

**SCIENTIFIC AND ENGINEERING FIRM  
“BACS”**

**ANALYZER  
Control software for chromatographic gas  
analyzers**

**02.02 version.**

**OPERATOR'S GUIDE**

**Samara, Russia**

**2009**



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## 1. Starting PC Software ANALYZER.



Make double-click on the ANALYZER icon on 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.

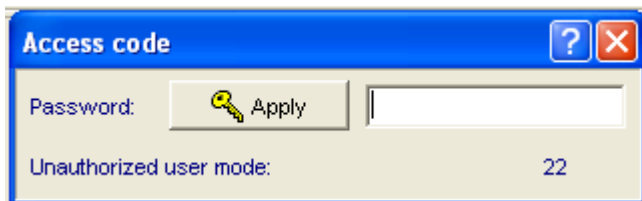


Figure 1.1.

## 2. Operating ANALYZER in Active Mode.

Access to **Active Mode** 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.

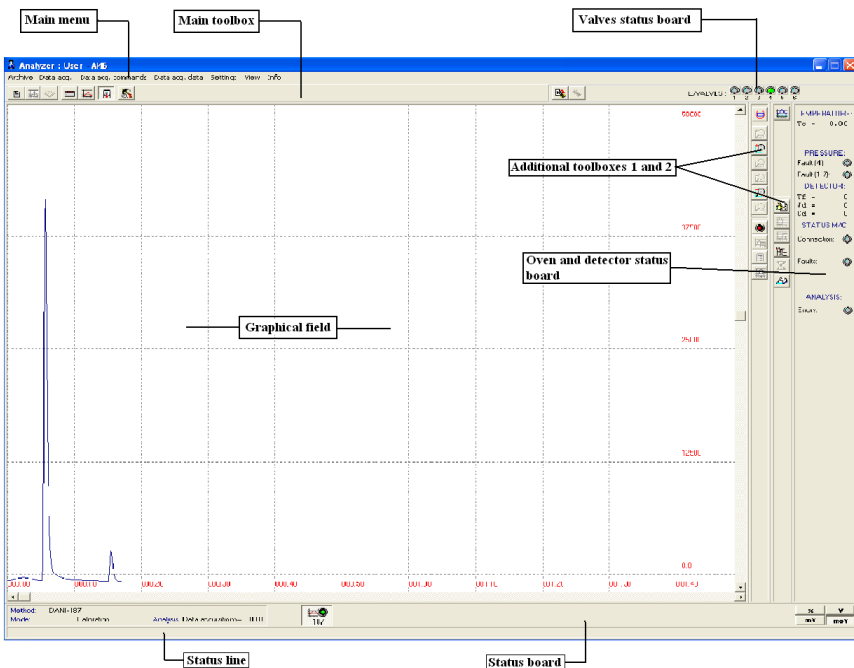

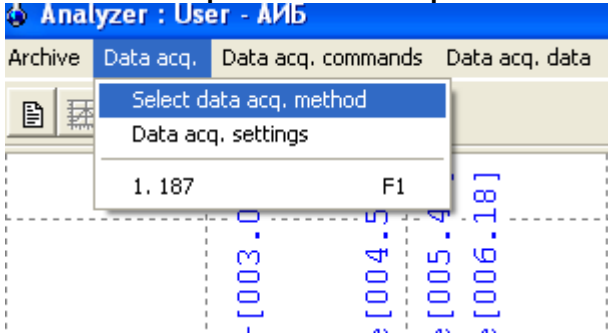


Figure 2.1.

## 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  on the *Main toolbox*;
- by **Main menu: Data acq. / Select data acq. method**



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*.

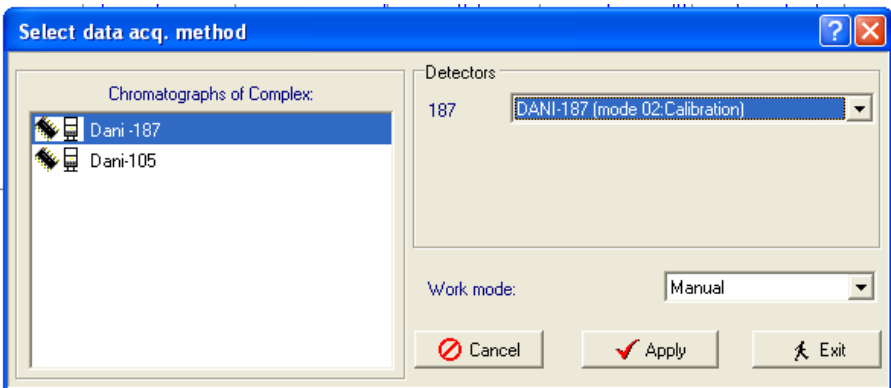



Figure 2.2.

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  button.

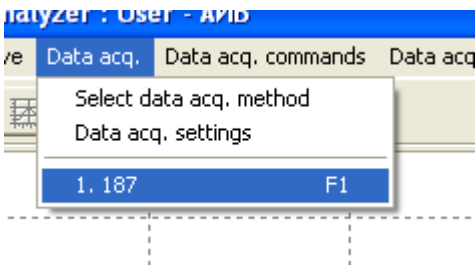
After that, buttons for the analyzers, will have appeared on *the Status board* (see Fig. 2.1). Every button is named in accordance with corresponding analyzer and equipped with a lamp, indicating the state of analysis:

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

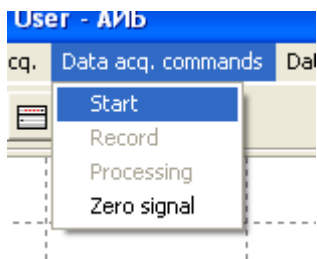
- by pressing a detector shortcut button , placed on *the State Board* (see Figure 2.1);
- by **Main Menu: Data acq. / N. Det-N** .



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

Icon  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  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.
- 

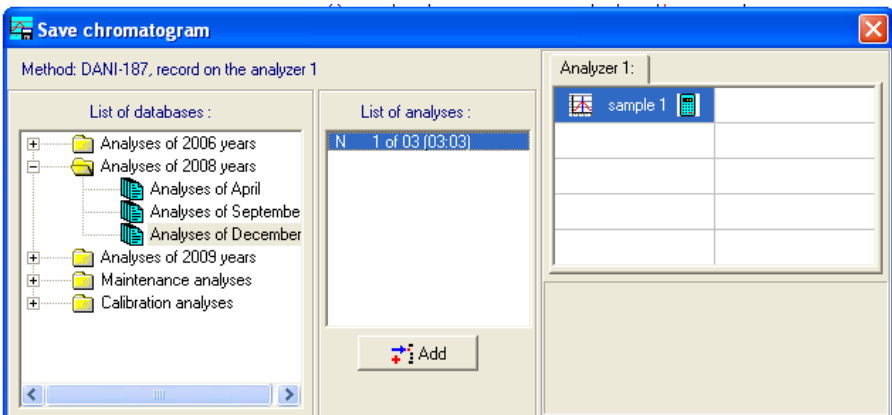



Figure 2.3.

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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 ways:

- 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 (overlying).**

To overlay any chromatogram onto current chromatogram, you should press  button, placed on *the Additional toolbox 2*.

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

### **2.9. Statistic protocols of analyses.**

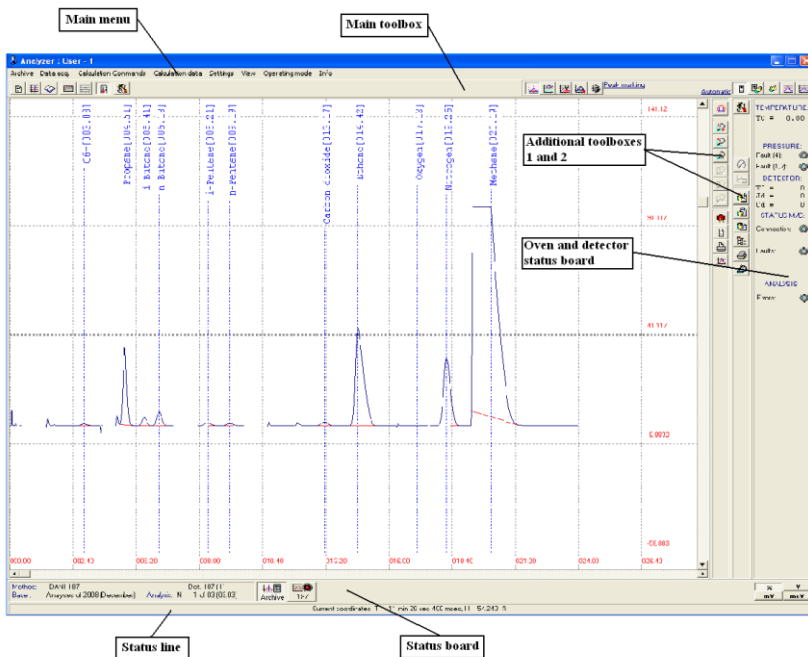
To view statistical protocols of analyses, use the «*Final measurement protocol*» expanded dialog box (see section 3.7):

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

### 3. Operating ANALYZER in Archive Mode.

Access to work in the **Archive** 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.



### **3.1. Starting Archive Mode.**

Initial load of new analysis from the archive could be fulfilled 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.

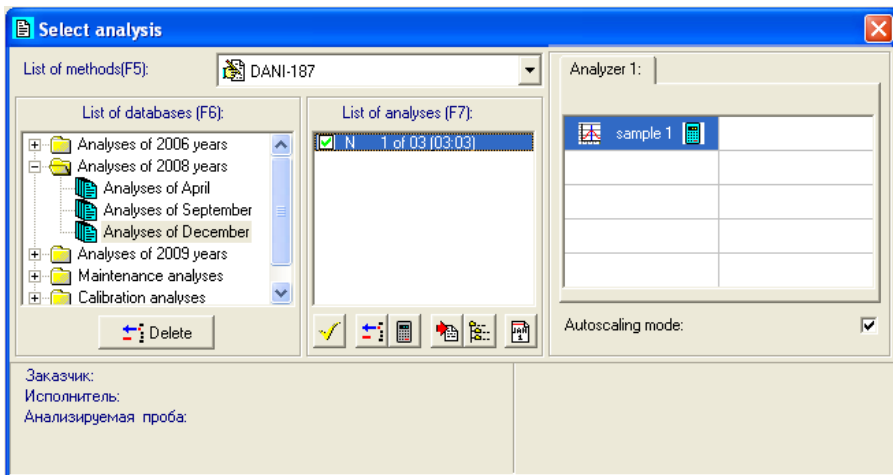




Figure 3.2.  
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Icon  situated to the left of sample number means that the chromatogram is still kept on the hard disk;

Icon  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  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*.

Identification. 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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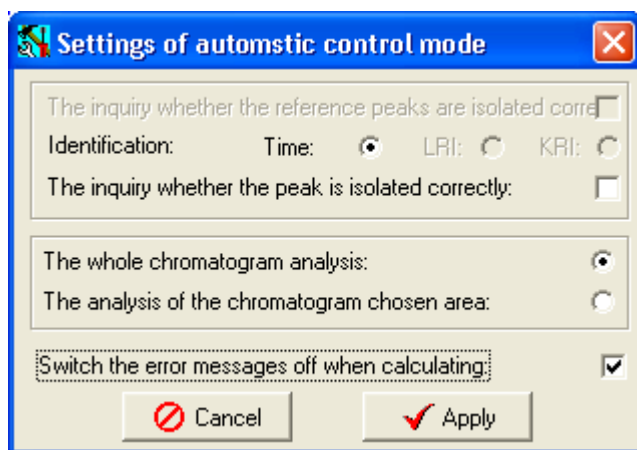


Figure 3.3.

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 **Calculation commands** / **Processing** 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:




- Go to previous reference peak.



- Go to next reference peak.

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.

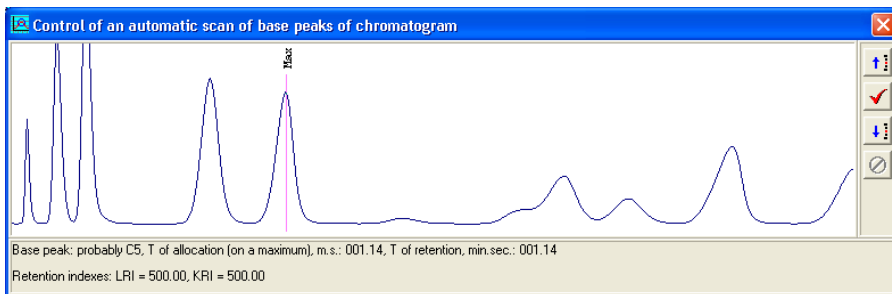



Figure 3.4.

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3. Drag 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.

If not, the «*Settings auto-search mode*» dialog box is activated (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  button for confirmation.

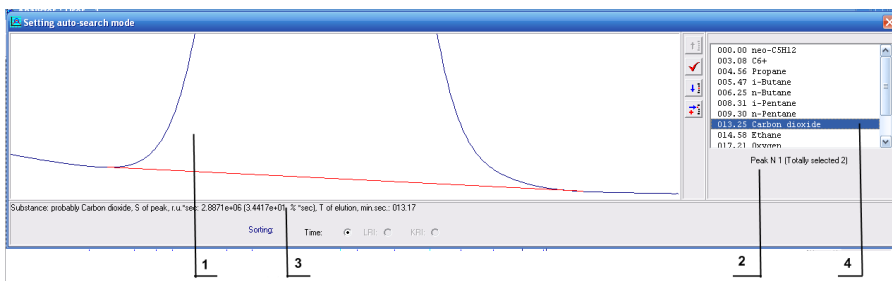




Figure 3.5.

### 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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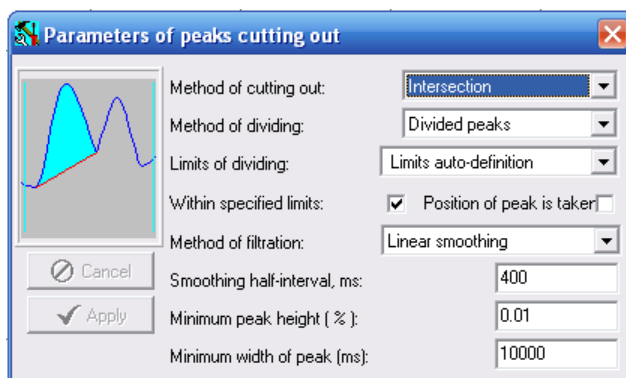


Figure 3.6.

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)

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

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 intersection method, there are two possible variants in the list:

- No division.
- Separate peaks (recommended).

For peaks that were cut out by 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 Smoothing half-interval. 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 Smoothing half-interval, 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 Smoothing half-interval should be about 600-800 ms. For the compounds with the concentration 1000-5000 ppm, the Smoothing half-interval should be about 400-500 ms. For the compounds with the concentration >5000 ppm, the Smoothing half-interval should be <400 ms. However, it is necessary to take into consideration that even for small peaks the value of Smoothing half-interval 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:

- Minimum peak height 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  or  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  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.**




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:





- the  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, drag 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  button.

After that the **Marking of peaks (manual)** 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  or  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  and  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



button on the *Additional toolbox 2*.

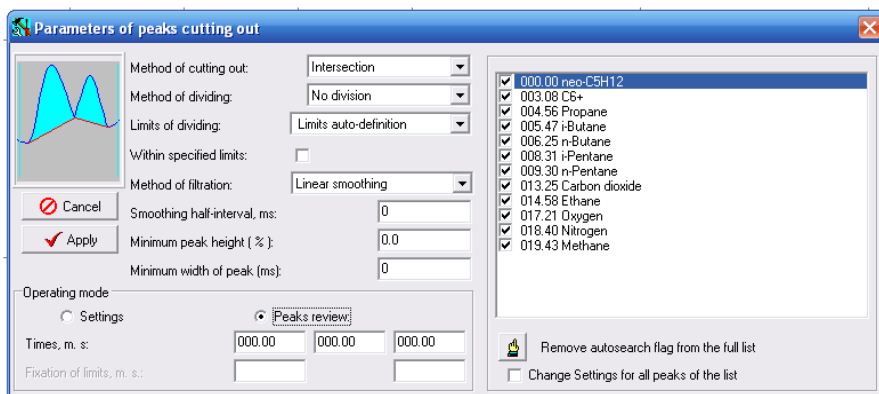



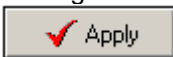
Figure 3.7.

27

The Settings 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 detailedly before (See section 3.3.2 ).

The Peak review 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  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 Settings 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  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.

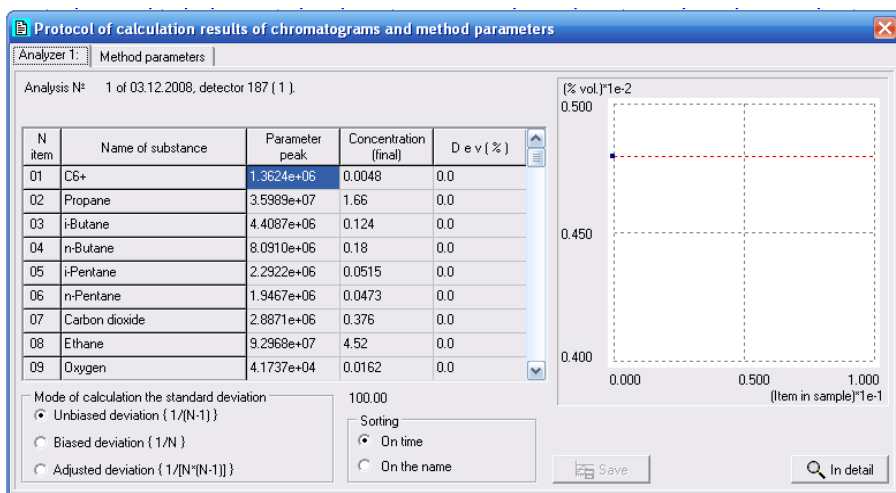



Figure 3.8.

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.

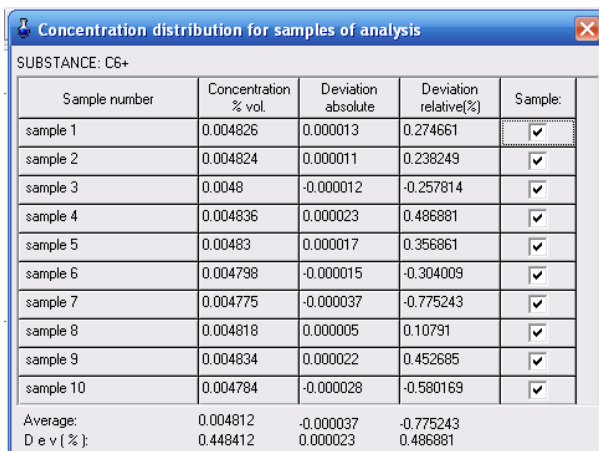


Figure 3.9.



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.

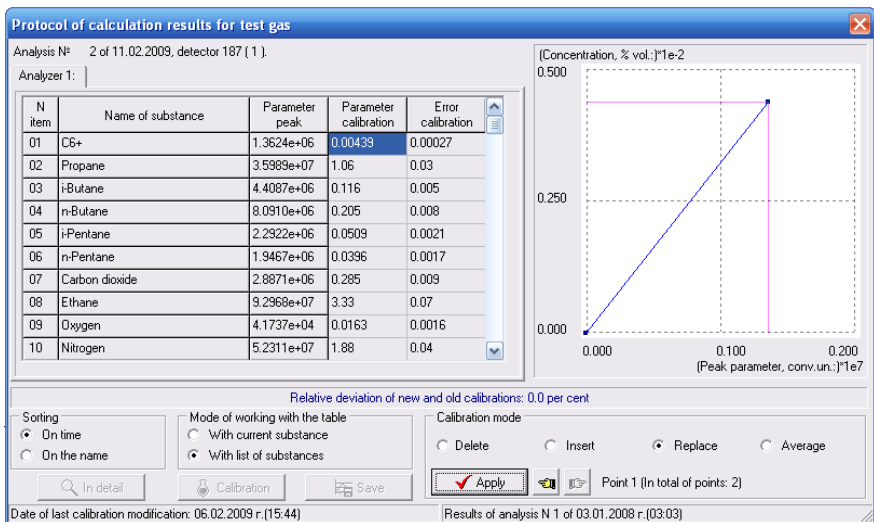


Figure 3.10.

By means of this dialog you can view new averaged points of calibration graph and select one of 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 (Delete option);
- insert new calibration point (Insert option);
- replace current calibration point with the new one (Replace option);
- recalculate value of current calibration point using the new data (Average option).

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

You can edit calibration graphs in accordance with specified *Mode of working* by pressing the  button.

If you activate the mode “With current substance”, you can open the «*Peak parameters distribution by the analysis samples*» dialog box for the selected substance by pressing the  button. There you can exclude manually the error chromatograms from the analysis.

## Direct work with the calibration file.

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

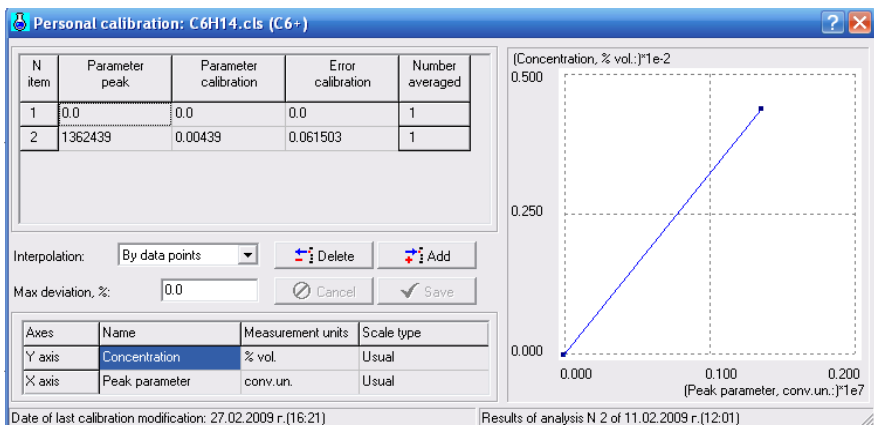

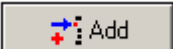


Figure 3.11.

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  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 least-squares 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*.

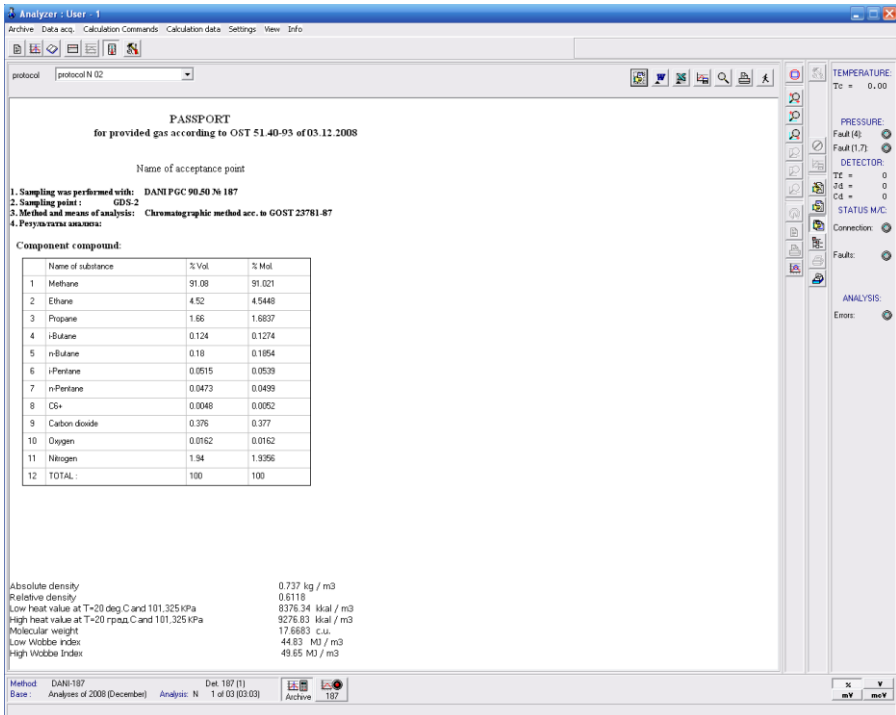





Figure 3.12.

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

You can edit the final protocol template or create a new one by means of the  button on the upper line of the Final Protocol dialog box.


You can export selected document into a new Microsoft Word document by means of the  button.


You can export selected document into a new Microsoft Excel document by means of the  button.


You also have an opportunity to:

- save selected document into CSV or HTML file;
- export its data into an existing Microsoft Excel or Open Office Calc document template

by means of the  button


You can open the «*Final analysis protocol preview and printing*» dialog box by means of the  button.

You can print the current final protocol by means of the  button.

You can finish working in the «*Final Protocol*» dialog box by means of the  button on the upper line of the dialog box.

### **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*.

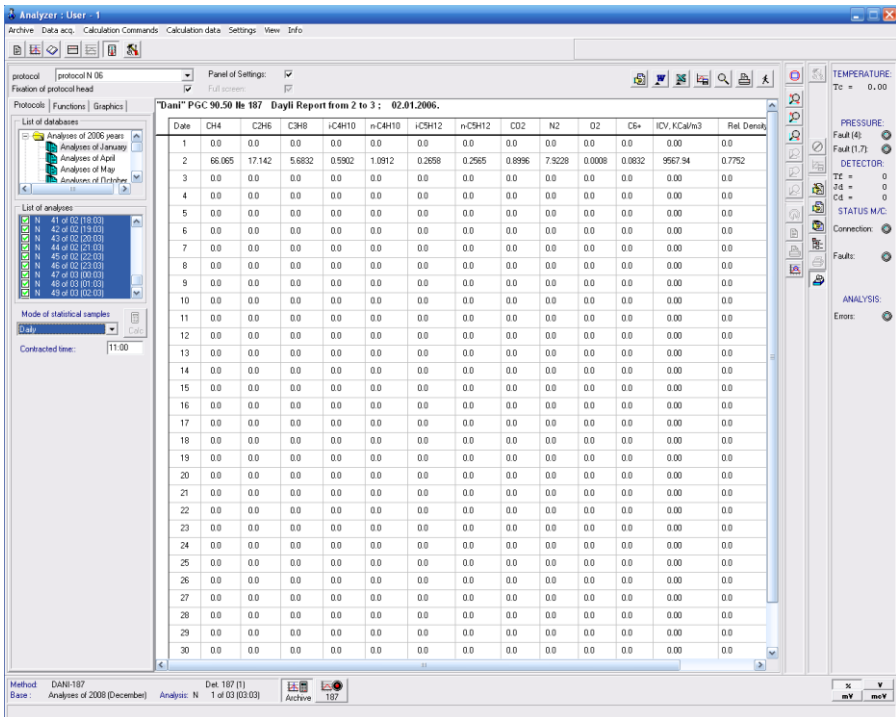


Figure 3.13.

**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).

“Points”. By means of this option you can specify the number of subdivisions for each graph axis.

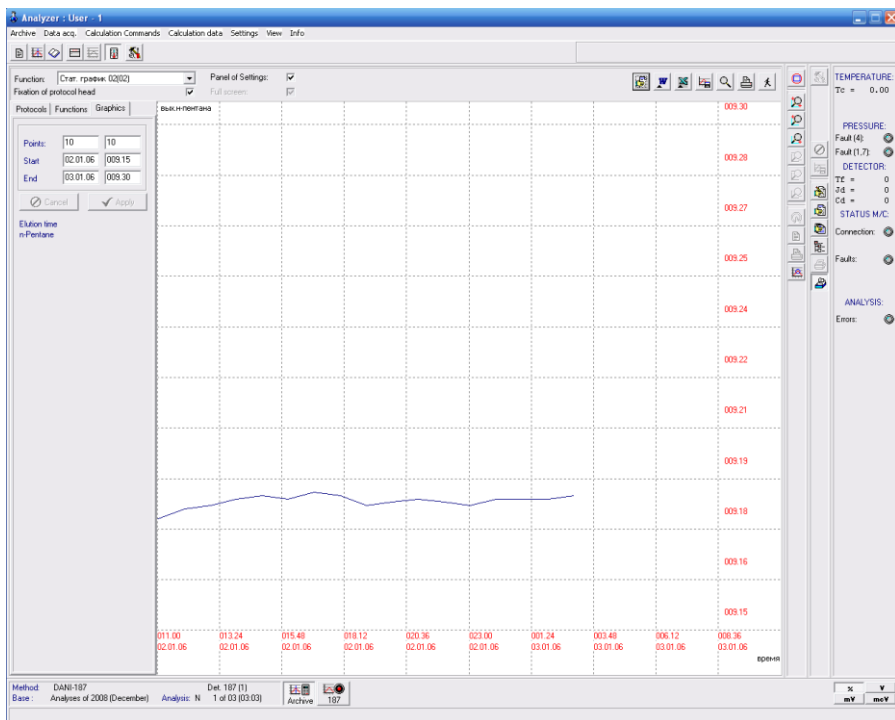




Figure 3.14.

“Start” and “End”. 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*.

To activate the «*Overlaying the chromatogram*» dialog box (see 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.

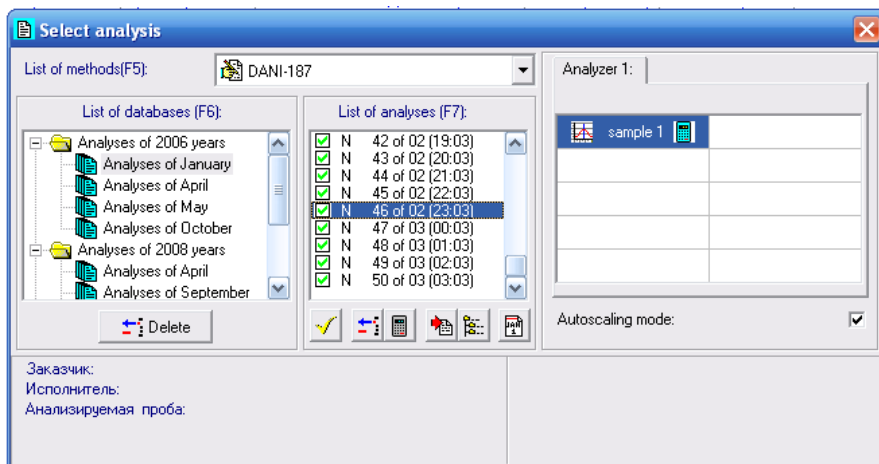







Figure 3.15.



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 comments to the analysis shot list.



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

- **«bold»**,
- *«italic»*,
- «underlined».


The «*Current graph*» panel shows the information on the analysis shot that is active at the moment. With the help of the Comment 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  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.

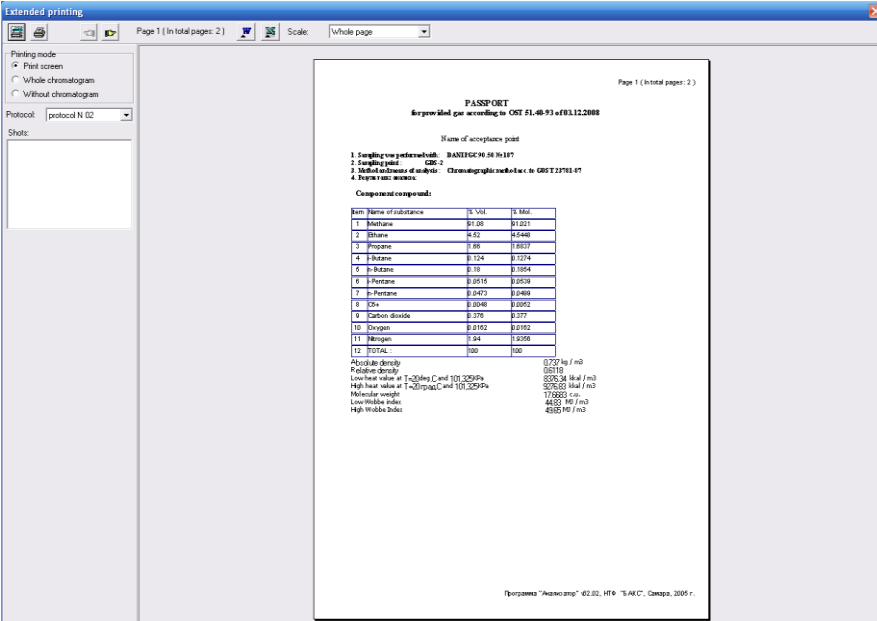
The  button is to activate the standard printing dialog box. By this dialog box you can choose a printer, change its settings and specify the number of copies to be printed.

The  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*.



Page 1 (In total pages: 2)

Scale: Whole page

Printing mode

Print screen

Without chromatogram

Without chromatogram

Protocol: protocol N 02

Shots:

Page 1 (In total pages: 2)

**PASSPORT**  
Сервисный газ according to GOST 51.48-93 of 01.11.2008

Name of acceptance point

1. Sampling was performed at: BANTEGHO 58 10 197  
2. Sampling point: GRS-2  
3. Method of analysis: Chromatographic method in GOST 23703.07  
4. Type of gas mixture:

Component composition:

Item	Name of substance	% Vol.	IS 360
1	Methane	97.99	0.021
2	Ethane	0.42	0.548
3	Propane	0.66	0.827
4	i-Butane	0.124	0.174
5	n-Butane	0.78	0.164
6	Pentane	0.0515	0.053
7	n-Pentane	0.0473	0.049
8	Hexa	0.0068	0.007
9	Carbon dioxide	0.375	0.377
10	Oxygen	0.0162	0.0162
11	Nitrogen	0.04	0.055
12	Hydrogen	0.00	0.00

Relative density 0.729 kg / m<sup>3</sup>  
65.115  
Low heat value at T=20 (kg C and 101.325 kPa) 55.924 kJ / m<sup>3</sup>  
High heat value at T=20 (kg C and 101.325 kPa) 57.653 kJ / m<sup>3</sup>  
Molecular weight 17.865 g / mol  
Low flammable index 48.93 M<sup>3</sup> / m<sup>3</sup>  
High flammable index 49.93 M<sup>3</sup> / m<sup>3</sup>

Программа "Анализатор" 02.02.1116 "АКС", Санкт-Петербург.

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 (Full chromatogram 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).

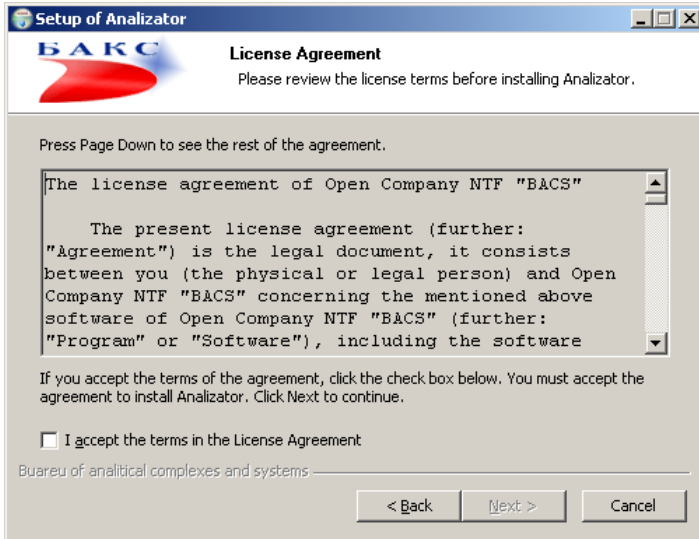
**APPENDIX. INSTALLING THE “ANALYZER” PROGRAM.**

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:

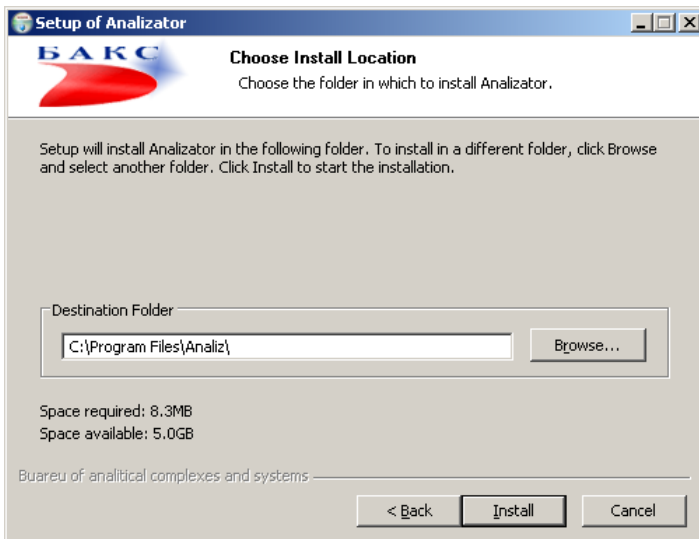


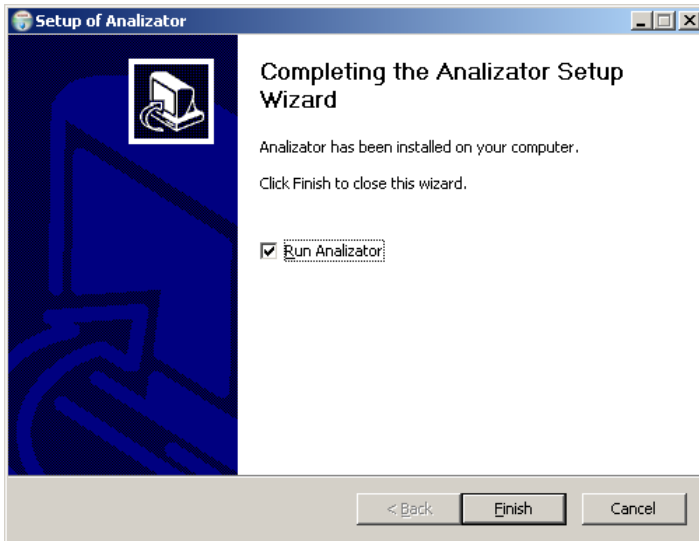
6. Press the “Next” button.
7. The «*License agreement*» window will appear:



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.

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

1. Press the "Start" button, mark "My computer", press the right-hand 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.