can choose required compound from the list that appears on the right panel of the dialog box.

The following buttons become accessible during changing the parameters:

- The Cancel button is to discard the last changes and restore the previous algorithm settings for automatic peak cutting out.
- The button is to save the new automatic cutting out settings.

If you wish to apply the settings of previous compound, you should:

- Choose required compound from the list;
- Go to the <u>Settings</u> mode;
- Save the selected parameters.

### Settings of peak auto-search algorithm.

Before you start working, enlarge required part of chromatogram and specify the peak auto-search parameters. You can activate the mode of setting of peaks auto-search parameters by means of:

- pressing the **I** button, placed on the Additional Toolbox 1;
- Main Menu: Calculation commands / Processing.

The button will remain pressed, meaning that the mode is activated.

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- To select the part of chromatogram for processing:
- Put the cursor to one of the bounds of the field;
- After the vertical bound marker will appear by the left mouse button, *drag* it to the opposite end of the area.
- Withdraw your finger from the left mouse button.

✓ If the Software finds the peak(s) in the specified part, the «Setting auto-search mode» dialog box automatically appears. In this dialog box you should identify the peak with compound from the list.

If the compound is simultaneously a reference one, you should additionally adjust the algorithm of search as a reference peak.

### 3.4. Protocols for unknown gas analyses.

You can view the results of the analyses and form the protocol by means of:

- Main Menu: Calculation data / Measurement Statistics or: •

  - the button on the Additional toolbox 2,

and the «Protocol of calculation results of chromatograms and method parameters» (see Fig.3.8) dialog window is activated.

With the help of this window you can browse through the calculation results, averaged by the analysis samples:

- final concentration of the analyzed mixture compounds; •
- integral mixture parameters. •

At the same time, you can see also graphs of distribution for the selected parameter values.

29

Đ	Pro	locol of calculation result	s of chromate	ograms and m	ethod paramo	eters				×
Ā	nalyze	r 1: Method parameters								
,	Analys	is № 1 of 03.12.2008, detecto	187 ( 1 ).				(% vol.)* 0.500	ʻ1e-2		
	N item	Name of substance	Parameter peak	Concentration (final)	Dev(%)					
	01	C6+	1.3624e+06	0.0048	0.0					
	02	Propane	3.5989e+07	1.66	0.0			1		
	03	i-Butane	4.4087e+06	0.124	0.0		0.450	ļ		
	04	n-Butane	8.0910e+06	0.18	0.0		0.400			
	05	i-Pentane	2.2922e+06	0.0515	0.0					
	06	n-Pentane	1.9467e+06	0.0473	0.0					
	07	Carbon dioxide	2.8871e+06	0.376	0.0					
ľ	08	Ethane	9.2968e+07	4.52	0.0					
Ī	09	Oxygen	4.1737e+04	0.0162	0.0	~	0.400	0.000	0.500	1.000
	Mode of calculation the standard deviation         100.00           © Unbiased deviation { 1/(N-1) }         Sortir           © Biased deviation { 1/(N + 1) }         © 0           © Adjusted deviation { 1/(N + 1) }         © 0				ame		s s		(Item in san	



By pressing the button the *«Parameter distribution for samples of analysis»* (see Fig.3.9) dialog box is activated, where you can see the distribution of the parameter between the chromatograms of analysis and exclude drop-out chromatograms from the analysis manually.

🕹 Concentration distribution for samples of analysis 🛛 🛛 🔀							
SUBSTANCE: C6+							
Sample number	Concentration % vol.	Deviation absolute	Deviation relative(%)	Sample:			
sample 1	0.004826	0.000013	0.274661	<b>•</b>			
sample 2	0.004824	0.000011	0.238249	<b>•</b>			
sample 3	0.0048	-0.000012	-0.257814	<b>I</b>			
sample 4	0.004836	0.000023	0.486881	<b>I</b>			
sample 5	0.00483	0.000017	0.356861	<b>I</b>			
sample 6	0.004798	-0.000015	-0.304009	<b>I</b>			
sample 7	0.004775	-0.000037	-0.775243	<b>I</b>			
sample 8	0.004818	0.000005	0.10791	<b>I</b>			
sample 9	0.004834	0.000022	0.452685	<b>I</b>			
sample 10	0.004784	-0.000028	-0.580169	<b>I</b>			
Average: Dev(%):	0.004812 0.448412	-0.000037 0.000023	-0.775243 0.486881				

New statistical data on the parameter distribution will be recalculated and displayed:

- the average value and mean-square deviation,
- minimum and maximum abmodality.

By pressing the Save button you can save the changes.

### 3.5. Protocols for test gas analyses.

If it was specified in the settings of the **Analysis mode**, the Software updates the calibration files automatically after finishing the analysis of test gas.

You can view the results of the analyses and form the protocol by means of:

• Main Menu: Calculation data / Measurement Statistics or;

• the button on the Additional toolbox 2,

and after this, the *«Protocol of calculation results for test gas»* (see Fig.3.10) dialog box is activated.

Protoco	Protocol of calculation results for test gas							
						(Concentration, % vol.:)*1e-2		
Analyzei	r1:					0.500		
N item	Name of substance	Parameter peak	Parameter calibration	Error calibration				
01	C6+	1.3624e+06	0.00439	0.00027				
02	Propane	3.5989e+07	1.06	0.03				
03	i-Butane	4.4087e+06	0.116	0.005		0.250		
04	n-Butane	8.0910e+06	0.205	0.008		0.200		
05	i-Pentane	2.2922e+06	0.0509	0.0021				
06	n-Pentane	1.9467e+06	0.0396	0.0017				
07	Carbon dioxide	2.8871e+06	0.285	0.009				
08	Ethane	9.2968e+07	3.33	0.07				
09	Oxygen	4.1737e+04	0.0163	0.0016		0.000	¥	
10	Nitrogen	5.2311e+07	1.88	0.04	✓		0.000 0.100 0.200	
							(Peak parameter, conv.un.:)*1e7	
		Relativ	e deviation of r	new and old calib	orations: (	).0 per cer	ent	
Sorting		orking with the t		Calibration	n mode -			
⊙ On		irrent substance t of substances		C Delete		O Ins	sert 📀 Replace 🔿 Average	
O Un	the name (• With its	t or substances					1	
	🔍 in detail 🛛 💧 Calibri	ation	Save	A	pply	<b>1</b>	Point 1 (In total of points: 2)	
Date of la	st calibration modification: 06.02.200	9 r.(15:44)		Results	of analys	is N 1 of C	03.01.2008 r.(03:03)	

Figure 3.10.

By means of this dialog you can view new averaged points of calibration graph and select one o them for editing.

At the same time, you can get following information for a selected compound:

- its current calibration graph;
- the new graph point is colored in red;
- relative value percentage deviation for the new and old calibrations.

By means of the *«Mode of working with the table»* panel you can specify whether you are working with:

- all substances of the analysis (With list of substances option) at once or
- with the selected substance only (With current substance option).

By means of the *«Calibration mode»* panel, you can specify the mode of editing the calibration graphs:

- delete current calibration point (<u>Delete</u> option);
- insert new calibration point (<u>Insert</u> option);
- replace current calibration point with the new one (<u>Replace</u> option);
- recalculate value of current calibration point using the new data (<u>Average</u> option).

Current point of the calibration graph is marked by axles and can be selected by means of and buttons.

You can edit calibration graphs in accordance with specified Mode

of working by pressing the Apply button.

If you activate the mode "<u>With current substance</u>", you can open the *«Peak parameters distribution by the analysis samples»* dialog

box for the selected substance by pressing the Local button. There you can exclude manually the error chromatograms from the analysis.

### Direct work with the calibration file.

If <u>"With current substance"</u> mode is active, you can open the «Personal Calibration» dialog box for chosen substance(see Fig. 3.11) by pressing the Lalibration button. Here you can view and manually edit the list of previously specified points of calibration graph.

8	Per	sonal	calibratio	n: C6H14	.cls (C6+)						? 🔀	
			Parameter calibration c.		on Number averaged	Γ	(Conce 0.500	ntration, % vol.:)*1e-	2			
	1	0.0		0.0	0.0		1	1			1	
	2	136243	39	0.00439	0.061503		1	1				
	erpola x dev	ation: viation, 3	By data p %: 0	points		Delete	Add Save		0.250			
4	Axes		Name		Measureme	nt units	Scale type					
	r axis		Concentratio	on	% vol.		Usual		0.000	¥		·····
E	< axis		Peak param	eter	conv.un.		Usual			0.000	0.100 (Peak parameter	0.200 ; conv.un.:)*1e7
Date of last calibration modification: 27.02.2009 r.(16:21) Results of analysis N 2 of 11.02.200								2009 r.(12:01)				

Figure 3.11.

By means of the table you can select the current point marked with axle markers on the calibration graph. The following parameters can be specified for the selected point:

- value of peak parameter,
- value of calibration parameter,
- absolute definition error of calibration parameter.

The button is to delete the current point of the calibration graph from the table.

The Add button is to add a new calibration point into the table.

Interpolation. By the help of this option you can give the Program instructions of how to work with the calibration graph:

- as a piece linear function;
- as a polynomial, calculated by graph points by means of the leastsquares method (if the number of points is more than the degree of polynomial).

### 3.6. Analysis final protocols.

To view the analysis final protocols you should open **The final measurement protocol** dialog box (see Fig. 3.12), activated by:

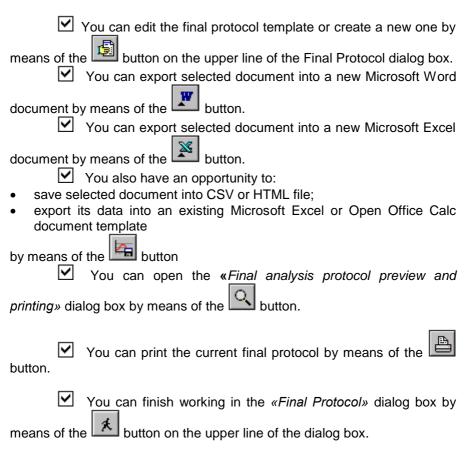
#### • Main Menu: Calculation data /Final protocols;

• the button on the Additional toolbox 2.

🕹 Ani	2 Analyzer : User - 1 📃 🗖 🗙									
Archive	Archive Data acq. Calculation Commands Calculation data Settings View Info									
Ð	▲	V 🗖 🗟 📓								
protoc	ol	protocol N 02	•			1	0 2	51	TEMPERATURE: Te = 0.00	
		for provided gas	of acceptance poi	nt	of 03.12.2008		<b>RRN</b>	<b>◎</b> 団 <b>◎</b>	PRESSURE: Fault (4) Fault (1.7) DETECTOR: TE = 0 3d = 0	
2. San 3. Mei 4. Per	mpli thed y.ra	ng was performed with: DANI ng point: GDS-2 and means of analysis: Chror raras anamera: ment compound:			23781-87		Ga	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Cd = 0 STATUS M/C: Connection:	
	-	-							Faults: 🕥	
		Name of substance	% Vol	% Mol.				2		
		Methane	91.08	91.021				~	ANALYSIS:	
2		Ethane	4.52	4.5448					Emors:	
3		Propane	1.66	1.6837					Eliois.	
4		i-Butane	0.124	0.1274						
5		n-Butane	0.18	0.1854						
6		i-Pentane	0.0515	0.0539						
2		n-Pentane	0.0473	0.0499						
8		C6+	0.0048	0.0052						
5		Carbon dioxide	0.376	0.377						
1		Oxygen	0.0162	0.0162						
1		Nitrogen	1.94	1.9356						
1	2	TOTAL :	100	100						
Absolute density 0.737 kg / m3 Reletive density 0.6118 Kow Nax T-20 deg C and 101.325 KPa 0.6118 Kow Nax T-20 deg C and 101.325 KPa 0.333 Mail / m3 Hybrinast value at T-20 deg C and 101.325 KPa 0.333 Mail / m3 Hybrinast value at T-20 deg C and 101.325 KPa 0.334 Mail / m3 Hybrinast value at T-20 deg C and 101.										
Methor Base :	Arehod         DAN-1107         Det. 167 (1)         LET         LOG         x         v           Sare:         Analysis of 2008 (December)         Analysis (N 1 of 03) (03.03)         Letters         187         wv         mvV									

Figure 3.12.

By means of the list of previously created final protocols you can choose one of protocol types to review the results of an analysis.



# 3.7. Statistical protocols.

To view the statistical protocols for several analyses, you should open the *«Statistical reports»* (see Fig. 3.13) dialog box, activated by:

- Main Menu: Calculation data/ Protocols review or;
- the *button on the Additional toolbox 2*.

col protocol N 06	•	Panel of S		V								6	<b>y</b> 🛛 🙀	Q 욥 *	0		TEMPERAT	UF	
tion of protocol head tocols   Functions   Graphics	⊽ Dani" Di	Full scree		M Dener	1 from 2 1	03; 02.0	11 2006								2		10 = 0		
ist of databases															2		PRESSU	00	
🚖 Analyses of 2006 years 🔼 🔸	Date	CH4	C2H6	C3H8	iC4H10	n-C4H10	iC5H12	n-C5H12	C02	N2	02	C6+	ICV, KCal/m3	Rel Density	8	. 1	Fault (4):		
Analyses of January Analyses of April	1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0		0	Fault (1,7):		
Analyses of May	2	66.065	17.142	5.6832	0.5902	1.0912	0.2658	0.2565	0.8996	7.9228	0.0008	0.0832	9567.94	0.7752	P		DETECT	)F	
Analyses of October	3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0			T£ = Jd =		
st of analyses	4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0		A P	Cd =		
N 41 of 02 (18:03)	5	0.0	0.0	0.0	0.0	0.0	0.0					0.0		0.0			STATUS		
N 42 of 02 (19:00) N 43 of 02 (20:00) N 44 of 02 (21:00) N 45 of 02 (22:00) N 45 of 02 (22:00) N 47 of 03 (00:00) N 47 of 03 (01:00)	6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0			Connection		
N 44 of 02 (21:03) N 45 of 02 (22:03)	7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0		8	Faults:		
N 46 of 02 (23.03) N 47 of 03 (00.03)	8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0	A =	8			
	9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0		8			
N 49 of 03 (02-03) 💌	10	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0			ANALYS	IS	
ode of statistical samples	11	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0		1	Errors:		
ly Calc	12	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0					
ontracted time: 11:00	13	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0					
	14	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0					
	15	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0					
	16	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0					
	17	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0					
	18	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0 0.0 0.00 0.0								
	19			0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0				
	20	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0					
	21	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0					
	22	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0					
	23	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0					
	23	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0					
	24	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0					
	-	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0					
	26																		
	27	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0					
	28 0.0 0.0		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0						
	29	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0					
	30	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0 🗸					

Figure 3.13.

Panel of Settings. By means of this option you can show or hide *«Panel of settings for Statistical Reports».* 

Full screen. By means of this option you can expand the dialog box up to the *Program Graphic field* or show it together with the chromatogram of the sample (accessible only for the sampling mode).

Functions of the set of auxiliary buttons have already been described (see item 3.6).

#### The «Protocols» bookmark (Panel of settings).

The «List of database» panel consists of the list of:

- working analyses monthly archive databases,
- or annual archive databases of calibration or supernumerary analyses.

The *«List of analyses»* panel consists of the previously performed analyses for the selected database.

The mode of statistical samples. By means of this list you can select one of the accessible intervals of the analyses sampling:

- switched off;
- daily;
- ten-day;
- monthly;
- the last analyses by the date;
- the last analyses by the time.

Protocol. When the mode of statistical sampling is switched off, it is a list of analysis final protocols. Otherwise it includes the list of previously created templates of statistical protocols for analyses samples.

When the mode of statistical sampling is switched off, you can review the final protocol of any set of analyses.

To review the statistical protocol,

- select necessary mode of statistical samples;
- select database;
- click the left-hand mouse button on any analysis of chosen sampling.

### The «Functions» bookmark (Panel of settings).

This bookmark gives us an opportunity to view the analyses results for a sample as a graph and contains the same set of settings.

Function. When the mode of statistical samples is switched off, this list consists of previously specified functions for the current mode of analysis. Otherwise, it includes the list of statistical protocols on the sampling analyses.

When the mode of statistical samples is switched off, you can view the functional graphs for any separate analysis of the chosen database.

To review the statistical graphs:

- select necessary mode of statistical samples;
- select the database;
- *Click the left-hand mouse button* on any analysis in selected sample.

### The «Graphics» bookmark (Panel of settings).

This bookmark helps us to set the parameters of system axes to represent the measurement results on the analyses samples graphically (see Fig. 3.14).

✓ "<u>Points</u>". By means of this option you can specify the number of subdivisions for each graph axis.

Analyzer : User - 1 Archive Data acq. Calculation Comman	de Colsulation d	ata Collinas Vie	u Iele										
	us calculation d	ata setungs vie	w 110										
Function: CTat. rpadvec 02(02) Fixation of protocol head	2	Panel of Settings: Full screem:	<b>र</b> ज								0 8		TEMPERATURE: Te = 0.00
Protocols Functions Graphics	вык.н-пентана									009.30	2		PRESSURE:
Points: 10 10 Start 02.01.06 009.15 End 03.01.06 009.30										009.28			Fault (4): O Fault (1,7): O DETECTOR: TE = 0
Cancel Apply										009.27	9	1	Jd = 0 Cd = 0 STATUS M/C: Connection:
n-Pentane										009.25		間:	Faults:
										009.24		ď	ANALYSIS: Errors:
										009.22			
										009.21			
										009.19			
				~						009.18			
										009.16			
										009.15			
	011.00 02.01.06	013.24 02.01.06	015.48 02.01.06	018.12 02.01.06	020.36 02.01.06	023.00 02.01.06	001.24 03.01.06	003.48 03.01.06	006.12 03.01.06	008.36 03.01.06 время			
Method: DANI-187 Base : Analyses of 2008 (December)	Analysis: N	let. 187 (1) 1 of 03 (03:03)	Archive 1	<b>9</b> 7									× ¥ m¥ mc¥

Figure 3.14.

"<u>Start</u>" and "<u>End</u>". With these options you can set the minimum and maximum values for each graph axis.

# 3.8. Chromatograms superposition mode.

This mode is to overlay any chromatogram on current one. You can activate it by:

- Main Menu: Operating mode / Analysis of Chromatogram / Overlaying the chromatogram;
- the 🚾 and 🖾 buttons on the Main toolbox.

Fig. 3.15), in which you can select a chromatogram to overlay:

- press the **button** from the Additional toolbox 1;
- use the Main Menu: Calculation commands / Processing.

During this procedure, the processing button will remain pressed, informing that the mode is active.

To overlay the chromatogram:

- select the database;
- select the analysis;
- put the mouse cursor on the needed sample field of the analyses table (right field of the window, see Fig. 3.15) and click twice on it.

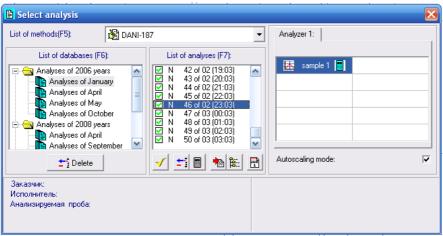


Figure 3.15.

# 3.9. Printing of the current chromatogram.

To print the current chromatogram, as well as to form the set of selected chromatogram shots you should activate the *«Current analysis chromatogram»* dialog box (see Fig. 3.16):

- by Main Menu: Calculation commands / Printing;
- by the button on the Additional toolbox 1;

# The «Graphs» bookmarks.

By means of the *«List of the shots of analysis»* panel you can view the set of previously saved chromatograms shots and choose one or two of them for placing on the printer's page model.

The button is to delete the active shot from the list. If the shot is not chosen, this button becomes inaccessible.

🖨 Current chromatogram of an	alysis ( detect. 187, sample 1)				🛛
Graphs Comments					
<b>3 6</b> 10 P	age 1 [ In total pages: 1 ]		🖉 Scale:	50%	•
✓ 01. Current chromatogram     ✓		MS Sans Senit 💌 8	: <u>B / U</u>	Ø Cancel	✔ Save
Current graph Current chromatogram Detector: 187 Sample: 1 Comment: Shot's comment					

Figure 3.16.

The button is to add the shot of the current chromatogram.

The button is to confirm the current set of shots and to form the printer's page model.

By means of the *«Shot's comment»* panel you can view and edit commentss to the analysis shot list.

The **B**, **M** and **W** buttons are to activate the corresponding styles of the type, accessible in the system:

- «bold»,
- «italic»,
- <u>«underlined»</u>.

The *«Current graph»* panel shows the information on the analysis shot that is active at the moment. With the help of the <u>Comment</u> self-opening list you can choose one of previously created typical comments for the graph. These typical comments are created by means of the *«Signs»* bookmark of this dialog box.

To form the pages for printing, you should:

- mark necessary set of graphs for printing with ticks;
- confirm the selection;
- if necessary, edit comments to the selected graphs.

The review of a multi-page printing model is performed by means of

and <sup>IIII</sup> buttons, used for choosing the previous or the next page of the current set of shots.

You can choose the scale for review in the Scale self-opening list.

The button is to activate the standard printing dialog box. By this dialog box you can choose a printer, change its settings and specify the number of <u>copies</u> to be printed.

ne 💷 button is to send the formed page to the printer.

#### 3.10. Printing of the protocols and chromatograms.

You can print the final protocol together with the selected chromatograms by the *«Expanded printing»* dialog box (see Fig. 3.17), activated by:

- the Main Menu: Calculation data / Expanded printing;
- the shortcut button on the Additional toolbox 2.

Print and       Print and         Print and       Print and         Which drawningan       Print in the cost of the 49 set of the	tended printing	Page 1 (In total pages: 2) 🖉 🛐 Scale:	K White page 💌
bit     Description     Description	Printing mode Print screen		
Image: Section of the sectio		1	
Compared.           File         <	nots:		1. Sangling var performelvrålt. DAXITGC 90.50 (51197 2. Sangling pråst: GBS-2 3. Medio hardness of andrefs: Ottomothermålsmetholse.c.to GBST22791.47
1         Mature         10 / 20           3         Mare         4.51         4.644           3         Mare         5.04         5.074           4         Mare         5.04         5.074           4         Mare         5.04         5.074           7         Mare         5.04         5.074           7         Mare         5.04         5.074           10         Mare         5.04         5.074           10         Mare         5.04         5.04           10         Mare         5.04         5.04           10         Same device         5.04         5.04           11         Mare         5.44         5.04           11         Mare         5.44         5.04           11         Mare         5.44         5.04           11         Mare         5.04         5.04           11         Mare         5.04         5.04           11         <			
1         Import         60         8007           4         Ansare         5134         5024           7         Ansare         513         5024           6         Ansare         5134         5024           7         Ansare         5137         5024           8         Ansare         5124         5024           1         Ansare         5127         5024           1         Borgen         5124         5024           1         Borgen         5124         5024           1         Borgen         5124         5024           1         Borgen         5142         5024           1         Borgen         5142         5024           1         Borgen         5142         5024           1         Borgen         5144         5024           1         Borgen         5024         5024           1			
0         Interna         Int         Interna           0         Interna         ID 551         ID 563           1         Interna         ID 647         ID 664           0         Interna         ID 647         ID 664           10         Interna         ID 642         ID 664           11         Interna         ID 642         ID 663           12         Interna         ID 644         ID 663           14         Interna         ID 644         ID 663           14         Interna         ID 644         ID 663           14         Interna         ID 644         ID 663           15         Interna         ID 664         ID 663           14         Interna         ID 664         ID 663           14         Interna         ID 664         ID 663           14 <t< td=""><td></td><td></td><td>3 Propane 1.66 1.603?</td></t<>			3 Propane 1.66 1.603?
7         Instrume         (0.477)         (0.467)           8         (0.467)         (0.467)         (0.467)           9         (0.466)         (0.79)         (0.77)           10         (0.466)         (0.79)         (0.77)           11         (0.466)         (0.79)         (0.77)           12         (0.466)         (0.17)         (0.77)           11         (0.466)         (0.17)         (0.166)           12         (0.466)         (0.17)         (0.166)           13         (0.466)         (0.17)         (0.166)           14         (0.166)         (0.17)         (0.166)           14         (0.166)         (0.17)         (0.166)           14         (0.166)         (0.17)         (0.166)           15         (0.166)         (0.17)         (0.166)           14         (0.166)         (0.17)         (0.166)           14         (0.166)         (0.17)         (0.166)           14         (0.166)         (0.17)         (0.166)           14         (0.166)         (0.17)         (0.166)           14         (0.166)         (0.17)         (0.166)			6 p-Butane 0.18 0.1854
Ibi         Jongon         J.0142         J.0142           11         Hampon         3.44         5.956           12         19574         900         900           24         4.956         900         900           15         19574         900         900           24         4.956         900         900           16         19574         900         900           17         19574         900         900           16         1959         900         900           17         1990         900         900           16         14         100         94         94           16         16         100         100         94         94           16         16         100         100         100         100           16         16         100         100         100         100           16         16         100         100         100         100           17         100         100         100         100         100           17         100         100         100         100         100 <td></td> <td></td> <td>7         P-Pentane         0.0493         0.0499           8         05+         0.0060         0.0052</td>			7         P-Pentane         0.0493         0.0499           8         05+         0.0060         0.0052
U         Instruct         Instruct         Instruct           Polytics for stratig         0000         00200         00200           Polytics for stratig         0000         00000         00000           Polytics for stratig         0000         00000         00000           Low how where if - 200% Cond 100,259Pa         00000 Mark / no0         00000         00000           Hey have use in - 7-200% Cond 100,259Pa         000000 Mark / no0         170000 Mark         00000           Hey have use in - 7-200% Cond 100,259Pa         000000 Mark         170000 Mark         00000         00000			10 Dxypen 0.0162 0.0162
Molecular 175533 cu. Low Webb index 4482 MJ /m3			12 TOTAL : 100 100 Abolue denoty 0.727 kg / m0 Roblem denoty 0.7118
			Molecular weight 170933 c.m. Low Wolden index 4433 MI / m3
Tporpants "Associate" 42.00, H19 % AVCT, Campa, 2005 r.			Decrement "Access root" 42.00 JBA T. 2017 Courses 1004 c
iporpama watwoanp occar, HV av&C, Canapa, 2005r.			ipogawes watwoattp: vozuz, HI v Iswer, Lawapa, duosr.

Figure 3.17.

By means of the *«Printing mode»* panel you can place to the page for printing:

- any fragment (Print Screen option);
- shooting sheet in the fragment scale (<u>Full chromatogram</u> option);

on the printer's page model of the current chromatogram.

Other details of work with this dialog box were given in the previous paragraphs (see items 3.6, 3.8).

### APPENDIX. INSTALLING THE "ANALYZER" PROGRAM.

To install the "Analyzer" Software:

- 1. Insert the disk into the CD-drive.
- 2. Open "My Computer".
- 3. Open the CD.
- 4. Click SETUP.EXE twice.
- 5. The «Welcome» window will appear:

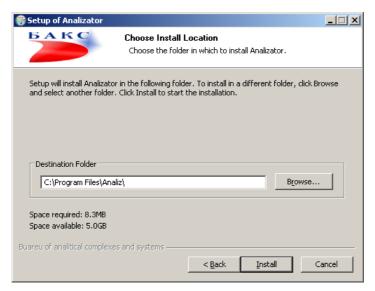
😽 Setup of Analizator	
	Welcome to the Analizator Setup Wizard
	This wizard will guide you through the installation of Analizator.
	It is recommended that you close all other applications before starting Setup. This will make it possible to update relevant system files without having to reboot your computer.
	Click Next to continue.
	<u>Next</u> Cancel

- 6. Press the "Next" button.
- 7. The «License agreement» window will appear:



8. If you agree with all terms of the license agreement, tick the «I agree with the terms of the agreement», then press the «Next» button.

9. The "Choosing the folder to install" window will appear





9. By means of the «Browse» button you can choose any other folder for installation of the program.

10. Press the button "Install".

11. After the process is finished, the *"The program has been installed"* window will appear.

12. Press the "Finish" button.

<u>Note.</u> If the program refuses to work with printing dialogs, you should do the following:

1. Press the "Start" button, mark "My computer", press the righthand mouse button and choose "Properties" command.

2. In the dialog "The system properties" that appear, choose the "Optional" bookmark and use the button "Variable media".

3. In the new dialog on the "Variable user's media..." panel with the help of a "Change" button one should replace values of TMP and TEMP variables for the full name of any already existing folder, i.e. C:\TEMP.

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