CONTENT.

1. INTRODUCTION.

Softberry Genome Explorer (SGE) provides the visual presentation and ability to work with multiple **genomic features** (e.g. known and predicted genes, mRNAs, EST, repeats etc.) in multiple genomic sequences.

The Classes of Objects localized on a genomic sequence (e.g. genes, EST, repeats etc.) are referred to as "**Feature Types**". The term "**Feature**" is used to define the single object of known type localized on a chromosome. For example, if the object is mRNA with ID AK001299 localized on chromosome 22 in positions from 14027013 to 14123757, then this mRNA is referred to as "Feature" and type of this feature is mRNA.

In order to make the information output more convenient for user, SGE, using the available databases, schematically shows all features localized on a chosen genomic fragment. At the moment Genome Explorer shows the features for preliminary Human Genome Sequence provided by UCSC Human Genome Project Team. In addition to publicly available information, Genome Explorer includes the genes predicted by Softberry's FGENESH++ program and some others.

Since the single genome region can contain several features of the same types (the overlapping features) thus, for convenience, these features are shown in multiple graphic layers.

Genome Explorer provides the following options:
- Selection of user defined chromosome region;
- Visual evaluation of available information on various genome regions;
- Retrieving of sequences sets of selected feature types;
- Retrieving of various sets of feature's sequences;
- Retrieving of information on feature expression;
- Retrieving of protein sequences encoded by features;
- Retrieving of features and their types description;
- Retrieving of references on features databases;
- Search for sequences in various genome regions;
- Alignment of sequences by Fmap and Scan2 programs and visualization of results;
- Gene search;

Softberry Genome Explorer includes the wide set of navigation and search facilities developed with special attention to subject knowledge field and user's requirements.

2. BASIC SYSTEM DESCRIPTION.
2.1. System Loading

To launch the **Softberry Genome Explorer** use one of the following ways:

1. Launch the Java-applet at the softberry.com server using hyperlink;
2. Launch the Java-applet at the softberry.com server using special HTML-code insert in HTML page.
3. Launch the local application from command line.

In general the launch script should looks as following:

1. Hyperlink (URL):

To call the cgi-bin program type the following in the browser location bar:

http://www.softberry.com/cgi-bin/genomexp.pl?parameter_name_1=value1&parameter_name_2=value2

2. HTML-code:

Insert the following code in your own HTML-page:

```
<APPLET    ARCHIVE="genomexp.jar"    CODE="softberry.project.genome_explorer.Base"
CODEBASE="/genomb/" WIDTH=10 HEIGHT=10>
<PARAM name="cgiFile" value="/cgi-bin/genomb/genome_get">
</APPLET>
```

Where:

ARCHIVE – the filename of archive with executable applet code;

CODE – the basic applet class;

CODEBASE – the catalog at the web-server where the archive with executable applet code is;

WIDTH – the width of applet on a browser screen in pixels (it is not recommended to set less than 10);

HEIGHT - the height of applet on a browser screen in pixels (it is not recommended to set less than 10);

PARAM – a certain applet parameter with the following attributes:

Name – parameter name

Value – parameter value

Several parameters are allowed. There is the one obligatory parameter with the name "cgiFile." The value for this parameter is a relative URL to cgi-bin file (data and request server). Applet will not work at incorrect indication of this parameter.

3. Command line:
General appearance:
```
java  -mx500m  -cp  .;genomexp.jar  softberry.project.genome_explorer.Base  E:\InetPub\cgi-
bin\genomb\genome_get.exe–parameter_name_1=value1–parameter_name_2=value2 ...
```

Example:

java -mx500m -cp .;genomexp.jar softberry.project.genome_explorer.Base E:\InetPub\cgi-bin\genomb\genome_get.exe

Parameters:
-mx500m – The maximum memory block size available for application
-cp – The archive key
.;genomexp.jar – The applet archive
softberry.project.genome_explorer.Base - Basic applet class
 E:\InetPub\cgi-bin\genomb\genome_get.exe – The path to the file "genome_get.exe" (data and requests server).

Loading parameters.

There are three different sets of parameters, which provide different loading ways:
1. Default region loading;
2. Loading of a region containing a feature with a certain ID;
3. Loading of a certain chromosome region.

1. **Default region loading.** This way makes the Softberry Genome Explorer to load a certain chromosome region, which was defined on default at the data and requests server. The hyperlink, HTML-code and command line scripts for this way should be as following:

   1. **Hyperlink (URL):**
      http://www.softberry.com/cgi-bin/genomexp.pl

   2. **HTML-код:**
      ```
      <APPLET          archive="genomexp.jar"          CODE="softberry.project.genome_explorer.Base"
      CODEBASE="/genomb/" WIDTH=10 HEIGHT=10>
      <PARAM name="cgiFile" value="/cgi-bin/genomb/genome_get">
      </APPLET>
      ```

   3. **Command line:**
      ```
      java -mx500m -cp .;genomexp.jar softberry.project.genome_explorer.Base
      E:\InetPub\cgi-bin\genomb\genome_get.exe
      ```

2. **Loading of a feature of a certain type, with a certain ID and localized on a certain chromosome.**

   For such a way the following parameters should be used:

   - **Feature_type** – The type of loading features. For example, if it is needed to load features of "fgenesh" type, the parameter should be set as following:

     ```
     feature_type=fgenesh
     ```

   - **Label** – The feature ID. For example, if it is needed to load all features of a certain type and containing C2200009 substring in their IDs, the parameter should be set as following:

     ```
     label=C2200009
     ```

- **Chrom** – The chromosome in which features will be searched for. For example, if it is needed to load features localized on the chromosome 22, the parameter should be set as following:

  ```
  chrom=chr22
  ```

- **Left_flank** – The length (size) of a loading region left flank

  ```
  left_flank=1000
  ```

- **right_flank** – The length (size) of a loading region right flank

  ```
  right_flank=1000
  ```

It is mandatory to define ALL parameters in HTML-code. If a single parameter is not defined, then features and chromosome region are being loaded "on default". If «left_flank» and «right_flank» are not defined in hyperlink, then default values (set on default at the data and requests server) for these parameters are used.

At the previously defined parameters the scripts for hyperlink, HTML-code and command line should be as following:

- **Hyperlink (URL):**
http://www.softberry.com/cgi-bin/genomexp.pl?feature_type=fgenesh&label=C2200009&chrom=chr22&left_flank=1000&right_flank=1000

- **HTML-code:**
```
<APPLET          archive="genomexp.jar"          CODE="softberry.project.genome_explorer.Base"
CODEBASE="/genomb/" WIDTH=10 HEIGHT=10>
<PARAM name="cgiFile" value="/cgi-bin/genomb/genome_get">
<PARAM name="feature_type" value="fgenesh">
<PARAM name="label" value="C2200009">
<PARAM name="chrom" value="chr22">
<PARAM name="left_flank" value="1000">
<PARAM name="right_flank" value="1000">
</APPLET>
```

- **Command line**
```
java  -mx500m  -cp  .;genomexp.jar  softberry.project.genome_explorer.Base
E:\InetPub\cgi-bin\genomb\genome_get.exe              -feature_type=fgenesh-
label=C2200009 -chrom=chr22 -left_flank=1000 -right_flank=1000
```

If the selected chromosome contains no features with such parameters, the message, that no features were found, appears (fig2.1.1) and loading of data does not occur.

Figure 2.1.1.

If a single feature is found, it will be loaded automatically without additional messages. If several features are found, the information window with the message on number of found features appears (fig.2.1.2). Upon the pressing of the "OK" button the dialog window with the list of found features is being opened (fig.2.1.3). In order to load a certain feature from the list select the required one and press the "Load" button (fig.2.1.3). The selected feature will be loaded.

Figure 2.1.2.
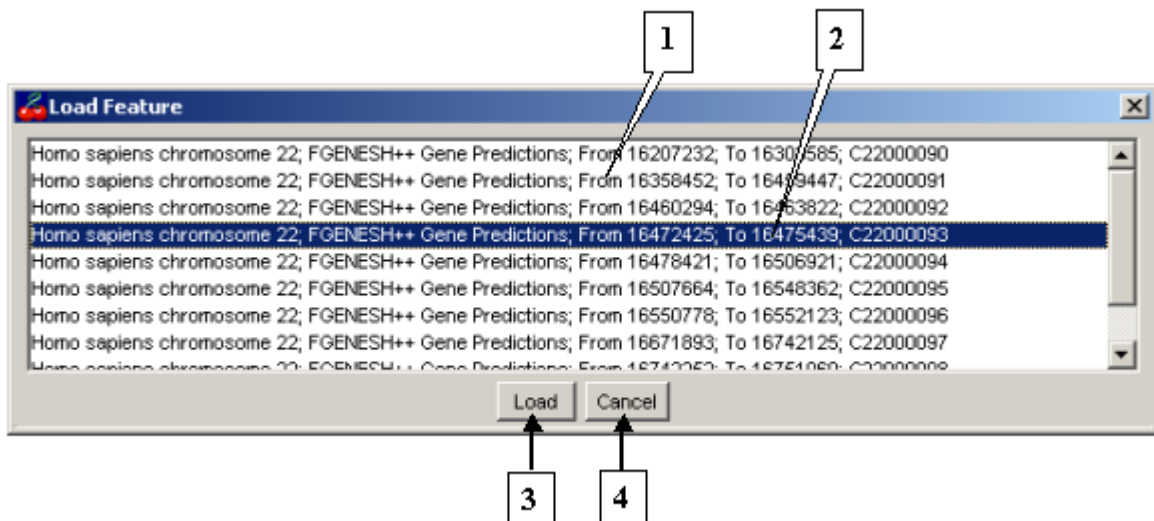
Figure 2.1.3.

1. The list of found features. **2.** The feature selected to be loaded. **3.** The button for loading. **4.** The button for aborting.

3. Loading of a certain region of a certain chromosome.

For such a way the following parameters should be used:

- **chrom** – The chromosome. For example, if it is needed to load the chromosome 22, the parameter should be set as following:

```
chrom=chr22
```

- **chrom_from** – The starting position of the loading region. For example, if it is needed to load the region, which starts from the position 14000000, the parameter should be set as following:

```
chrom_from=14000000
```

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- **chrom_to** – The ending position of the loading region. For example, if it is needed to load the region, which ends at the position 15000000, the parameter should be set as following:

```
chrom_to=15000000
```

- **show_from** – The starting position, from which the loaded region must be displayed. For example, if it is needed to display the loaded region from the position 14000000, the parameter should be set as following:

```
show_from=14000000
```

- **show_to** – The ending position, up to which the loaded region must be displayed. For example, if it is needed to display the loaded region up to the position 14500000, the parameter should be set as following:

```
show_to=14500000
```

At the previously defined parameters the scripts for hyperlink, HTML-code and command line should be as following:

- **Hyperlink (URL):**
http://www.softberry.com/cgi-bin/genomexp.pl?chrom=chr22&chrom_from=14000000&chrom_to=15000000&show_from=14000000& show_to=14500000

- **HTML-code:**
```
<APPLET archive="genomexp.jar" CODE="softberry.project.genome_explorer.Base"
CODEBASE="/genomb/" WIDTH=10 HEIGHT=10>
<PARAM name="cgiFile" value="/cgi-bin/genomb/genome_get">
<PARAM name="chrom" value="chr22">
<PARAM name="chrom_from" value="14000000">
<PARAM name="chrom_to" value="15000000">
<PARAM name="show_from" value="1400000">
<PARAM name="show_to" value="14500000">
</APPLET>
```

- **Command line:**
java -mx500m -cp .;genomexp.jar softberry.project.genome_explorer.Base   -chrom=chr22 -chrom_from=14000000 -chrom_to=15000000 -show_from=14000000 -show_to=14500000

Once being set, these parameters will cause the loading of the chromosome 22 from the starting position at 14000000 up to the ending position at 15000000. At the same time, all features localized in this region will be loaded also, but only those localized between the positions 14000000 and 14500000 will be displayed.

In the case when the "show_from" and "show_to" parameters are not defined in hyperlink, then they automatically gain the "chrom_from" and "chrom_to" values respectively.

It is mandatory to define ALL parameters in HTML-code. If a single parameter is not defined, then features and chromosome region are being loaded "on default".

If any of the parameters was assigned an invalid value the data loading will not occur.

2.2. Main Window.

The title line of the main window contains the following (fig.2.2.1):

- The program name (Softberry Genome Explorer);
- The loaded chromosome name (the loaded region size/full length of the chromosome)

In the window the main parts, which are placed one below another in the following order, can be distinguished (fig.2.2.1):

- **Main menu**
- **Toolbar**
- **Graphic navigation bar**
- **Map**
- **Precise navigation bar**
- **Information bars**

Main Window.

Figure 2.2.1.

1. Main menu. **2.** Toolbar. **3.** Graphic navigation bar. **4.** Auxiliary map areas. **5.** Map. **6.** Precise navigation bar. **7.** Information on a current pointer position. **8.** Left information bar. **9.** Right information bar. **10.** Status line.
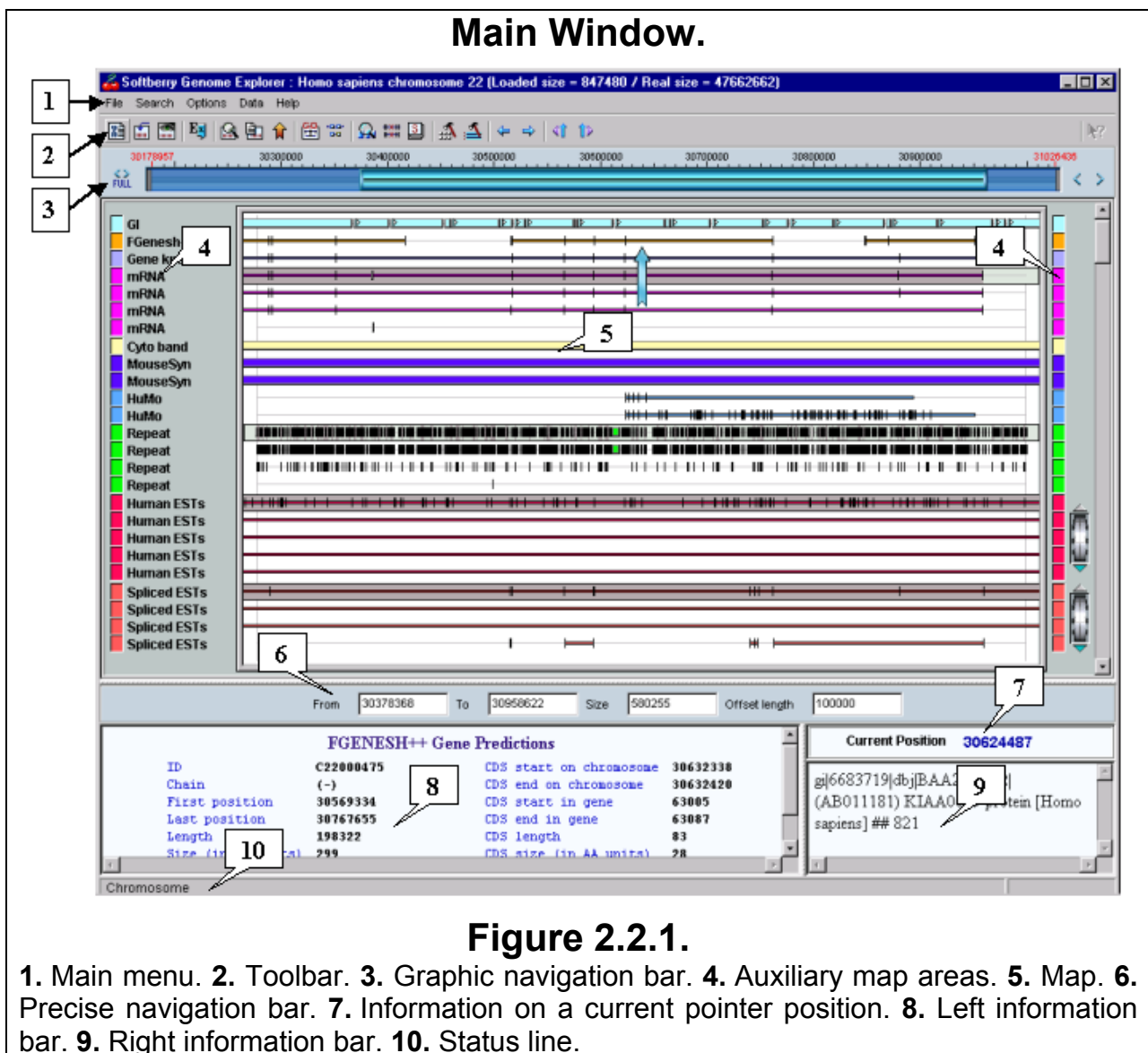
Comment.

In order to displace the lower map edge, pick it by pressing the mouse left button and drag to a new location. The first double click on the lower map edge causes information bars to be hided, while the second one restores them.

In order to displace the right edge of the left information bar, pick it by pressing the mouse left button and drag to a new location. The first double click on the right edge of the left information bar causes the right information bar to be hided, while the second one restores it.

2.3. Main Menu.

The Main menu contains several groups (menus) of commands:
- The "File" menu contains the single command "Exit", which provides exit the program (Fig.2.3.1);

«File» menu.

Figure 2.3.1.

1. Exit the Softberry Genome Explorer.

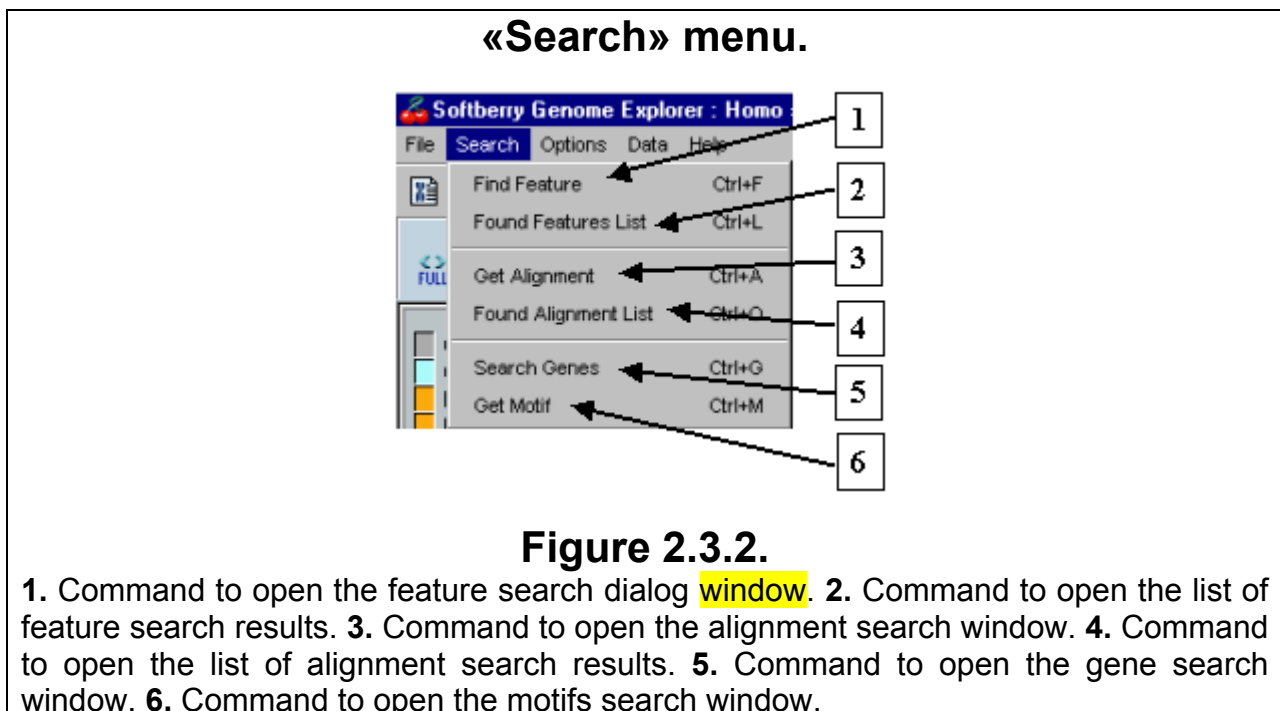---
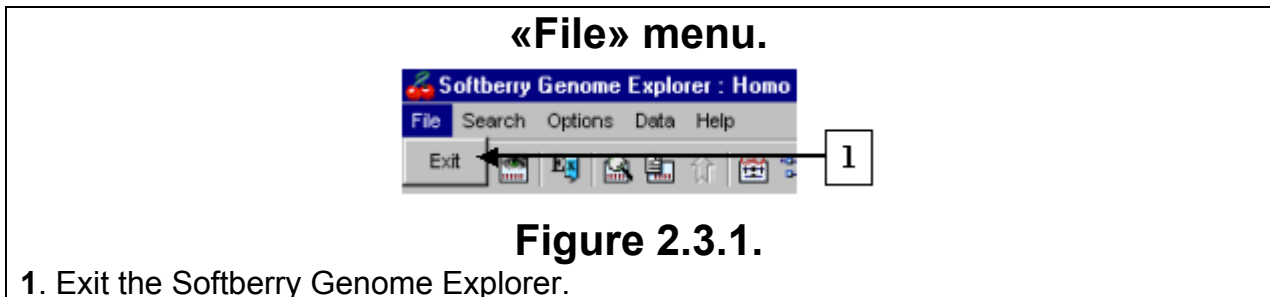
- The "Search" menu contains six commands (fig.2.3.2), which are:
  1. "Find Feature" – opens the feature search dialog window. The hot keys combination for this command is <Ctrl+F>;
  2. "Found Feature List" – opens the dialog window with the list of feature search results. The hot keys combination for this command is <Ctrl+L>;
  3. "Get Alignment" – opens the dialog window with alignment options menu. The hot keys combination for this command is <Ctrl+A>;
  4. "Found Alignment List" – opens the dialog window with the lists of found alignments. The hot keys combination for this command is <Ctrl+O>;
  5. "Search Genes" – opens the dialog window with genes search options. The hot keys combination for this command is <Ctrl+G>;
  6. "Get Motif" – opens the dialog window with motives search options. The hot keys combination for this command is <Ctrl+M>;

«Search» menu.

Figure 2.3.2.

1. Command to open the feature search dialog window. **2.** Command to open the list of feature search results. **3.** Command to open the alignment search window. **4.** Command to open the list of alignment search results. **5.** Command to open the gene search window. **6.** Command to open the motifs search window.

- The "Options" menu (fig. 2.3.3.) contains the following commands:

1. "Chromosome" – opens the dialog window for selection of a chromosome and its region to be loaded;
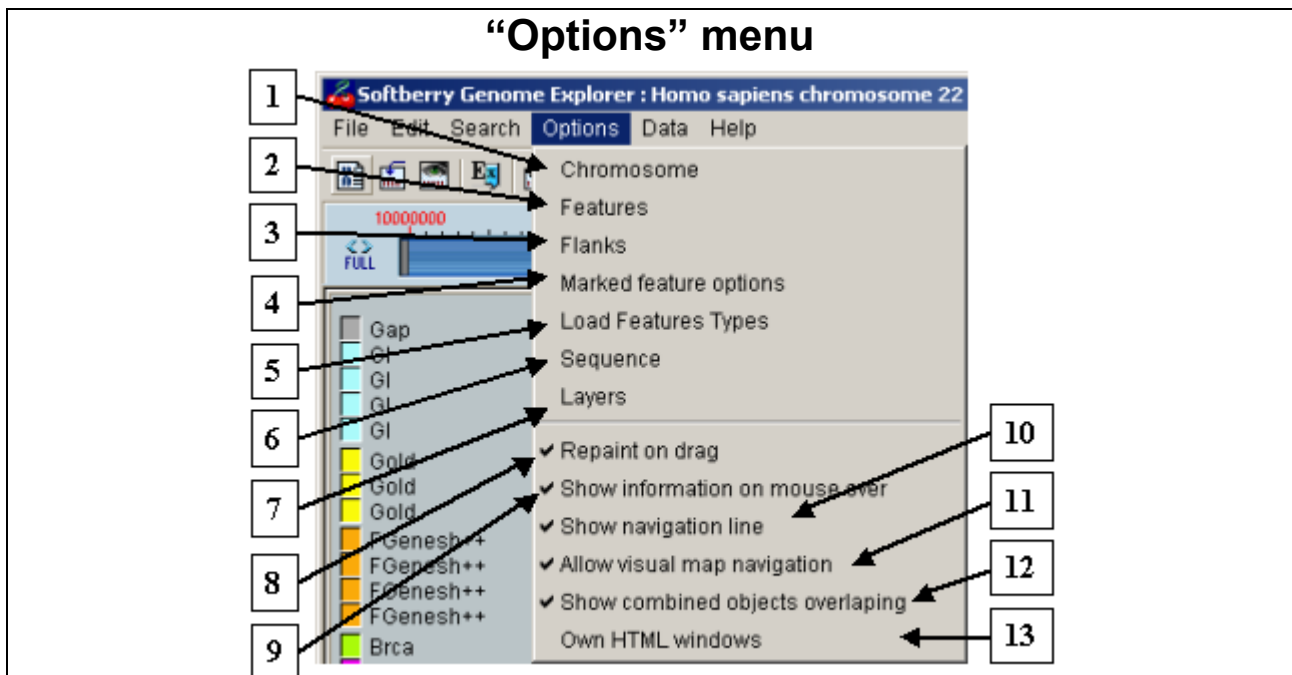
"Options" menu

Figure 2.3.3.

1. Chromosome selection dialog <mark>window</mark>. **2.** Feature types to be displayed selection window. **3.** "Flanks" dialog window. **4.** Feature marking parameters setup dialog window. **5.** Feature types to be loaded selection window. **6.** Nucleotide sequence output setup window. **7.** Layers visualization setup window. **8.** Map redrawing mode switch. **9.** Information display mode switch. **10.** Enabling current mouse pointer position display mode. **11.** Enabling visual map navigation mode. **12.** Enabling coloring mode of combined layers overlapping. **13.** Enabling of own HTML windows.

2. "Features" – opens the dialog window for selection of a feature(s) to be displayed;
3. "Flanks" – opens the "Side intends options" dialog window (fig.2.3.4). The "Left flank" and "Right flank" fields are proposed for setting up of the loading options for a chromosome region, in which the found feature or alignment is localized (see also 3.4 and 3.5). In this term, the loading region is a region, which contains the found feature or alignment, plus the lengths of left and right flanks;
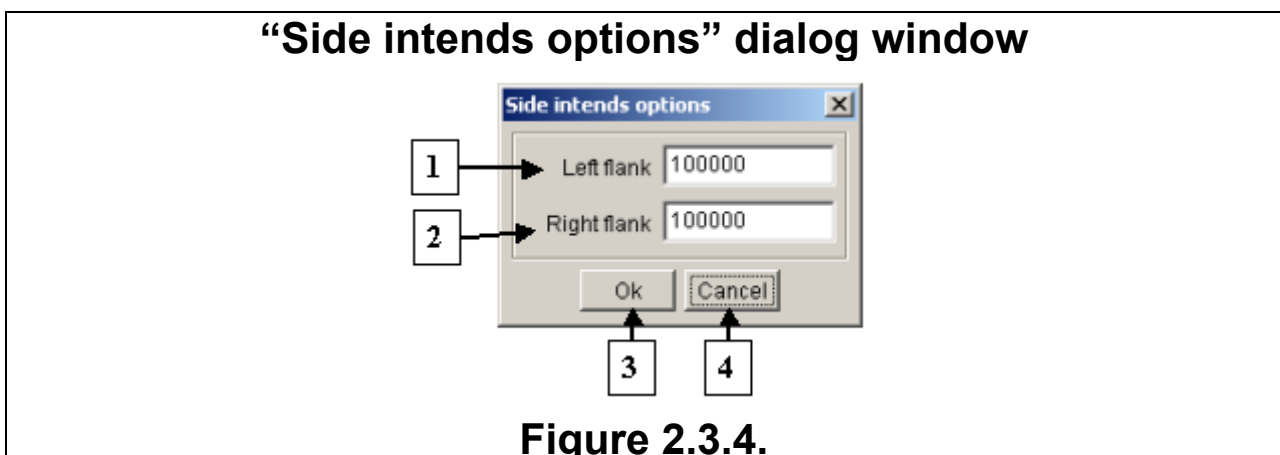
"Side intends options" dialog window

Figure 2.3.4.

1. Field for definition of the left flank length. **2.** Field for definition of the right flank length. **3.** Confirmation button. **4.** Rejecting button.

4. "Marked feature options" – opens the dialog window proposed for setting up of the feature marking parameters;
5. "Load Features Types" – opens the dialog window with the list of loadable feature types and their display order.
6. "Sequence" – opens the dialog window proposed for setting up the nucleotide sequence output options.
7. "Layers" – opens the dialog window proposed for setting up the layers visualization options.
8. "Repaint on drag" [disabled on default] – when enabled, the map redrawing occurs simultaneously with either runner dragging by mouse or movement of pointer along the map at pressed mouse left button. When disabled, the map redrawing occurs just after mouse button is released.
9. "Show information on mouse over" [enabled on default] – when enabled, the information on feature appears in Information bar automatically upon the placement of mouse pointer over the Feature. When disabled, the information on Feature appears only after click on required site.
10. "Show navigation line" [enabled on default] – enabling in the map window of a vertical line (current horizontal position line), that moves synchronously with mouse pointer.
11. "Allow visual map navigation"[enabled on default] – enabling of navigation by mouse in the map window.
12. "Show combined objects overlapping" – enabling of overlapping features regions display in combined (multiple) layer.
13. "Own HTML windows" – when disabled, information appears in the window of a browser used to launch Java-applet. When enabled, application uses it's own windows.

- The "Data" menu (fig. 2.3.5.) contains two commands, which are:
  1. "Sample Sequences" – opens the dialog window with options for retrieving of sets of feature sequences. The hot keys combination for this command is <Ctrl+S>;
  2. "Show Expression" – opens the dialog window with data on the gene expression. The hot keys combination for this command is <Ctrl+E>;

"Data" menu

Figure 2.3.5.

1. Dialog window with options for retrieving of sets of feature sequences. **2.** Dialog window with data on the gene expression.
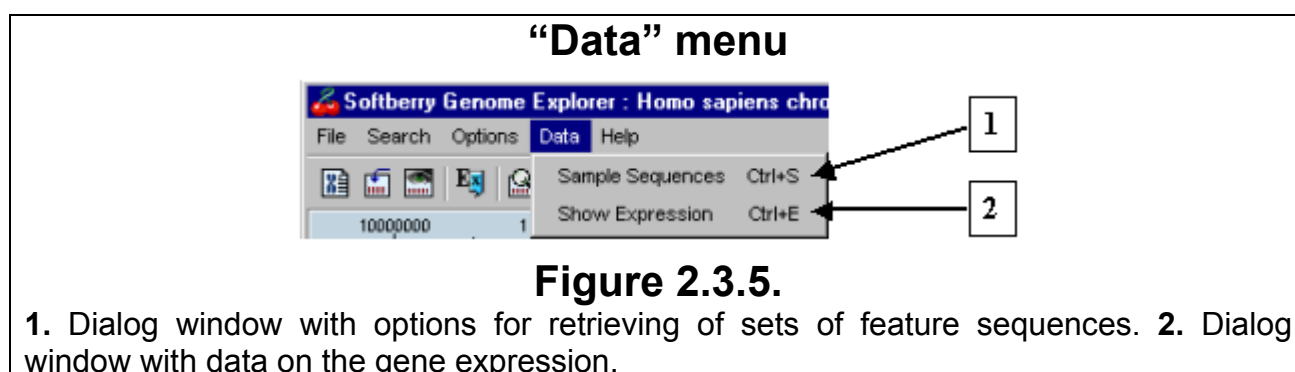
- The "Help" menu (fig. 2.3.6.) contains the single command "About", which provides the information on the current program version (fig. 2.3.7.).
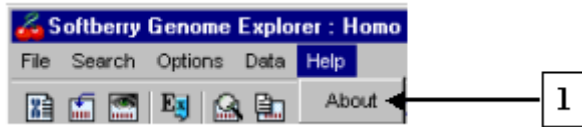
"Help" menu

Figure 2.3.6.

1. Information window with current version of the Softberry Genome Explorer.
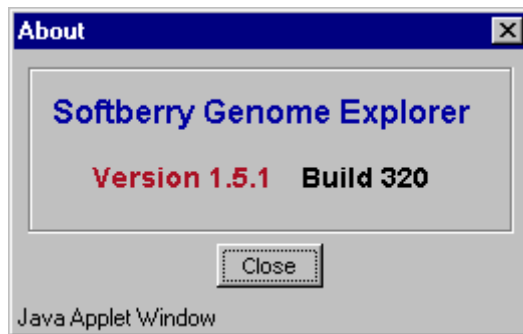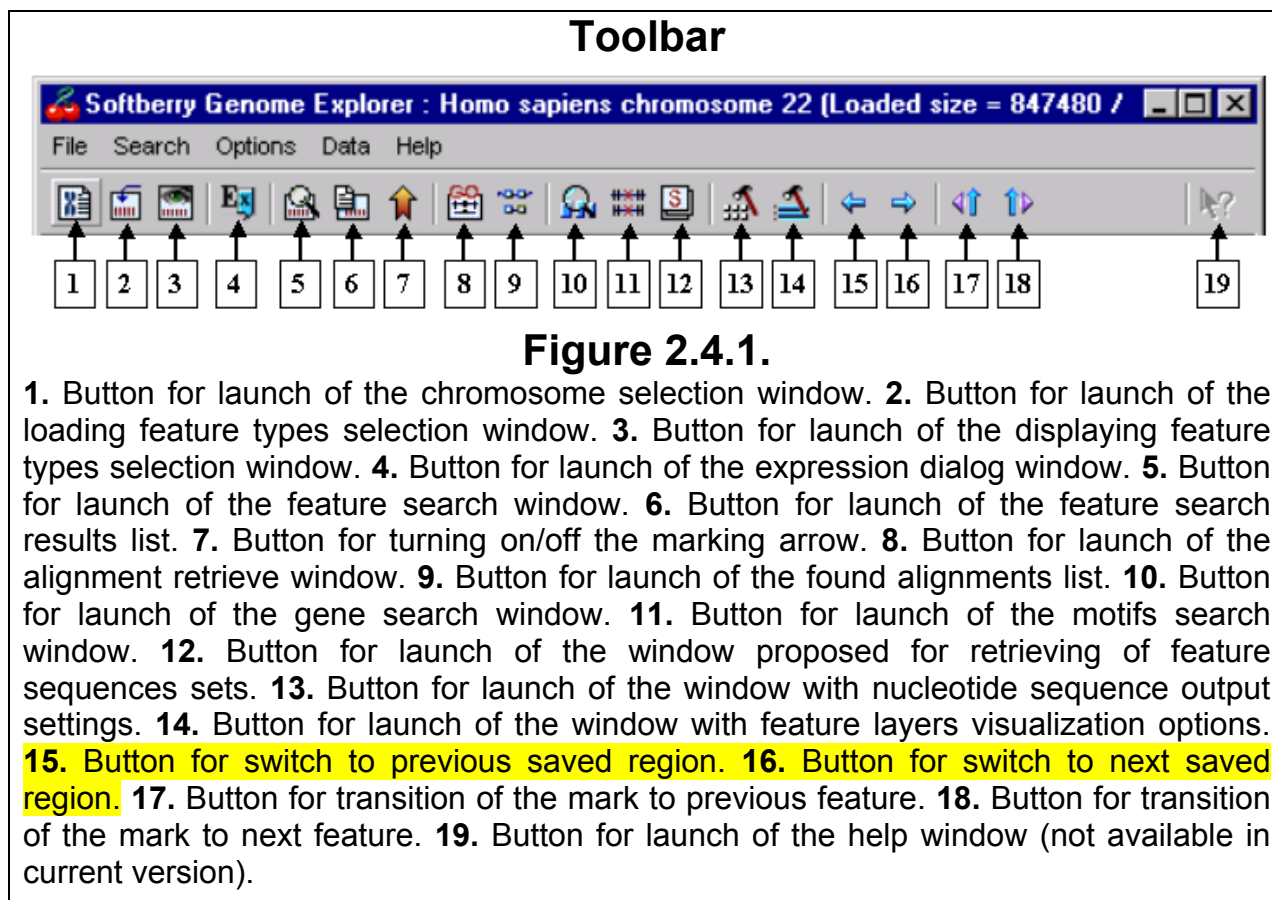
Dialog window with current version.

Figure 2.3.7.

2.4. Toolbar.

The toolbar is proposed for quick launch of certain dialog windows (fig. 2.4.1.).

Toolbar

Figure 2.4.1.

1. Button for launch of the chromosome selection window. **2.** Button for launch of the loading feature types selection window. **3.** Button for launch of the displaying feature types selection window. **4.** Button for launch of the expression dialog window. **5.** Button for launch of the feature search window. **6.** Button for launch of the feature search results list. **7.** Button for turning on/off the marking arrow. **8.** Button for launch of the alignment retrieve window. **9.** Button for launch of the found alignments list. **10.** Button for launch of the gene search window. **11.** Button for launch of the motifs search window. **12.** Button for launch of the window proposed for retrieving of feature sequences sets. **13.** Button for launch of the window with nucleotide sequence output settings. **14.** Button for launch of the window with feature layers visualization options. **15.** Button for switch to previous saved region. **16.** Button for switch to next saved region. **17.** Button for transition of the mark to previous feature. **18.** Button for transition of the mark to next feature. **19.** Button for launch of the help window (not available in current version).

The Toolbar contains the following buttons most of which have the same functions as the commands of main menu:

	"Chromosome" – opens the dialog window for selection of a chromosome and its region to be loaded. Has the same purpose as the «Options->Chromosome» command of main menu.
	"Load Features Types" – opens the dialog window with the list of loadable feature types and their display order. Has the same purpose as the «Options->Load Feature Types» command of main menu.
	"Features" – opens the dialog window for selection of a feature(s) to be displayed on the map. Has the same purpose as the «Options->Feature» command of main menu.
	"Show Expression" – opens the dialog window with data on the feature expression. Has the same purpose as the «Data->Show Expression» command of main menu or the «Show Expression» command of feature popup menu.
	"Find Feature" – opens the feature search dialog window. This window is proposed for setting up the options for feature search by elements, which present in the feature name or description, or in brief information on a feature. Has the same purpose as the «Search->Find Feature» command of main menu.
	"Found Features List" – opens the dialog window with the list of previously found features. Has the same purpose as the «Search->Found Features List» command of main menu.

⬆	"Hide Arrow" – hides or reveals the arrow, which marks the position on the map where the found feature or alignment is localized.
🔍	"Search Genes" – opens the dialog window with genes search options. Has the same purpose as the «Search-> Search Genes» command of main menu.
▥	"Get Motif" – opens the dialog window with motifs search options. Has the same purpose as the «Search->Get Motif» command of main menu.
▦	"Get Alignment" – opens the dialog window with alignment options menu. Has the same purpose as the «Search->Get Alignment» command of main menu.
▦	"Found Alignment List" – opens the dialog window with the lists of previously found alignments. Has the same purpose as the «Search->Found Alignment List» command of main menu.
▤	"Sample Sequences" – opens the dialog window with options for retrieving of sets of feature sequences. Has the same purpose as the «Data->Sample Sequences» command of main menu.
▨	"Sequence Options" – opens the dialog window proposed for setting up the nucleotide sequence output options. Has the same purpose as the «Options->Sequence» command of main menu.
▨	"Layers Options" – opens the dialog window proposed for setting up the layers visualization options. Has the same purpose as the «Options->Layers» command of main menu.
⬅	"Back" – returns to the previous map position.
➡	"Forward" – cancels the effect of "Back" button.
◁⇑	"Previous feature" – marks the previous feature with an arrow.
⇑▷	"Next feature" – marks the following feature with an arrow.
▸?	"Help" – not available in current version.

Comment. Upon the placing of mouse pointer over a certain toolbar button the name of button will appear in the main window status line (fig.2.2.1).
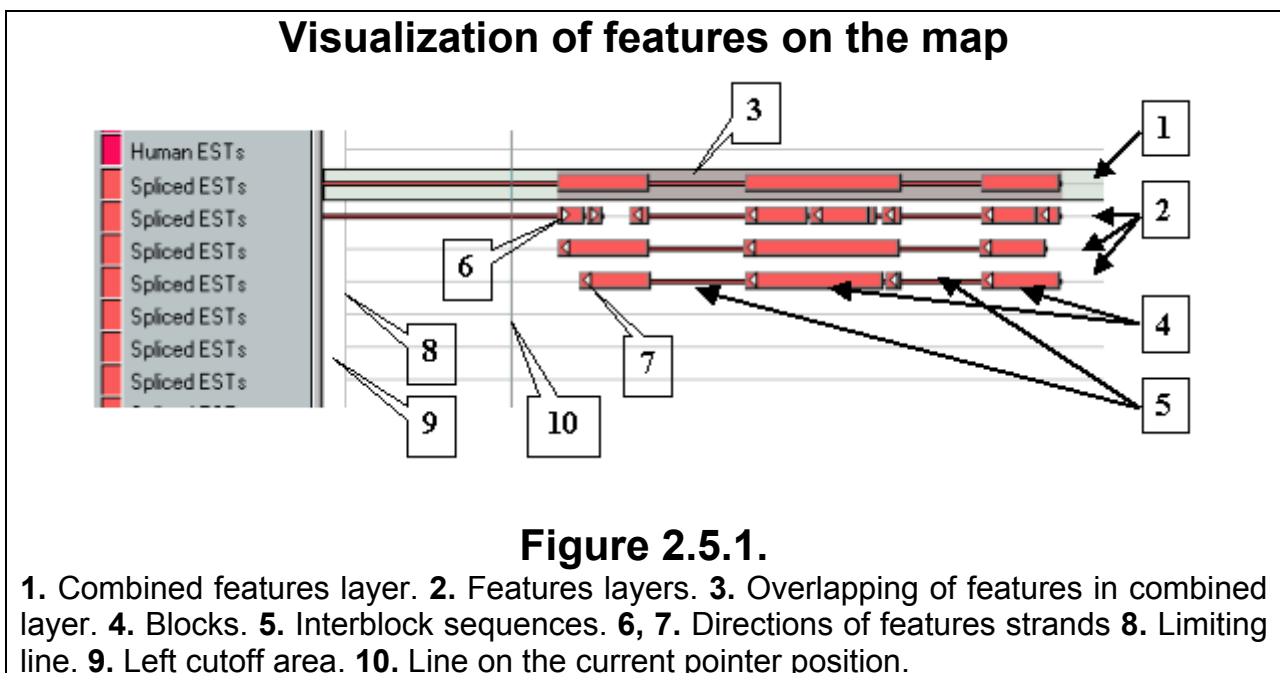
2.5. Map

The map is purposed for schematic visualization of the loaded data and retrieving of the information on features in a form convenient for user. The map allows the scaling and the navigation of the loaded region. The map elements provide information on the loaded feature types, e.g. the information on a number of layers possessed by a certain feature type, or the brief information on features types, or visualization of the complete profile of all features of a given type. These elements also provide data on a certain features, e.g. sets of features sequences, sequences of proteins encoded by features, data on features expression, alignment of sequences to a certain genome region, types of features, strands directions, links to databases etc.

Map utilizes the majority of the main window space. To the left and to the right of the main map window there are the auxiliary map areas purposed for layers setup and providing of information on feature types.

The map area (Features Display Area) is used for displaying of features. In the case when features of the same type are overlapping, they are displayed in several layers, which are placed one over another (fig.2.5.1). The number of layers is equal to the maximum number of overlappings of features of a given type in the loaded genome region. The order in which features of different types are displayed corresponds to that selected in "Load Features Types" window.

The types of features can be combined into the following classes of type species:
- Block features, e.g. mRNAs, ESTs etc.
- Non-block or simple features, e.g. Cyto, band, Gap etc.
- Graphic features, e.g. VISTA.

Visualization of features on the map

Figure 2.5.1.

1. Combined features layer. **2.** Features layers. **3.** Overlapping of features in combined layer. **4.** Blocks. **5.** Interblock sequences. **6, 7.** Directions of features strands **8.** Limiting line. **9.** Left cutoff area. **10.** Line on the current pointer position.

For block features, blocks are represented as colored rectangles, while interblock sequences are represented as thin colored lines between rectangles. The arrow direction on a block shows the direction of the strand in which the current feature is localized (fig. 2.5.1). If an arrow doesn't appear in a block, it might require to enlarge the map scale. If the map scale is maximal but an arrow still doesn't appear, it means the block size is too small to display an arrow. In this case the direction of a strand can be seen in the information bar (see 2.8).

Non-block features are represented on the map as colored rectangles without interblock sequences.

Graphic features are represented as a plot or histogram.

Over the gray background combined layers of features are displayed (if «Combined» or «Combined+All» options are enabled). Regions, where two or more different features of the same type (which, of course, are in different layers) are overlapping each other, are displayed in dark gray color. Combined layers exist not for all features types, but when "Combined" mode is enabled, then for all types displayed either combined layer (if it exists for this type), or layers are being combined (if there is no combined layers for this type, then results of combination are being displayed over the white background, not over the gray one).

The feature display area itself consists of three parts:
- The left cutoff area;
- The central part;
- The right cutoff area.

The restriction lines separate these areas from each other. The central part of the features area has the horizontal gridlines, a number of which is consistent with that of displayed layers, and corresponds to coordinates of the displayed region. In the cutoff areas only those features are being displayed which actually present in the selected region, but extend beyond its edges. These areas are necessary for visual identification of the features, which completely are inside the selected region, and those ones, which extends beyond its boundaries (in this case the feature continues in the cutoff area).

The maximal map scale corresponds to a single chromosome position (single nucleotide) per pixel.

If the mouse pointer is in the central area of features display, then in the left information bar (see below), in the «Current position» field, the current chromosome position is being displayed. At the enabled "Show navigation line" mode the current chromosome position is being marked with a vertical line which never leaves from the central features area.

At the enabled "Allow visual map navigation" mode the map navigation can be carried out using a mouse and control keys via operating the map itself (except the layers layout area). At that, if "Repaint on drag" is enabled, the map redrawing occurs simultaneously with movement of mouse pointer (left mouse button must be hold down), otherwise it occurs just after mouse button is released.

There are several operations available:
- o To move along the map to the left or right without pressing any control key;
- o To hold down the "Shift" key and smoothly change the map scale by movement of mouse pointer. Scaling occurs from the center of map. Movement of mouse pointer to the right causes upscaling and vice versa. Pressing or releasing of the "Shift" key during the mouse movement leads to switch from navigation to scaling or vice versa correspondingly.
- o To hold down the "Ctrl" key and left-click at any map space. It will cause the change of scale to maximum and one of the following regions will be displayed:
  - Region to the right of the point clicked in the case when previous scale was too small;
  - Region, which includes the point clicked if previous scale was not significantly different from maximum.
- o To hold down the "Ctrl" key and select some map area drawing a rectangle by mouse movement. The left and right borders of rectangle

designate the region of map, which will be scaled up after release of mouse button.

Comment. The "Ctrl" key must be pressed at all operations with mouse (from pressing to releasing of mouse button), otherwise operation will not be completed.

The left and right auxiliary map areas are purposed for layers layout and retrieving of information on features types. In the right area there is a color layout (colored rectangles) only. In the left one along a color layout there are the brief feature types names. If the number of layers of a certain features type is larger than it's displayed (i.e. at enabled «Compact mode»), then in the right area appears the layer-scrolling tool, which can be used for transition to the layer of interest. In the right area there is also the vertical scrolling bar, which is purposed for scrolling of the map up and down (fig.2.5.2).

Right auxiliary area

Figure 2.5.2.

1. Layer-scrolling tool. **2.** Map-scrolling bar. **3.** Features types **4.** Layers of features of the same type.
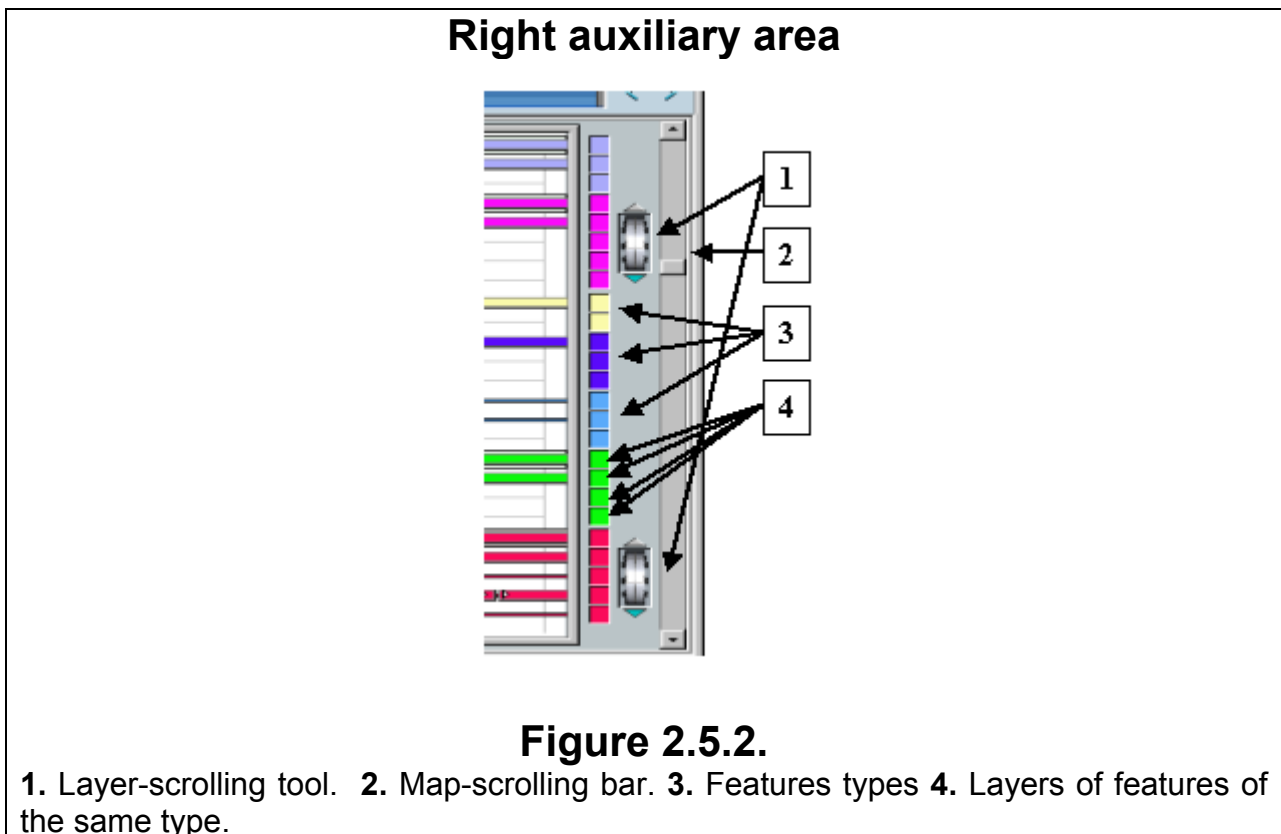
2.6. Graphic navigation bar

Using the graphic navigation bar (fig.2.6.1) an approximate length of displayed region can be assigned. This bar allows operating the loaded chromosome region only.

At enabled "Repaint on drag" the map redrawing occurs on displacement of runner by mouse right button (at navigation by mouse); in this mode the bar acts as a horizontal scrolling bar with variable runner size. At disabled "Repaint on drag" the map redrawing occurs on mouse right button releasing only.
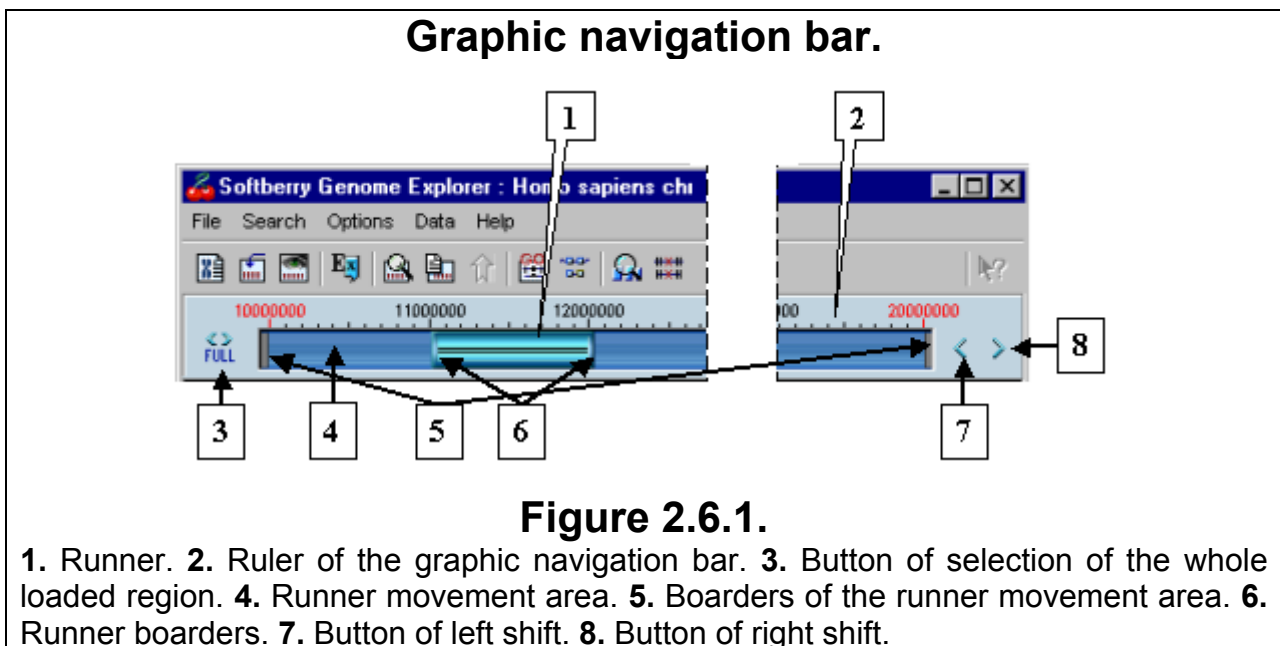
Area of runner movement corresponds to loaded chromosome region. Boarders of the moving area are for superposing with the runner boarders (at the ultimate left or right position of the runner its boarders are being superposed with the moving area ones).

Operating the graphic navigation bar is being performed by means of mouse. The rectangle of runner shows what the part of loaded region is displayed; boarders are not included in this part. Boarders and/or scale of this part can be changed (using the runner) by one of the following ways:

- Drag it to the left of right by mouse;
- Drag an appropriate boarder (left or right) by mouse and thus change it.

At the pressed "Shift" key and dragging of runner boarder by mouse both boarders change – the runner becomes clenched to the center or stretched from it.

To the left of navigator there is the button ![FULL] («Full») (fig.2.6.1) at the pressing of which the whole loaded region becomes selected. In this case, runner occupies the whole movement area.

Graphic navigation bar.

Figure 2.6.1.

1. Runner. **2.** Ruler of the graphic navigation bar. **3.** Button of selection of the whole loaded region. **4.** Runner movement area. **5.** Boarders of the runner movement area. **6.** Runner boarders. **7.** Button of left shift. **8.** Button of right shift.

A minimal region, which the runner represents, depends on size of the application window. In this case between the navigator boarders the red line instead of rectangle appears. It means the runner cannot be stretched further.

To the right of navigator there are shift buttons - ![<] and ![>]. At pressing on one of them the selected region (and the runner itself) shifts in appropriate direction accordingly to the number of positions defined in the «Offset length» field (fig.2.7.1) on the precise navigation bar.

Mouse left-click on the runner movement area to the left or right of runner leads to scrolling of shown map area in appropriate direction. Scrolling distance corresponds to shown map width.

2.7. Precise navigation bar.

The **Precise Navigation Bar** (fig.2.7.1) provides the ability to set the exact borders of region to be displayed and consists of several text fields directly below the map. In these fields the parameters of region selected using the Graphic Navigation Bar are automatically being displayed.

- Field "From" – the start position of displayed region
- Field "To" – the end position of displayed region
- Field "Size" – the size of displayed region

Precise Navigation Bar

| 1 | 2 | 3 | 4 |

From 10209923   To 11154579   Size 944657   Offset length 100000

Figure 2.7.1.

1. Field of the start position of displayed region. **2.** Field of the end position of displayed region. **3.** Field of the displayed region size. **4.** Field of the displayed region shift.
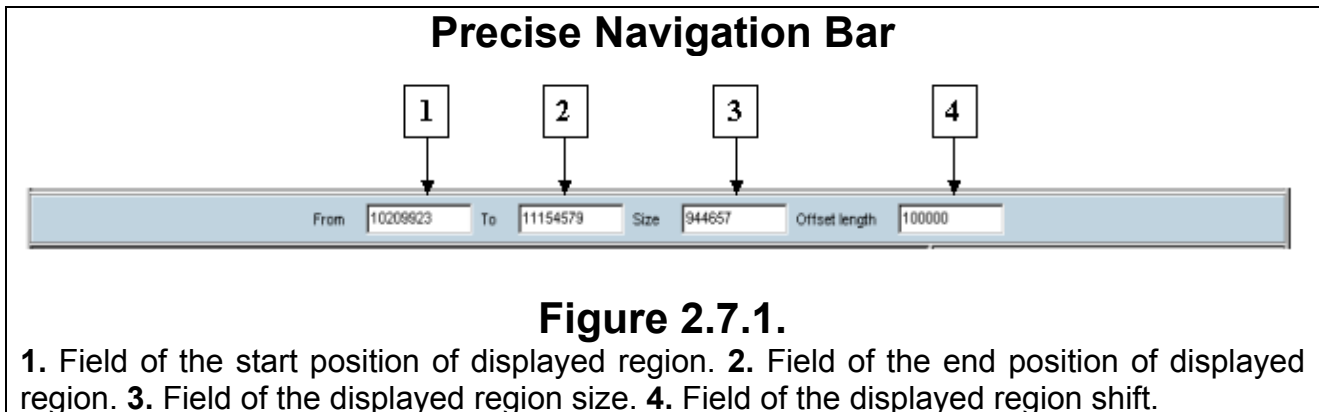
Comment. Changing of a value in a field (more definitely – fixing of entered value) occurs on either entering of a numerical value in a field and pressing of the "Enter" key, or quitting a field (removing of the cursor to another field). After entering the value is being corrected accordingly to restriction, resulted from a chromosome length, and revealed anew.

Comment. If a value has been changed in one of the fields it may cause the automatic value changes in another one.

If a value has been changed in the «Size» field it causes the recalculating of a value in the «To» field, while that one in the «From» field remains unchanged.

If a value has been changed in the «From» field it causes the recalculating of a value in the «Size» field, while that one in the «To» field remains unchanged.

If a value has been changed in the «To» field it causes the recalculating of a value in the «Size» field, while that one in the «From» field remains unchanged.

Comment. Changes in field values automatically cause changes of the size and location in the navigator of a rectangle, which represents the selected region, and redrawing of the map. In turn, change of a region using the navigator or scrolling of the map using a mouse causes visualization of the corrected positions in the appropriate fields.

2.8. Information bars.

Information bars are purposed for visualization of information on features or feature types, which are currently pointed by mouse.

Figure 2.8.1.
A. Appearance of the information bar in the case of a block feature. **B.** Appearance of the information bar in the case of a non-block feature.
1. Left information bar. **2.** Right information bar. **3.** Position currently pointed out.
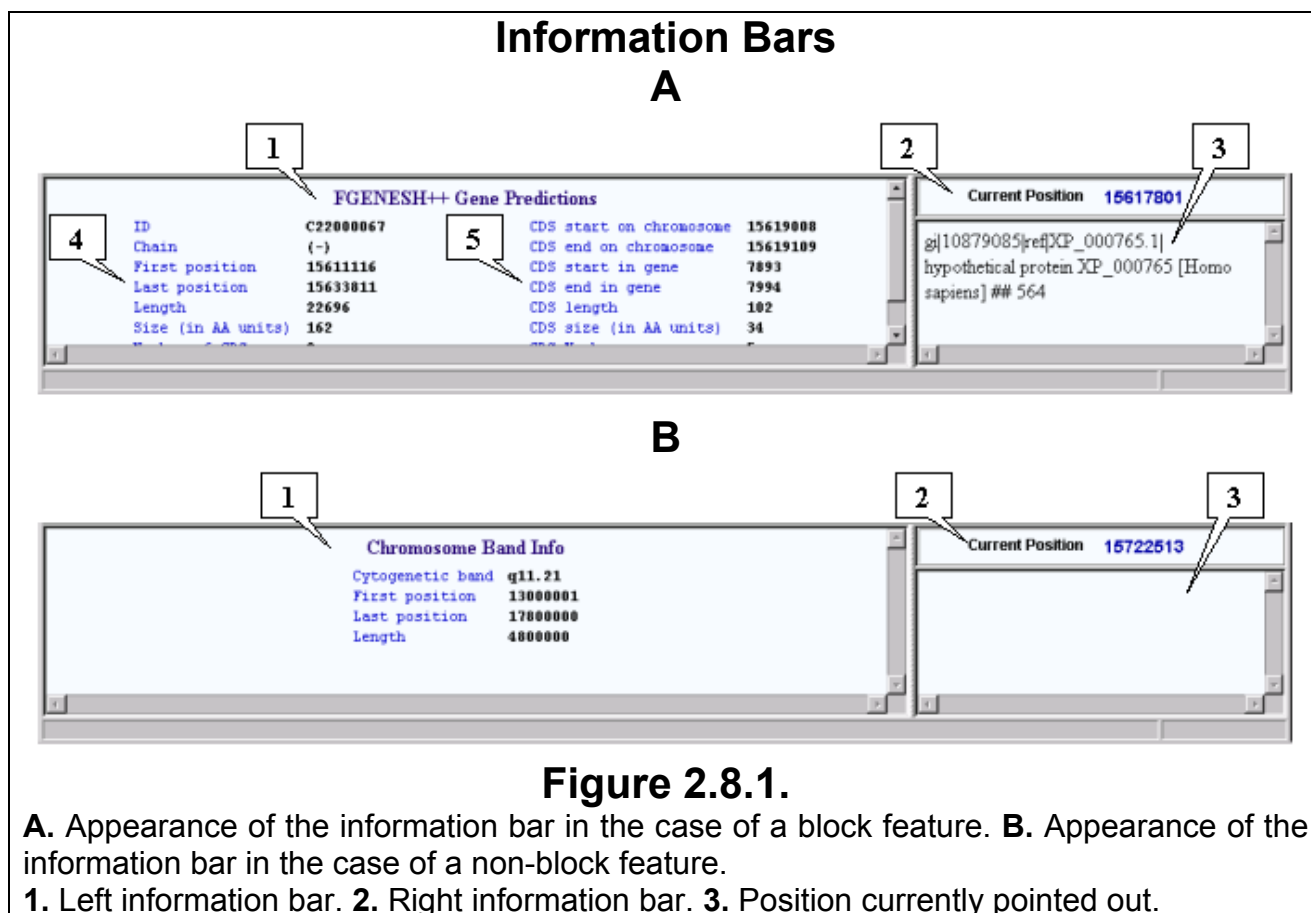
The left information bar (fig.2.8.1) displays the information on a feature (at the top there is the title with a feature type indication, below the title the data on a feature, such as ID, nucleotide chain direction, the starting and ending positions, feature length etc., are displayed). These data reiterate the information available via the «Show Description» command of the feature popup menu (see below). If features of a given type may consist of several blocks the information will be displayed on the left part of the bar (fig. 2.8.1.A). Otherwise (non-block features, such as Cyto band) the information will be displayed in the center of the bar (fig. 2.8.1.B). If a feature consists of blocks and mouse pointer is over one of them, then on the left part of the bar will be displayed the information on a feature, and on the right one – the information on a block (fig. 2.8.1.A).

At the top of the right information bar there is the «Current Position» field, in which displayed the number of currently pointed chromosome position. Current position is being displayed only in the case, when the pointer is inside the central part of the Feature Display Area (space between the left and right cutoff areas).

Below the «Current Position» field brief information on either a feature (it is completely identical to a content of the «Short info» bar of the «Description» window, which can be opened using the «Show Description» command of the feature popup menu (see below)), or a feature type is displayed. Information display occurs on the placing of the mouse pointer over a subject (feature or feature type).

When the "Show information on mouse over" option is enabled information on a feature (both brief and full) is being displayed on the placing of the mouse pointer over a feature. Otherwise it is being displayed only after the mouse clicking on a feature.

Information on the last feature is automatically being saved and thus is being displayed until the pointer is placed over another one. If the pointer is placed in an area, which doesn't contain any feature, the information bar doesn't become clear, but contains information on the last feature pointed out.

3. SYSTEM OPERATING

3.1. Data loading.

3.1.1. Selection of feature types and display order.

It is important to select the required feature types correctly. Loading of data from the server and, respectively, displaying on the map will occur only for those types, which were selected for. It is better to select for loading the required feature types only, but do not load all of available ones, since it may significantly affect the data loading time and system resources, such as memory, usage. On a necessity it is always possible to add and load new feature types without reloading of old ones. In certain cases the application may independently add some feature types to the loading list.

All these operations are available in the appropriate dialog window (Window for selection of loading feature types and their display order, fig.3.1.1.1). This window can be opened using one of the following methods:

- o Using the «Options->Load Features Types» command of main menu;
- o Using the 🖻 button at the toolbar.

In order to select feature types for loading the following operations should be performed:

1. To select the required feature types in the «Non-loading feature types» list by mouse clicking on them (deselection occurs on a recurring click);

2. To press the ⟩ button (button for including of selected feature types to the loading list) on the lists operating bar. At this the selected types will be moved from the list of non-loading types to the end of list of loading ones. The types will be placed in the same order as they were in the non-loading types list.

It's allowed to add all types at the time. To do so, press the ⟩⟩ button (button for including of all feature types to the loading list) on the lists operating bar.

In order to exclude certain feature types from being loaded the following operations should be performed:

1. To select the required feature types in the «Feature types to load» list by mouse clicking on them (deselection occurs on a recurring click);

2. To press the ⟨ button (button for excluding of selected feature types from the loading list) on the lists operating bar. At this the selected types will be moved from the list of loading types to the end of list of non-loading ones. The types will be placed in the same order as they were in the loading types list.

It's allowed to exclude all types at the time. To do so, press the ⟨⟨ button (button for excluding of all feature types from the loading list) on the lists operating bar.

The feature types display order will be the same as in the loading list. In order to change it use the buttons for displacement of selected feature types («Up» and «Down») in the list of loading feature types and their display order. On a pressing of a certain button the displacement of the selected types for a single position in appropriate direction will occur.

Window for selection of loading feature types and their display order.
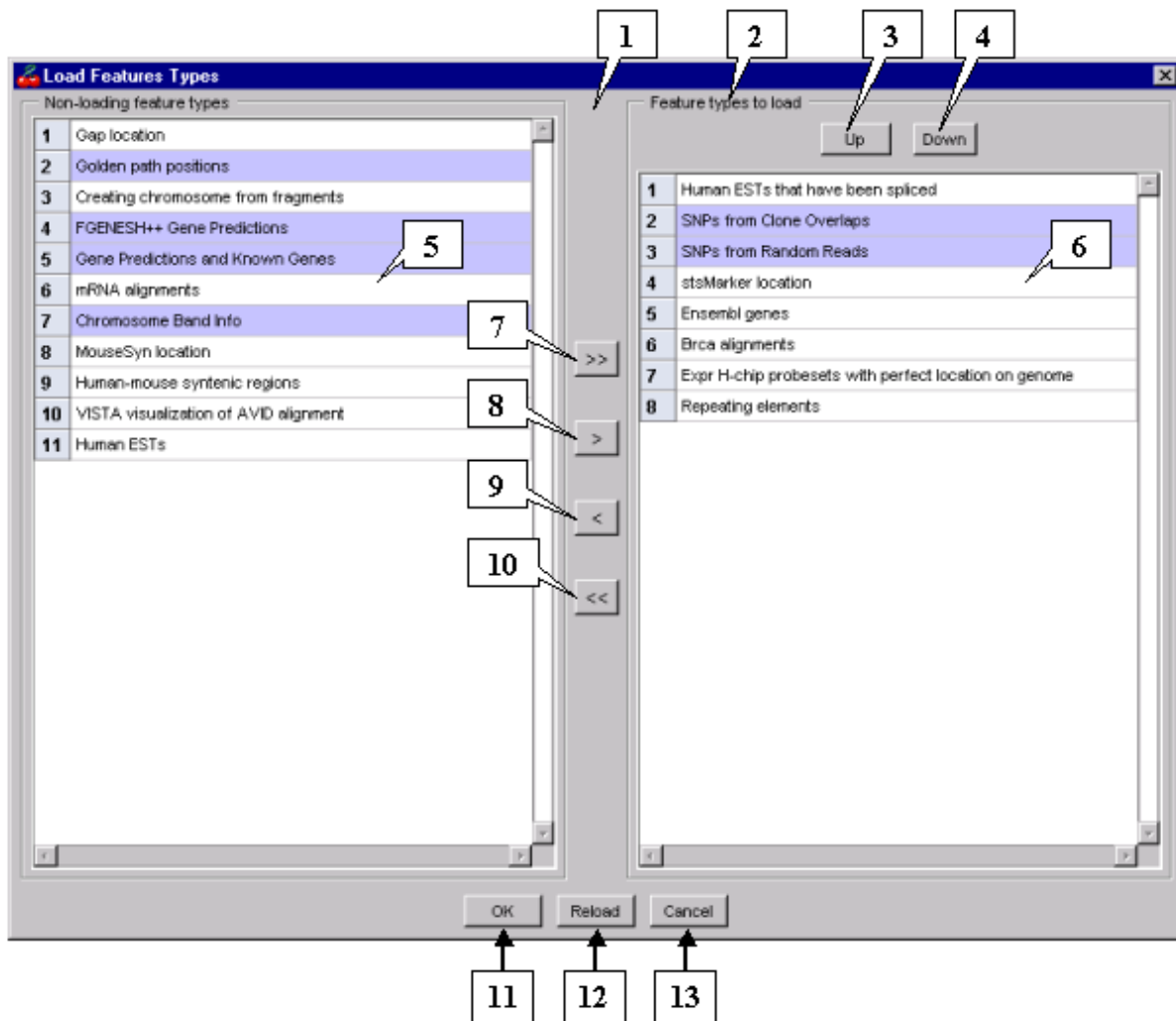
Figure 3.1.1.

1. The lists operating bar. **2.** The bar for definition of types order in the list. **3.** Button for upward displacement of the selected feature types. **4.** Button for downward displacement of the selected feature types. **5.** The list of non-loading feature types. **6.** The list of loading feature types and their display order. **7.** Button for including of all feature types to the loading list. **8.** Button for including of selected feature types to the loading list. **9.** Button for excluding of selected feature types from the loading list. **10.** Button for excluding of all feature types from the loading list. **11.** Confirmation button. **12.** Confirmation and reloading button. **13.** Rejecting button.

3.1.2. Selection of chromosome and its region for loading.

The dialog window for chromosome selection can be opened using one of the following methods:

- Using the «Options->Chromosome» command of main menu;
- Pressing the ▦ button on the toolbar.

In the appeared window select the required chromosome from the drop down list (fig. 3.1.2.1). Further, define the region for data loading. In order to select the whole chromosome use the ⟨⟩FULL button. Loading of data from the server will occur for the selected region only.

Comment. The data loading process may take a certain time, which depends on the selected region size and a number of feature types included to loading (see chapter 3.1.1). Any change in the loading region parameters will be accompanied by data reloading. The process of data loading may be significantly time-consuming, thus, in the necessity of work with different regions of the same chromosome, it makes sense to define the region boarders, which include all these regions.
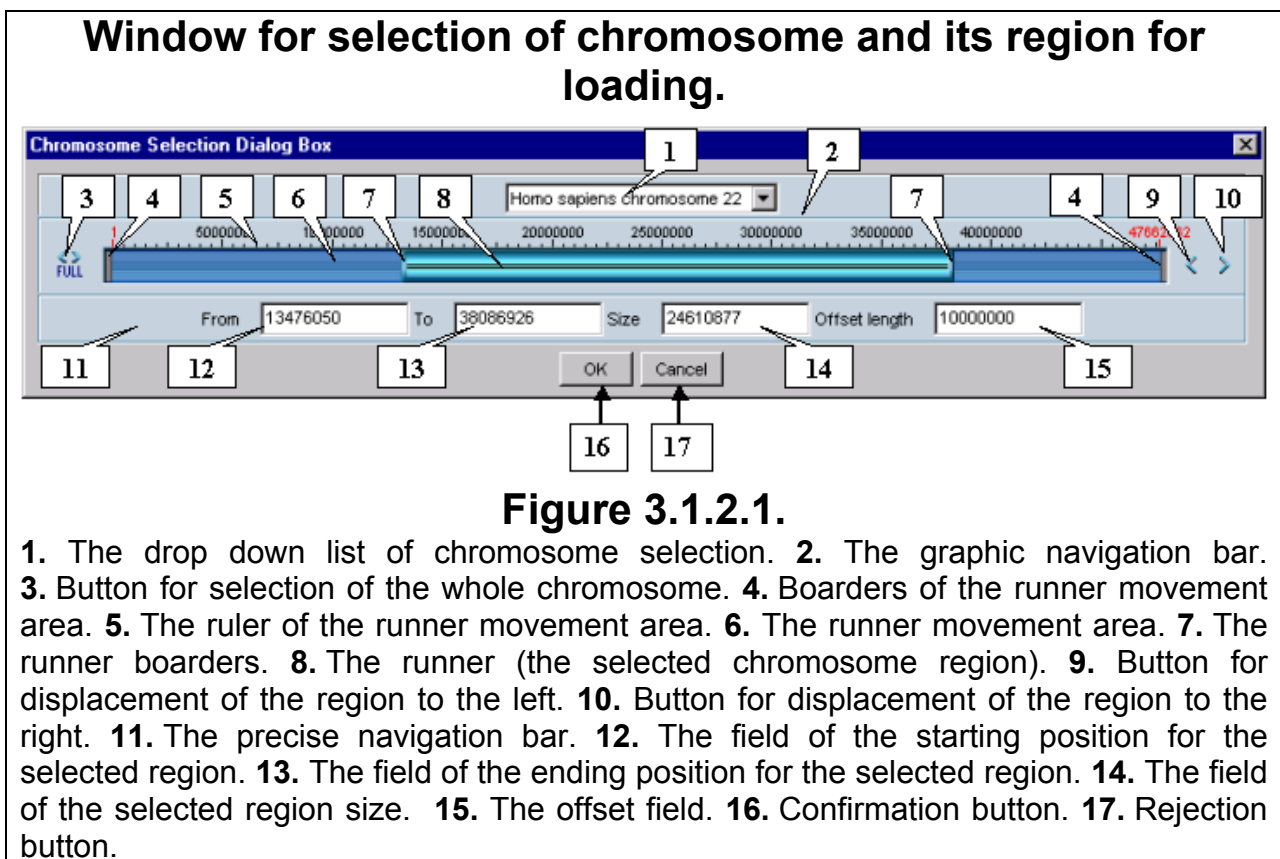
Window for selection of chromosome and its region for loading.

Figure 3.1.2.1.
1. The drop down list of chromosome selection. **2.** The graphic navigation bar. **3.** Button for selection of the whole chromosome. **4.** Boarders of the runner movement area. **5.** The ruler of the runner movement area. **6.** The runner movement area. **7.** The runner boarders. **8.** The runner (the selected chromosome region). **9.** Button for displacement of the region to the left. **10.** Button for displacement of the region to the right. **11.** The precise navigation bar. **12.** The field of the starting position for the selected region. **13.** The field of the ending position for the selected region. **14.** The field of the selected region size. **15.** The offset field. **16.** Confirmation button. **17.** Rejection button.

The region can be selected by several ways:
- Using the graphic navigation bar;
- Using the precise navigation bar;
- Using the rough and precise navigation bar.

The scale of the graphic navigation bar corresponds to the whole chromosome. The filled rectangle, which is also referred to as the runner, corresponds to the loading region (the runner boarders are not being included in this region). The graphic navigation bar doesn't allow precise definition of the loading region. For such a purpose use the precise navigation bar. At any change in the runner size the values in the precise navigation bar

fields (fields of the starting and ending positions as well as region size field) are automatically being changed in accordance to the region boarders defined in navigator. And vice versa, any changes in the precise navigation bar fields automatically lead to changes in the runner size and location.

There are several ways to change the loading region using the runner:
- To displace the region of current size presented in navigator to the right or left. To do so, pick the runner by mouse and move it in appropriate direction. On mouse click to the left or right of the runner in its movement area it will be shifted in appropriate direction for the distance corresponding to the runner's length.
- To change any of current region boarders and thus to make the region wider or shorter regarding to its left or right boarder. To do so, pick the appropriate runner's boarder by mouse and move it in appropriate direction.
- To change the region size regarding to its center. To do so, press the «Shift» key, then pick any of the runner's boarders by mouse and move it. If the runner's boarder is being moved to the center of navigator the region becomes shorter, otherwise it becomes wider.

When the choice is made press the "OK" button. Upon this the data loading will occur. The loading process is being accompanied by appearance of the information window, which contains the «Please wait while loading data» message (fig.3.1.2.2) and automatically disappears on data loading is finished. Data loading takes some time, which depends on the selected region size and loading parameters.

The loading region can be changed using the appropriate fields (starting and ending positions, and region size fields) on the precise navigation bar as well as the whole chromosome selection button and the offset buttons. There are several rules, which determine the changes in values in the fields of starting and ending positions, and region size, if such values were defined directly.
1. Input values can be automatically changed by system on their fixing (such cases described below);
2. Fixing of a value in appropriate field occurs on either "Enter" key pressing, while the cursor is within that field, or exit the field using any other way (loss of entering focus);
3. If changing of a value in one of the fields results in that the value in the ending position field is less than that in the starting position field (or vice versa), then on fixing values substitute each other.
4. If changing of values in fields of the starting/ending positions or the region size results in that any of boarders exceed those valid for current chromosome, then it is being set accordingly to the appropriate chromosome boarder.
5. At change in the region size field automatically occurs the value change in the ending position field, while the value in the starting position field remains unchanged.
6. If a value being entered in any field exceeds the maximum allowable integer value (~2'000'000'000), then on fixing this field value is being considered as false and changed to the previous one.
7. By pressing the "whole chromosome selection" button it is available to set the region's boarders corresponding to those of the chromosome, i.e. to select the whole chromosome for loading.
8. At pressing the buttons for displacement of the region's boarders to the left or right, positions of the region are being changed accordingly to a value in the offset field. A value in the offset field is a subject for changing. If displacement of the region for a given value results in exceeding the allowable chromosome boarders, then it occurs to the appropriate chromosome boarder only.

Loading of data begins on pressing the choice confirmation button. At this, the chromosome selection window disappears and, instead of it, the data loading process-indicating window (fig.3.1.2.2) appears.

Window of data loading indication.

Please wait while loading data

Figure 3.1.2.2.
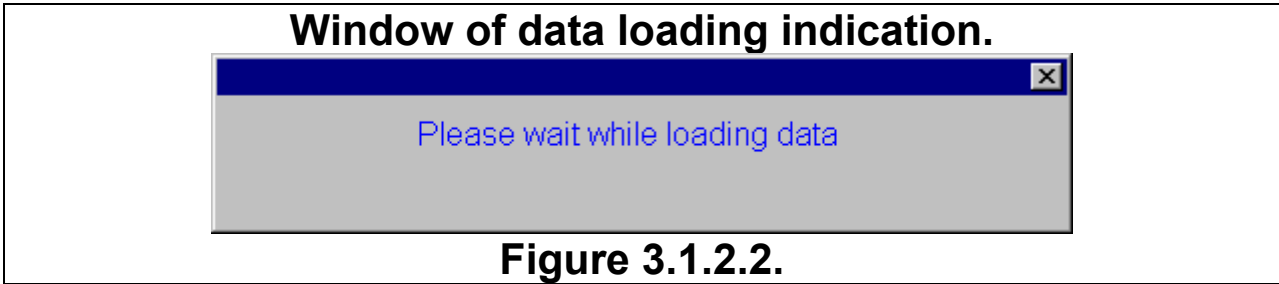
3.2. Chromosome map operating.

3.2.1. Temporal removal of feature types from being displayed on the map.

The «Features» dialog window purposed for selection of feature types for visualization (fig.3.2.1.1) can be opened using either of the following ways:

- Using the "Options->Features" commands of main menu;
- Pressing the 🖳 button on the toolbar.

In order to include or exclude a certain feature type it is required to click on it by mouse. The "Select All" button allows synchronous inclusion of all feature types, while the "Deselect All" button synchronously removes such a selection from all feature types. Upon a selection of required feature types press the "OK" button to confirm a choice. If any chromosome region had been loaded prior to, then upon a confirmation of feature types selection the map will be refreshed in accordance with such a selection.

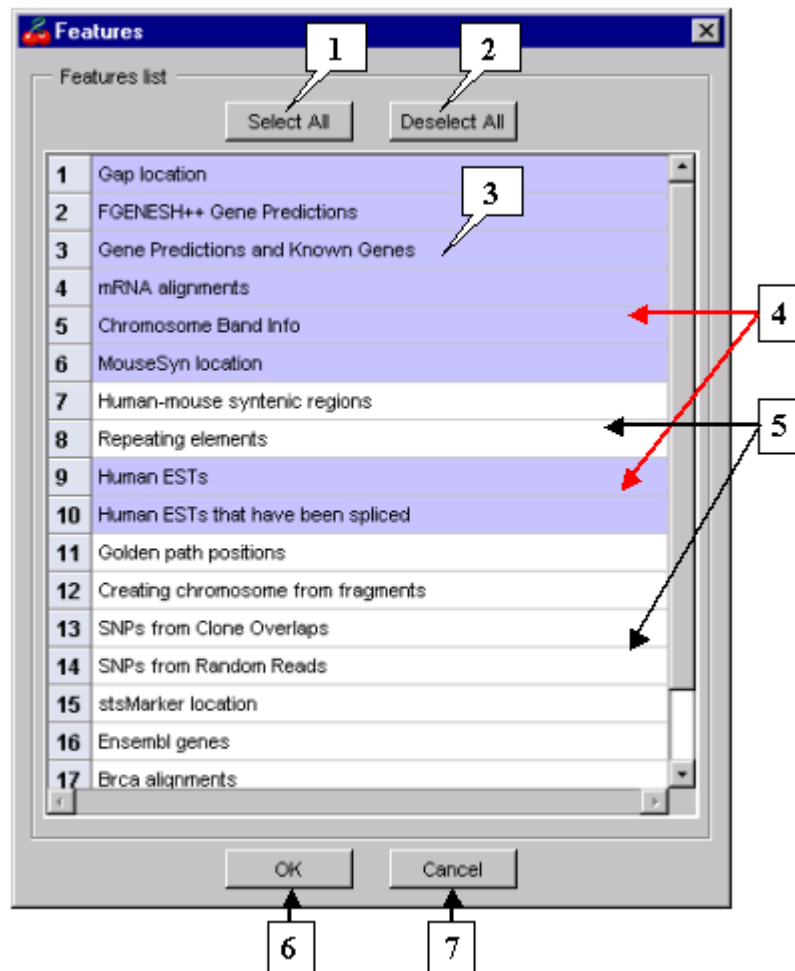## Window for selection of displayed feature types.

Figure 3.2.1.1.

1. Button for selection of all feature types. **2.** Button for deselection of all selected feature types. **3.** List of feature types to be loaded. **4.** Feature types selected to be displayed. **5.** Feature types not selected to be displayed. **6.** Confirmation button. **7.** Cancel button.

The number and order of feature types are similar both in the «Features» dialog window and in the «Load Features Types» one. If the list in the "Load Features Types" window has been changed, then automatically the same changes occur in the list in the «Features» one.

Upon the loading of a new genomic region only those feature types will be displayed, which were previously included in the display list.

3.2.2. Setting up the feature mark

In order to set a mark on a feature, select the "Mark feature" command of feature popup menu. A feature will be marked with an arrow.
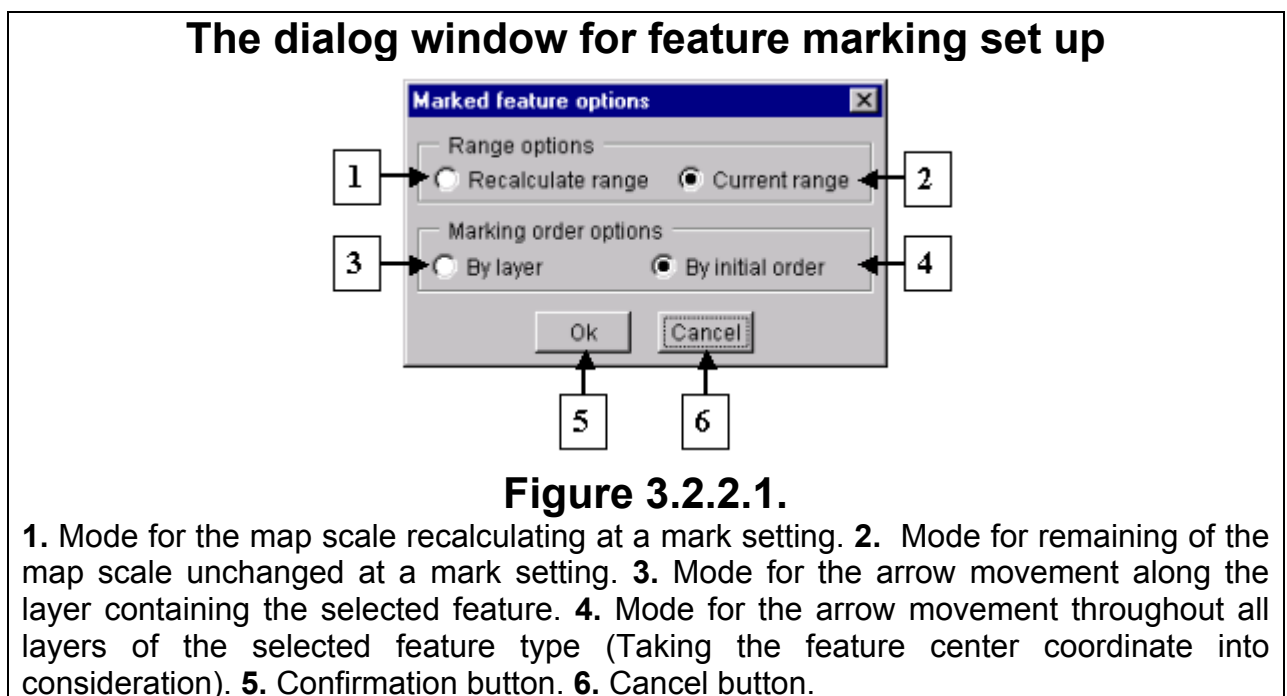
In order to move the arrow to the previous feature, press the ⬙ button.

In order to move the arrow to the next feature, press the ⬘ button.

Movement of the arrow occurs inside the loaded chromosome region and between the features of the same type only. If the marked feature is the first (last) one inside the loaded region, then the ⬙ (⬘) button becomes inactive.

The arrow movement modes can be set up in the "Marked feature options" dialog window (fig. 3.2.2.1), which in turn can be opened using the "Options>Marked feature options" command of main menu. In this dialog window the following parameters can be set up:

1. The "Range options" bar:
- The "Recalculate range" option. If this option is selected, then upon a mark setting the map scale is being changed so that a feature starts to be displayed in the center of the map and occupied the half of visible area if possible;
- The "Current range" option. If this option is selected, then upon a mark setting the map scale remains unchanged.

The dialog window for feature marking set up

Figure 3.2.2.1.
1. Mode for the map scale recalculating at a mark setting. **2.** Mode for remaining of the map scale unchanged at a mark setting. **3.** Mode for the arrow movement along the layer containing the selected feature. **4.** Mode for the arrow movement throughout all layers of the selected feature type (Taking the feature center coordinate into consideration). **5.** Confirmation button. **6.** Cancel button.

---

2. The "Marking order options" bar:

- The "By layer" option. If this option is selected, then the arrow moves along the layer containing the selected feature until the last feature of this layer is reached. Upon this, the arrow moves to the first feature of the next layer and all operations are being repeated (fig. 3.3.1.2.A);
- The "By initial order" option. If this option is selected, then the arrow moves throughout all layers of the selected feature type. In this case the order of the arrow movement is being determined by the center feature coordinates (fig.3.3.1.2.B)

Order of the marking arrow movement

A

B

Figure 3.3.1.2.

A. Order of the arrow movement in the "By layer" mode. **B.** Order of the arrow movement in the "By initial order" mode.
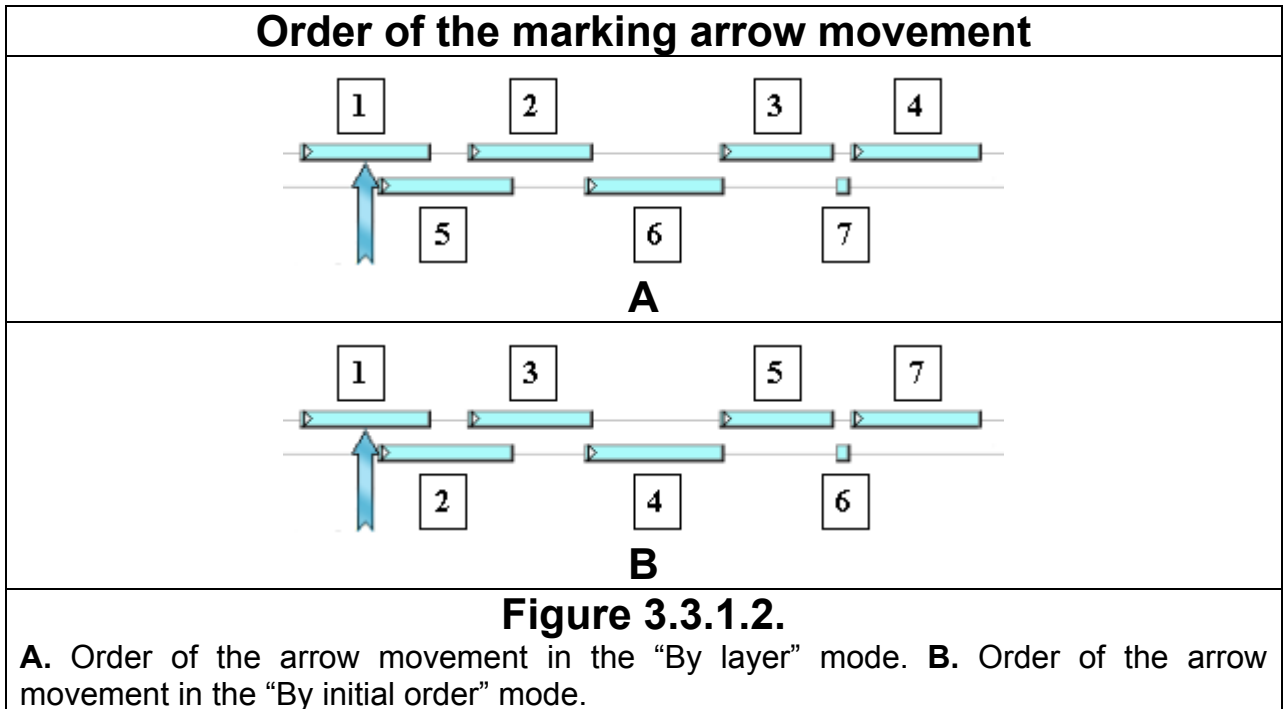
3.3. Getting information on features
3.3.1. Feature types

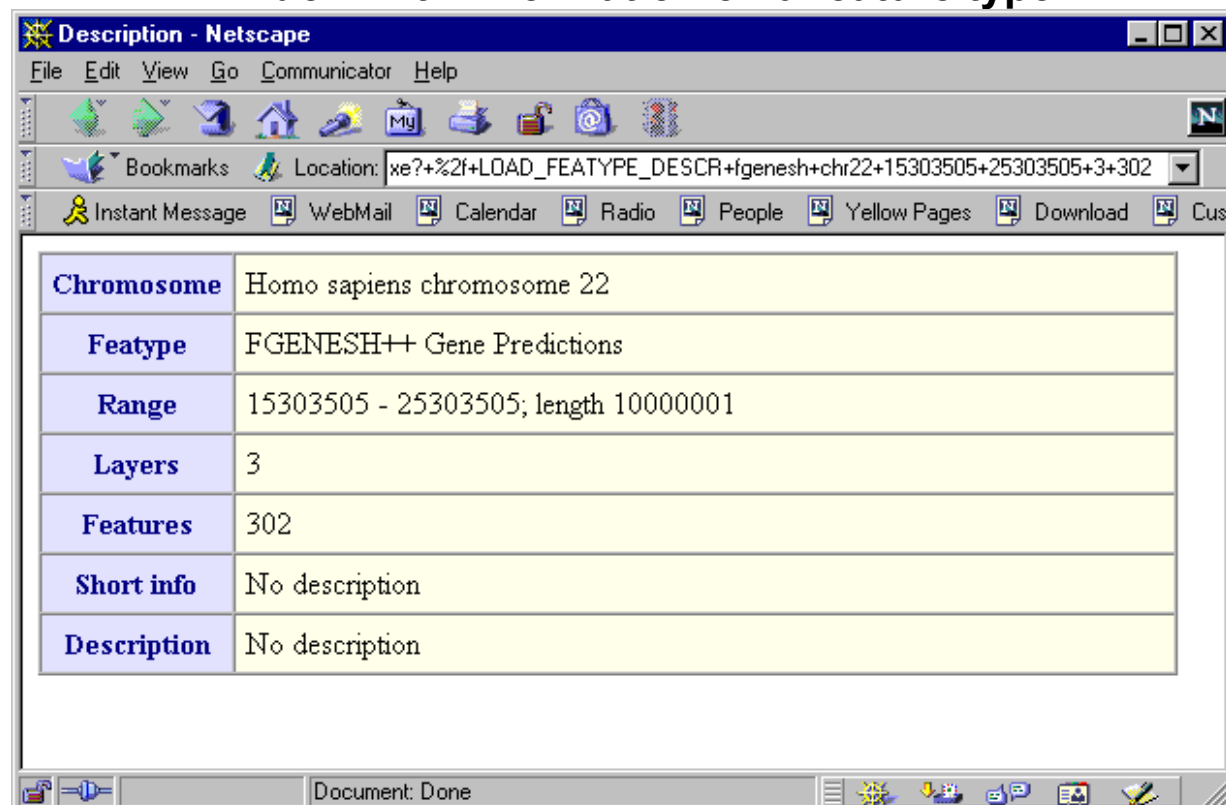In order to **get information on a features type** place the mouse pointer over a filled rectangle on either of the auxiliary map areas. At this the name of a feature or its brief description will appear in the right information bar. The mouse right-click will cause the appearance of the features type popup menu (fig.3.3.1.1). This menu contains the commands, which provide information on a feature type as well as allow changing of the feature display mode or color layout.

Feature type popup menu

Figure 3.3.1.1.

1. The command providing information on a features type. **2.** Menu for the selection of graphic data visualization mode. **3.** The command allowing the color layout set up. **4.** Mode for visualization of graphic data in a histogram manner. **5.** Mode for visualization of graphic data in a plot manner (profile diagram).
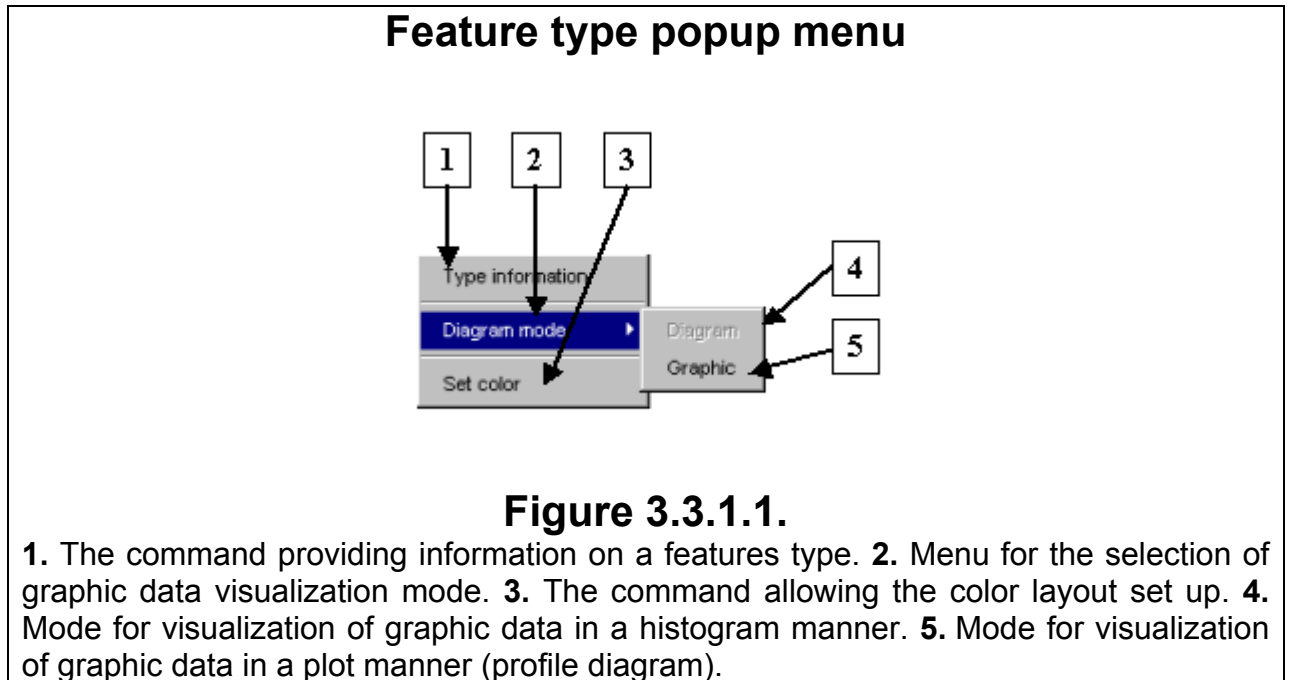
- The «Type information» command opens the window with information on a current type (fig.3.3.1.2). The data set includes the following fields: the selected chromosome, the feature type, the loaded region, the number of layers of a given type, the number of features of a given type, the brief information, the description.
- For the graphic type of features the value of any parameter for each position (nucleotide) can be defined. The «Diagram mode» command offers to show such data on features as either a histogram (the «Diagram» command) (fig.3.3.1.3a) or a plot (the «Graphic» command) (fig.3.3.1.3b). If one of the commands is selected then the remaining one is automatically being disabled, i.e. both diagram and plot can't be displayed concurrently.
- The «Set color» command opens the «Color dialog» window (see 3.10), which allows setting of a new color for feature type representation.

Window with information on a feature type

Chromosome	Homo sapiens chromosome 22
Featype	FGENESH++ Gene Predictions
Range	15303505 - 25303505; length 10000001
Layers	3
Features	302
Short info	No description
Description	No description

Figure 3.3.1.2.

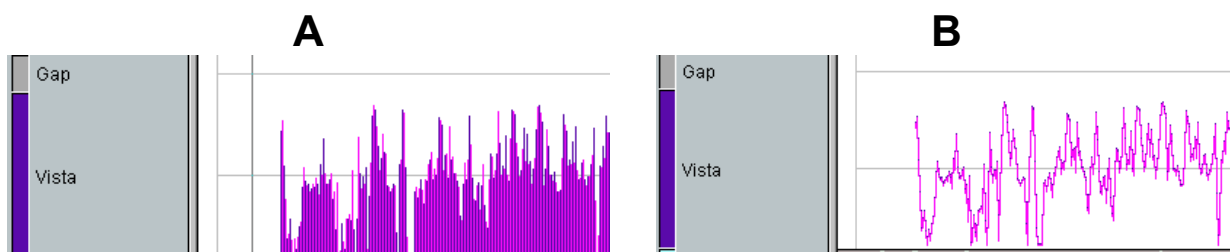## Visualization of graphic data

A   **B**

Figure 3.3.1.3.
A – Visualization of data as a histogram. **B** – Visualization of data as a plot (profile diagram).

3.3.2. Setting up visualization of features layers

The number and height of displayed feature types can be changed in accordance to a user's wish.

The window for setting up the layers output can be opened using either the "Options->Layers" command of main menu or the ⛏ button on the toolbar. In this window the following display parameters can be changed:
- The maximal number of displayed layers;
- The maximal number of layers being displayed for features in the compact mode;
- The maximal height of feature (in pixels);
- The type of layers to be displayed (all, combined or all+combined);
- The display mode (full or compact).
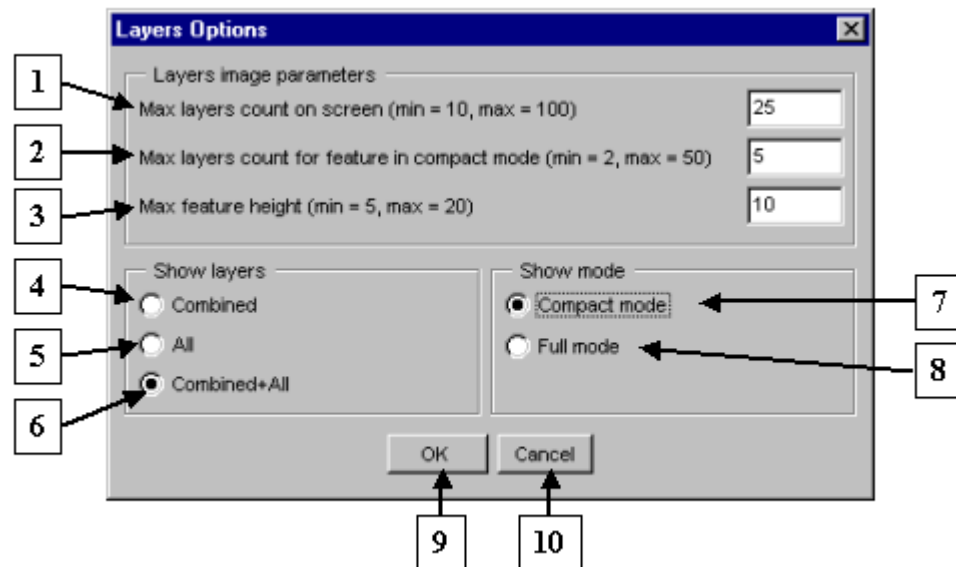
Window for setting up the layers output.

Figure 3.3.2.1.
1. The maximal number of displayed layers. **2.** The maximal number of layers being displayed for feature type in the compact mode. **3.** The maximal height of feature. **4.** Mode for display of combined layers only. **5.** Mode for display of all layers (without combined). **6.** Compact layers display mode (including combined). **7.** Compact mode for features types display. **8.** Mode for display of all feature layers. **9.** Confirmation button. **10.** Rejection button.

     Comment. If upon the made changes the visualization of layers disappeared, it means the current display resolution doesn't allow the visualization of currently set number of layers. Change the value in the "Max layers count on screen" field to a smaller one or set the higher display resolution.

     Comment. If in the "Max layers count on screen" field will be entered a value beyond the minimal or maximal allowed, then the application will automatically change it to a minimal (if entered value was lesser than minimal) or maximal (if entered value was greater than maximal) allowed one.

     If the number of layers is larger than that displayed on the map (e.g. at the compact display mode 5 layers of 946 are shown), then in the right auxiliary map area, to the left of color layout of feature types, the layers scrolling tool appears. Upon a placing of the mouse pointer over this tool the hint containing information on numbers of currently displayed layers appears (e.g. layers 70-74 of 946 available for current feature type).

     Layers can be navigated through by the following ways:
- One layer up or down using the scrolling buttons (fig.3.3.2.2);
- Several layers up or down using the scrolling wheel;
- To the first/last layer. In order to do so, click the right mouse button on the scrolling wheel and in appeared popup menu (fig.3.3.2.3) select the «First position»/«Last position» command;
- To a certain layer. In order to do so, select the «Set position» command of scrolling wheel popup menu. In the appeared dialog window (fig.3.3.2.4) enter the number of a required layer and press the «OK» button.

Layers scrolling tool.
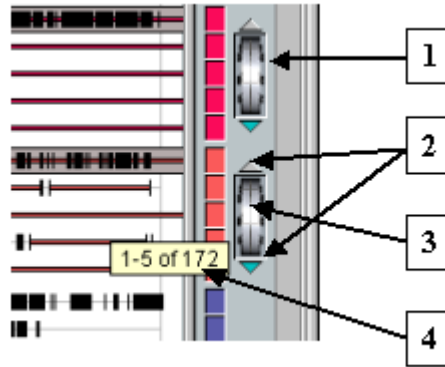
Figure 3.3.2.2.
1. Scrolling tool. **2.** Scrolling buttons. **3.** Scrolling wheel. **4.** Popup hint.
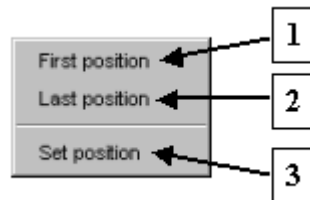
Scrolling tool popup menu.

Figure 3.3.2.3.
1. Command for jump to the first layer. **2.** Command for jump to the last layer.
3. Command for jump to a certain layer.
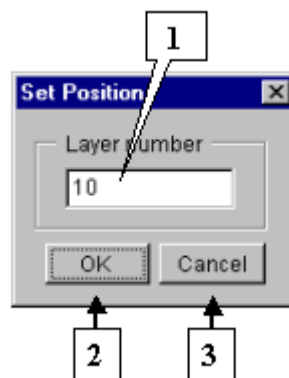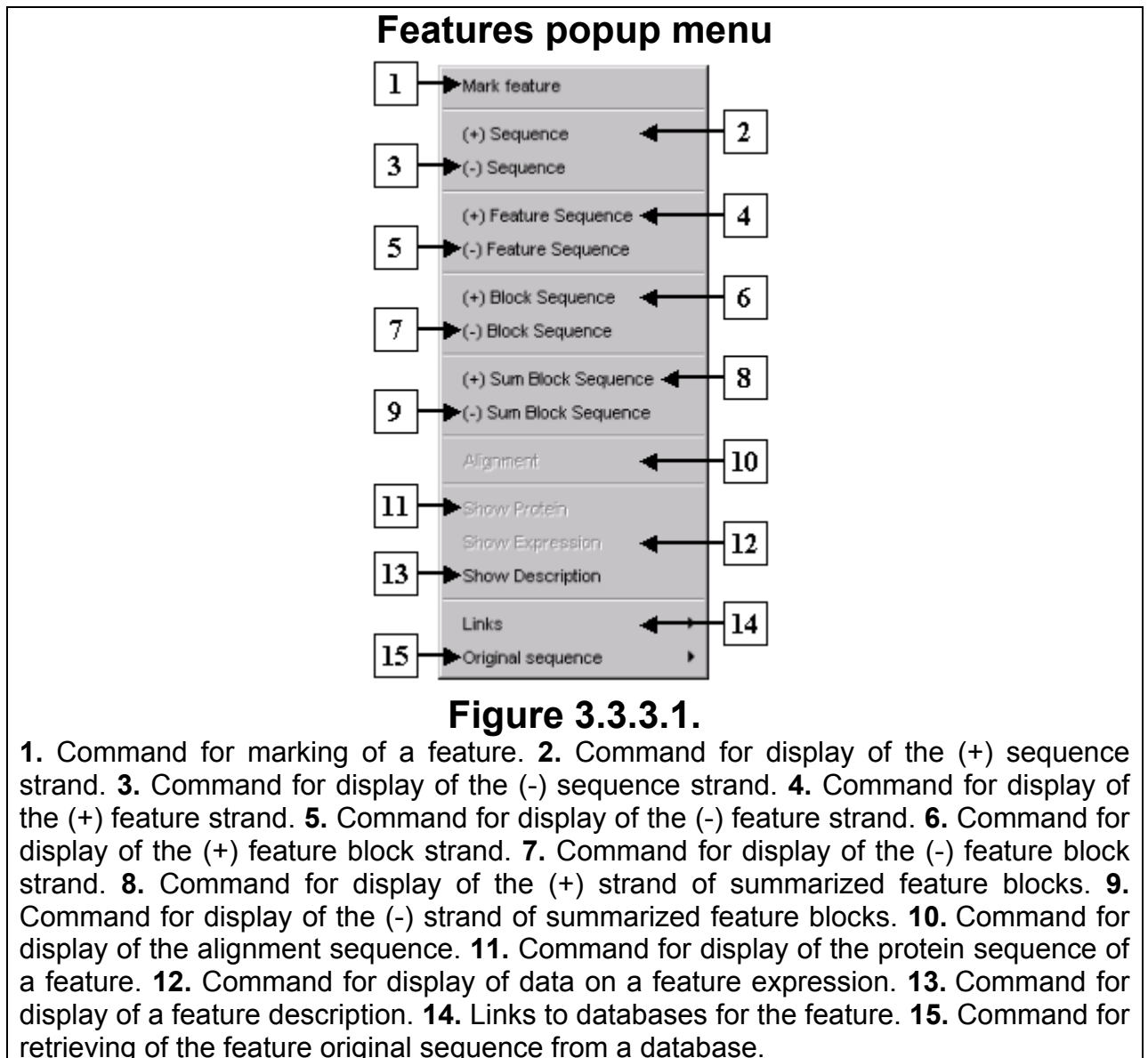
Dialog window for definition of the layer number.

Figure 3.3.2.4.
1. Field for entering of the layer number. **2.** Confirmation button. **3.** Rejection button.

3.3.3. Features popup menu.

Besides the information on a certain feature displayed in the information bar, the Softberry Genome Explorer allows retrieving of additional data on a feature of interest. Such information can be retrieved via the commands of feature popup menu (fig.3.3.3.1). This menu can be opened using the mouse right click on a feature. Some commands of this menu may be unavailable for a certain features types.

Features popup menu

Figure 3.3.3.1.

1. Command for marking of a feature. **2.** Command for display of the (+) sequence strand. **3.** Command for display of the (-) sequence strand. **4.** Command for display of the (+) feature strand. **5.** Command for display of the (-) feature strand. **6.** Command for display of the (+) feature block strand. **7.** Command for display of the (-) feature block strand. **8.** Command for display of the (+) strand of summarized feature blocks. **9.** Command for display of the (-) strand of summarized feature blocks. **10.** Command for display of the alignment sequence. **11.** Command for display of the protein sequence of a feature. **12.** Command for display of data on a feature expression. **13.** Command for display of a feature description. **14.** Links to databases for the feature. **15.** Command for retrieving of the feature original sequence from a database.

3.3.3.1. «Mark feature»

The **«Mark feature»** command makes the feature to be marked with an arrow. The ◁⇑ button moves the arrow to the previous feature of a given type, the ⇑▷ button – to the next one. Parameters of the arrow transition can be defined in the "Marked feature options" dialog window (see 3.2.2)

3.3.3.2. «Unmark feature»

The **«Unmark feature»** command removes the marking arrow from a feature.

3.3.3.3. «(+) Sequence»

The **«(+) Sequence»** command causes the (+) strand (sense strand, virulent strand) of a sequence to be displayed. This command opens the window containing the (+) strand of that chromosome region, which is currently pointed by mouse (fig. 3.3.3.3.1). Parameters of the displayed region are to be defined in the «Sequence Options» dialog window (see 3.3.4).

3.3.3.4. «(-) Sequence»

The **«(-)Sequence»** command causes the (-) strand (antisense strand, complimentary strand) of a sequence to be displayed. This command opens the window containing the (-) strand of that chromosome region, which is currently pointed by mouse (fig. 3.3.3.3.1). Parameters of the displayed region are to be defined in the «Sequence Options» dialog window (see 3.3.4).
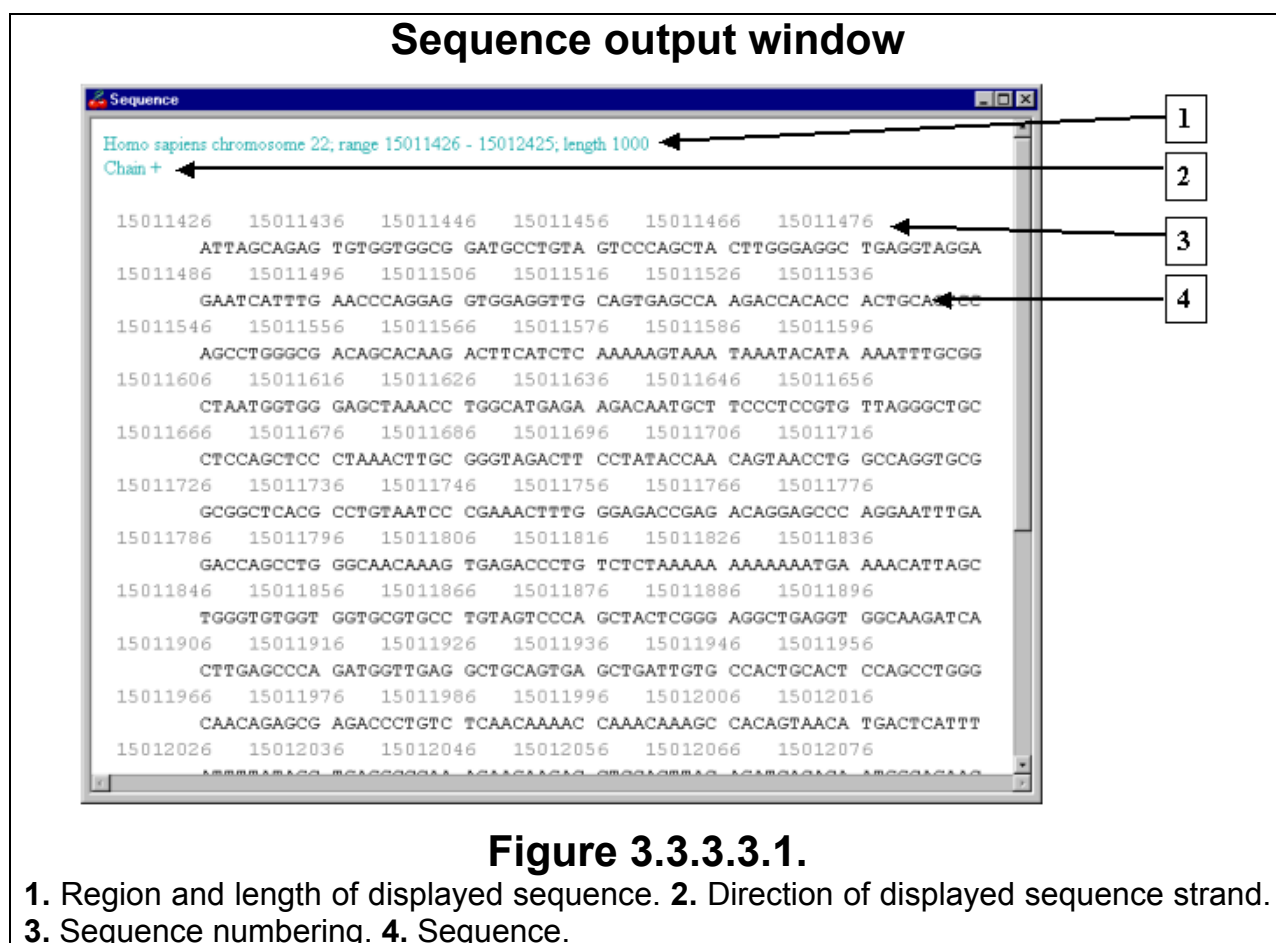

Sequence output window
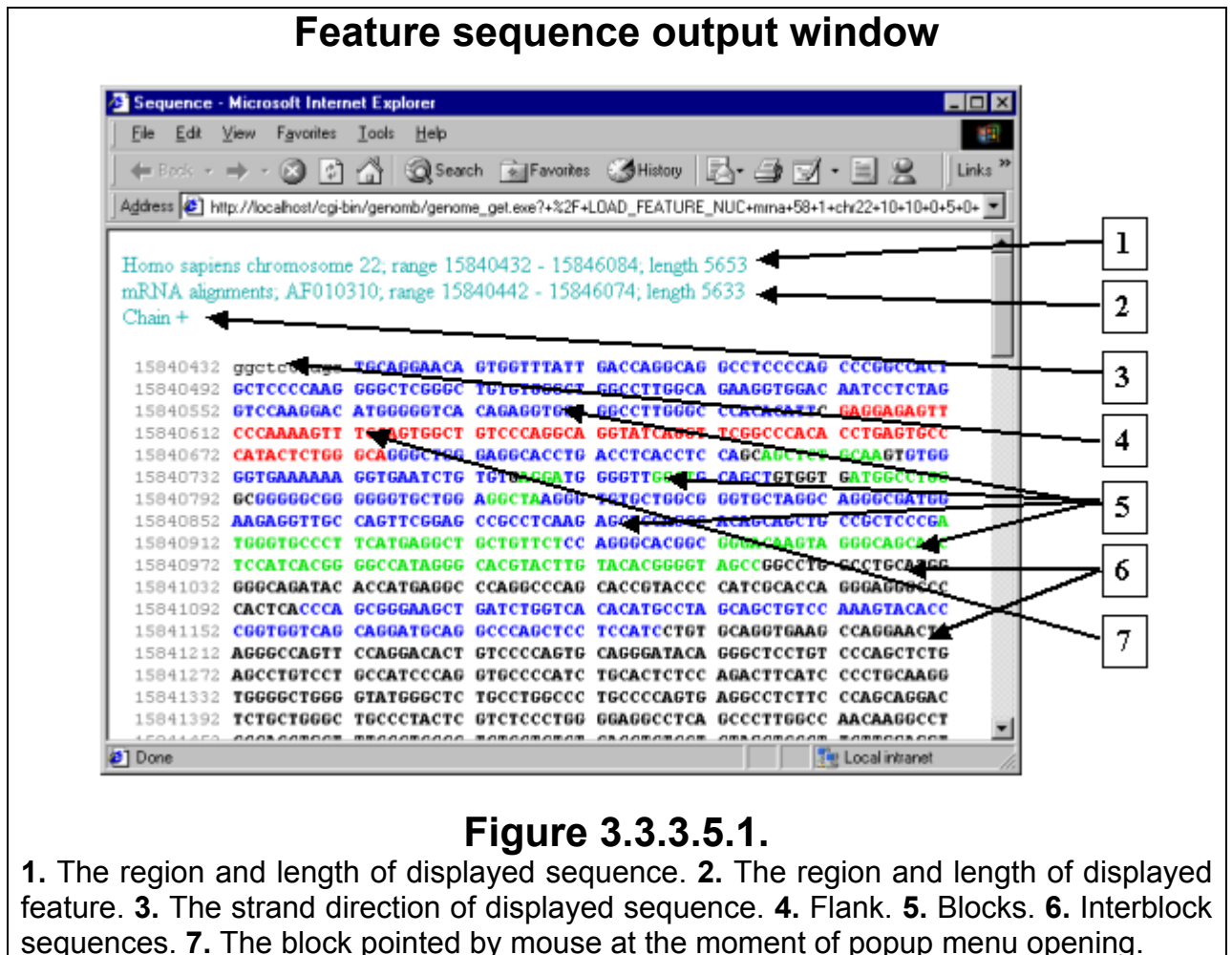
Figure 3.3.3.3.1.
1. Region and length of displayed sequence. **2.** Direction of displayed sequence strand. **3.** Sequence numbering. **4.** Sequence.

3.3.3.5. «(+) Feature Sequence»

The **«(+) Feature Sequence»** command causes the (+) strand of a feature sequence to be displayed. This command opens the window containing the (+) strand of that feature, which is currently pointed by mouse (fig.3.3.3.5.1). In the sequence output window lowercase letters are used for flanking sequences, while the sequence of a feature itself is shown in bold uppercase letters. In a feature sequence the alternating block sequences are highlighted with blue and green colors, while the interblock ones are shown in black. Red color is used to mark the block pointed at the moment of popup menu opening. In a case, when no block was pointed at the moment of popup menu opening, there is nothing marked with red color. Parameters of the output region are to be defined in the «Sequence Options» dialog window (see 3.3.4)

3.3.3.6. «(-) Feature Sequence»

The **«(-) Feature Sequence»** command causes the (-) strand of a feature sequence to be displayed. This command opens the window containing the (-) strand of that feature, which is currently pointed by mouse (fig. 3.3.3.5.1). The color layout in the sequence output window will be the same as for (+) strand. Parameters of the output region are to be defined in the «Sequence Options» dialog window (see 3.3.4).

Feature sequence output window

Figure 3.3.3.5.1.

1. The region and length of displayed sequence. **2.** The region and length of displayed feature. **3.** The strand direction of displayed sequence. **4.** Flank. **5.** Blocks. **6.** Interblock sequences. **7.** The block pointed by mouse at the moment of popup menu opening.

3.3.3.7. «(+) Block Sequence»

The **«(+) Block Sequence»** command causes the (+) strand of a feature block sequence to be displayed. This command opens the window containing the (+) strand of that feature block, which is currently pointed by mouse.

In the block sequence output window the sequence of a feature block itself will be highlighted with a color. The flanking sequence, which is a part of a feature, will be displayed in bold uppercase letters, while the flanking sequence, which is not a part of a feature, will be displayed in lowercase ones (fig. 3.3.3.7.1). Parameters of the output region are to be defined in the «Sequence Options» dialog window (see 3.3.4).

3.3.3.8. «(-) Block Sequence»

The **«(-) Block Sequence»** command causes the (-) strand of a feature block sequence to be displayed. This command opens the window containing the (-) strand of that feature block, which is currently pointed by mouse. Parameters of the output region are to be defined in the «Sequence Options» dialog window (see 3.3.4).

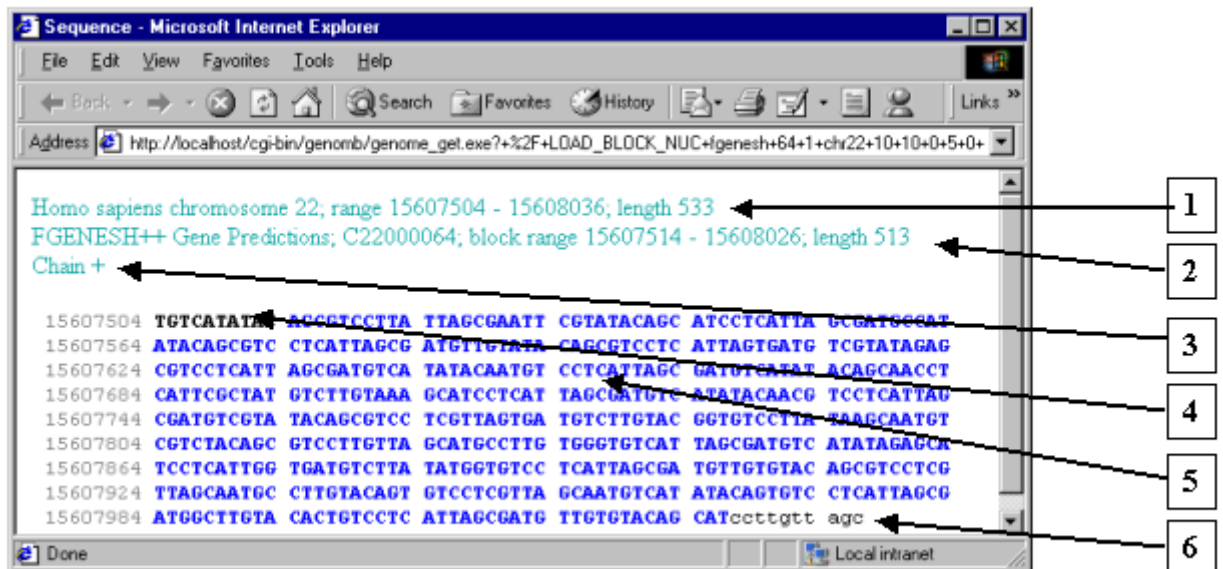**Feature block sequence output window**

Figure 3.3.3.7.1.
1. The region and length of displayed sequence. **2.** The region and length of displayed block sequence. **3.** The strand direction of displayed sequence. **4.** Flank, which is a part of a feature. **5.** Block. **6.** Flank, which is not a part of a feature.

3.3.3.9. «(+) Sum Block Sequence»

The **«(+) Sum Block Sequence»** command causes the (+) strand of a summarized (combined) feature blocks sequence to be displayed. This command opens the window containing the (+) strand of a summarized blocks sequence of that feature, which is currently pointed by mouse.

In the sequence output window the sequences of feature blocks will be displayed in bold uppercase letters and alternating blue and green colors (fig. 3.3.3.9.1), while the flanking sequence will be displayed in lowercase ones. Parameters of the output region are to be defined in the «Sequence Options» dialog window (see 3.3.4).

3.3.3.10. «(-) Sum Block Sequence »

The **«(-) Sum Block Sequence»** command causes the (-) strand of a summarized feature blocks sequence to be displayed. This command opens the window containing the (-) strand of a summarized blocks sequence of that feature, which is currently pointed by mouse. Parameters of the output region are to be defined in the «Sequence Options» dialog window (see 3.3.4).

3.3.3.11. «Alignment»

The **«Alignment»** command opens the window containing the obtained alignment results (for details see 3.7).

3.3.3.12. «Show Protein»

The **«Show Protein»** command opens the «Protein» dialog window containing the information on a feature and the sequence of a protein encoded by this feature (fig. 3.3.3.12.1).

Protein sequence output window

Chromosome	Homo sapiens chromosome 22
Feature	Gene Predictions and Known Genes
Range	17013602 - 17014508; length 907
Chain	Chain +
ID	C.ctg22fin3-000000.19.0
Description	C.ctg22fin3-000000.19.0
Protein	METDESPSPLPCGPAGEAVMESRARPFQALPREQSPPPPLQTSSGAEVMDVGSGGDGQSE LPAEDPFNFYGASLLSKGSFSKGRLLIDPNCSGHSPRTARHAPAVRKFSPDLKLLKDVKI SVSFTESCRSKDRKVLYTGAERDVRAECGLLLSPVSGDVHACPFGGSVGDGVGIGGESAD KKDEENELDQEKRVEYAVLDELEDFTDNLELDEEGAGGFTAKAIVQRDRVDEEALNFPYE VCWQPLL

Figure 3.3.3.12.1.

3.3.3.13. «Show Expression»

The **«Show Expression»** command opens the dialog window containing the data on a feature expression (see 3.9).

3.3.3.14. «Show Description»

The **«Show Description»** command opens the «Description» dialog window containing the following information on a feature (fig.3.3.3.14.1):

Feature description window

Chromosome	Homo sapiens chromosome 1
Feature	FGENESH++ Gene Predictions
Range	10388843 - 10403127; length 14285
Chain	Chain -
ID	C1000189
Short info	gi|8923303|ref|NP_060236.1| hypothetical protein FLJ20321 [Homo sapiens] ## 1044
Description	Not available

Figure 3.3.3.14.1.

- The chromosome, which contains the feature;
- The name of the feature type;
- The numbers of the first and the last feature positions and the length of the feature;
- The strand direction (if available);
- ID (if available);

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- If for a given feature the description is available on a server, then two additional points will be displayed:
  1. The brief information on a feature;
  2. The description of a feature.

Upon a placing of the mouse pointer over a feature image the detailed data on this feature will be shown in the information bar windows.

3.3.3.15. «Links»

The **«Links»** menu contains the list of links to web servers containing additional information on a current feature (fig. 3.3.3.15.1, 3.3.3.15.2). If no links available this menu remains inactive, otherwise the list of available links is displayed.
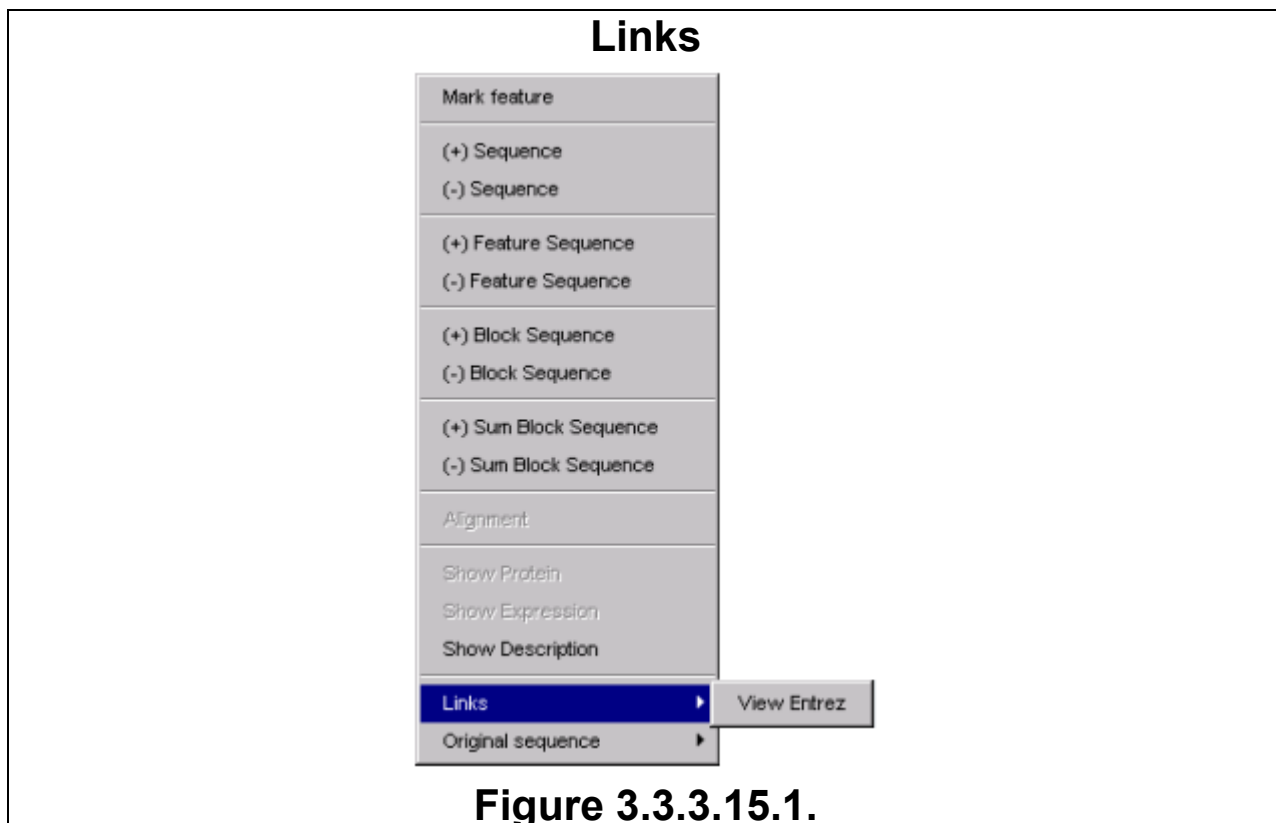

Figure 3.3.3.15.1.
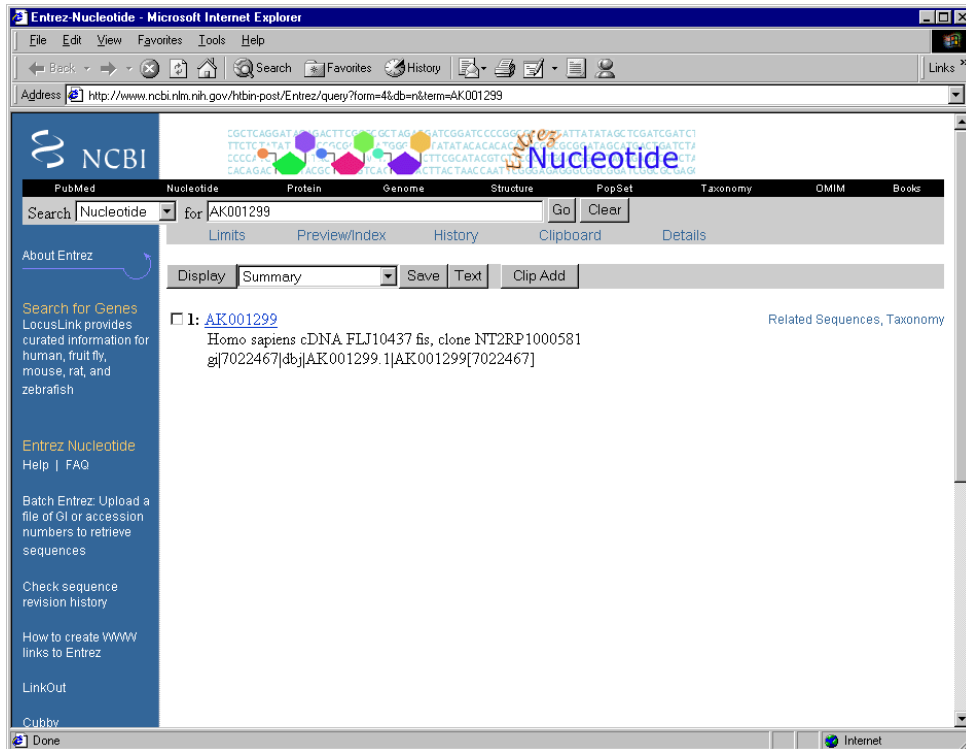
Enter to the "NCBI" database.

Figure 3.3.3.15.2.

3.3.3.16. «Original Sequence»

The **«Original Sequence»** menu provides the possibility to load the original feature sequence from a database (there are may be several links to databases). During the data loading process the information window is being displayed (fig. 3.3.3.16.1). As the data loading is finished, the «Get Alignment» dialog window appears. The retrieved sequence in FASTA-format is being displayed in the «Sequence» field of this window and the ID of a feature, to which the loaded sequence belongs, is shown in the «Current alignment» one (fig. 3.3.3.16.2). It allows the immediate aligning of the loaded feature sequence to be made. The operating the «Get Alignment» window is described in the chapter 3.7, «Getting alignment».
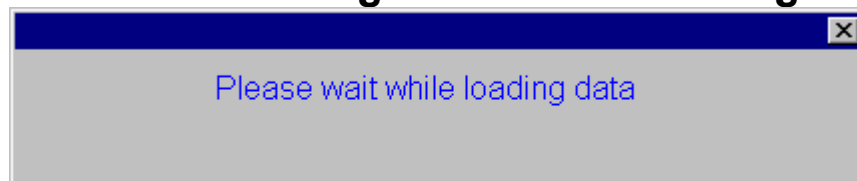
The data loading information message.

Please wait while loading data

Figure 3.3.3.16.1.

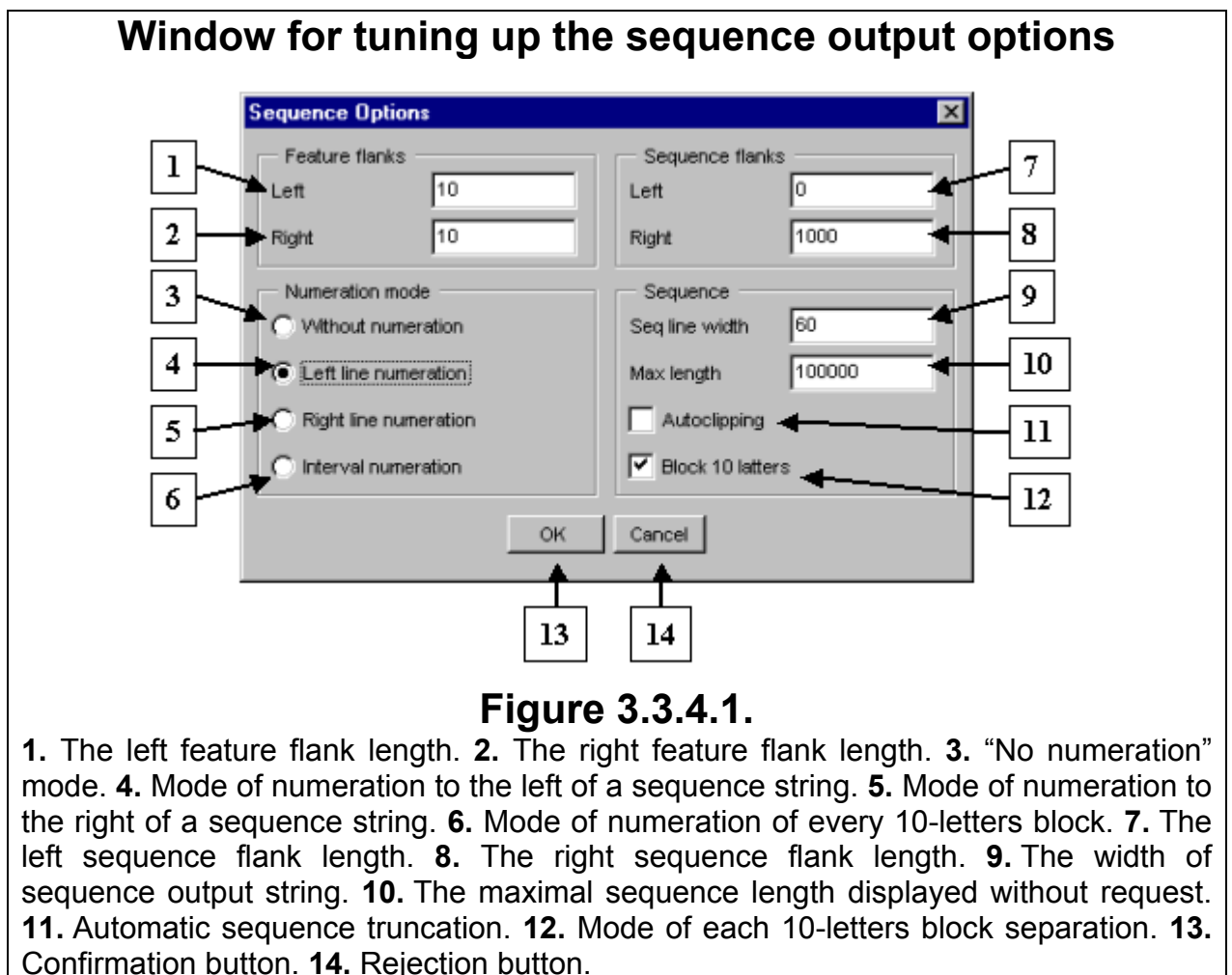# Original feature sequence.

Figure 3.3.3.16.2.
1. Feature ID. **2.** The original feature sequence loaded from a database.
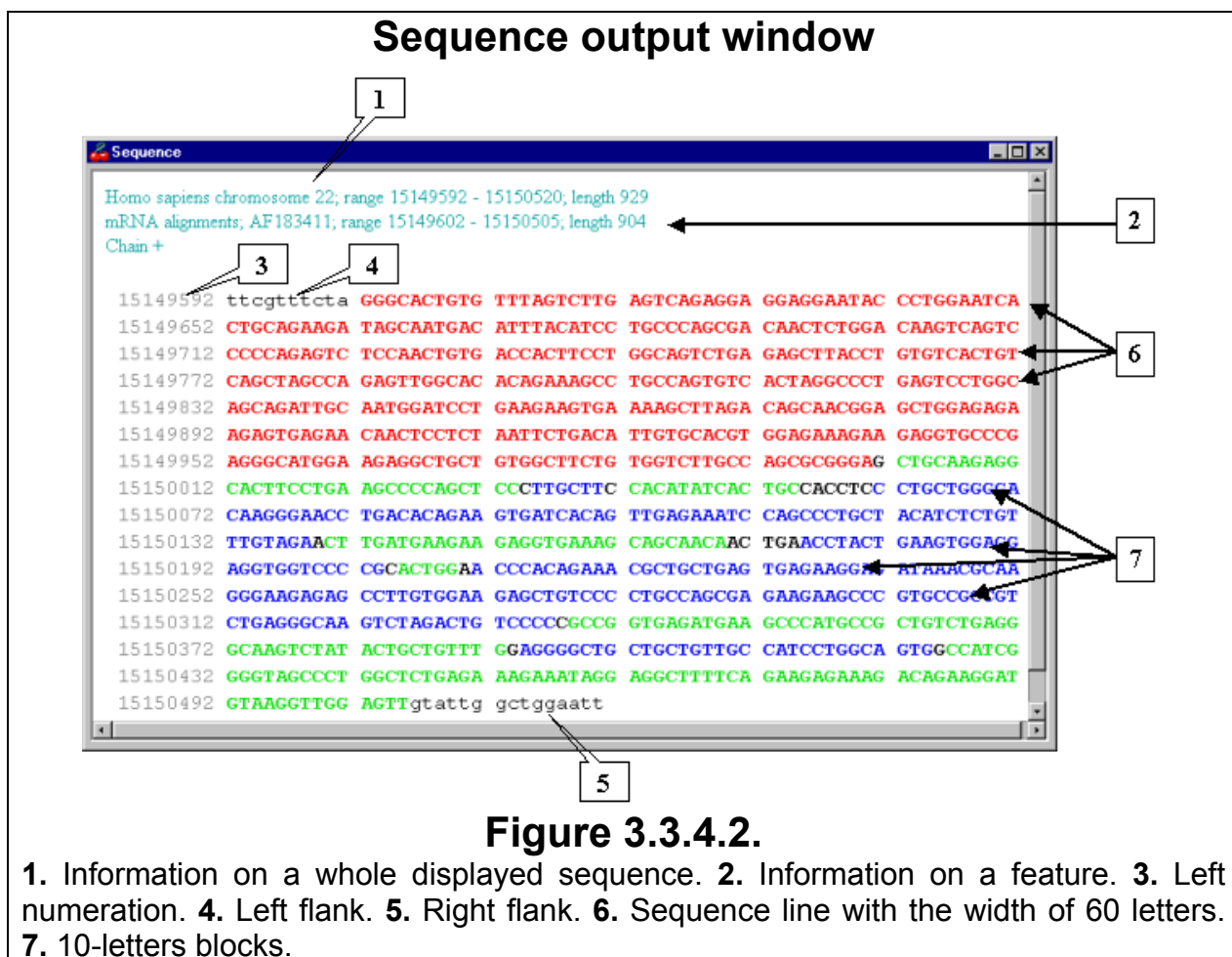
3.3.4. Tuning up the sequence output options

The dialog window for changing the sequence output options can be opened using either the «Options->Sequence» command of main menu, or the ⚒ button on the toolbar. In the appeared «Sequence Options» dialog window the following parameters can be defined (fig.3.3.4.1):

1. The lengths of the right and left flanking sequences for either a feature (in the «Feature flanks» fields), or a sequence, which was pointed by mouse at the moment of the popup menu opening (in the «Sequence flanks» fields). If a feature (or a sequence) is located in the very beginning or ending of a chromosome, then the length of one of flanks will be zero.
2. The sequence «Numeration mode». Using the switches the following modes can be selected:
   - No numeration;
   - Put the numeration to the left of a sequence string;
   - Put the numeration to the right of a sequence string;
   - To numerate every 10-letters block (the position numbers are being placed above the first, eleventh, twenty first etc. positions).
3. The required width of a sequence output string. It requires the entering of an appropriate value into the «Seq line width» field. In order to get a sequence in a single line set the string width to zero.

Window for tuning up the sequence output options

Figure 3.3.4.1.

1. The left feature flank length. **2.** The right feature flank length. **3.** "No numeration" mode. **4.** Mode of numeration to the left of a sequence string. **5.** Mode of numeration to the right of a sequence string. **6.** Mode of numeration of every 10-letters block. **7.** The left sequence flank length. **8.** The right sequence flank length. **9.** The width of sequence output string. **10.** The maximal sequence length displayed without request. **11.** Automatic sequence truncation. **12.** Mode of each 10-letters block separation. **13.** Confirmation button. **14.** Rejection button.

4. The maximal length of displayed sequence. It requires the entering of an appropriate value into the «Max length» field. Если в поле введен 0, последовательность выводится в виде одной строки.
5. The mode for automatic sequence truncation. It requires the checking in the «Autoclipping» checkbox. The sequence will be shortened up to the length defined in the «Max length» field.
6. Placing of a gap after every 10-letters block. It requires the checking in the «Block 10 letters» checkbox.

The fig. 3.3.4.2 shows the way of feature sequence visualization, which occurs at parameters set in the «Sequence options» window as shown on fig. 3.3.4.1.

Figure 3.3.4.2.

1. Information on a whole displayed sequence. **2.** Information on a feature. **3.** Left numeration. **4.** Left flank. **5.** Right flank. **6.** Sequence line with the width of 60 letters. **7.** 10-letters blocks.

Comment. If the length of displayed sequence is larger than that defined in the «Max length» field, then, on a request to display a sequence, the «Long sequence» dialog window (window of request for a long nucleotide sequence display) will appear. It proposes either to cut the sequence up to the defined length, or to display the complete sequence (fig. 3.3.4.3). In order that sequence was always truncated up to the defined length, it requires the checking in the «Autoclipping» checkbox of the sequence output tuning window. Pressing of the «Cancel» button will cause the rejection of sequence display.

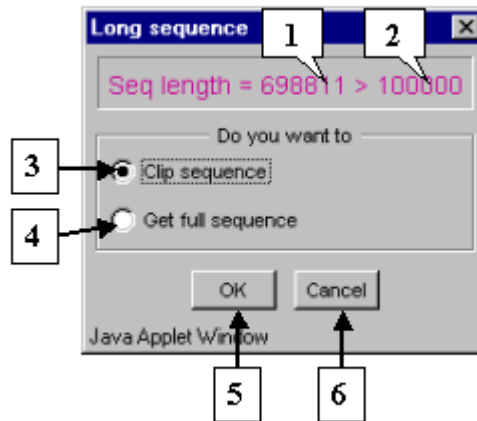# Window of request for a long nucleotide sequence display.

Figure 3.3.4.3.

1. The length of a sequence to be displayed. **2.** The maximal sequence length displayed without request. **3.** Sequence truncation option. **4.** The whole sequence display option. **5.** Confirmation button. **6.** Rejection button.

3.4. Feature search

Softberry Genome Explorer provides the facilities for search for a feature in any genome region. Moreover, a wide set of features types can be used in a search. A feature can be searched for by the following fields: feature ID, feature description or brief information on it.

3.4.1. "Find Feature" dialog window

The "Find Feature" dialog window (fig.3.4.1.1) can be opened using either of the following means:

- Selecting the "Search->Find Feature" command of main menu.
- Pressing the 🔍 button on the toolbar.
- The <Ctrl+F> hot keys.

On the search is done, its parameters and results are automatically being saved.

In the upper part of the window there is the «Saved searches» drop down list of the previously saved search requests IDs. On a selection of one of IDs, parameters of this request become displayed in the window. The «Remove» button allows a single request to be deleted from the list. The «Remove all» button allows all requests to be deleted from the list. On a pressing of any of these buttons, an appropriate of two dialog windows (fig.3.4.1.2 A, B) appears.

Below the «Saved searches» list there is the field with the current request ID («Current search name»).

The «Chromosomes» list contains the names of chromosomes available for searching in.

The «Features» list contains the names of features types available for searching for.

In the lower part of features search window there are the "Match" and "Search attributes" panels, purposed for setting the search parameters.

The "Match" panel contains the search modes switches:

- "Match word start" – search for string start.
- "Match whole word only" – precise search for string.
- "Match substring" - search for substring.

The " Search attributes" panel contains:

- "Find what" – field for definition of the search value.
- "Find in" – drop down list for selection of the field (ID (Label), Short info, Description), to be searched by.
- "Match case" – checkbox for turning on/off the symbol case sensitivity.
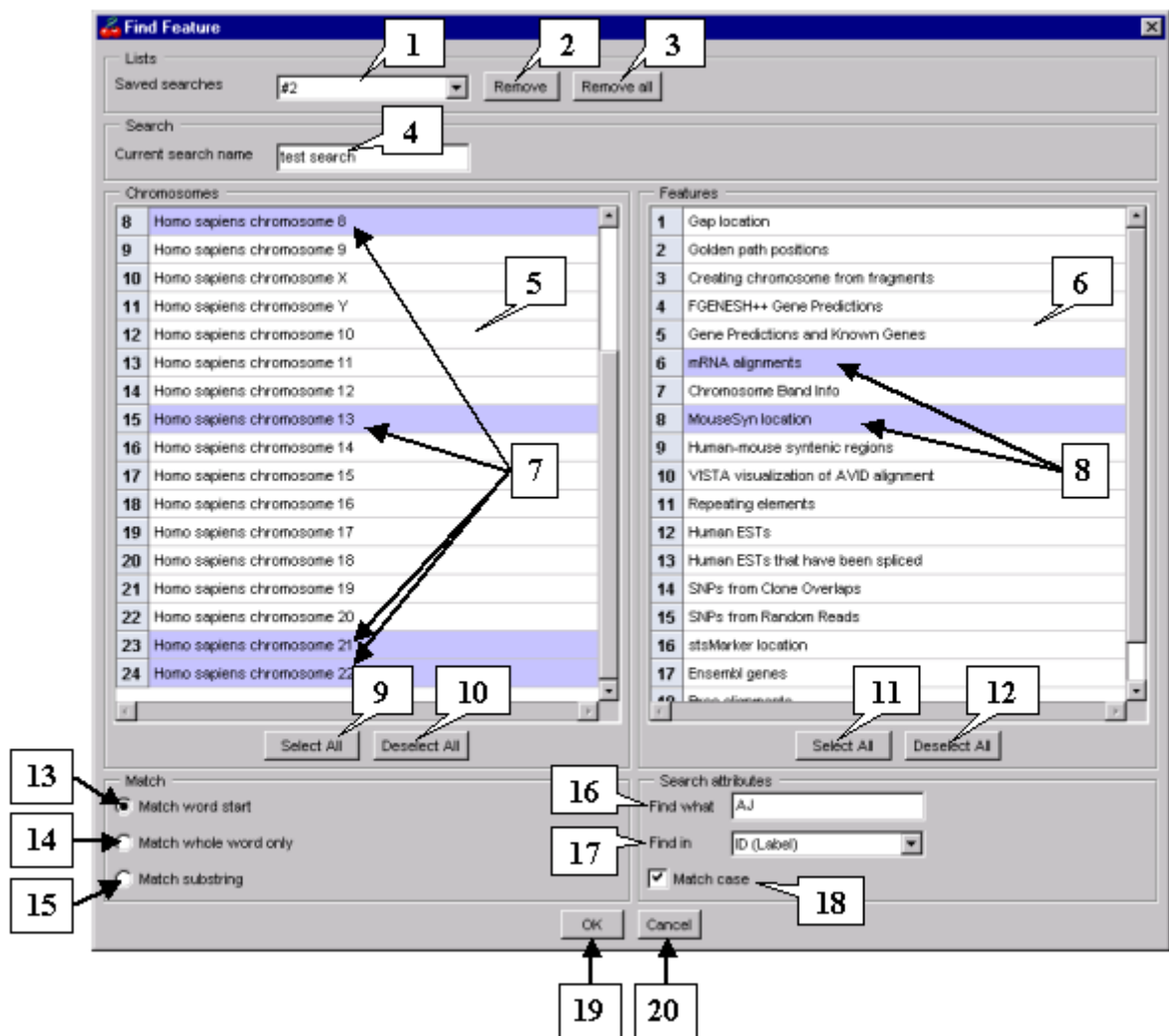
Feature search dialog window.

Figure. 3.4.1.1.

1. Drop down list with IDs of saved search results. **2.** Button for removing of a single search result from the list. **3.** Button for removing of all search results from the list. **4.** Field for ID of the current search request. **5.** List of chromosomes. **6.** List of feature types. **7.** Chromosomes, selected to be searched in. **8.** Feature types, selected to be searched for. **9.** Button for inclusion of all chromosomes in a search list. **10.** Button for exclusion of all chromosomes from a search list. **11.** Button for inclusion of all feature types in a search list. **12.** Button for exclusion of all feature types from a search list. **13.** String start search mode. **14.** Precise string search mode. **15.** Substring search mode. **16.** Field for definition of the search value. **17.** Drop down list for selection of the field, to be searched by. **18.** Turn on/off a symbols case sensitivity in a search. **19.** Start search button. **20.** Cancel search and close window button.

Dialog windows with requests for saved search results removal confirmation

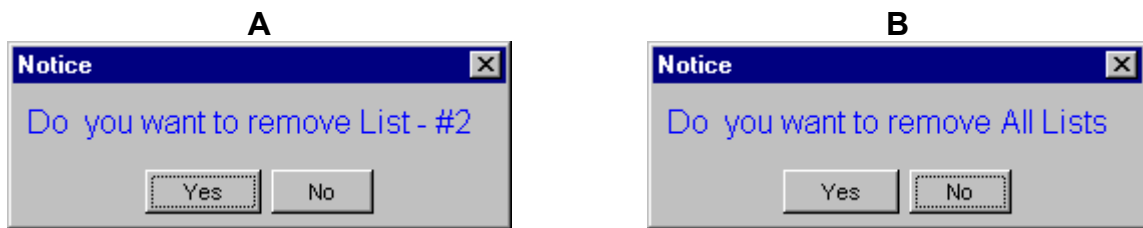A   B

Figure. 3.4.1.2.

A. Request for removing of a single result. **B.** Request for removing of all results.

To make a search do the followings:

1. Enter the search request name into the «Current search name» field. If a request with this name already exists, then results of a new search will be written over the old ones.
2. Select the chromosomes, which will be searched for a feature, by the clicking on appropriate chromosomes names (recurring click removes selection). The «Select all» and «Deselect all» buttons allow all chromosomes to be selected or unselected respectively at the time.
3. Select the types of features, to be searched for, by the clicking on appropriate ones (recurring click removes selection). The «Select all» and «Deselect all» buttons allow all features types to be selected or unselected respectively at the time.
4. Select the search mode (precise string search, string start search, substring search) (fig.3.4.1.1).
5. Enter the search value into the "Find what" field.
6. Select the field, by which a feature to be searched for, from the "Find in" drop down list (fig.3.4.1.3). The following fields are available: feature ID, brief information on a feature, feature description.

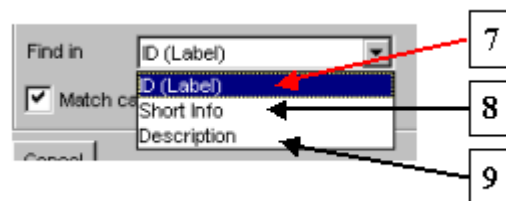
Drop down list of the search attributes.

Figure. 3.4.1.3.

1. ID. **2.** Brief information. **3.** Description.

7. Check in/out the symbols case sensitivity checkbox («Match case»).
8. Press the «OK» button.
9. On this is done, the window, containing the message on data searching process, appears (fig.3.4.1.4).

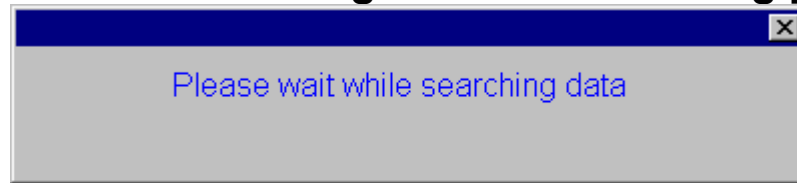## Window with the message on data searching process

Figure. 3.4.1.4.

10. On the search is done, the window with the message on a number of found features, meeting the search request parameters, appears (fig. 3.4.1.5).

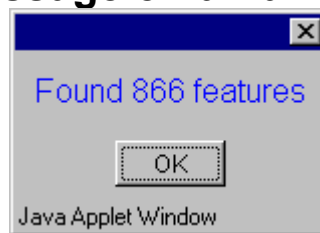## Window with the message on a number of found features

Figure. 3.4.1.5.

11. Pressing the «OK» button causes the "Found Features List" to appear.

3.4.2. Found features list

In the upper part of the "Found Features List" window (fig. 3.4.2.1) there are the drop down list of search results IDs and the field with the ID of feature, loaded on the main window map.

The "Found Features List" window contains two tabs:

- The "Features map" tab is purposed for visualization of the search results.
- The "Features list" tab is purposed for visualization of found features in the manner of a list.

3.4.2.1. "Features map" tab

The "Features map" tab consists of three parts: the chromosomes map, the found features map and the information bar.

3.4.2.1.1. Chromosomes map

The map of chromosomes provides the general visualization of the search results. Chromosomes on the map are shown as rectangles. Height of a rectangle is proportionate to a corresponding chromosome length. Inside of a rectangle the features, found in an appropriate chromosome, are depicted in accordance to their localization on the chromosome. Above a rectangle the number of features, found in an appropriate chromosome, is displayed, below a rectangle – the chromosome brief name.

If the "All" button is pressed, then all chromosomes are shown on the map of chromosomes. Chromosomes, in which features were found, are marked with a color. Chromosomes, in which features were not found, are colorless. If the button is not pressed, then only those chromosomes, in which features were found, are shown on the map.

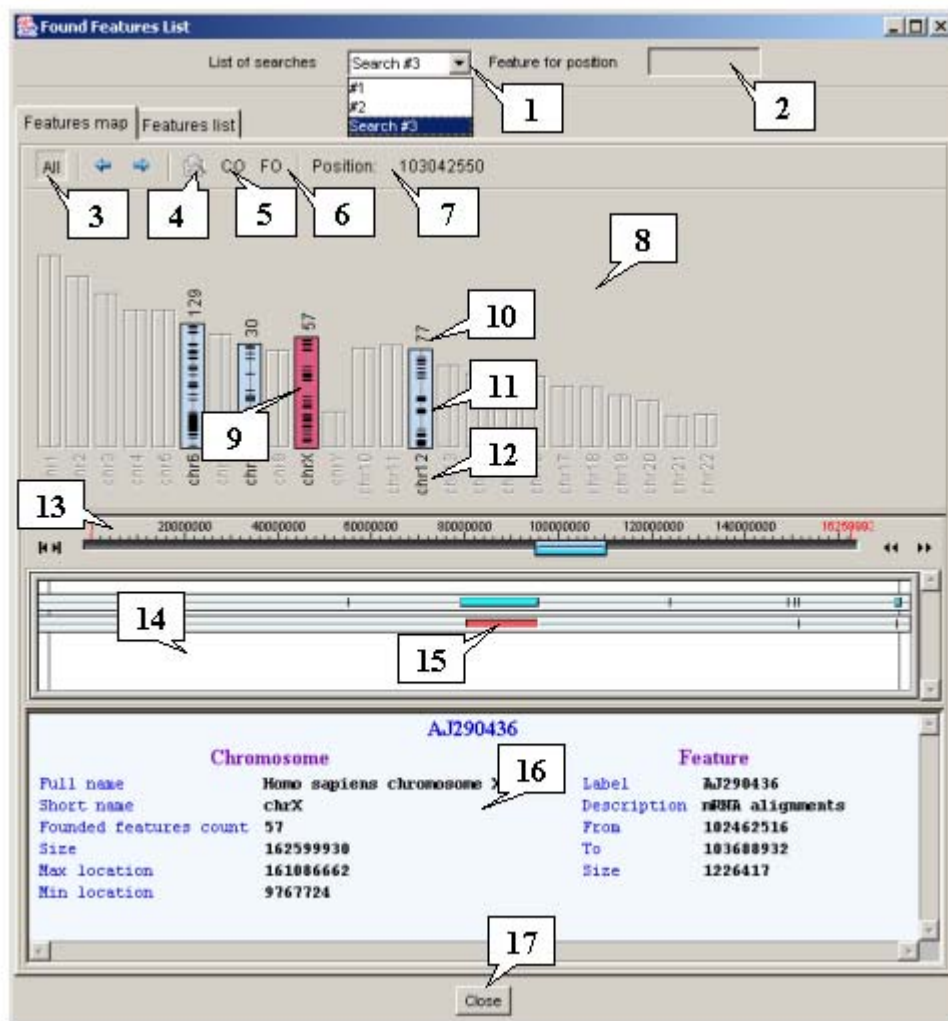## "Found Features List" dialog window, "Features map" tab

Figure. 3.4.2.1.

1. List of search results IDs. **2.** Field with the ID of feature, loaded on the main window map. **3.** Switch between the chromosomes visualization modes. **4.** Button for visualization of the selected feature visibility range. **5.** Button for opening of the chromosomes map settings dialog window. **6.** Button for opening of the features map settings dialog window. **7.** Current position of the mouse pointer on the features map. **8.** Chromosomes map. **9.** Chromosome, selected for visualization on the map. **10.** Number of features, found in a chromosome. **11.** Found features. **12.** Brief chromosome name. **13.** Features map control bar. **14.** Features map. **15.** Selected feature. **16.** Information bar. **17.** Close window button.

Parameters for visualization of the chromosome map elements are to be defined in the "Options" dialog window (see 3.4.2.1.2), which can be opened by pressing the CO button.

In order to select a chromosome for visualization, click the mouse left button on the chromosome of interest. The chromosome will be selected, and features, found in this chromosome, will be displayed on the features map.

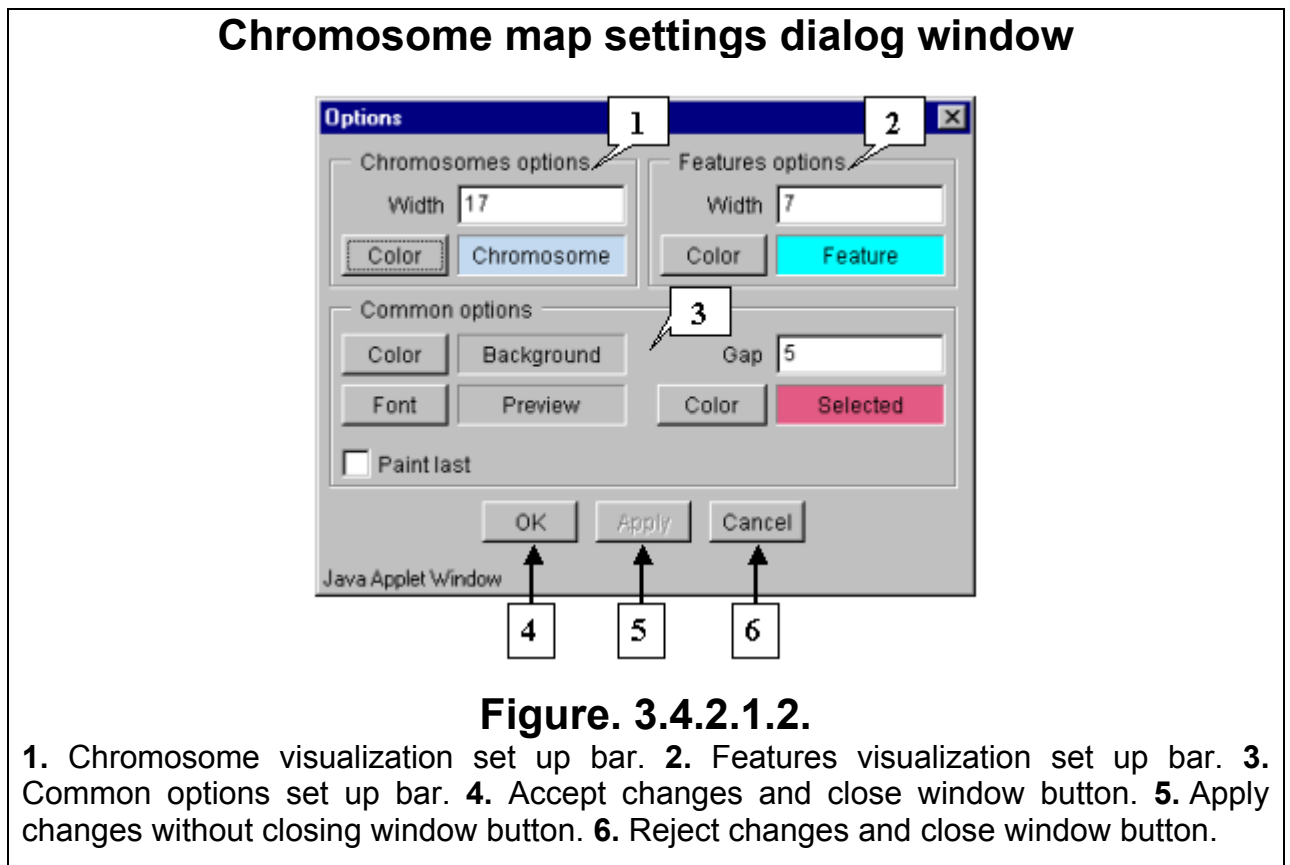### 3.4.2.1.2. Chromosome map settings dialog window.

The "Options" dialog window (fig.3.4.2.1.2), purposed for setting up the parameters of the chromosome map, can be opened using the CO button.

In this window the following parameters can be changed:

Chromosomes visualization set up bar ("Chromosomes options"):

- The "Width" field allows the width (in pixels) of a rectangle, representing a certain chromosome, to be set.
- The «Color» button allows the color of a chromosome to be set. On the button is pressed, the "Color dialog" window, purposed for the color selection, is opened. The selected color is displayed on the "Chromosome" preview bar.

Features visualization set up bar ("Features options"):

- The "Width" field allows the width (in pixels) of a feature to be set.
- The «Color» button allows the color of a feature to be set. On the button is pressed, the "Color dialog" window, purposed for the color selection, is opened. The selected color is displayed on the "Feature" preview bar.

Chromosome map settings dialog window

Figure. 3.4.2.1.2.

1. Chromosome visualization set up bar. **2.** Features visualization set up bar. **3.** Common options set up bar. **4.** Accept changes and close window button. **5.** Apply changes without closing window button. **6.** Reject changes and close window button.

Common options set up bar ("Common options"):

- The «Color» button to the left of the "Background" preview bar allows the background color of the chromosomes map to be set. On the button is pressed, the "Color dialog" window, purposed for the color selection, is opened. The selected color is displayed on the "Background" preview bar.
- The «Font» button allows the font for the chromosomes map legends to be selected. On the button is pressed, the "Font" window, purposed for the font selection, is opened. The selected font is displayed on the preview bar.
- The "Gap" field allows the definition of the space (in pixels) between chromosomes.
- The «Color» button to the left of the "Selected" preview bar allows the color of the selected chromosome to be set. On the button is pressed, the "Color dialog" window, purposed for the color selection, is opened. The selected color is displayed on the "Selected" preview bar.

- The "Paint last" checkbox. If it is not checked in, then only those columns are displayed, which can be completely fit into the chromosomes map area. Differently, the last visible column is also displayed.

Dialog window control buttons:
- "OK" – accept the selected options and close the window.
- "Apply" – apply the selected options without closing the window.
- "Cancel" – reject all selected options and close the window.

3.4.2.1.3. Features map

The map provides visualization of the features, located on a selected chromosome, and selection of loading feature. If features of the same type overlap each other, then they are displayed in multiple layers, one below another.

Selection of the displayed chromosome region and scaling of the image can be carried out using:
- The graphic navigation bar. The bar operating means are the same as that of the main application window (see chapter 2.6).
- The mouse and control keys (if the "Map navigation" checkbox of the "Options" dialog window is checked in) as described in 2.5. At enabled "Repaint on drag" the map redrawing occurs on the mouse movement. Differently, it occurs on the mouse button releasing only

The central part of the map area corresponds to coordinates of the selected for visualization region. Beyond the restriction lines only those features are displayed, which are in the selected region, but extend beyond its boarders.

If the pointer is in the central part of the map area, then in the «Position» field the current position of the pointer on a chromosome is displayed. Differently, the «Position» field contains multiple dashes only.

If the "Navigation line" mode is enabled, then the current pointer position on the map is marked with the vertical line, which never goes beyond the restriction lines.

To select a feature, click the mouse left button on it. On this is done, the feature will be highlighted with a color (color can be set in the "Options" dialog window (see 3.4.2.1.4), which can be opened by pressing the FO button). The selected feature will automatically be selected in the list on the "Features list" tab.

The ⇐ button allows the jump to the previous map position.

The ⇒ button allows the jump to the next map position.

The button allows the visualization of the selected feature visibility range.

The popup menu of the features map can be opened by clicking the mouse right button on the map. It contains the following commands:
- To position – load a selected feature.
- Select all – select all features.
- Deselect all – remove a selection from all features.
- Sample sequence – retrieve the sequences of selected features.
- Copy – copy the selected feature to the editable list of features.

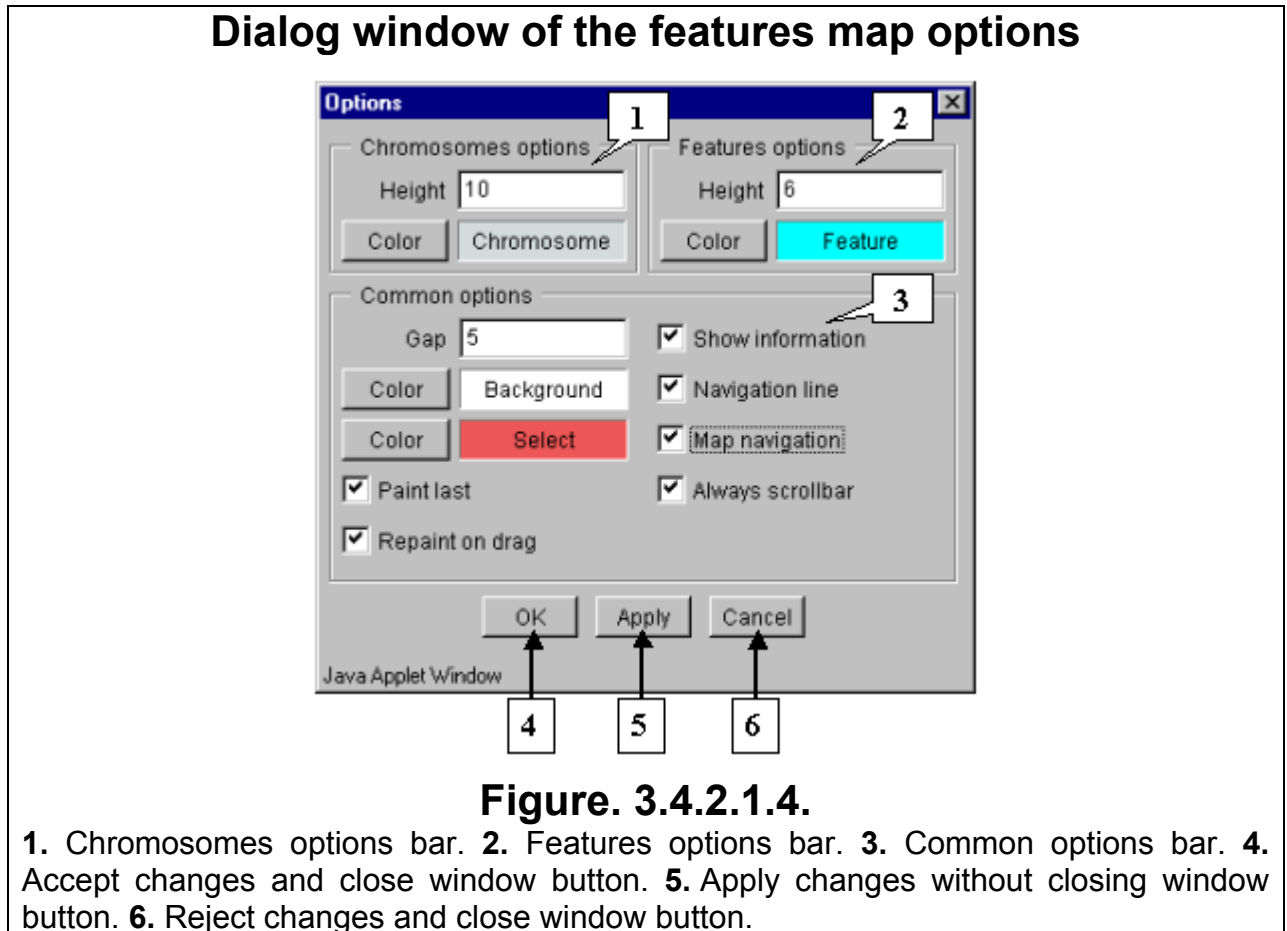### 3.4.2.1.4. Dialog window of the features map options.

The "Options" dialog window (fig.3.4.2.1.4), purposed for setting up the features map visualization parameters, can be opened using the FO button.

In this window the following options can be changed:

Bar for setting up the chromosome visualization options ("Chromosomes options"):
- The "Height" field allows the definition of features layers height (in pixels).

- The «Color» button allows the visualization color for features layers to be set. On the button is pressed, the "Color dialog" window, purposed for the color selection, is opened. The current color is displayed on the "Chromosome" preview bar.

Bar for setting up the features visualization options ("Features options"):
- The "Height" field allows the definition of features height (in pixels).
- The «Color» button allows the visualization color for features to be set. On the button is pressed, the "Color dialog" window, purposed for the color selection, is opened. The current color is displayed on the "Feature" preview bar.

Dialog window of the features map options

Figure. 3.4.2.1.4.

1. Chromosomes options bar. **2.** Features options bar. **3.** Common options bar. **4.** Accept changes and close window button. **5.** Apply changes without closing window button. **6.** Reject changes and close window button.

Bar for setting up the common visualization options ("Common options"):
- The "Gap" field allows the definition of the space (in pixels) between layers.
- The «Color» button and the "Background" field allow the map background color to be set. On the button is pressed, the "Color dialog" window, purposed for the color selection, is opened. The current color is displayed on the "Background" preview bar.
- The «Color» button and the "Select" field allow the selected feature color to be set. On the button is pressed, the "Color dialog" window, purposed for the color selection, is opened. The current color is displayed on the "Select" preview bar.
- The "Paint last" checkbox. If it is not checked in, then only those layers are displayed, which can be completely fit into the map area. Differently, the last visible layer is also displayed.
- The "Repaint on drag" checkbox. If it is checked in, then map redrawing occurs simultaneously with movement of the mouse pointer at pressed mouse left button. Differently, it occurs on a releasing of the mouse left button.

- The "Show information" checkbox. If it is checked in, then information on a feature automatically becomes displayed in the information bar on a placing of the mouse pointer over the feature. Differently, it becomes displayed on a click on the feature.
- The "Navigation line" checkbox. If it is checked in, then the vertical line (line of the current horizontal position), which moves along with the mouse pointer, becomes displayed in the map window. Differently, the line of the current horizontal position remains invisible.
- The "Map navigation" checkbox. If it is checked in, then the visual navigation on the map by mouse becomes available. Differently, it does not work and for navigation use the map toolbar (fig.3.4.2.1).
- The "Always scrollbar" checkbox. If it is checked in, then the scrolling lines are always displayed. Differently, they are displayed only when there is no room on the map for all layers of found features.

Dialog window control buttons:
- "OK" – accept the selected options and close the window.
- "Apply" – apply the selected options without closing the window.
- "Cancel" – reject all selected options and close the window.

3.4.2.1.5. Information bar

The information bar is purposed for display of the following information:
- On a chromosome, currently targeted by the mouse pointer on the chromosomes map: full and brief names, number of found in this chromosome features, size, positions of the first and last localized features.
- On a feature: information on a chromosome, in which a given feature was found, ID of a feature, its type, the starting and ending positions, size a feature.

If in the dialog window of the map options ("Options") the "Show information" checkbox is checked in, then on the information bar the information on a feature automatically becomes displayed on the placing of mouse pointer over the feature. Differently, the information becomes displayed on the mouse click only.

The popup menu of the information bar can be opened by the mouse right click and contains the following commands:
- "Save target as…" – N/A in the current version.
- "Copy" – copy the selected information to the clipboard.
- "Select all" – select the whole information, displayed on the bar.

3.4.2.2. "Features list" tab

The "Features list" tab (fig. 3.4.2.2.1) contains the list of found features. In this list the following items are indicated: the name of chromosome, in which a feature is localized, type of a feature, the feature starting and ending positions on a chromosome and ID of a feature.

Feature can be selected from the list by mouse left click. If one or more features located in the same chromosome are selected in the list, then at the "Features map" tab occurs the following:
- The chromosome, to which selected feature(s) belongs, becomes selected on the chromosome map;
- The first of the selected features becomes displayed on the features map;
- Data on this feature become displayed on the information bar.

If selected features belong to different chromosomes, then the features map and information bar become empty, and chromosomes do not become selected on the chromosomes map.

The popup menu of the list can be opened by the mouse right click on it and contains the following commands:

- To position – load the selected feature.
- Select all – select all features.
- Deselect all – remove selection from all features.
- Sample sequence – retrieve the sequences of selected features.
- Copy – copy the selected feature to the editable layer of features.

"Found Features List" dialog window, "Features list" tab
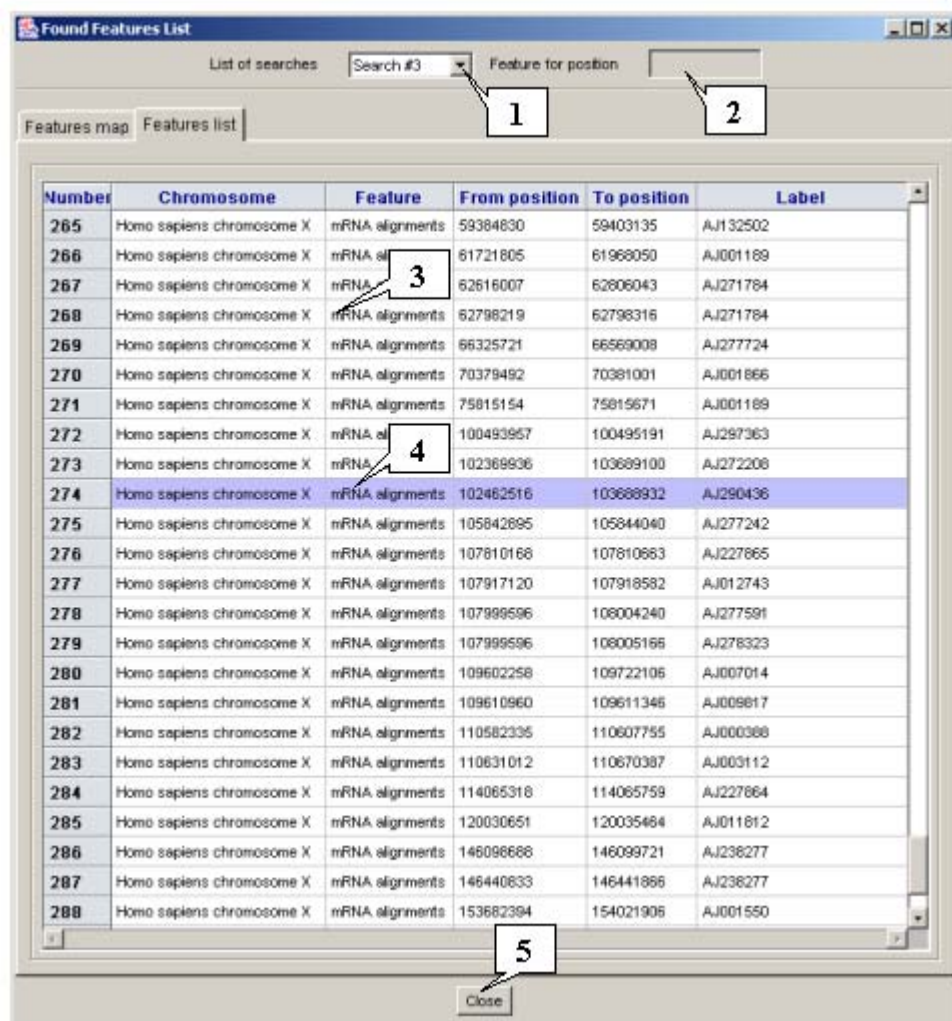
Figure. 3.4.2.2.1.

1. Drop down list of search requests IDs. **2.** Field with the ID of the feature, loaded on the map of the main application window. **3.** List of found features. **4.** Selected feature. **5.** Close button.

3.4.2.3. The "Found Features List" dialog window control buttons

- The "Close" button makes the "Found Features List" window to be closed with the following return to the main application window.

3.4.2.4. "Found Features List" window operating order

3.4.2.4.1. Feature loading

In order to load one of found features the following operations are required:

1. To select a feature using one of following means:
   - On the "Features map" tab of the chromosome map select the chromosome, in which the required feature is localized. Layers of found in the chromosome features will be displayed on the features map. Select the required feature and click the left mouse button.
   - On the "Features list" tab feature can be selected from the list by mouse left click (selection can be removed by recurring mouse left click).
   Comment. Feature, selected on the "Features list" tab, is automatically being selected on the "Features map" one.
   Comment. Feature, selected on the "Features map" tab, is automatically being selected on the "Features list" one.
2. To open the popup menu of the map or list of features and select the "To position" command.
3. The window with message on data loading (fig. 3.4.2.4.1.1) will appear.
4. The selected feature will be displayed on the map of main application window. Location of the feature will be marked with the pointing arrow (fig. 3.4.2.4.1.2). The ⬆ button on the toolbar allows switch of this arrow on and off.
   Comment. Size of the loading chromosome region, in which the selected feature is localized, can be defined in the "Side intends options" dialog window, which, in turn, can be opened using the "Options>Flanks" command of main menu.

Window of data loading message

Please wait while searching data
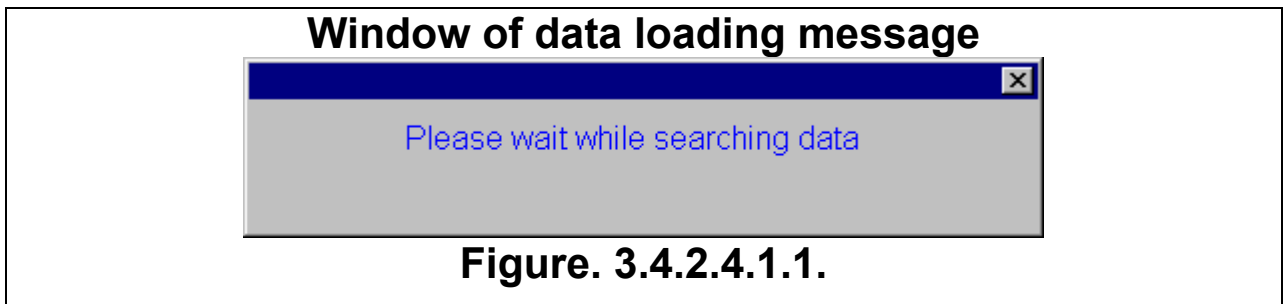
Figure. 3.4.2.4.1.1.
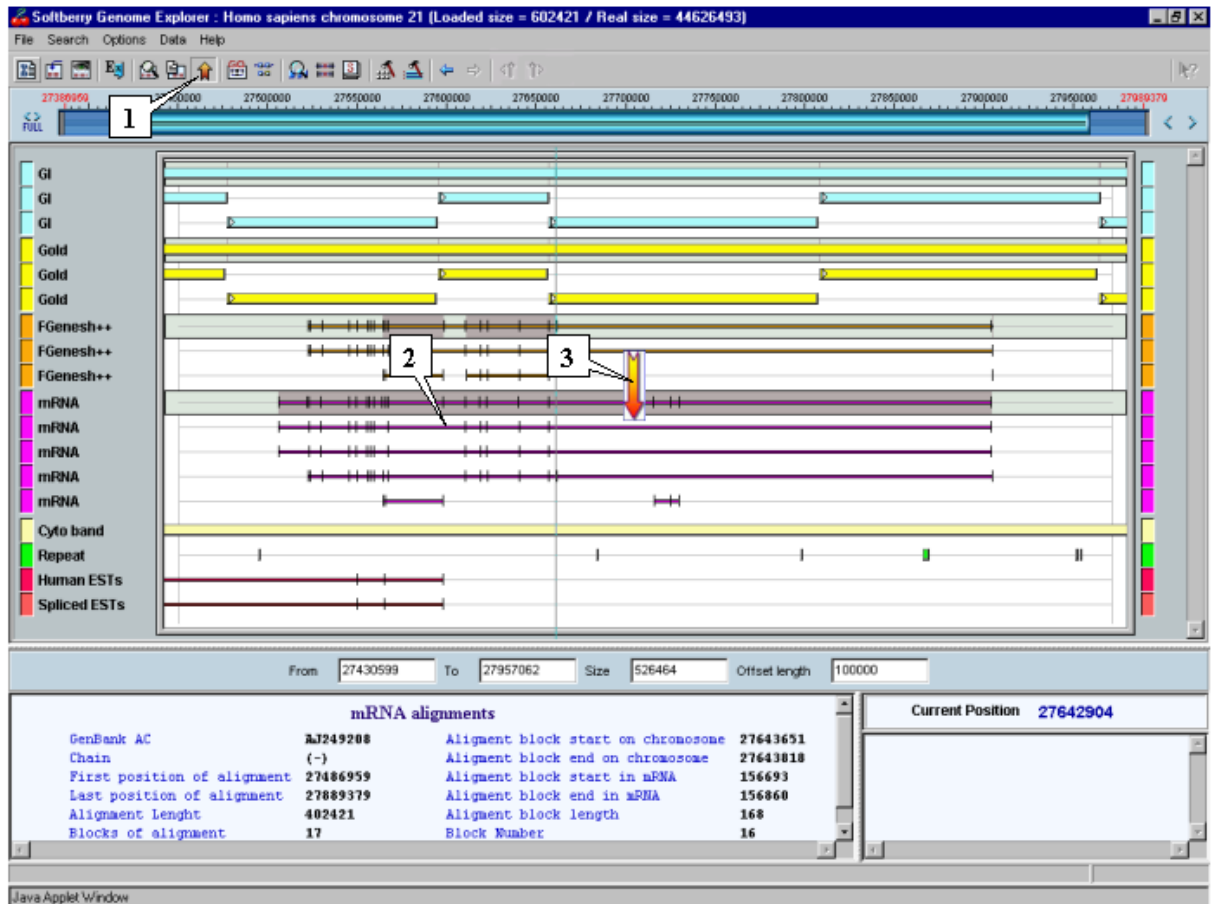

Visualization of the found feature

Figure. 3.4.2.4.2.
1. Turn on/off the marking arrow button. **2.** Loaded feature. **3.** Feature-marking arrow.

3.4.2.4.2. Retrieving of sets of found features sequences

To retrieve sets of found features sequences do the following:
1. Select features by clicking on them (to select all features use the "Select all" command of popup menu).
2. Select the "Sample sequence" command of popup menu.
3. As a result the "Sample sequences" dialog window, in which sequence output parameters are to be defined (description of parameters see in 3.5), will appear.
4. Press the "OK" button.

3.5. Retrieving of feature sequence sets

Softberry Genome Explorer provides the facility for retrieving of both a whole feature sequence and sequences of features' blocks.

3.5.1. Retrieving of sequence sets for selected chromosomes and features types.

To get a required sequence do the followings:

1. Open the «Sample Sequences» dialog window (fig.3.5.1.1) using one of the following means:
   - The «Data->Sample Sequences» command of main menu;
   - The 🖥️ button on the toolbar;
   - The <Ctrl+S> hot keys.
2. Set one of the search region selection modes:
   - Select chromosomes from the list mode. To activate this mode select the «Chromosomes» switch. This mode allows the search to be performed in all selected chromosomes.
   - Current chromosome mode (fig. 3.5.1.2). To activate this mode select the «Current chromosome & screen range» switch. The search will be performed in the currently displayed region of the currently loaded chromosome only. On a selection of this mode, the «Chromosomes» list becomes inactive.
3. As the select chromosomes from the list mode is set, in the «Chromosomes» list select the chromosomes, which will be searched for features sequences. The «Select all» and «Deselect all» buttons allow all chromosomes to be selected or unselected respectively at the time.
4. Select features types, for which sequences must be retrieved, in the «Feature Types» list by clicking on them. The «Select All» button allows all types in the list to be selected. The «Deselect All» one removes a selection from all features types.
5. Using the appropriate switches, select the part of sequences to be retrieved: complete sequences (Full feature), summarized (combined) sequences of all features' blocks (Lace blocks) or certain fragments of certain blocks (Block data). As the «Block data» mode is set, two drop down lists become active (fig. 3.5.1.2). The first of them, «Block data type», offers to find either complete blocks sequences, or starting/ending blocks regions. The «Data location» one allows the output requesting of either all features' blocks, or only first/last/inner blocks of feature.
6. Select the required strand of a feature sequence («Chain(+)»,«Chain(-)»,«Original Chain»).
7. In the «Left flank» and «Right flank» fields set a required length of appropriate flanks.
8. Define the sequence output format:
   - Set the width of a sequence string in the «Seq line width» field.
   - Turn on/off the separators between features in a text by checking in/out the «Delimiters» checkbox.
   - Enable/disable the color layout of features by checking in/out the «Color formatting» checkbox

   Comment. The flanks direction depends on that of sequence strand. If the mode of block's start visualization and chain(+) are selected, then after the left flank will be shown as much block sequence letters, as defined in the «Right flank» field. If the mode of block's end visualization and chain(-) are selected, then before the right flank will be shown as much block sequence letters, as defined in the «Left flank» field.
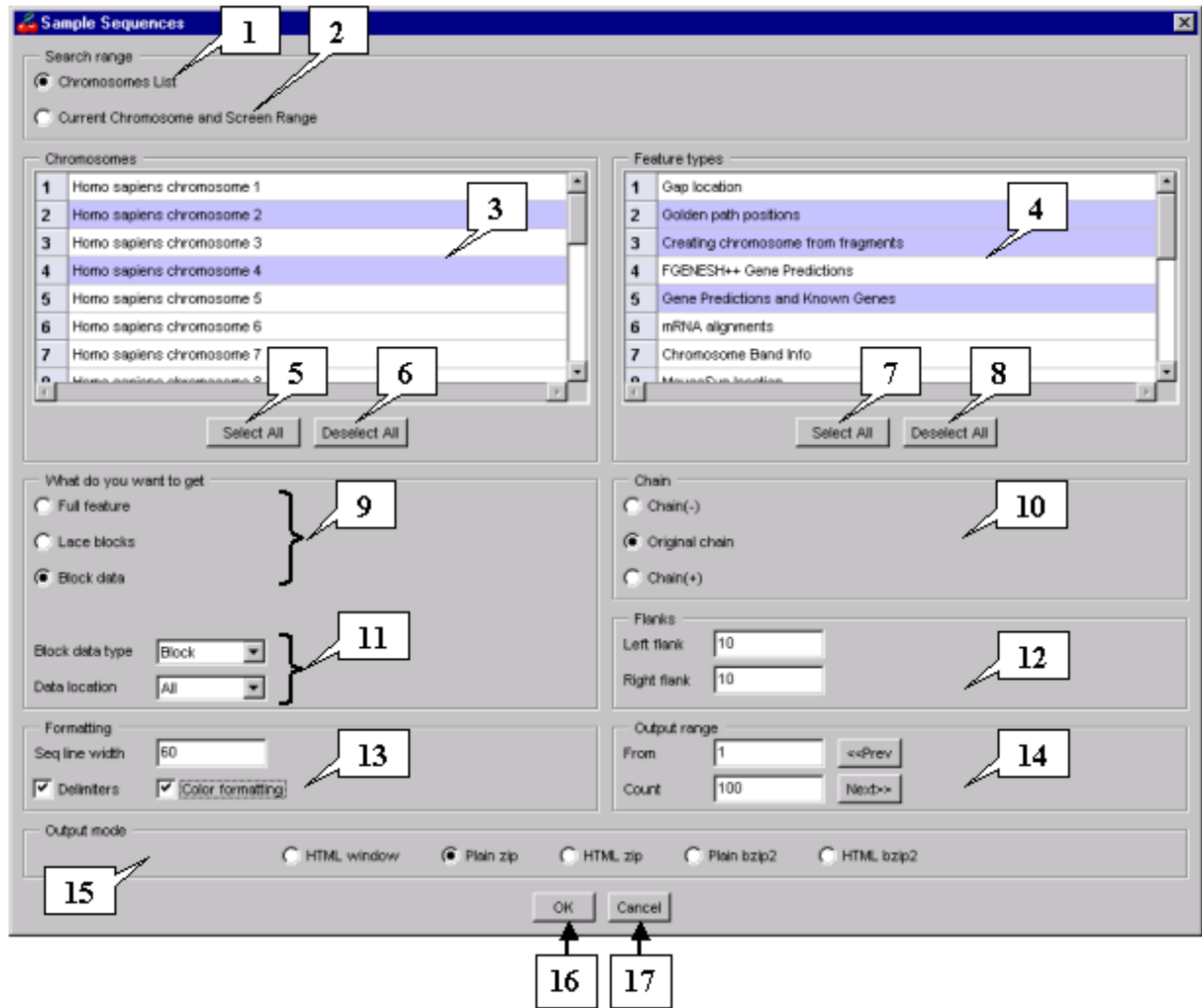
Sequence retrieving dialog window

Figure 3.5.1.1.

1. Chromosomes list mode. **2.** Current chromosome mode. **3.** Chromosomes list. **4.** Features types list. **5.** Select all chromosomes button. **6.** Deselect all chromosomes button. **7.** Select all features types button. **8.** Deselect all features types button. **9.** Modes for retrieving of various fragments of feature sequences. **10.** Panel for selection of a sequence strand. **11.** Lists of feature blocks and block regions. **12.** Sequence flanks length set up bar. **13.** Sequence output format set up bar. **14.** Sequence output parameters set up bar. **15.** Sequence output mode selection bar. **16.** Search start button. **17.** Cancel button.

9. Set the sequence output parameters. In the fields below the «Output range» title the number of a feature to be used as the beginning for data output as well as total number of features, for which the data must be displayed, can be defined. Enter a required number into the «From» field (the default value is 1, i.e. data output is being started from the first found feature). Then enter a required number into the «Count» field to define the number of features, for which data must be displayed. The maximally allowed number is 1000. On entering a greater number, it will automatically be changed to 1000. Pressing the «Prev>>» button causes the increase of the «From» value for that in the «Count» field, while pressing the «<<Prev» button decreases it for the same value.

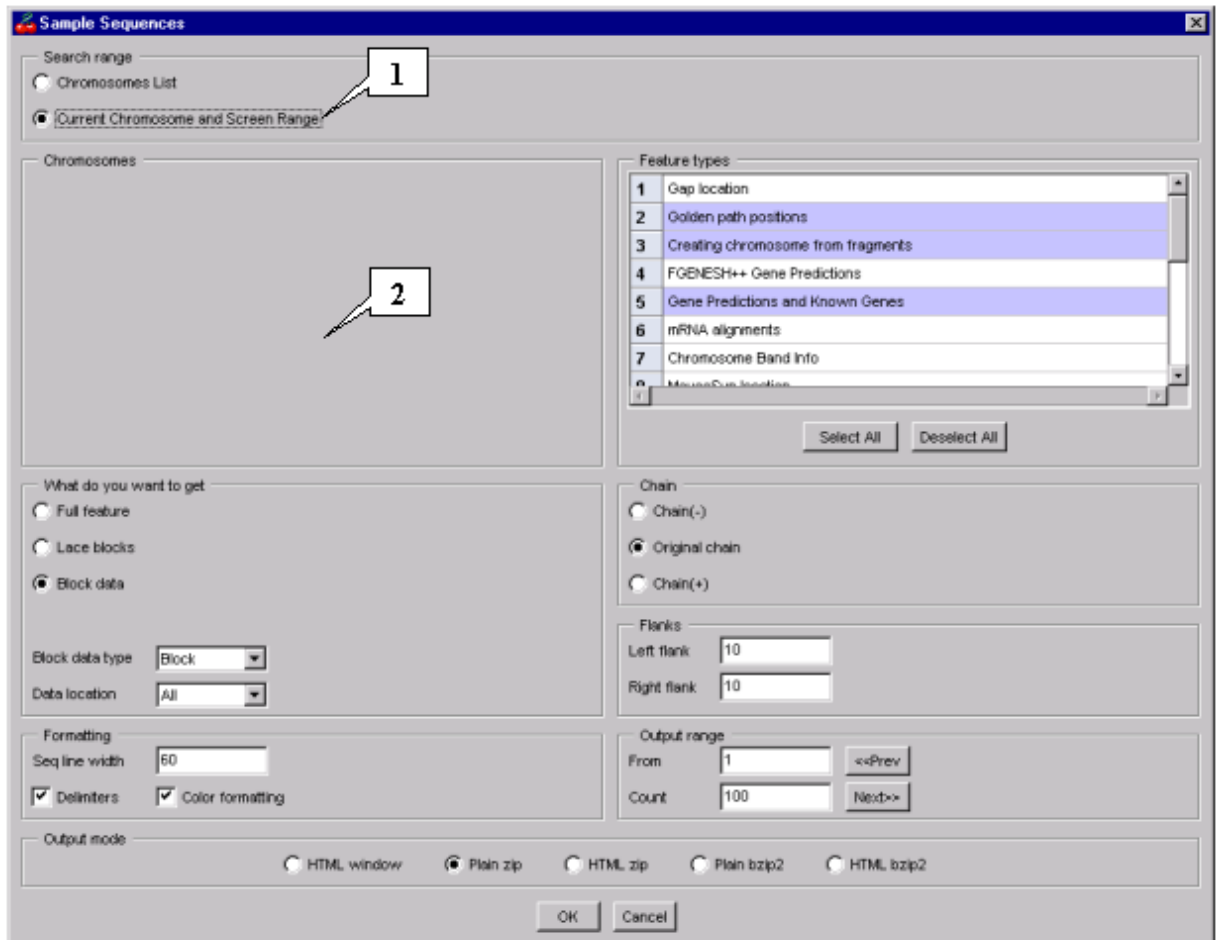# Dialog window for retrieving of sequences

Figure 3.5.1.2.

1. Activated mode of searching in the currently displayed region. **2.** Inactivated list of chromosomes selection.
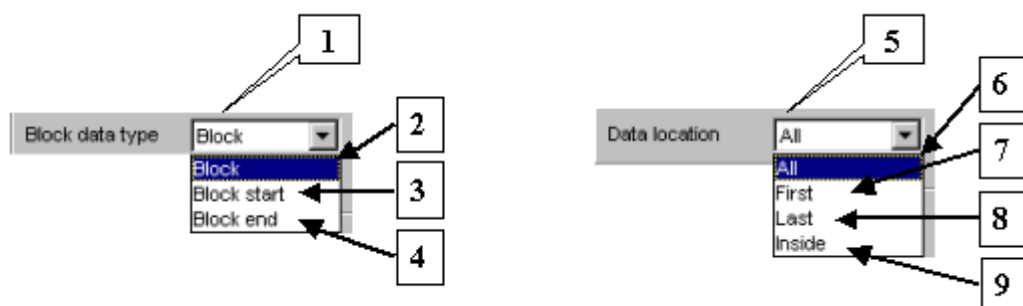
Blocks sequences output modes

Figure 3.5.1.3.

1. List for selection of features' blocks regions. **2.** Mode for retrieving of complete sequences of features' blocks. **3.** Mode for retrieving of starting sequences of features' blocks. **4.** Mode for retrieving of ending sequences of features' blocks. **5.** List for selection of features' blocks. **6.** Mode for retrieving of all blocks of features. **7.** Mode for retrieving of first blocks of features only. **8.** Mode for retrieving of last blocks of features only. **9.** Mode for retrieving of inner blocks of features only.

10. Set up the data output mode using switches below the «Output Mode» title:
  - «HTML-window» - data will be displayed in a separate HTML-window.
  - «Plain ZIP» - in the HTML-window will be displayed the link to a ZIP-archive with data file in normal text format.
  - «HTML ZIP» - in the HTML-window will be displayed the link to a ZIP-archive with data file in HTML format.
  - «Plain BZIP2» - in the HTML-window will be displayed the link to a BZIP2-archive with data file in normal text format.
  - «HTML BZIP2» - in the HTML-window will be displayed the link to a BZIP2-archive with data file in HTML format.
11. Press the «OK» button.

As the search is launched, the window, which contains either the selected features sequences (fig.3.5.1.4A) or the link to data archive (fig.3.5.1.4B) (it depends on data output mode), will be displayed. The file archive is on the web or local server. All sequences are displayed in FASTA-format.

Figure 3.5.1.4.
A. Window with selected features sequences. **B.** Window with the link to file archive with selected features sequences.
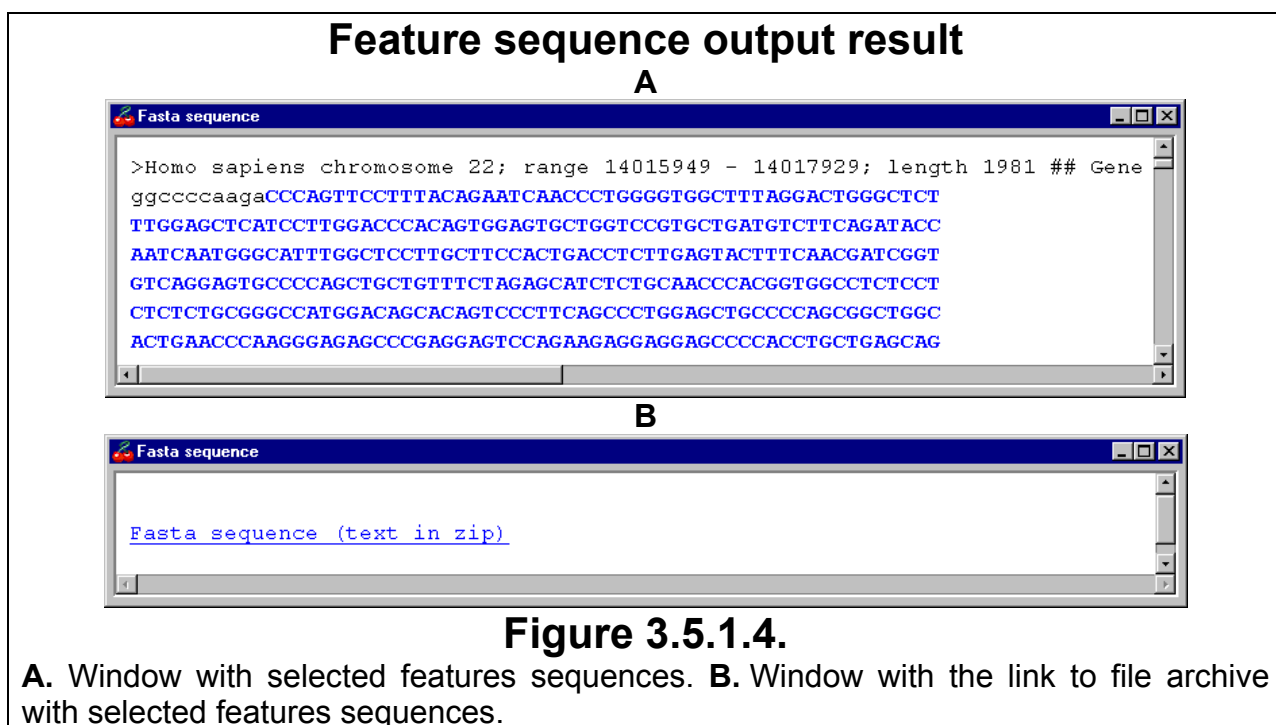
3.5.2. Retrieving of sets of found features sequences.

There is a possibility to retrieve sets of sequences of previously found features. In details, if a search for features had been performed (see 3.4), then it is allowed to open the window with the search results (see chapter 3.4 and fig 3.4.6), to select a required search request ID and to select features of interest. On this is done, select the "Sample sequences" command of popup menu. It will result in appearance of the "Sample sequences" dialog window (fig.3.5.2.1), in which sequence output parameters are to be defined. On the parameters definition is completed, press the "OK" button. Operating this window is exactly the same as that defined in 3.5.1 (fig.3.5.1.1).
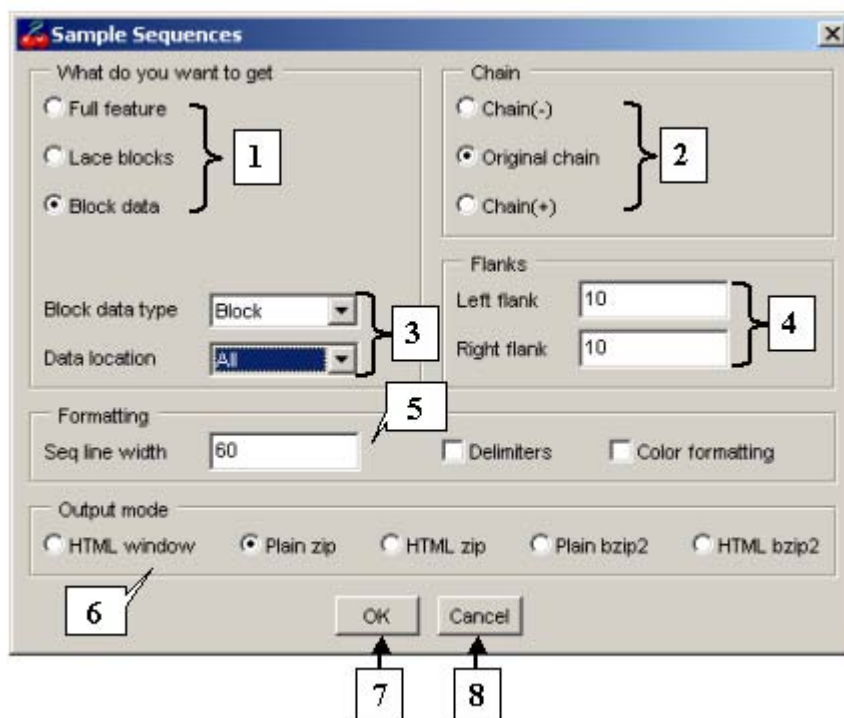
Retrieving of the found features sequences
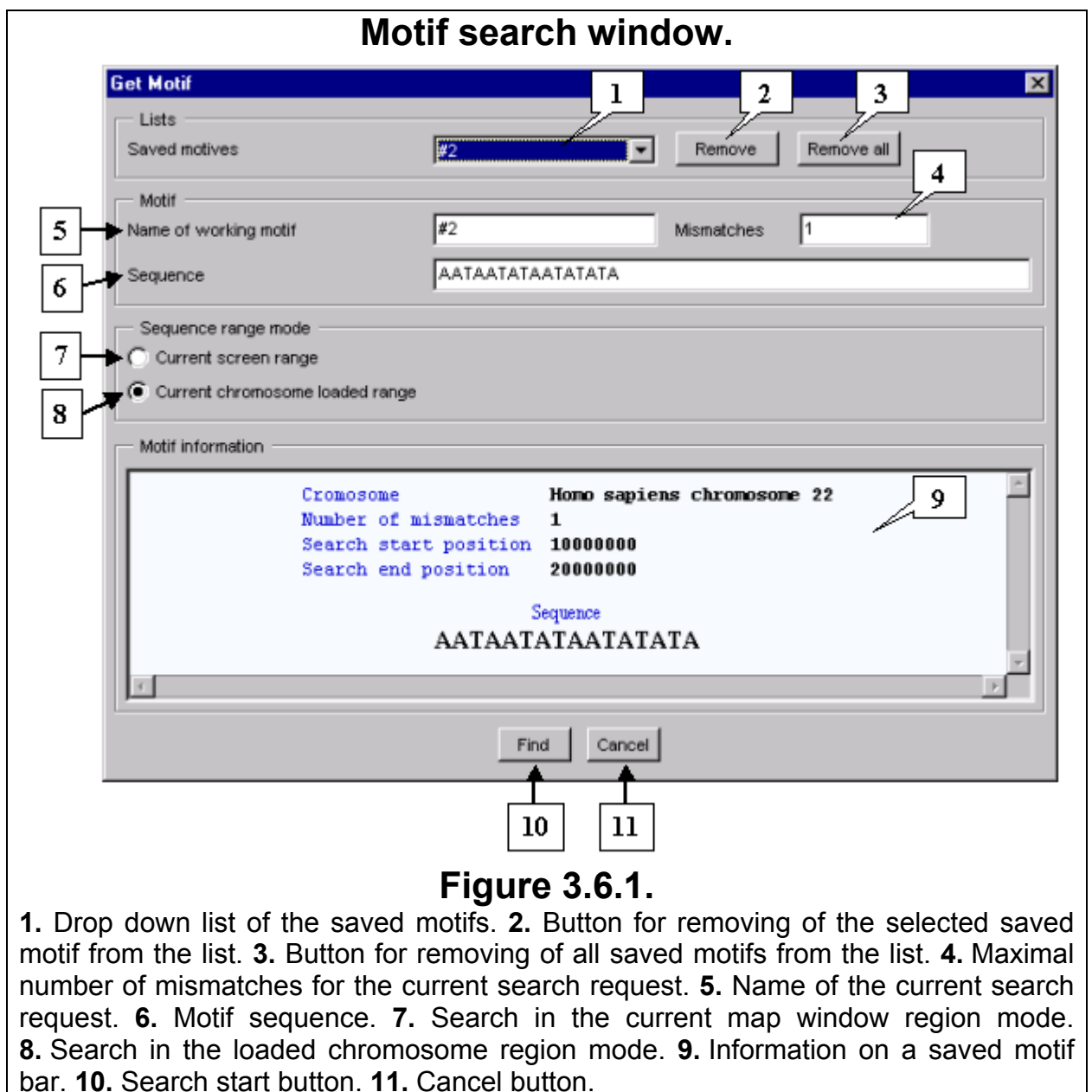

Figure 3.5.2.1.

1. Mode for retrieving of feature sequence fragments. **2.** Sequence strand selection bar. **3.** Lists of feature blocks and block regions. **4.** Sequence flanks length set up bar. **5.** Sequence output format set up bar. **6.** Sequence output mode selection bar. **7.** Search start button. **8.** Cancel button.

3.6. Motifs search

Softberry Genome Explorer provides the facility for search for a certain sequence in a certain genome region.

To find a motif do the followings:

1. Open the motif search dialog window using one of the following means:
   - The «Search->Get Motif» command of main menu.
   - The <Ctrl+M> hot keys.
   - The ![icon] button on the toolbar.
2. Enter the ID of current motif into the «Name of working motif» field of the appeared dialog window (fig.3.6.1).
3. Set the maximally allowed number of mismatches in the «Mismatches» field.
4. Enter the sequence to be searched for (sequence must not contain gaps, since otherwise motif will not be found) in the «Sequence» field.

Motif search window.

Figure 3.6.1.

1. Drop down list of the saved motifs. **2.** Button for removing of the selected saved motif from the list. **3.** Button for removing of all saved motifs from the list. **4.** Maximal number of mismatches for the current search request. **5.** Name of the current search request. **6.** Motif sequence. **7.** Search in the current map window region mode. **8.** Search in the loaded chromosome region mode. **9.** Information on a saved motif bar. **10.** Search start button. **11.** Cancel button.

5. Set the region, to be searched in, using the switches:
    - «Current screen range» - currently displayed region;
    - «Current chromosome loaded range» - currently loaded region.
6. Press the «Find» button. On this is done, the window with the message on data receiving (fig.3.6.2) appears. On the search is done, the window with the message on the number of found motifs (fig. 3.6.3) appears.
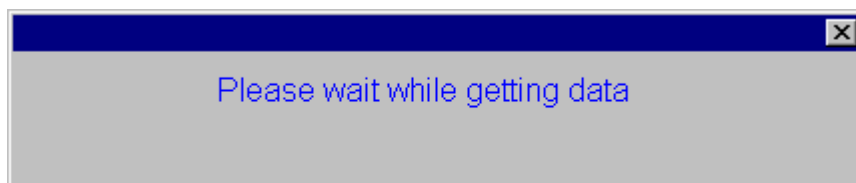
Window with the message on data receiving

Please wait while getting data

Figure 3.6.2.

Window with the message on the number of found motifs

Found 63 Motifs

OK
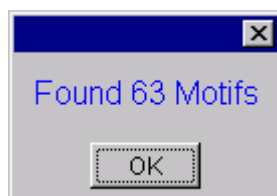
Figure 3.6.3.

7. The new type with the name, which was assigned to the current search request, will appear in the map area (e.g. <#1>). This type may contain both one and several layers (fig. 3.6.4). The information on a type is available via the popup menu of feature types. It may be multiple types of motives.

For example, on the figure 3.6.4 the second type of motives, designated as «#2», contains 63 features (or found motifs, meeting the set search parameters), which are in two layers. The combined layer of features is also available for this type of motives.

Comment. Types of motives are placed in the upper positions of the lists of the «Load Features Types» and «Features» dialog windows, which are used to define the parameters of features types loading and visualization on the map.

Comment. In the motives search dialog window, below the title, there is the list of IDs of the previously found motives. On a selection of one of them, in the information bar appears the information on this search request: the search region, number of mismatches and the sequence, which was searched for. The «Remove» and «Remove all» buttons allow the removing of one or all search results respectively from the list of saved motives. On a pressing of these buttons, the dialog windows with confirmation requests appear (fig.3.6.5).
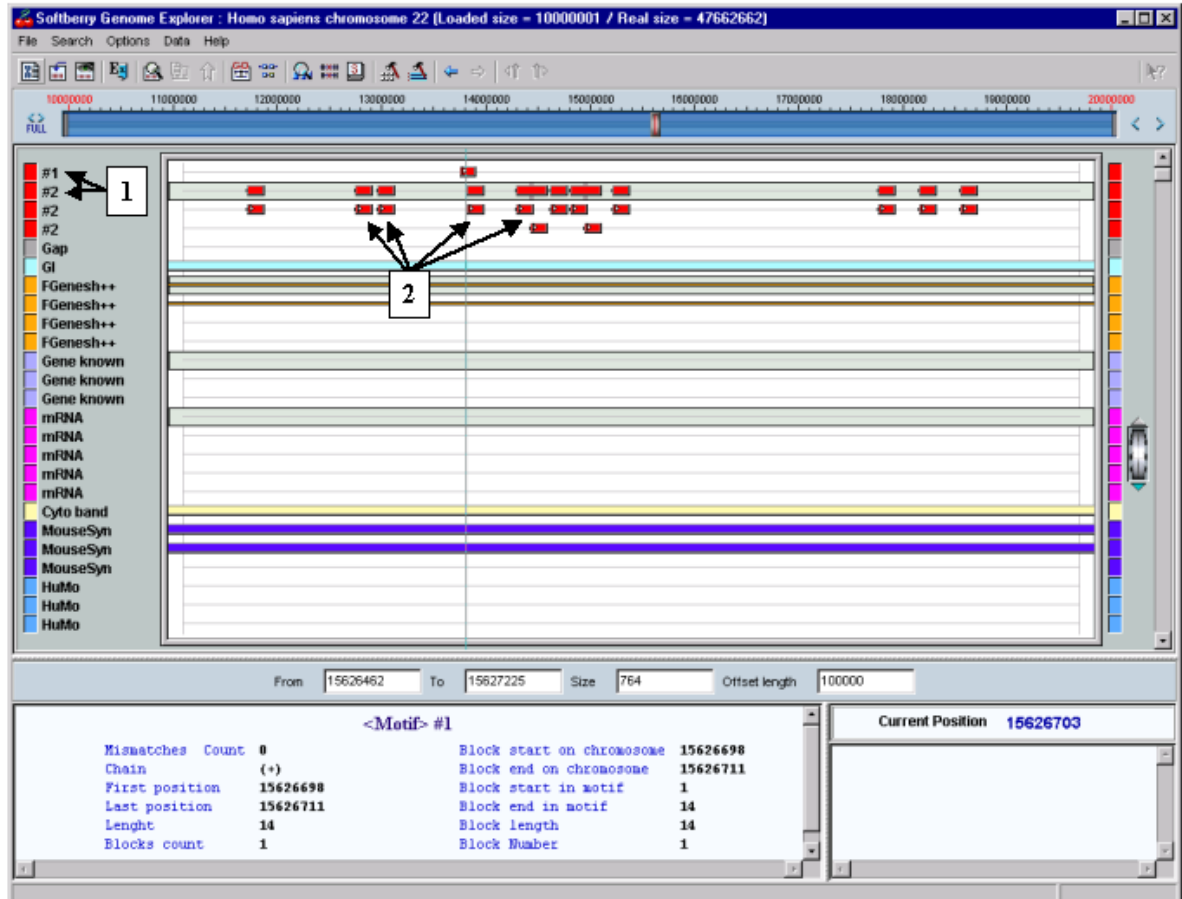
Motif search result.

Figure 3.6.4.

1. Types of found motifs. **2.** Some of found motifs.

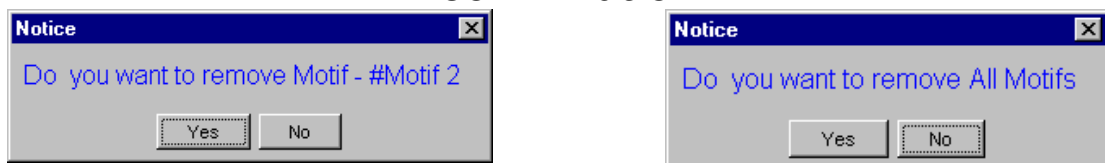# Dialog windows with requests for saved motifs removal confirmation

Figure 3.6.5.

3.7. Getting alignment

Softberry Genome Explorer provides the facility for sequence alignment. Moreover, the user is allowed to change multiple search parameters. For the current system two different algorithms are developed. The first algorithm is fast, but gives very "rough" results, i.e. it finds the clear homology, but may miss some small blocks (FMap). The other one finds all possible homology blocks, but works significantly slower (Scan2). The Scan2 program has the modification, which is pronounced for the mapping of mRNA/EST on a chromosome (EST-Map). It often makes sense to find at first the "rough" region (using the FMap), which contains an alignment, and then to find the complete alignment in this region (using Scan2).

If at a given set of parameters one or several alignments were found, the assemblage of these alignments forms a new type of features, the name of which is identical to that of search request (e.g. #1, #Alignment 2, etc.).

In order to find (get) an alignment of a sequence the followings must be done:

1. Open the dialog window of an alignment search (fig.3.7.1) using one of the following means:
   - Using the «Search->Get Alignment» command of main menu.
   - Using the 🔳 button on the toolbar.
   - Using the <Ctrl+A> hot keys.
2. In the «Current alignment» field of the appeared window enter the ID of a current alignment.
3. In the «Chromosomes» list select the chromosomes, which will be searched for an alignment. The «Select all» and «Deselect all» buttons allow all chromosomes to be selected or unselected respectively at the time (fig.3.7.1).
4. Enter a sequence into the «Sequence» field. The «Clear» button makes the field empty.
5. Select required alignments parameters.
   1. Chose the similarity level using the «Normal», «Strong», «Weak» or «Custom» switches. If the «Custom» mode is selected, the «Set Custom» button becomes active. On a pressing of this button, the «Set Custom Alignment Mode» dialog window, in which the user can set the required alignment parameters (the window description see below), appears. This window allows also to check the default values of parameters for normal, strong or weak modes of similarity level search.
   2. Set the maximal width of a chromosome region, which may be covered by an alignment, in the «Width Level Area Alignment» field.
   3. Select the optimization method from the appropriate («Optimization method») drop down list (fig.3.7.2).
   4. Checking in the «EST Mode» checkbox activates the EST-Map mode instead of Scan2.
   5. Select the required alignment mode using one of the following switches:
      - «FMap» - the rough alignment mode.
      - «FMap+Scan2» - the combined mode, when at first the search region is being searched for clear homology, and then the found region is being searched for fine homology.
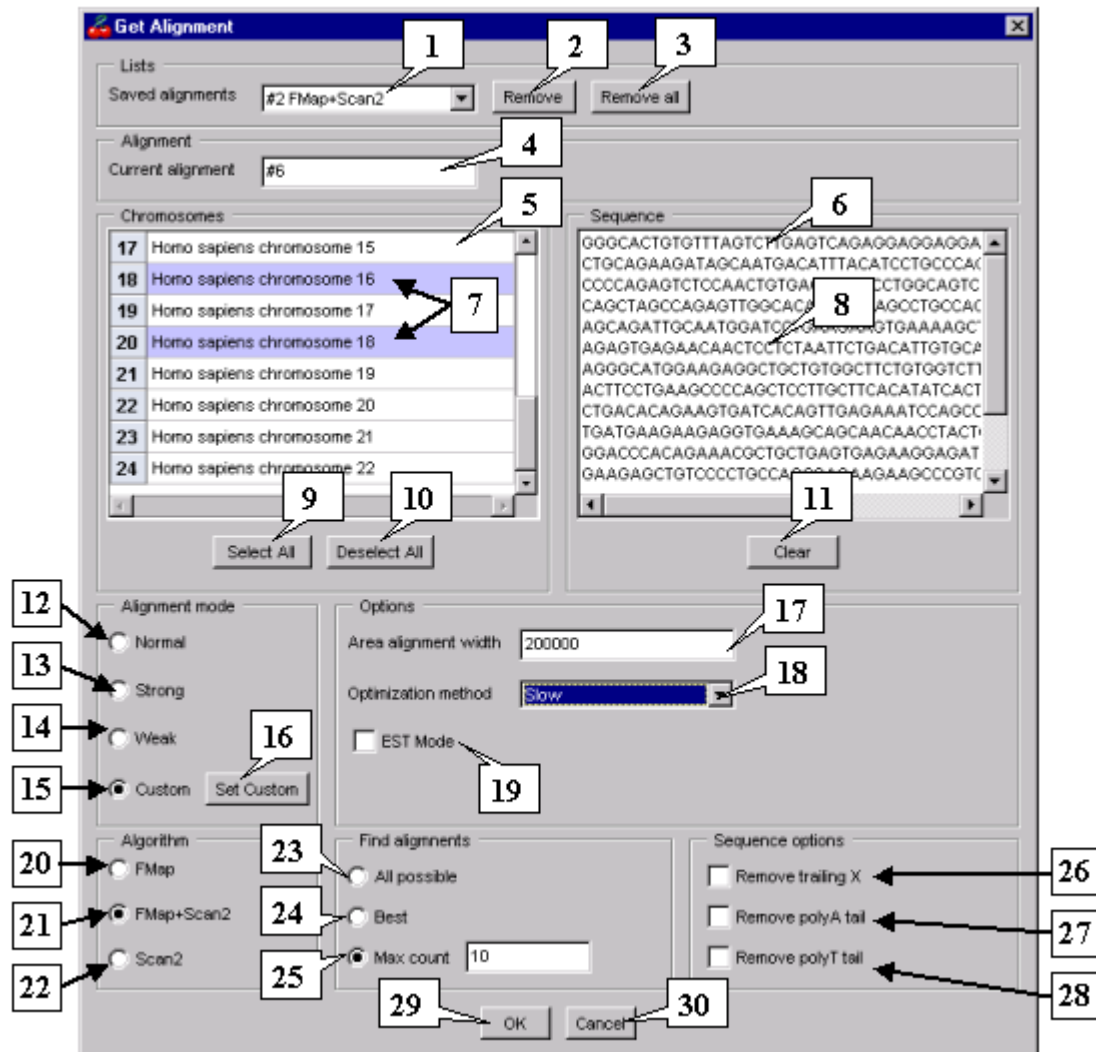   - «Scan2» - the fine alignment mode.

Alignment search window

Figure 3.7.1.

1. Drop down list with IDs of saved alignments. **2.** Button for removing of a single element from the drop down list. **3.** Button for removing of all elements from the drop down list. **4.** ID of the current alignment. **5.** List of chromosomes, available for alignment. **6.** Sequence field. **7.** Selected chromosomes. **8.** Sequence, which is being aligned. **9.** Button for selection of all chromosomes. **10.** Button for deselection of all chromosomes. **11.** Button for clearing of the sequence field. **12.** Mode of the search with normal similarity level. **13.** Mode of the search with strong similarity level. **14.** Mode of the search with weak similarity level. **15.** Mode of the search with custom set of parameters. **16.** Button for opening the dialog window for setting the custom parameters. **17.** Maximal width of a chromosome region, which may be covered by an alignment. **18.** Drop down list of the optimization methods. **19.** Switch to EST-Map instead of Scan2. **20.** Switch to the fast search algorithm (Fmap). **21.** Switch to the combined search algorithm (FMap+Scan2). **22.** Switch to the slow search algorithm (Scan2). **23.** To find all possible alignments. **24.** To find the best alignment only. **25.** To find not more than N of the best alignments. **26.** Remove flanking poly-X. **27.** Remove terminal poly -A. **28.** Remove terminal poly -T. **29.** Button for the search launch. **30.** Button for rejection of the search.

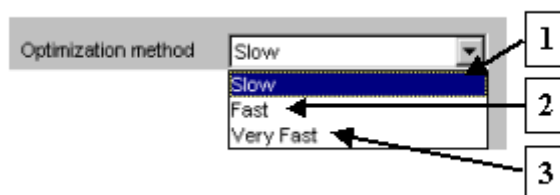**Drop down list of the optimization methods**

Figure 3.7.2.

1. Slow optimization method. **2.** Fast optimization method. **3.** Fastest optimization method.

6. Set the limitation of the found alignments number:
   - «Best» - to find the best alignment only. Only the one ("The best") alignment per chain is displayed, thus not more than two alignments can be retrieved in this mode.
   - «All possible» - to find and to display all possible alignments.
   - «Max count» - to find and to display not more alignments, than it was defined in the «Max count» field. This number refers to that of alignments, found in one of the chromosome nucleotide chains, e.g. if to set 5 in this field, then it will be found not more than 10 alignments: 5 per (+) strand and 5 per (-) one.
7. Set (or do not) removing of the flanking poly-X or terminal poly-A and poly –T sequences by checking in the «Remove trailing X», «Remove poly-A tail» and «Remove poly-T tail» checkboxes.
6. Press the «OK» button.
7. On the button is pressed, the window with the message on data receiving process (fig.3.7.3) appears. On the process is finished the window with the message on the number of found alignments (fig.3.7.4) appears.
8. On the «OK» button is pressed (or after a lapse of certain time), appears the dialog window with the list of found alignments ("Found Alignment List"), in which data on either currently found alignment, or alignments found before (they can be selected from the drop down list "List of searches") can be selected.

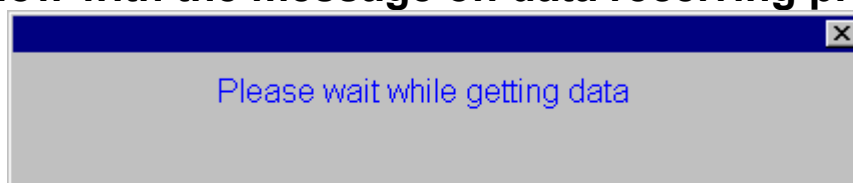**Window with the message on data receiving process**

Figure 3.7.3.

Window with the message on the number of found alignments

Figure 3.7.4.

3.7.1. List of found alignments

In the upper part of the "Found Alignment List" window (fig. 3.7.1.1) there are the drop down list of alignments IDs and the field with the score of alignment, loaded on the main window map.

The "Found Alignment List" window contains two tabs:

- The "Features map" tab is purposed for visualization of the search results.
- The "Features list" tab is purposed for visualization of found local features of alignment in the manner of a list.

3.7.1. "Features map" tab

The "Features map" tab consists of three parts: the chromosomes map, the found features map and the information bar (fig. 3.7.1.1).

3.7.1.1. Chromosomes map

The map of chromosomes provides the general visualization of the search results. Chromosomes on the map are shown as rectangles. Height of a rectangle is proportionate to a corresponding chromosome length. Inside of a rectangle the features (alignments), found in an appropriate chromosome, are depicted in accordance to their localization on the chromosome. Above a rectangle the number of alignments, found in an appropriate chromosome, is displayed, below a rectangle – the chromosome brief name.

If the "All" button is pressed, then all chromosomes are shown on the map of chromosomes. Chromosomes, in which alignments were found, are marked with a color. Chromosomes, in which alignments were not found, are colorless. If the button is not pressed, then only those chromosomes, in which alignments were found, are shown on the map.

Parameters for visualization of the chromosome map elements are to be defined in the "Options" dialog window (see 3.7.1.2), which can be opened by pressing the CO button.

In order to select a chromosome for visualization, click the mouse left button on the chromosome of interest. The chromosome will be selected, and features (alignments), found in this chromosome, will be displayed on the features map.
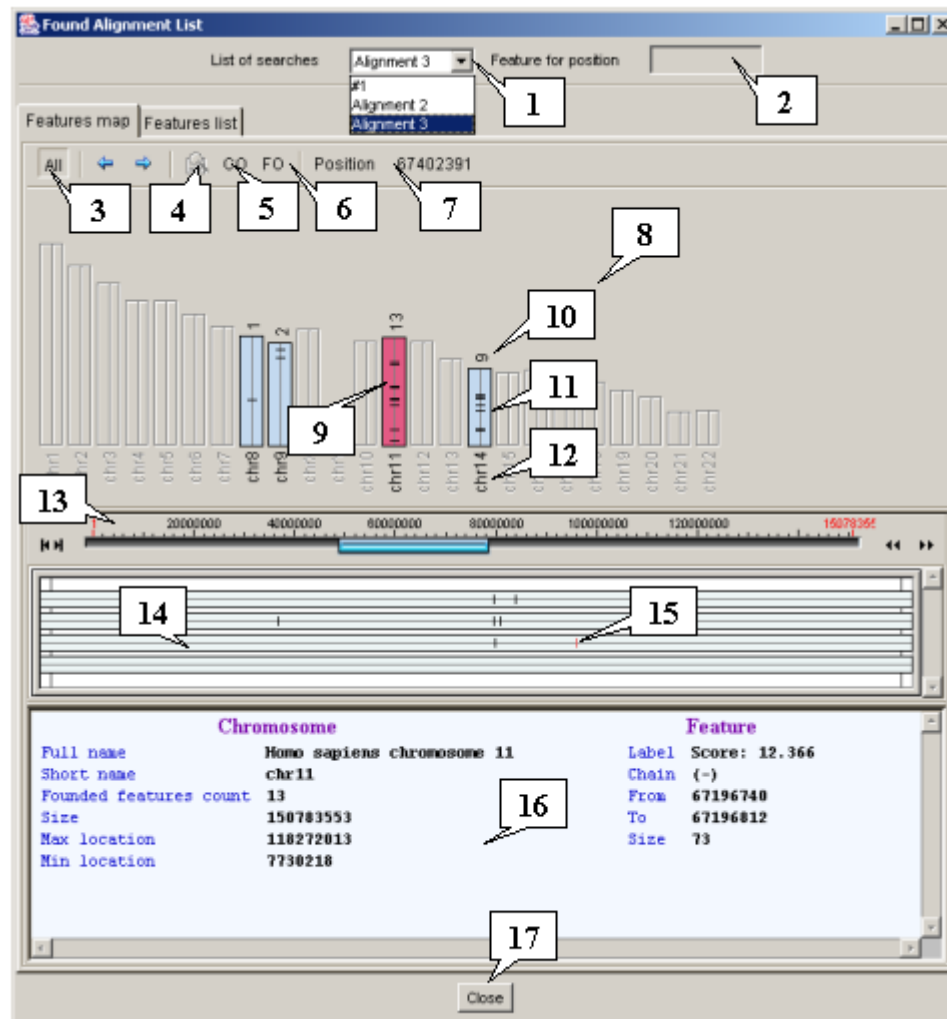
Found alignments list

Figure. 3.7.1.1.

1. List of alignments IDs. **2.** Field with the score of alignment, loaded on the main window map. **3.** Switch between the chromosomes visualization modes. **4.** Button for visualization of the selected local feature of alignment visibility range. **5.** Button for opening of the chromosomes map settings dialog window. **6.** Button for opening of the features map settings dialog window. **7.** Current position of the mouse pointer on the features map. **8.** Chromosomes map. **9.** Chromosome, selected for visualization on the map. **10.** Number of alignments, found in a chromosome. **11.** Found alignments. **12.** Brief chromosome name. **13.** Features map control bar. **14.** Features map. **15.** Selected alignment. **16.** Information bar. **17.** Close window button.

3.7.1.1.2. Chromosome map settings dialog window.

The "Options" dialog window (fig. 3.7.1.2), purposed for setting up the parameters of the chromosome map, can be opened using the CO button.

In this window the following parameters can be changed:
Chromosomes visualization set up bar ("Chromosomes options"):
- The "Width" field allows the width (in pixels) of a rectangle, representing a certain chromosome, to be set.
- The «Color» button allows the color of a chromosome to be set. On the button is pressed, the "Color dialog" window, purposed for the color selection, is opened. The selected color is displayed on the "Chromosome" preview bar.
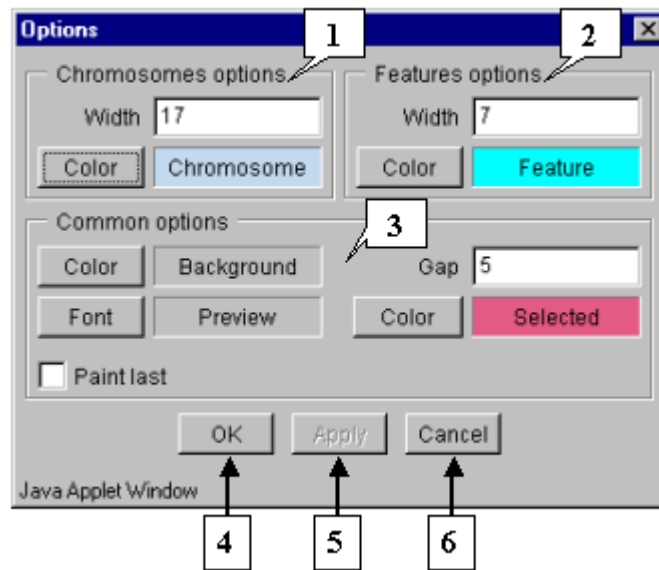
Chromosome map settings dialog window

Figure. 3.7.1.1.2.

1. Chromosome visualization set up bar. **2.** Features (alignments) visualization set up bar. **3.** Common options set up bar. **4.** Accept changes and close window button. **5.** Apply changes without closing window button. **6.** Reject changes and close window button.

Features visualization set up bar ("Features options"):
- The "Width" field allows the width (in pixels) of an alignment to be set.
- The «Color» button allows the color of an alignment to be set. On the button is pressed, the "Color dialog" window, purposed for the color selection, is opened. The selected color is displayed on the "Feature" preview bar.

Common options set up bar ("Common options"):
- The «Color» button to the left of the "Background" preview bar allows the background color of the chromosomes map to be set. On the button is pressed, the "Color dialog" window, purposed for the color selection, is opened. The selected color is displayed on the "Background" preview bar.
- The «Font» button allows the font for the chromosomes map legends to be selected. On the button is pressed, the "Font" window, purposed for the font selection, is opened. The selected font is displayed on the preview bar.
- The "Gap" field allows the definition of the space (in pixels) between chromosomes.
- The «Color» button to the left of the "Selected" preview bar allows the color of the selected chromosome to be set. On the button is pressed, the "Color dialog" window, purposed for the color selection, is opened. The selected color is displayed on the "Selected" preview bar.
- The "Paint last" checkbox. If it is not checked in, then only those columns are displayed, which can be completely fit into the chromosomes map area. Differently, the last visible column is also displayed.

Dialog window control buttons:
- "OK" – accept the selected options and close the window.
- "Apply" – apply the selected options without closing the window.
- "Cancel" – reject all selected options and close the window.

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3.7.1.3. Features map

The map provides visualization of the local features of alignment (further - alignments), located on a selected chromosome, and selection of loading alignment. If alignments overlap each other, then they are displayed in multiple layers, one below another.

Selection of the displayed chromosome region and scaling of the image can be carried out using:

- The graphic navigation bar. The bar operating means are the same as that of the main application window (see chapter 2.6).
- The mouse and control keys (if the "Map navigation" checkbox of the "Options" dialog window is checked in) as described in 2.5. At enabled "Repaint on drag" the map redrawing occurs on the mouse movement. Differently, it occurs on the mouse button releasing only

The central part of the map area corresponds to coordinates of the selected for visualization region. Beyond the restriction lines only those alignments are displayed, which are in the selected region, but extend beyond its boarders.

If the pointer is in the central part of the map area, then in the «Position» field the current position of the pointer on a chromosome is displayed. Differently, the «Position» field contains multiple dashes only.

If the "Navigation line" mode is enabled, then the current pointer position on the map is marked with the vertical line, which never goes beyond the restriction lines.

To select an alignment, click the mouse left button on it. On this is done, the alignment will be highlighted with a color (color can be set in the "Options" dialog window (see 3.7.1.4), which can be opened by pressing the FO button). The selected alignment will automatically be selected in the list on the "Features list" tab.

The ← button allows the jump to the previous map position.

The → button allows the jump to the next map position.

The button allows the visualization of the selected alignment visibility range.

The popup menu of the features map can be opened by clicking the mouse right button on the map. It contains the following commands:

- To position – load a selected alignment.
- Select all – select all alignments.
- Deselect all – remove a selection from all alignments.
- Copy – copy the selected alignment to the editable list of features.

3.7.1.4. Dialog window of the features map options.

The "Options" dialog window (fig. 3.7.1.4), purposed for setting up the features map visualization parameters, can be opened using the FO button.

In this window the following options can be changed:
Bar for setting up the chromosome visualization options ("Chromosomes options"):

- The "Height" field allows the definition of features (alignments) layers height (in pixels).
- The «Color» button allows the visualization color for features (alignments) layers to be set. On the button is pressed, the "Color dialog" window, purposed for the color selection, is opened. The current color is displayed on the "Chromosome" preview bar.

Bar for setting up the features visualization options ("Features options"):

- The "Height" field allows the definition of features (alignments) height (in pixels).

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- The «Color» button allows the visualization color for features (alignments) to be set. On the button is pressed, the "Color dialog" window, purposed for the color selection, is opened. The current color is displayed on the "Feature" preview bar.

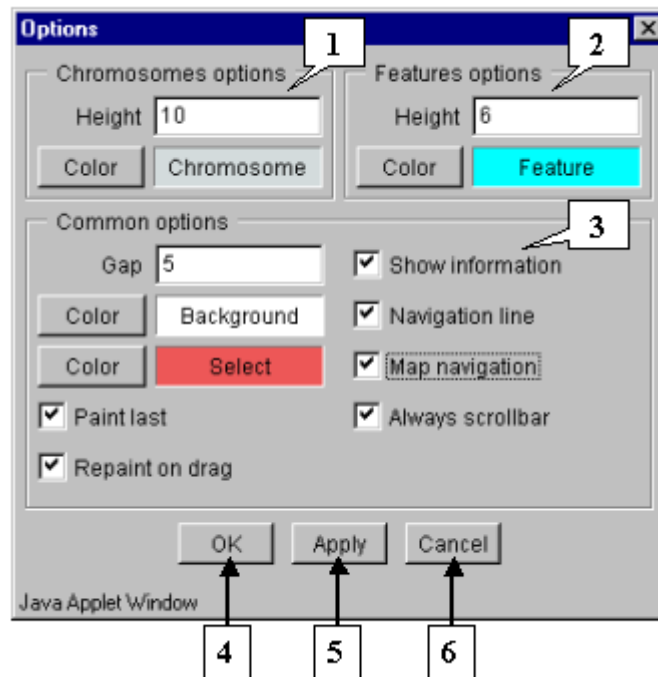**Dialog window of the features map options**

Figure 3.7.1.4.
1. Chromosomes options bar. **2.** Features options bar. **3.** Common options bar. **4.** Accept changes and close window button. **5.** Apply changes without closing window button. **6.** Reject changes and close window button.

Bar for setting up the common visualization options ("Common options"):
- The "Gap" field allows the definition of the space (in pixels) between layers.
- The «Color» button and the "Background" field allow the map background color to be set. On the button is pressed, the "Color dialog" window, purposed for the color selection, is opened. The current color is displayed on the "Background" preview bar.
- The «Color» button and the "Select" field allow the selected alignment color to be set. On the button is pressed, the "Color dialog" window, purposed for the color selection, is opened. The current color is displayed on the "Select" preview bar.
- The "Paint last" checkbox. If it is not checked in, then only those layers are displayed, which can be completely fit into the map area. Differently, the last visible layer is also displayed.
- The "Repaint on drag" checkbox. If it is checked in, then map redrawing occurs simultaneously with movement of the mouse pointer at pressed mouse left button. Differently, it occurs on a releasing of the mouse left button.
- The "Show information" checkbox. If it is checked in, then information on an alignment automatically becomes displayed in the information bar on a placing of the mouse pointer over the alignment. Differently, it becomes displayed on a click on the alignment.
- The "Navigation line" checkbox. If it is checked in, then the vertical line (line of the current horizontal position), which moves along with the mouse pointer,

becomes displayed in the map window. Differently, the line of the current horizontal position remains invisible.

- The "Map navigation" checkbox. If it is checked in, then the visual navigation on the map by mouse becomes available. Differently, it does not work and for navigation use the map toolbar (fig.3.7.1.1).
- The "Always scrollbar" checkbox. If it is checked in, then the scrolling lines are always displayed. Differently, they are displayed only when there is no room on the map for all layers of found features.

Dialog window control buttons:

- "OK" – accept the selected options and close the window.
- "Apply" – apply the selected options without closing the window.
- "Cancel" – reject all selected options and close the window.

3.7.1.5. Information bar

The information bar is purposed for display of the following information:

- On a chromosome, currently targeted by the mouse pointer on the chromosomes map: full and brief names, number of found in this chromosome alignments, size, positions of the first and last localized alignments.
- On an alignment: score, strand direction, the starting and ending positions, size of the region, taken by an alignment.

If in the dialog window of the map options ("Options") the "Show information" checkbox is checked in, then on the information bar the information on an alignment automatically becomes displayed on the placing of mouse pointer over the alignment. Differently, the information becomes displayed on the mouse click only.

The popup menu of the information bar can be opened by the mouse right click and contains the following commands:

- "Save target as…" – N/A in the current version.
- "Copy" – copy the selected information to the clipboard.
- "Select all" – select the whole information, displayed on the bar.

3.7.2. "Features list" tab

The "Features list" tab (fig. 3.7.2) contains the list of found alignments. In this list the following items are indicated: the name of chromosome, in which an alignment is localized, the alignment starting and ending positions on a chromosome, strand direction and the score of a given alignment.

Alignment can be selected from the list by mouse left click. If one or more alignments located in the same chromosome are selected in the list, then at the "Features map" tab occurs the following:

- The chromosome, to which selected alignment (s) belongs, becomes selected on the chromosome map;
- The first of the selected alignments becomes displayed on the features map;
- Data on this alignment become displayed on the information bar.

If selected alignments belong to different chromosomes, then the features map and information bar become empty, and chromosomes do not become selected on the chromosomes map.

The popup menu of the list can be opened by the mouse right click on it and contains the following commands:

- To position – load the selected alignment.
- Select all – select all alignments.
- Deselect all – remove selection from all alignments.
- Copy – copy the selected alignment to the editable layer of features.
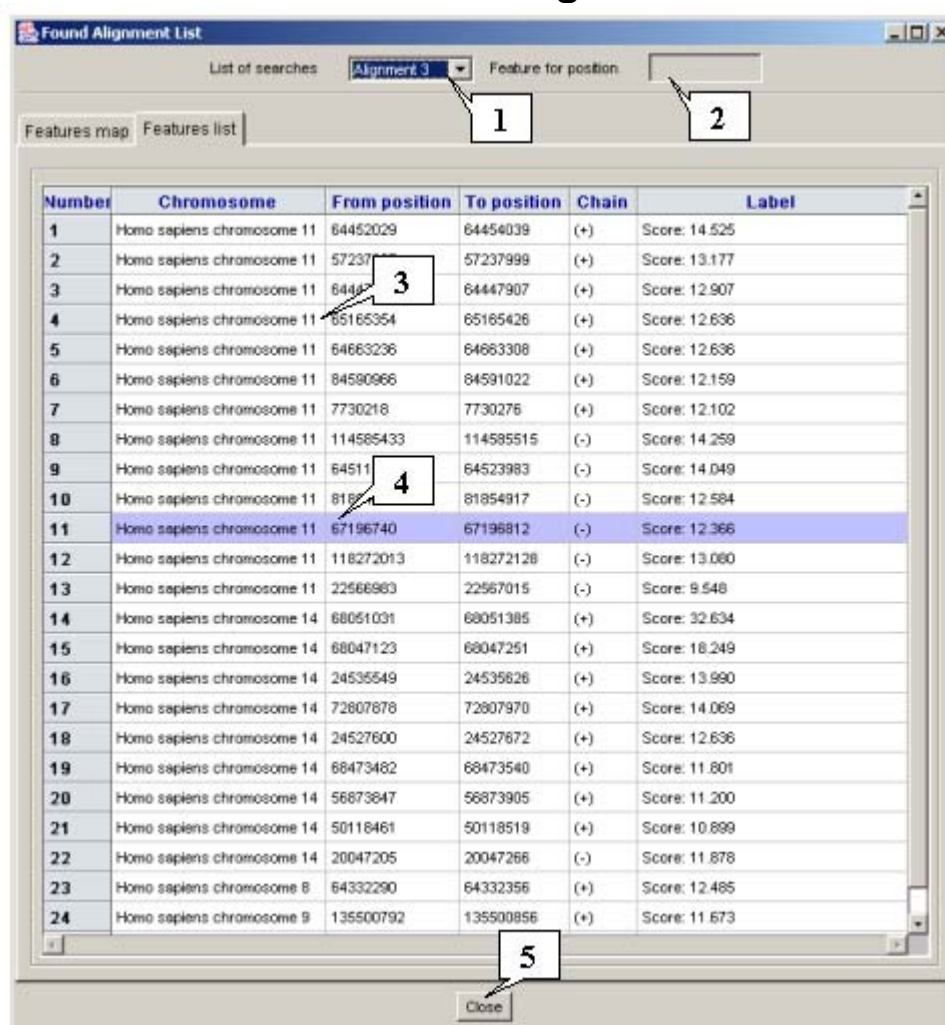
List of found alignments

Figure 3.7.2.
1. Drop down list of alignment requests IDs with the selected ID of a certain request result (alignment type). **2.** Field with the score value of the alignment, loaded on the map of the main application window. **3.** List of found alignments. **4.** Selected alignment. **5.** Close button.

3.7.3. Window operating order.

In order to load one of found alignments the following operations are required:
1. To select an alignment using one of following means:
   - On the "Features map" tab of the chromosome map select the chromosome, in which the required alignment is localized. Layers of found in the chromosome alignments will be displayed on the features map. Select the required alignment and click the left mouse button.
   - On the "Features list" tab alignment can be selected from the list by mouse left click (selection can be removed by recurring mouse left click).
   Comment. Alignment selected on the "Features list" tab is automatically being selected on the "Features map" one.
   Comment. Alignment selected on the "Features map" tab is automatically being selected on the "Features list" one.

2. To open the popup menu of the map or list of features (alignments) and select the "To position" command.
3. The window with message on data loading (fig. 3.7.6) will appear.

Window of data loading message

Please wait while loading data
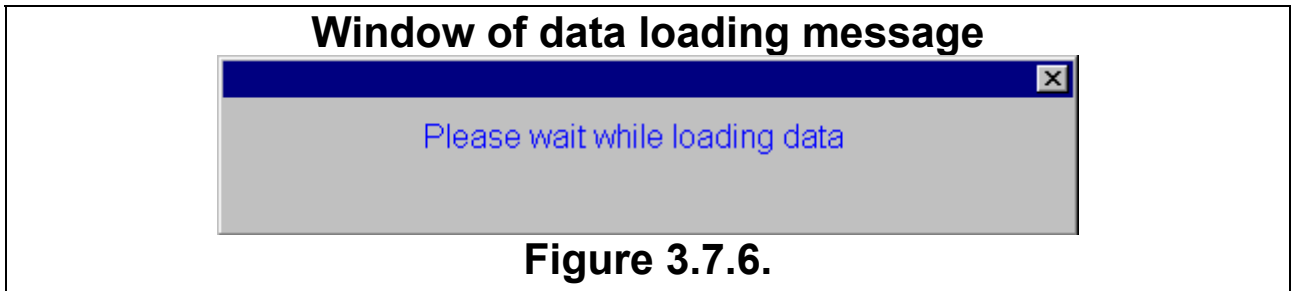
Figure 3.7.6.

4. In the map area of the main window the loaded chromosome region, in which the selected alignment is localized, will be displayed and this alignment will be marked with the pointing arrow (fig. 3.7.7). The ⬆ button on the toolbar allows switch of this arrow on and off. Size of the loading chromosome region, in which the selected alignment is localized, can be defined in the "Side intends options" dialog window, which, in turn, can be opened using the "Options>Flanks" command of main menu.

Alignment localization
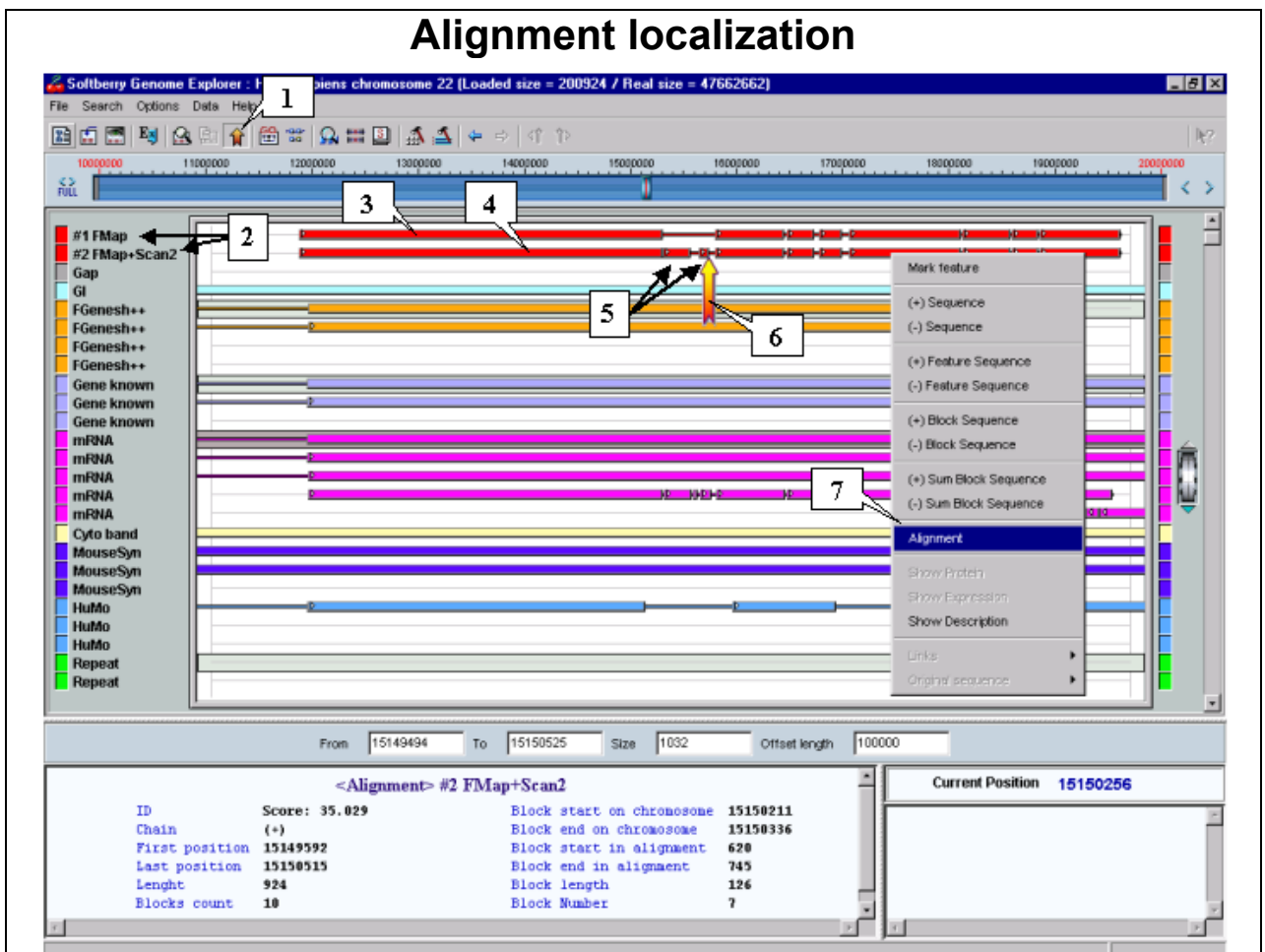
Figure 3.7.7.

1. Button for switch of pointing arrow on/off. **2.** Types of found alignments. **3.** Found in search (Using the Fmap mode) and loaded feature (alignment). **4.** Found in search (Using the Fmap+Scan2 combined mode) and loaded feature (alignment). **5.** Small homologies blocks. **6.** Alignment-pointing arrow. **7.** Popup menu.

5. For look-up the loaded alignment click the mouse right button on the block marked with an arrow and select the «Alignment» command in appeared popup menu.
6. In appeared window the alignment will be displayed (fig. 3.7.8).

   Comment. There can be several types of alignments. Every successful alignment search request provides an additional alignment features type. This type includes as much features as alignments satisfying the request parameters is found. Features types (alignments) are automatically being placed at the top of lists containing features types. These lists are in the «Load Features Types» and «Features» dialog windows, in which features types loading and visualization parameters can be defined.

   On the figure 3.7.7 the result of two alternative alignment search modes is shown. The "#1 Fmap" alignment was found using the Fmap mode, the "#2 Fmap+Scan2" one – using the combined mode (Fmap+Scan2). It's obvious that combined mode provides more precise result since small homologies blocks are found, which were missed at the Fmap mode.

Sequence of found alignment and information on it
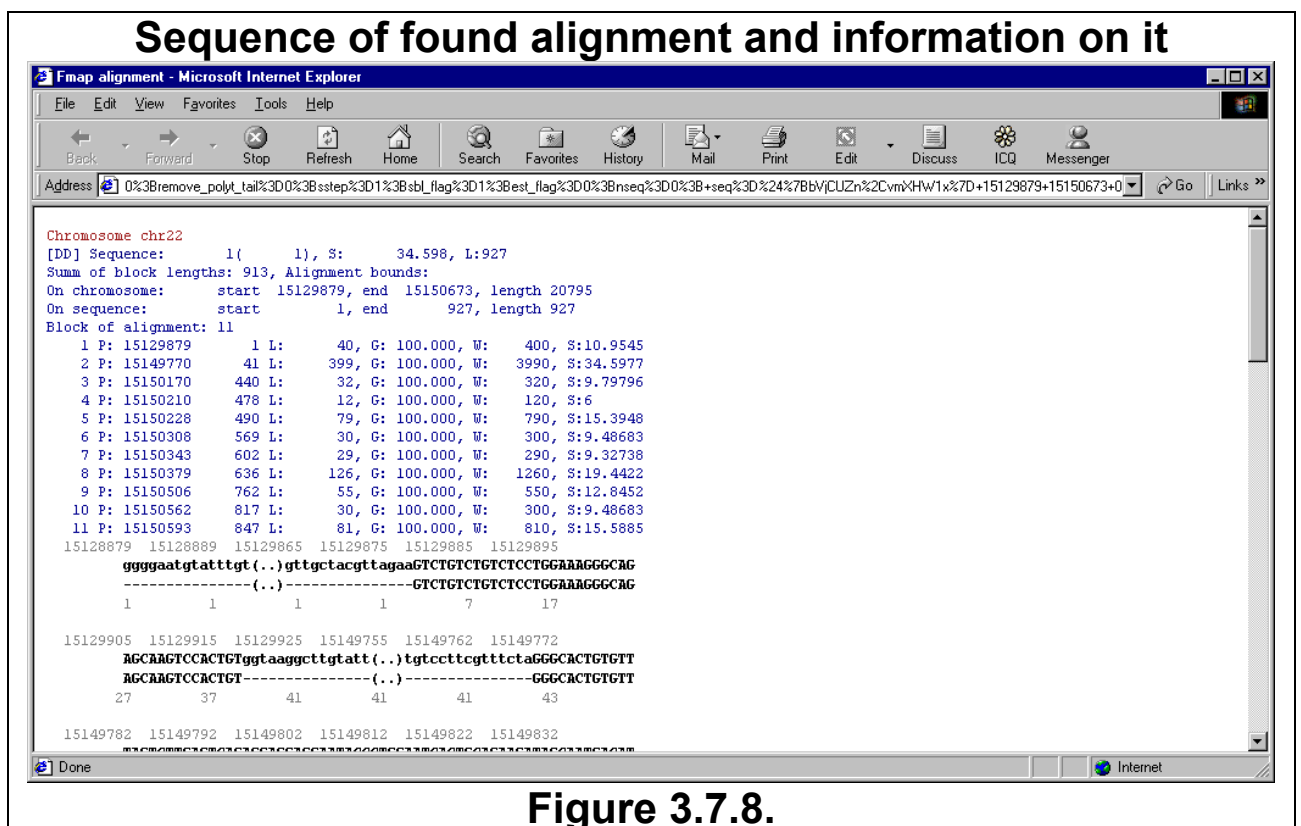
Figure 3.7.8.

3.7.4. Alignment of multiple sequences

The Softberry Genome Explorer provides the possibility of simultaneous aligning of several sequences to a chromosome. To run such an alignment enter the required multiple sequences (instead of a single one) in FASTA-format (fig. 3.7.9) into the «Sequence» field of the alignment search dialog window.
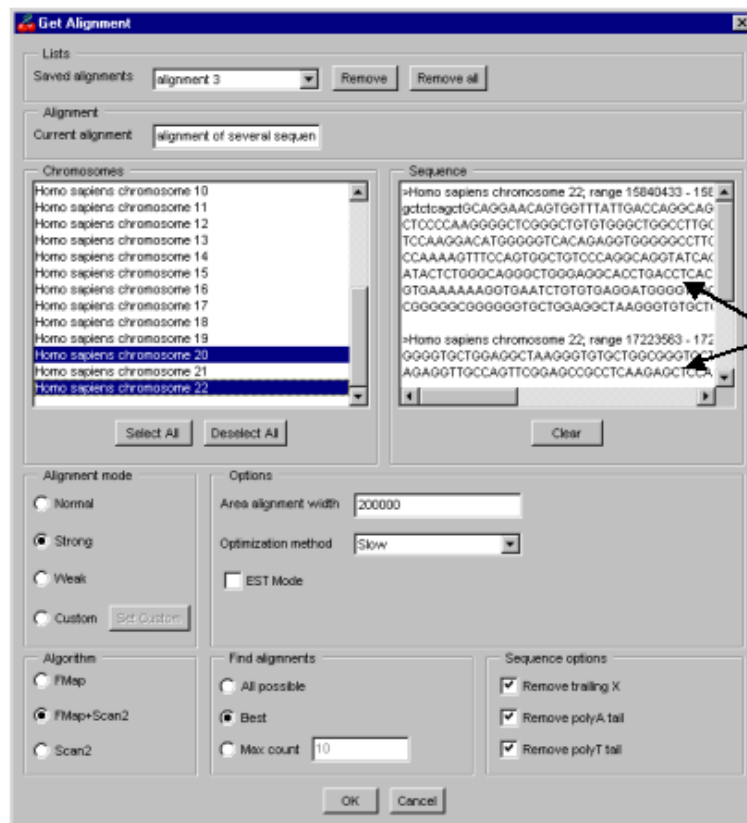
Alignment of multiple sequences

Figure 3.7.9.

1. Sequences in the FASTA-format.

3.7.5. Dialog window for user-defined alignment mode

Upon a selection of user-defined alignment mode the «Set Custom» button, which opens the «Set Custom Alignment Mode» dialog window, becomes available. In this window the following alignment parameters can be defined (fig. 3.7.10):

1. The minimally allowable length of considered block (diagonal element). It requires the entering of appropriate values into the «for best block» and «for all another blocks» fields below the «Minimal considered block length» title. This parameter means that considered blocks should be not less than it's defined in appropriate fields, and is being defined separately for the best block and all others.
2. The minimally allowable score of considered block. It requires the entering of appropriate values into the «for best block» and «for all another blocks» fields below the «Minimal considered block score» title. This parameter means that considered block score should be not less than it's defined in appropriate fields.
3. The minimally allowable number of matches between L-pletts (tracts) on a diagonal element. This parameter can be defined in the «for best block» and «for all another blocks» fields below the «Minimal needed L-plett matches» title.
4. The number of the first ("best") potential diagonal elements to be taken for scanning. It can be defined in the «Scan only N best potential diagonal elements» field.
5. The minimal threshold for sequence similarity, which can be defined in the «Threshold for similary» field.
6. The minimally allowable length of considered L-pletts, which can be defined in the «Use L-plett of length» field.
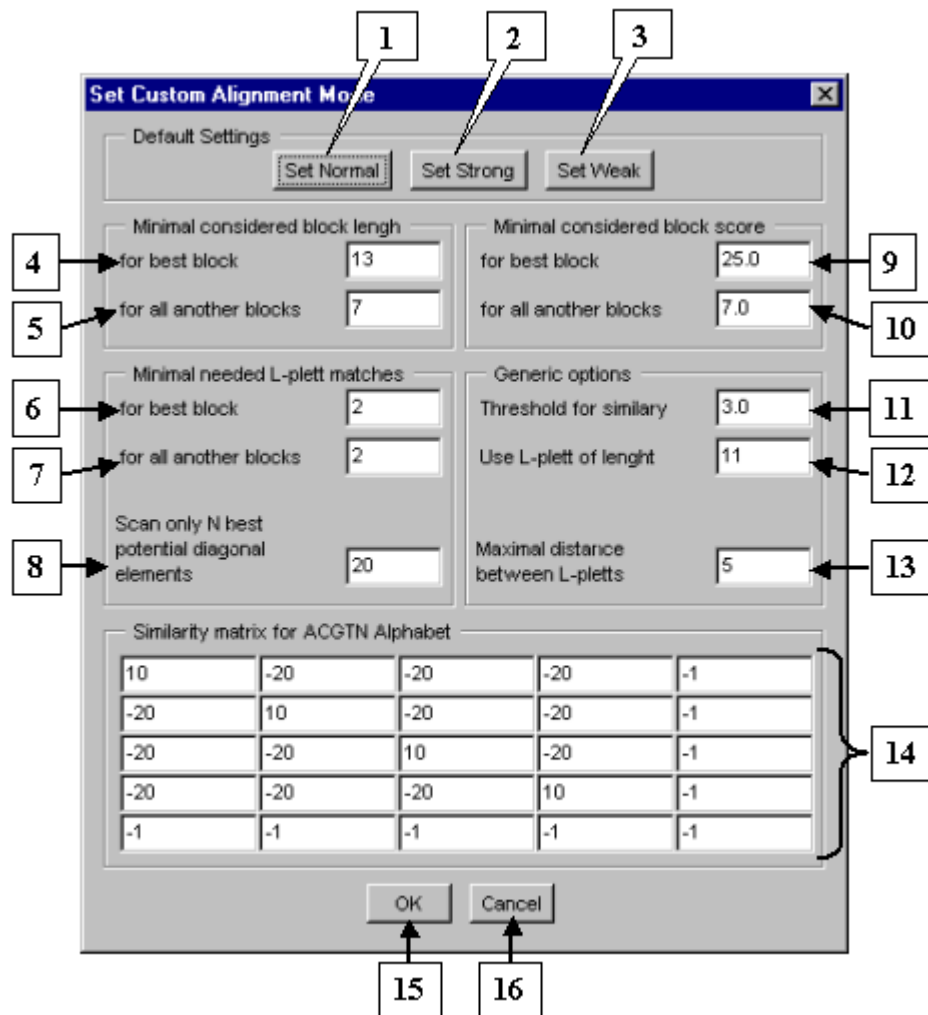
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Dialog window for user-defined alignment mode

Figure 3.7.10.

1. Button for setting the regular similarity degree. **2.** Button for setting the strong similarity degree. **3.** Button for setting the weak similarity degree. **4.** Setting the «best block not less then...» parameter. **5.** Setting the «all another blocks not less then...» parameter. **6.** The minimally allowable number of matches in L-pletts (tracts) for the "best" block. **7.** The minimally allowable number of matches in L-pletts (tracts) for all another considered blocks. **8.** The number of the first ("best") potential diagonal elements to be taken for scanning. **9.** Setting the «best block score not less than...» parameter. **10.** Setting the «all another blocks score not less than...» parameter. **11.** The minimal threshold for sequence similarity. **12.** The minimally allowable length of considered L-pletts. **13.** The maximal length of interval on a diagonal, which must contain at least as much L-pletts matches as defined in the fields «6» and «7». **14.** Similarity matrix for ACGTN Alphabet (The matrix mathematical expectation should be negative). **15.** Confirmation button. **16.** Rejection button.

7. The length of interval, which must contain at least as much L-pletts matches as defined in the fields below the «Minimal needed L-plett matches» title. This length can be defined in the «Maximal distance between L-pletts» field. If a diagonal contains no intervals satisfying the set parameters, then it's being not considered.
8. The required values in the «Similarity matrix for ACGTN Alphabet». The matrix mathematical expectation should be negative.

9. Press the «OK» button.

In order to check up the values of parameters used for regular, strong or weak similarity degree press the «Set Normal», «Set Strong», or «Set Weak» buttons of the «Set Custom Alignment Mode» dialog window respectively. In the fields the values of parameters used for a selected mode will appear.

3.8. Gene search

The Softberry Genome Explorer allows a genomic sequence to be searched for regions, which could be genes. For such an analysis the PPD software is used.

The gene search dialog window can be opened using one of the following means:
- Using the «Search->Search Genes» command of main menu.
- Using the [button] button on the toolbar.
- Using the <Ctrl+G> hot keys.

In the appeared gene search dialog window (fig. 3.8.1) the following should be done:

1. To set a gene search region using switches. It could be:
   - The region displayed on the map.
   - The whole loaded region.

   The displayed region is selected by default.
2. To press the «Find» button.

Gene search dialog window

Figure 3.8.1.

1. Search in the region displayed on the map. **2.** Search in the loaded chromosome region. **3.** Search launch button. **4.** Rejection button.

---
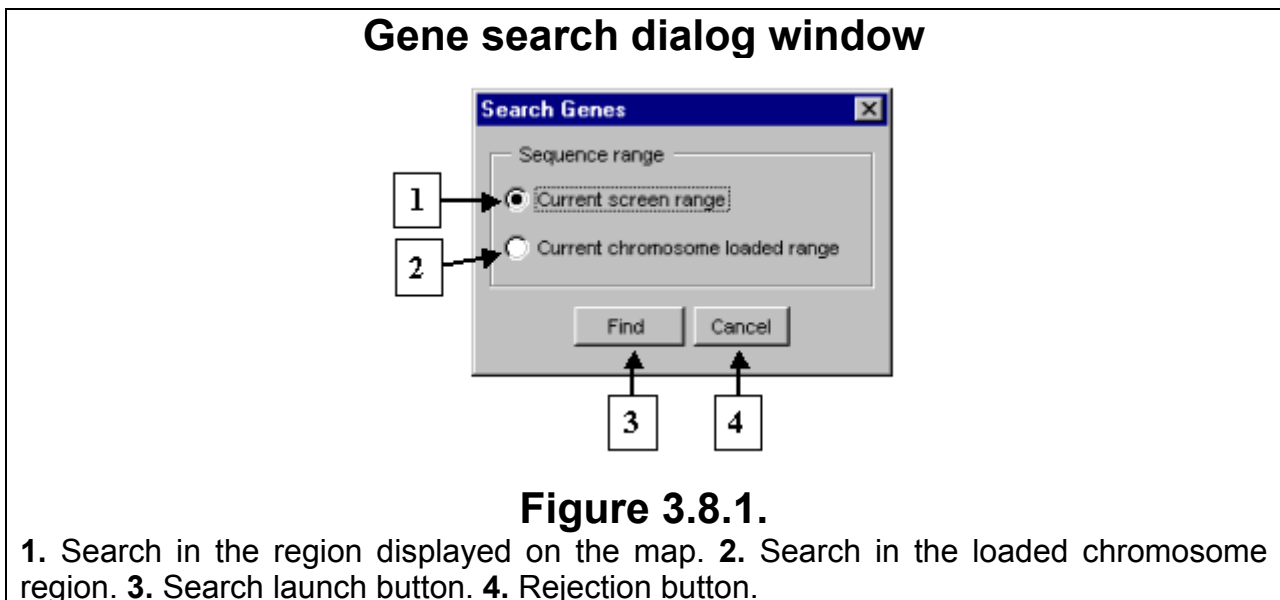
3. The information window with a message on data search process will appear (fig. 3.8.2).

Data search process information window

Figure 3.8.2.

---
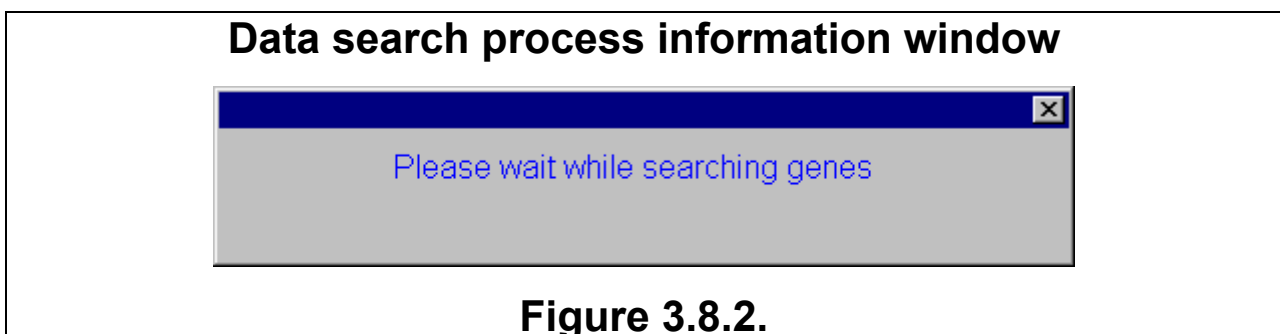
4. Upon a search is done the dialog window with a message on a number of found genes will appear (fig. 3.8.3).
5. Found genes will be displayed on the map (fig. 3.8.4). Upon a placing of the mouse pointer over the one of found sequences information on a corresponding gene will be revealed on the right information bar
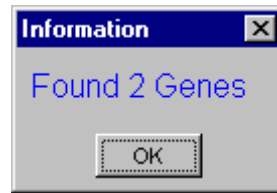
Gene search information window

Information ✕

Found 2 Genes

OK

Figure 3.8.3.

Comment. By default the gene search result is being added to the beginning of feature types lists of the «Load Features Types» and «Features» dialog windows, in which loading of the feature types and their display on the map are regulated. But in contrast to found motifs and alignments, which may be of different types (in dependence on a number of performed search requests), the type of genes found in a single chromosome always the same and has the standard name.

Found genes localization
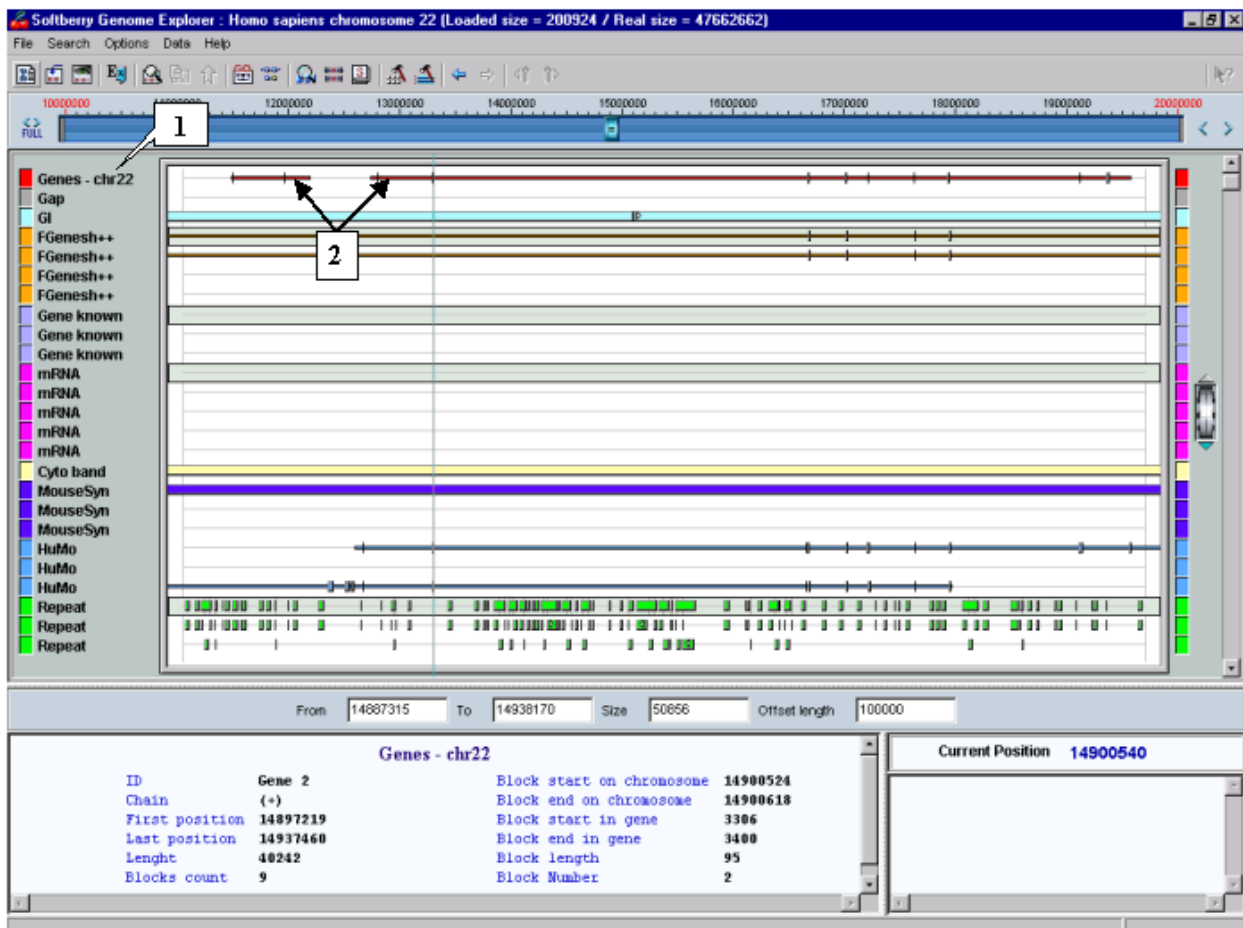
Figure 3.8.4.
1. The layer of found genes type. **2.** Found genes.

3.9. Expression

The expression dialog window can be opened using one of the following means:

- Using the «Data->Show Expression» command of main menu.
- Using the «Show Expression» command of feature popup menu.
- Using the ⬛ button on the toolbar.
- Using the <Ctrl+E> hot keys.

Figure 3.9.1.

1. Histogram mode. **2.** Profile diagram with data markers mode. **3.** Profile diagram mode. **4.** Dot diagram mode. **5.** Vertical grid lines display mode. **6.** Horizontal grid lines display mode. **7.** Pseudo-3D plot mode (for diagram only). **8.** Button for opening the "Expression options" dialog window. **9.** Button for removing of all elements from being displayed. **10.** Button for adding of all elements to being displayed. **11.** Button for removing of selected elements from the features list. **12.** Button for removing of all elements from the features list. **13.** Button for adding of a feature to the list by ID. **14.** Button for adding of a feature from the map to the list. **15.** Common profile of all groups. **16.** Plot area. **17.** Drop down list of features types. **18.** List of features (for current type). **19.** Button for exclusion of all data groups. **20.** Button for turn on the minimum and maximum for all data groups. **21.** Button for turn on the list mode for all data groups. **22.** Button for inclusion of all data groups. **23.** List of groups. **24.** Information bar.

In the expression dialog window data on features expression are displayed (fig. 3.9.1). It consists of three parts: the plot, the list of features and the list of data groups.

3.9.1. Plot

On the top of expression dialog window, above the plot area, there are the buttons, which allow the data visualization mode to be changed in accordance to the results of experiments. Data can be visualized by the following means:

- As a histogram (fig.3.9.2.A, 3.9.3.A) (Button).
- As a profile diagram with data markers (plot with data markers) (fig.3.9.2.B, 3.9.3.B) (Button).
- As a profile diagram (plot) (fig.3.9.2.C, 3.9.3.C) (Button).
- As a dot diagram (fig.3.9.2.D, 3.9.3.D) (Button).

The button allows horizontal grid lines in the build area, the button – vertical ones. The button allows a pseudo-3D mode for the plot (available for histogram only). The button opens the dialog window for options setting.

Below the build area there is the **information bar of the expression dialog window**. Information starts to be displayed in this bar on a placing of the mouse pointer over a plot element (or on a click on it – depends on current settings). At the top the chromosome name and ID of feature, for which the data are shown, are being displayed. The right column contains information on the group of data (elements), which is currently being pointed by mouse, (brief name, full name, number of elements in a group, minimal and maximal expression value for the elements of this group). The left column contains information on the element, which is currently being pointed by mouse, (brief name, full name and expression value).

Comment. There are two modes of data visualization:
- Single visualization of feature expression.
- Multiple visualization of feature expression.

Switch between these modes can be performed in the list of features.

In the single mode of feature expression visualization (fig.3.9.2) the coloring of appropriate plot elements corresponds to that of data groups. Above the plot the minimal and maximal values for all groups of data on a feature expression are being displayed. In the upper part of plot there is a common profile of all groups of data on feature expression. In the upper part of plot there is a markup of all data groups. The markup color corresponds to that of data group. The ordinate axis shows the expression value (zero corresponds to a certain expression level and thus values for elements can be negative, as shown on the fig.3.9.1, 3.9.3). The abscissa axis shows the brief names of experiments.

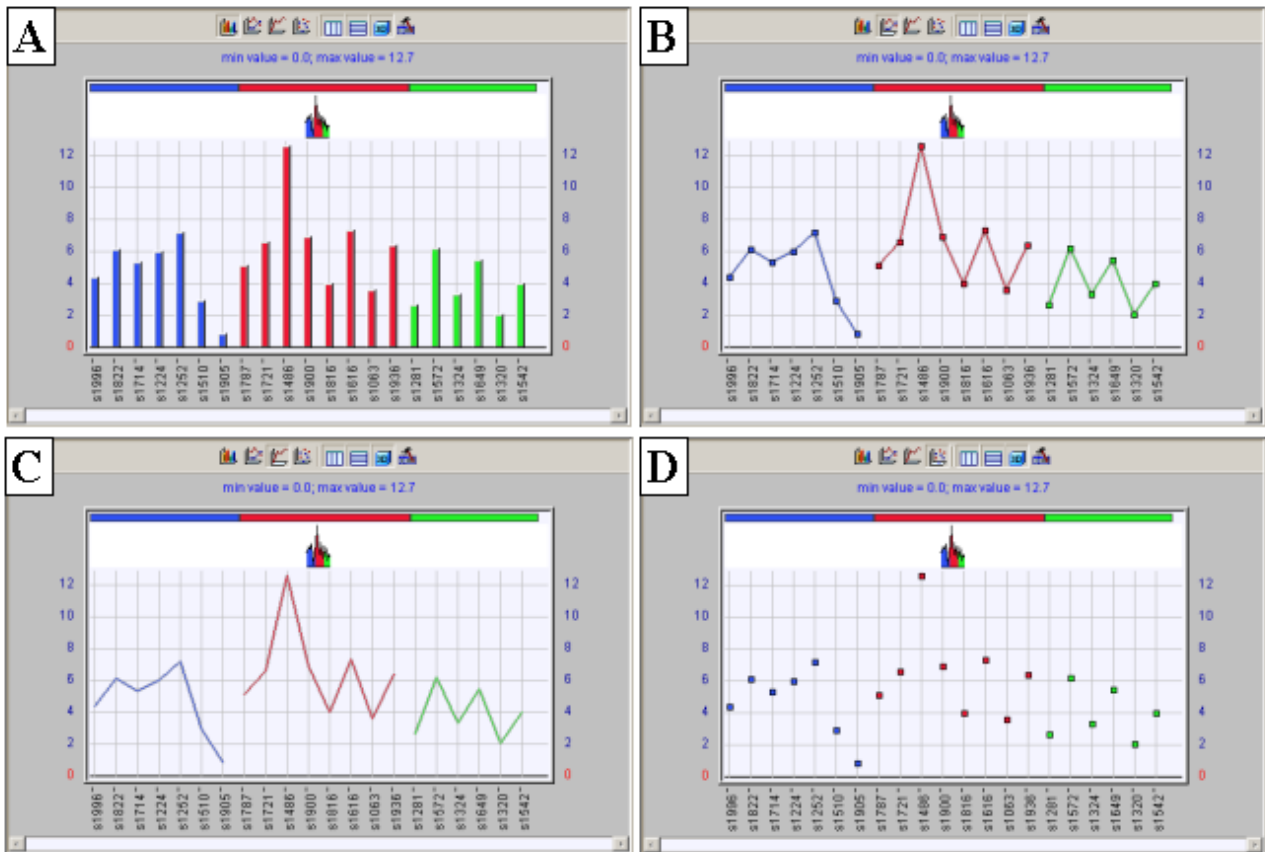**Single mode of visualization of feature expression**

Figure 3.9.2.
A. Histogram mode. **B.** Profile diagram with data markers mode. **C.** Profile diagram mode.
D. Dot diagram mode.

In the multiple visualization mode data for one and more features are being displayed. In this mode (fig.3.9.3), the coloring of appropriate plot elements corresponds to that of features (genes). Above the plot the minimal and maximal values for all groups of data on all features in the list (independently on which ones were selected to be displayed) are being displayed. In the upper part of plot there is a markup of all data groups. The markup color corresponds to that of data group. In the histogram mode the data for each experiment are being displayed by series and columns overlaps for a half. In a front there is the element (column) of data group for that gene, which occupies the most upper position in the list. On the mouse left click on any of elements the gene expression profile corresponding to a selected element will be highlighted with a color, which was set in the "Expression options" dialog window.
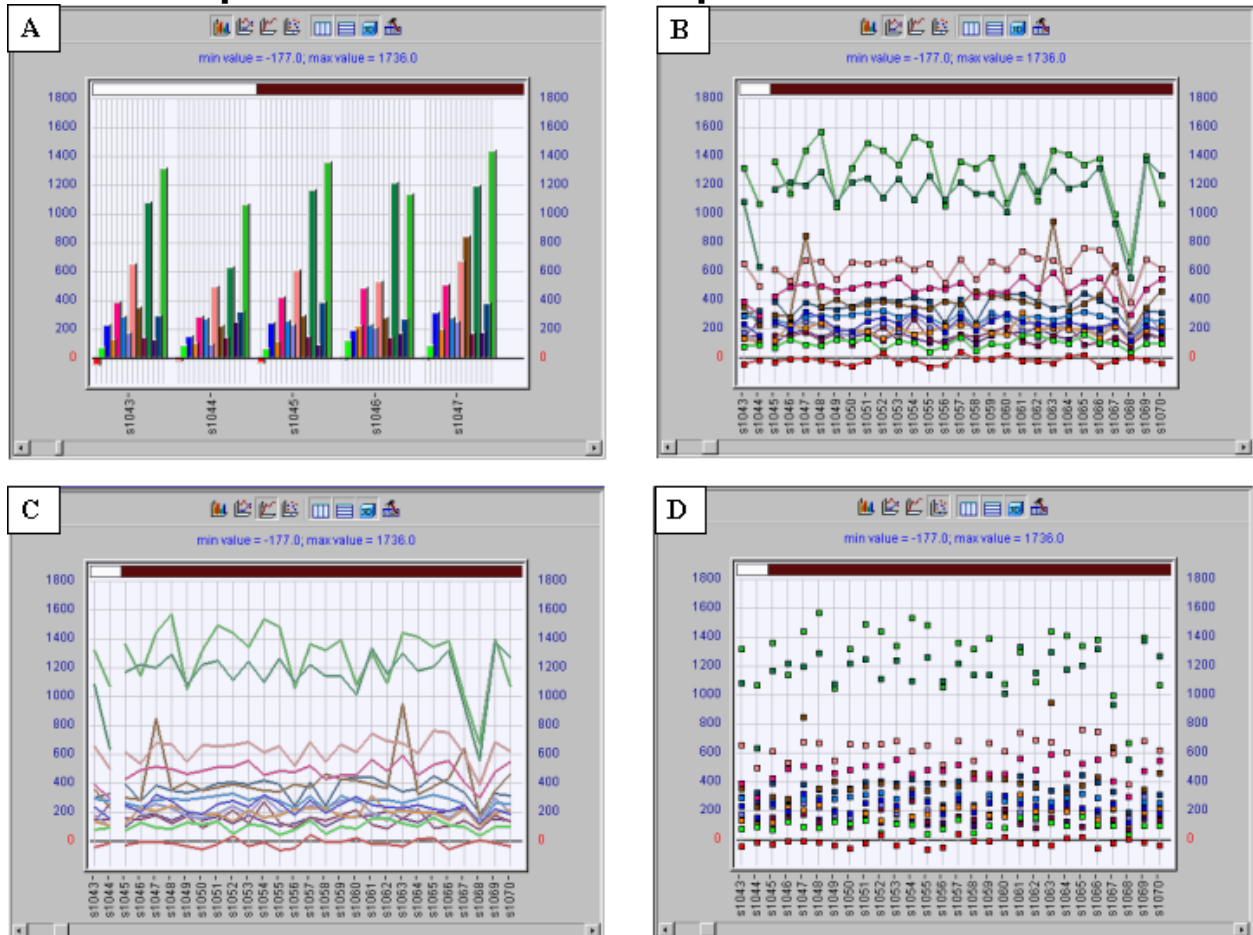
Figure 3.9.3.

A. Histogram mode. **B.** Plot with data markers mode. **C.** Simple plot mode. **D.** Dot diagram mode.

3.9.2. Features list

In the upper right part of the expression dialog window there is the features list. The buttons to the left of features names (color of a button corresponds to that of a feature) allow operating every feature separately. Each button consists of two parts. The square part is the status indicator (switches through in a cycle manner by mouse clicks) and the rectangle one is the working part. These buttons provide the following facilities:

- Switch to the <mark>single</mark> mode of feature expression visualization by pressing the working part. The button at this will appear drowned (fig. 3.9.1). At the time a single button only can be pressed (on a pressing another button the previous one releases).
- Switch to the multiple mode of feature expression visualization by releasing of all buttons (fig.3.9.4). Switch from detailed to multiple mode occurs on releasing of that feature button, which currently is in detailed mode of visualization.
- Inclusion of a feature to visualization. To achieve this click on the button status indicator until the black square appears (■▭).
- Exclusion of a feature from visualization. To achieve this click on the button status indicator until the white square appears (▢▭). If all features are excluded from visualization, the build area will remain empty independently on a selected visualization mode, either detailed or multiple.
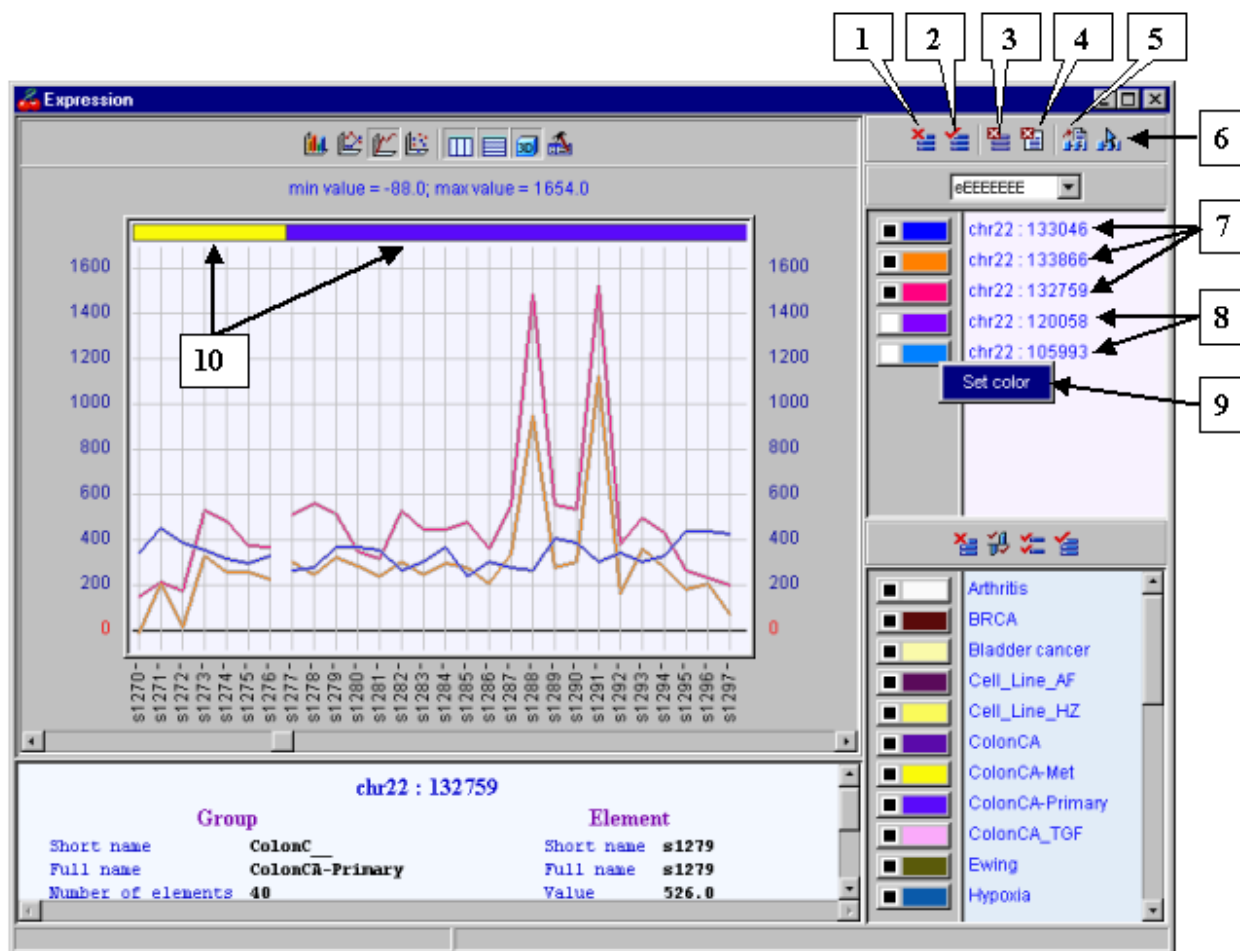
Features list

Figure 3.9.4.
1. Button for exclusion of all list elements. **2.** Button for inclusion of all list elements. **3.** Button for exclusion of selected elements from the features list. **4.** Button for exclusion of all elements from the features list. **5.** Button for inclusion of a feature to the list by ID. **6.** Button for inclusion of a feature to the list from the map. **7.** Features, included for visualization. **8.** Features, excluded from visualization. **9.** Popup menu. **10.** Data groups markup.

In order to change the color of visualized feature click the mouse right button on a rectangle part of button. In the appeared popup menu select the «Set color» command and then, using the color set dialog window, set a desired color (color set dialog window operating is described in 3.3.1).

Above the list of features (fig. 3.9.4) there is the set of buttons, which allow the list parameters to be changed.

The ▤ button allows the simultaneous exclusion of all features from visualization.

The ▤ button allows the simultaneous inclusion of all features to visualization.

The ▤ button allows the exclusion of selected features from the list. Feature can be selected (or unselected) by clicking on its name.

The ▤ button allows the exclusion of all features from the list.

3.9.3. Data groups list

In the lower right part of the expression dialog window there is the list of data groups. The buttons to the left of data groups' legends (color of button corresponds to that of data group, controlled by the button) allow operating each data group separately. Each button consists of two parts. The square part is the status indicator (switches through in a cycle manner by mouse clicks) and the rectangle one is the working part. These buttons provide the following facilities:

- Turn off the visualization mode for a group of data. To achieve this click on the button status indicator until the white square appears (▢▬). If this mode is selected for a group, no elements of the group will be displayed on the plot.
- Turn on the visualization of minimal and maximal data group values only. To achieve this click on the button status indicator until the white square with black boarders appears (▫▬). If this mode is selected for a group, then elements of the group with minimal and maximal values only will be displayed on the plot.
- Turn on the visualization of elements, selected in the list of the current group (visualization "by the list"). To achieve this click on the button status indicator until the grey square with black boarders appears (▣▬). If this mode is selected for a group, then on the plot will be displayed only those elements, which have been selected in the list of the group elements (fig. 3.9.5, 3.9.6). The list can be opened using the group popup menu (see below).
- Turn on the visualization of all elements of data group. To achieve this click on the status indicator until the black square appears (■▬). If this mode is selected for a group, then all elements of the group will be displayed on the plot.
- Turn on the visualization of a certain data group. To achieve this click on the working area of the button, which corresponds to the desired data group. The button at this will appear drowned and in the build area the selected data group only will be displayed. At the time a single button only can be pressed (on a pressing another button the previous one releases). In order to quit this mode, release the button of currently displayed group.

Visualization of elements of a certain group depends on the mode selected for a group. Fig. 3.9.5 shows different states of buttons and corresponding ways of graphic data visualization. For "BRCA1" group turned on the visualization mode of elements with minimal and maximal values only (white square with black boarders on the button status indicator). For "BRCA2" group turned on the visualization mode of all elements (black square on the button status indicator). For "Sporadic" group turned on the visualization mode of those elements only, which have been selected for visualization in the list of group elements (fig. 3.9.6) (grey square with black boarders on the button status indicator). "Sporadic/Meth BRCA1" group of data is excluded from visualization (white square on the button status indicator).

In order to open the popup menu of a group (fig. 3.9.5) click the mouse on the working part of corresponding button.
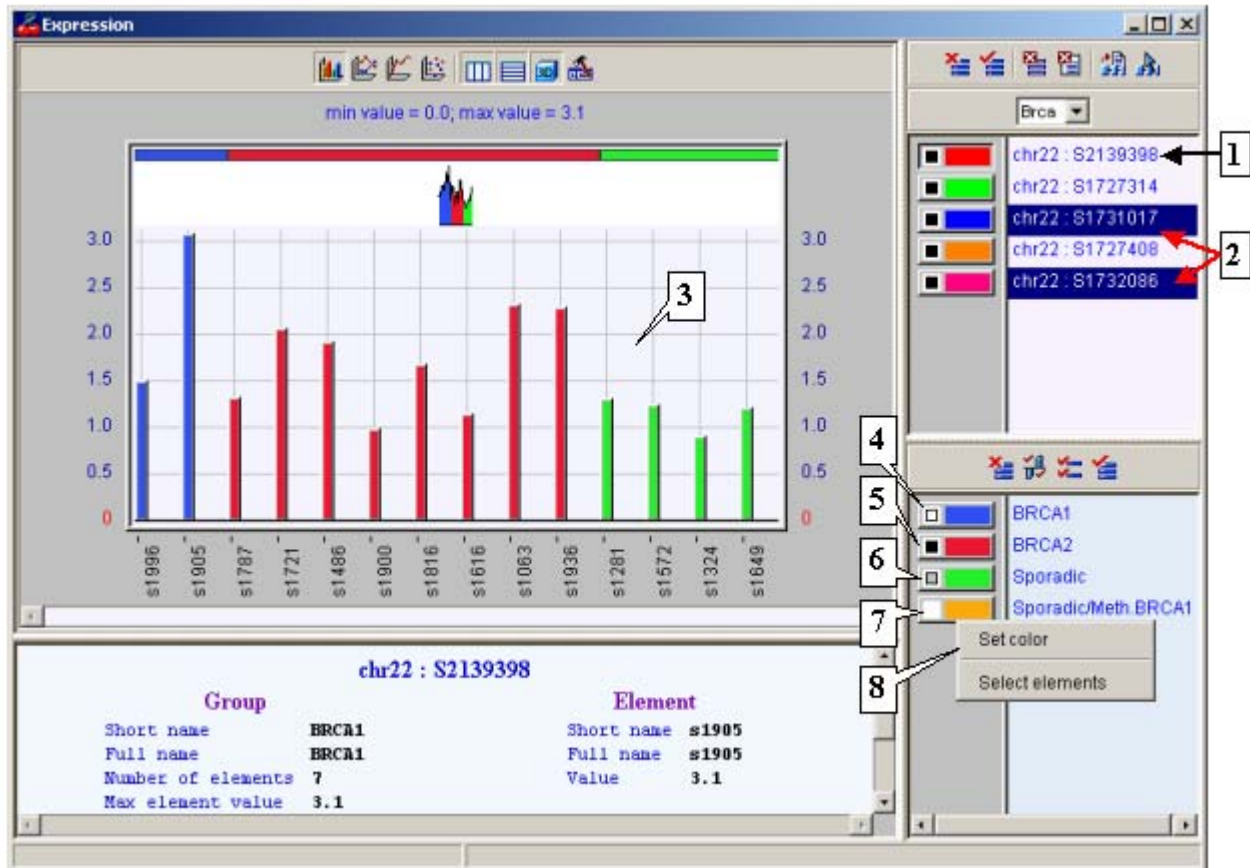
Data groups

Figure 3.9.5.
1. Feature, selected for visualization. **2.** Selected features. **3.** Build area with displayed data groups. **4.** Mode of group's minimum and maximum visualization. **5.** Mode of visualization of all group elements. **6.** Mode of visualization of elements, selected in the list of the current group. **7.** Groups of data, excluded from visualization. **8.** Popup menu of data group.

In order to select the elements of the group for visualization, launch the «Select elements» command of group popup menu. It will open the window with the list of group elements. The title of the window will contain the full group name. To select required elements (fig. 3.9.6) click on the status indicator to the left of element name. Black square in the indicator area means the element is selected for visualization, differently - the element is not selected. The 🗹 button provides the simultaneous selection of all elements of the list. The 🗙 button allows the deselection of all elements of the list. Press the «OK» button to confirm the selection. This set of elements, selected for visualization, is valid for visualization "by the list" mode only.

In order to change the color of data group visualization select the «Set color» command of group popup menu. In the appeared dialog window set the desired color (the dialog operating is described in chapter 3.3.1).
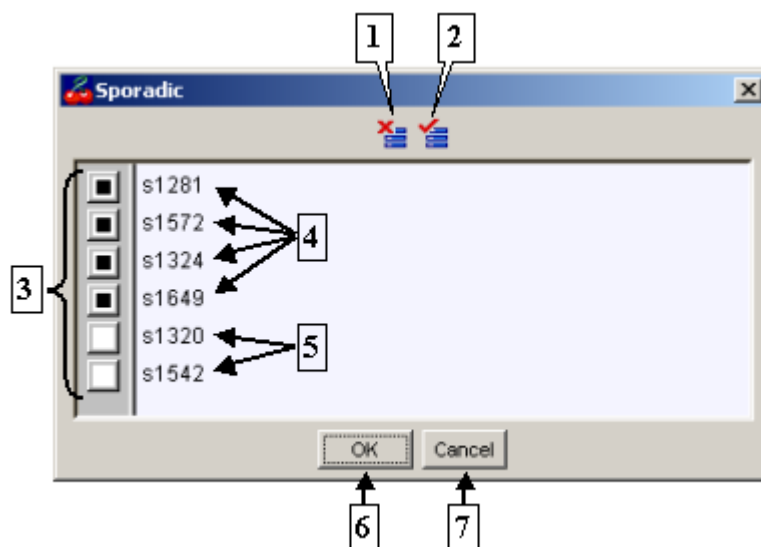
Group elements list

Figure 3.9.6.
1. Button for deselection of all elements of the list. **2.** Button for selection of all elements of the list. **3.** Elements status indicators. **4.** Elements, selected for visualization. **5.** Non-displayed elements. **6.** Confirmation button. **7.** Rejection button.

Above the list of group elements there is the set (line) of buttons, which allow the visualization parameters of all data groups, displayed in the build area, to be changed.

The ⊞ button allows the simultaneous exclusion of all data groups from visualization.

The ⊞ button allows the simultaneous switch to display only the elements with minimum and maximum values of all data groups.

The ⊞ button provides the simultaneous turn on the displaying mode of selected elements for all data groups (fig. 3.9.5, 3.9.6).

The ⊞ button provides the simultaneous turn on the displaying mode of all elements for all data groups.

3.9.4. Features types

Above the list of features there is the drop down list containing the features types (fig. 3.9.1). In this list the type, to be operated with, can be selected.

3.9.5. Adding of a feature to the list

Feature can be added to the list from the map using the «Show Expression» command of feature popup menu. At this the plot automatically switches to detailed mode for selected feature.

The ⊞ button allows a feature to be added to the list by its ID. On the button is pressed, the dialog window (fig. 3.9.7) appears. In this window there are the field, in which the feature ID (or its part) must be entered, and switches of the search regions (all chromosomes or the current one). During the search will be retrieved all features meeting the search parameters. Search does not depend on a symbols case.
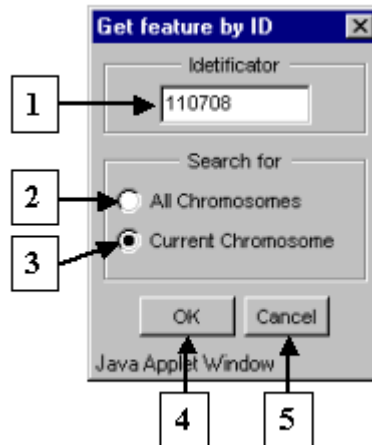
Features list dialog window

Figure 3.9.7.

1. Feature ID field. **2.** Search of features in all chromosomes. **3.** Search of features in the current chromosome. **4.** Confirmation button. **5.** Rejection button.

Found features will be added to the list. If there are no features meeting the set search conditions in a selected region, then error message window will appear (fig. 3.9.8).
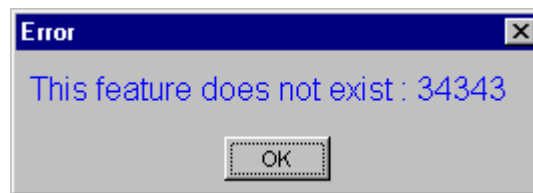
Error message window

Figure 3.9.8.

The ⏧ button allows a feature to be added to the list by its selection on the map. In order to do so, press this button and then click on a required feature on the map. Adding occurs for features of the selected type only.

3.9.6. Options dialog window

The ⏧ button opens the "Expression options" dialog window (fig. 3.9.9). This window allows the following parameters to be set:

- A feature can be added to the list from the map both for current features type and for all ones. For adding to the list of current type press the «For current type only» button. While in this mode, attempts to add a feature of another type to the list will be ignored by the application. At the pressed «For all types» button occurs the automatic switch to the list of features of that type, to which the selected on the map feature belongs.
- To turn on the mode, in which the confirmation for deleting of genes (features) from the list (fig.3.9.10) is being requested. The request mode can be turned on either for deleting of several genes (for this purpose switch to «Deleting genes by list»), or for deleting of all genes from the list (for this purpose switch to «Deleting all genes»).
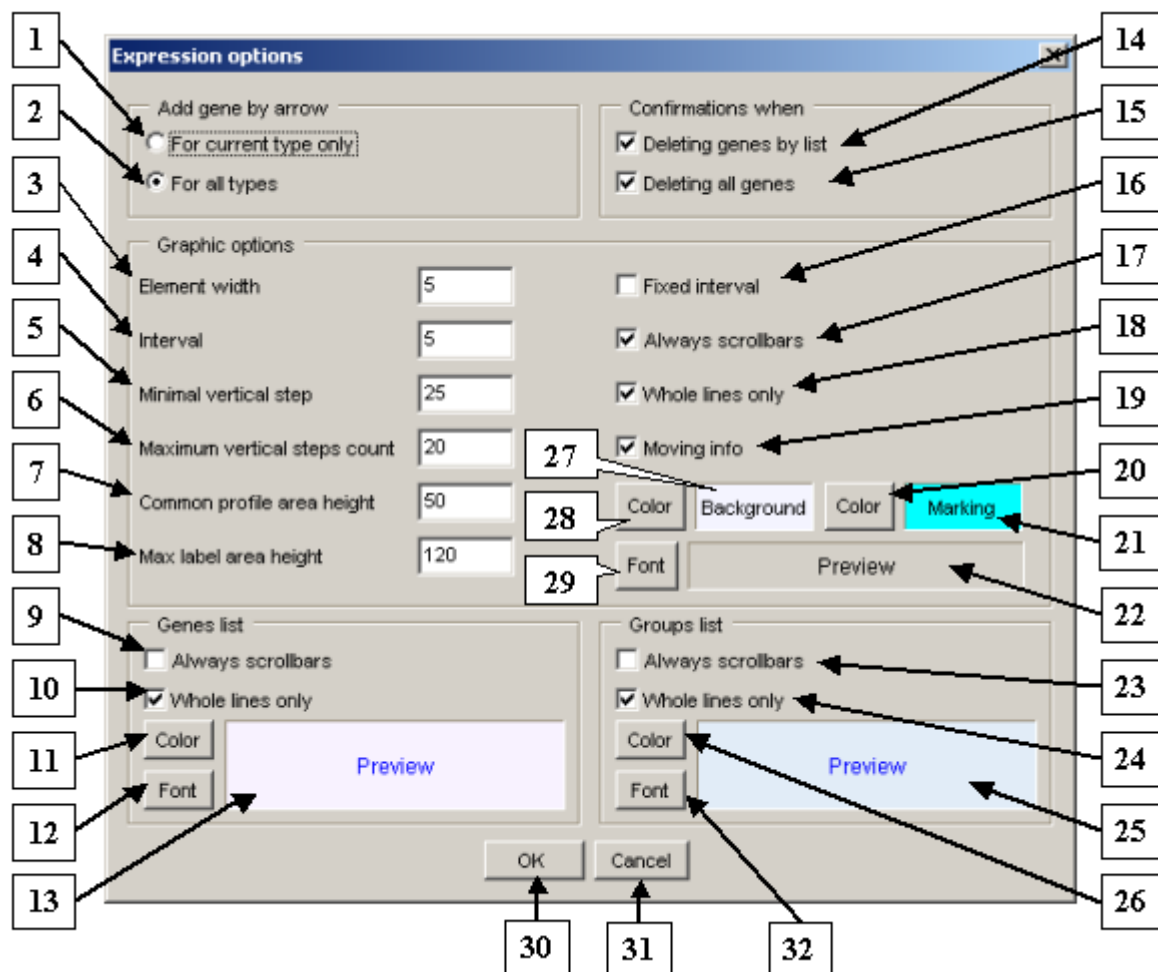
Expression options dialog window

Figure 3.9.9.

1. Add a gene by the arrow to the list of current feature type only. **2.** Add a gene by the arrow to the lists of all features types. **3.** Width of element on the plot. **4.** Gap between elements. **5.** Minimal vertical step along the ordinate axis. **6.** Maximal number of vertical steps along the ordinate axis. **7.** Height of total data profile. **8.** Maximal height of font for data element legend. **9.** Always display the scrollbars in the list of genes. **10.** Display only the complete strings in the list of genes. **11.** Button for setting of the genes list background color. **12.** Button for setting of the genes list font. **13.** Preview bar for the list of genes (features). **14.** Request the confirmation for removing of several genes from the list. **15.** Request the confirmation for removing of all genes from the list. **16.** Set the fixed gap between elements. **17.** Always display the scrollbars in the build area. **18.** Display only the complete strings in the build area. **19.** Display the information on a data element at the mouse pointer movement. **20.** Button for setting the color of a selected gene profile. **21.** Color preview bar for the selected gene profile. **22.** Font preview bar for the plot. **23.** Always display the scrollbars in the list of groups. **24.** Display the complete strings in the list of data groups. **25.** Preview bar for the list of data groups. **26.** Button for setting of the data groups list background color. **27.** Preview bar for the background color of the build area. **28.** Button for setting of the build area background color. **29.** Button for setting of the plot font. **30.** Confirmation button. **31.** Rejection button. **32.** Button for setting of the data groups list font.

Tuning up the plot:

- «Element width» - the width (in pixels) of data element on the plot.

- «Interval» - the interval (gap) (in pixels) between data elements (or data series for visualization of several genes) on the plot.
- «Minimal vertical step» - the minimally allowed step (in pixels) between the legends of values on the ordinate axis.
- «Maximum vertical steps count» - the maximal number of the legends of values on the ordinate axis.
- «Common profile area height» - the height (in pixels) of the total data profile. This value is strictly fixed.
- «Max label area height» - restriction of the data legend size (in pixels) under the plot. Since the legends are vertically oriented, then all brief names of all group elements are being looked through and the maximal length of legend for all groups is being taken. If lengths of all names are shorter than that is defined, the height of data legend will be equal to the maximal legend length for all groups. If legend is longer than defined value, it is being truncated.
- «Fixed interval» - when checked in, the gap between data elements (or data series for visualization of several genes) becomes strictly fixed.
- «Always scrollbars» - when checked in, the scrolling lines are always displayed on the plot independently on their activity status.
- «Whole lines only» - when checked in, only the complete columns or series of columns (for visualization of several genes) are shown, differently, columns or series of columns are truncated.
- «Moving info» - when checked in, the information on a data element is automatically being displayed in the information bar on the placing of mouse pointer over this element. Differently, the information becomes displayed on the mouse click only.
- The «Color» button to the left of the "Background" preview bar allows the background color of the plot to be set. On the button is pressed, the "Color dialog" window, purposed for the color selection (see chapter 3.10), is opened. The selected color is displayed on the "Background" preview bar.
- The «Color» button to the left of the "Marking" preview bar allows the color of the selected on the plot gene profile to be set. On the button is pressed, the "Color dialog" window, purposed for the color selection (see chapter 3.10), is opened. The selected color is displayed on the "Marking" preview bar.
- The «Font» button allows the font for the plot to be selected. On the button is pressed, the "Font" window, purposed for the font selection (see chapter 3.11), is opened. The selected font is displayed on the preview bar.

Request for removing of features from the list

Figure 3.9.10.
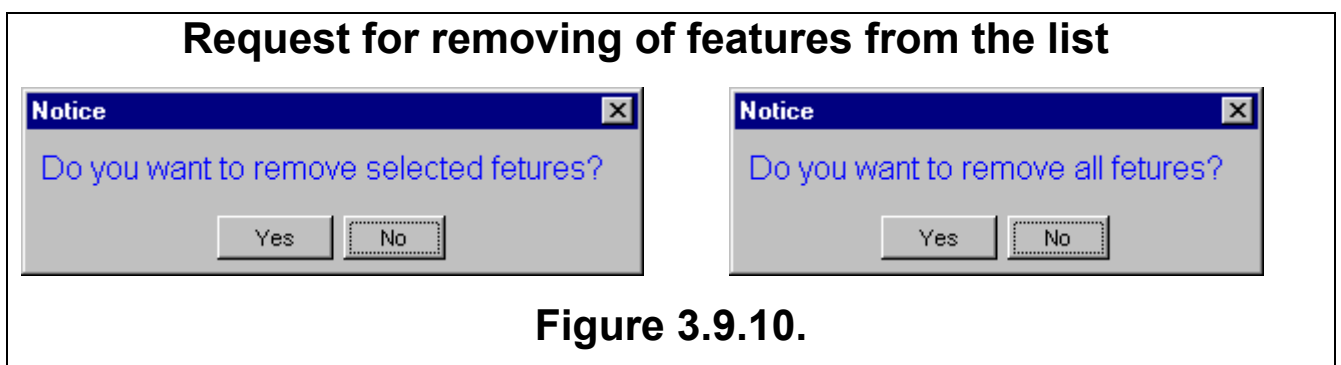
Tuning up the list of genes (features):

- «Always scrollbars» - when checked in, the scrolling lines are always displayed independently on their activity status.

- «Whole lines only» - when checked in, the complete strings of list are shown, differently, strings are truncated.
- The «Color» button allows the background color of the genes list to be set. On the button is pressed, the "Color dialog" window, purposed for the color selection (see chapter 3.10), is opened.
- The «Font» button allows the font for the genes list to be selected. On the button is pressed, the "Font" window, purposed for the font selection (see chapter 3.11), is opened.
- Selected background color and font for the genes list are displayed on the preview bar.

Tuning up the data groups list:

- «Always scrollbars» - when checked in, the scrolling lines are always displayed independently on their activity status.
- «Whole lines only» - when checked in, the complete strings of data groups list are shown, differently, strings are truncated.
- The «Color» button allows the background color of the data groups list to be set. On the button is pressed, the "Color dialog" window, purposed for the color selection (see chapter 3.10), is opened.
- The «Font» button allows the font for the data groups list to be selected. On the button is pressed, the "Font" window, purposed for the font selection (see chapter 3.11), is opened.
- Selected background color and font for the data groups list are displayed on the preview bar.
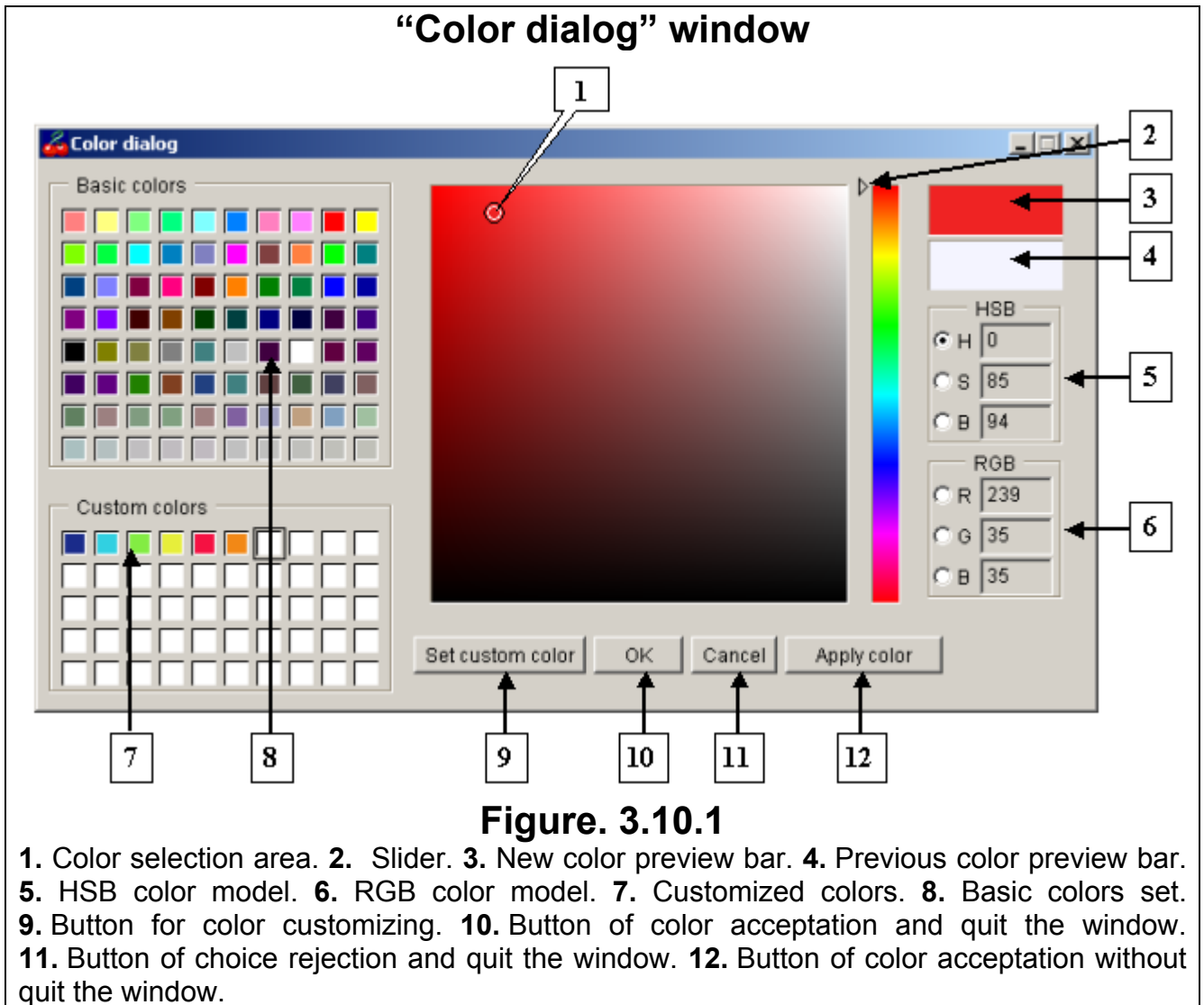
3.10. "Color dialog" window

The «Color dialog» window (fig. 3.10.1) provides the color selection. Color can be selected by several means:
- Using the basic colors set. It requires the clicking on the square with desired color. The selected color will appear on the new color preview bar. To accept the choice press the «OK» or «Apply» buttons.
- Using the customized colors set. It requires the clicking on the square with desired color of this set. The selected color will appear on the new color preview bar. To accept the choice press the «OK» or «Apply» buttons. It's allowed to change the set of colors. It requires the clicking on a square of this set. Using slider and switches of HSB and RGB models fields select a desired color. Upon the «Set Custom Color» button is pressed the selected color will appear in a selected square of the set and on the new color preview bar.
- Using the new color selection. For this purpose use the slider and switches of HSB and RGB color models fields. The selected color will appear on the new color preview bar. To accept the choice press the «OK» or «Apply» buttons.

If it's required to be back to old color click the mouse on the previous color preview bar and press the «OK» or «Apply» buttons.

Comment. The «OK» button provides the acceptation of changes made and quit the window. The «Cancel» button provides the rejection of changes made and quit the window. The «Apply color» button provides the acceptation of changes made without quit the window.

"Color dialog" window

Figure. 3.10.1

1. Color selection area. **2.** Slider. **3.** New color preview bar. **4.** Previous color preview bar. **5.** HSB color model. **6.** RGB color model. **7.** Customized colors. **8.** Basic colors set. **9.** Button for color customizing. **10.** Button of color acceptation and quit the window. **11.** Button of choice rejection and quit the window. **12.** Button of color acceptation without quit the window.

3.11. "Font" Dialog window

The "Font" dialog window (fig. 3.11.1) provides the setting of font parameters.

- The "Font" list provides the selection of a desired font.
- The "Font style" list provides the selection of the font style.
- The "Size" list provides the selection of the font size.
- The «Choose color» button opens the color set dialog window (see 3.10), in which the font color can be selected
- The «Preview» bar provides the preview of selected font.
- The «OK» button provides the acceptation of changes made and quit the window.
- The «Apply font» button provides the acceptation of changes made without quitting the window.
- The «Cancel» button provides the rejection of changes made and quit the window.
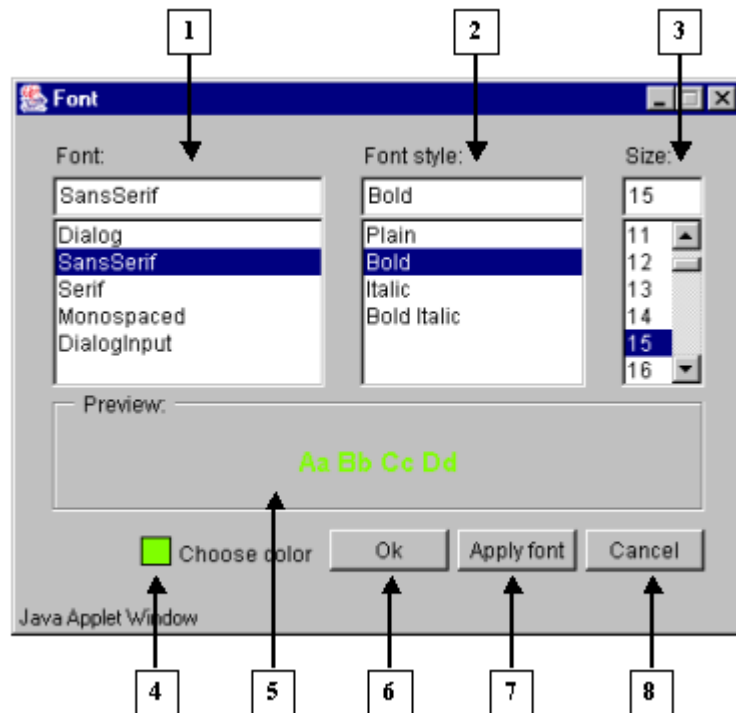
Font parameters dialog window

Figure. 3.11.1.

1. List of font selection. **2.** List of font style selection. **3.** List of font size selection. **4.** Button of font color selection. **5.** Font preview bar. **6.** Button of changes acceptation and window quit. **7.** Button of changes acceptation without window quit. **8.** Rejection button.