



User's Guide



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Preface

What is SignalMap?

SignalMap™ enables you to visualize NimbleGen array data. It provides the ability to:

- ◆ Import one or more GFF (General Feature Format) files.
- ◆ Visualize tracks of data organized into panes and tracks.
- ◆ See peak correlations between your data and annotation tracks.
- ◆ Link to a web site with detailed information for a selected gene.
- ◆ Export a subset of your data.
- ◆ Print and export screen captures.

Licensing

You can use SignalMap to visualize NimbleGen array data. Usage of this program or its components for other commercial/non-commercial entities purposes is strictly prohibited. Read license.txt on the SignalMap software CD for details on your current licensing agreement. Contact a NimbleGen representative for more information or to extend your license.

Requirements

SignalMap runs on computers with the Microsoft® Windows® operating system. Following are the system recommendations and requirements:

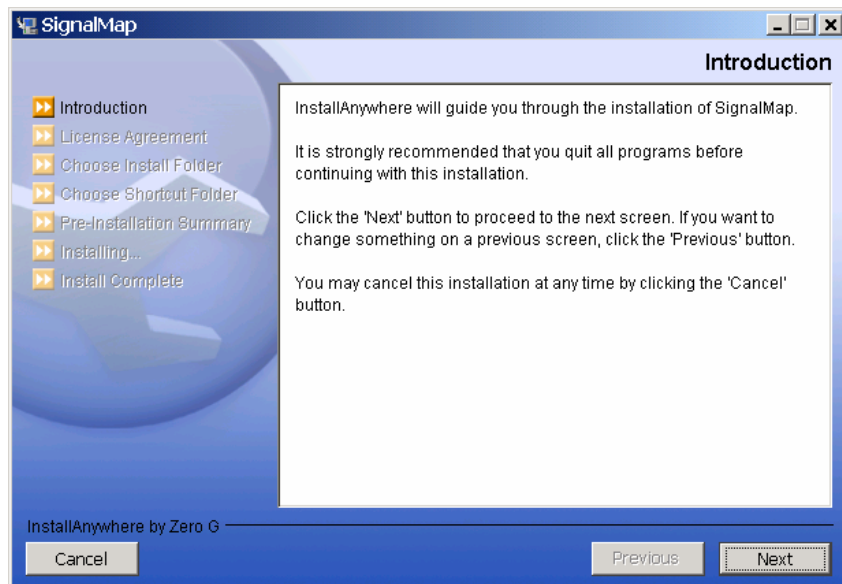
- ◆ Pentium III 600 MHz (Pentium II 450 MHz minimum) or equivalent
- ◆ 384 MB (256 MB minimum) RAM
- ◆ 384 MB (256 MB minimum) Virtual RAM
- ◆ 10 MB free space on your hard drive
- ◆ Microsoft Windows 98/ME/2000®XP® (Windows 98 minimum)
- ◆ SXGA 1280x1024 with 16-bit colors (SVGA 800x600 minimum)
- ◆ Hardware graphics drivers recommended
- ◆ Standard keyboard and 2-button mouse

Note: *SignalMap performs best with large amounts of memory. To increase efficiency, close other programs while using SignalMap.*

Installing SignalMap

You must install SignalMap from the CD or from files downloaded from NimbleGen's web site.

Click Install.bat to launch the installation program. Follow the on-screen installation instructions.



For detailed installation instructions, see ReadMe.txt on the CD or NimbleGen's web site.

! **CAUTION:** *Although NimbleGen has performed every effort towards providing a stable product, the Company is not responsible for system errors or data corruption from using this software.*

Technical Support

If you have trouble working with SignalMap, email your questions to technical-services@NimbleGen.com.

To report SignalMap software errors, see Appendix B, Reporting Bugs.

Chapter 1. Basic Concepts

To use SignalMap effectively and efficiently, you need to understand the basic concepts underlying this software. In this chapter, you learn about:

- ◆ A typical session for using the software
- ◆ The elements in the SignalMap interface
- ◆ GFF (General Feature Format) files
- ◆ Printing your data

Using SignalMap: A Typical Session

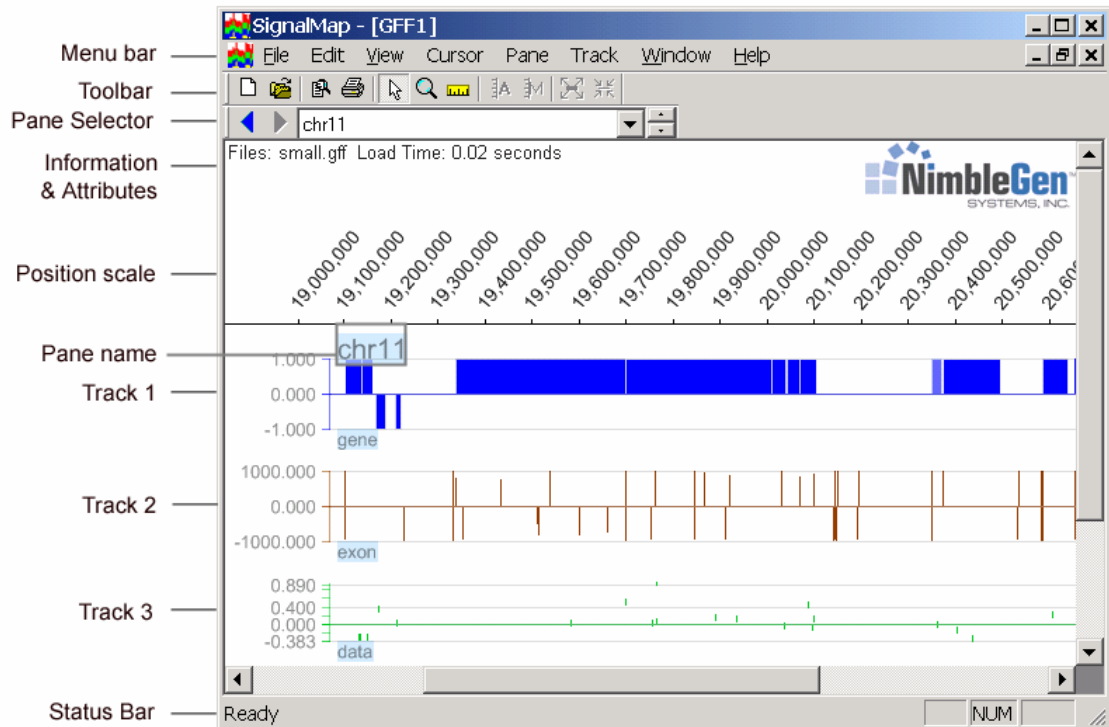
The following is a broad overview of a typical session using SignalMap.

To use SignalMap:

1. Start the SignalMap software. The SignalMap program window appears.
2. Choose File -> New to create a new document window.
3. Import your data files. For more information, see “Importing Data” in Chapter 2, Importing Your Data.
4. Browse your data. For more information, see “Viewing Panes and Tracks” in Chapter 3, Browsing Your Data.
5. Export your data or screen capture. For more information, see “Exporting Your Data” in Chapter 4, Exporting Your Data.
6. Print a screen. For more information, see “Printing Your Data” in this chapter.

The SignalMap Interface

When you import files into SignalMap, a window similar to the following appears:



Toolbar

Use the buttons on the toolbar to quickly access SignalMap features.

Tip: You can display or hide the toolbar by choosing View -> Toolbar.

Tip: You can move the pane selector by dragging it with the mouse.



Create a new document

Creates a new document (or window) in which to import data. The first new document window is called GFF1. Subsequent windows opened in the same session are named sequentially, GFF2, GFF3, and so on.



Import Files

Imports existing GFF files, saved with either a GFF or TXT filename extension. You can import several GFF files at a time.



Print Preview

Displays a preview of the current display before you print.



Print

Prints the current display to the selected printer.



Pointer

Click to select data or genes.

For locations on the gene track annotated with web addresses, double-click to activate the hyperlink.



Magnifier

Use to zoom in or out of the display in the selected pane. Be aware your magnification selections will *not* affect other panes.

- ◆ Click in the display to double the magnification around the center of the click.
- ◆ Press the Ctrl key then click to halve the magnification.
- ◆ Click and drag to magnify an area.



Auto Scale

Enables the automatic scaling of the y axis for the selected tracks.



Manual Scale

Displays the Manual Scale dialog box, from which you can change the minimum and maximum y-axis scale for the selected tracks.



Increase Point Size

Increases the height of the data to make it more visible.



Decrease Point Size

Decreases the height of the data.

Panes and Pane Selector

SignalMap displays the data from a GFF file in panes. Each pane contains information corresponding to one seqname defined in the GFF file. Typically, a seqname will be the chromosome or region name for NimbleGen-supplied data.

You can select individual panes from the selection box in the pane selector. Choosing the All Tracks button displays all tracks.

! **CAUTION:** *SignalMap replaces an empty seqname with a space.*



Back (Pane History)

Displays the previous pane in your browsing history.



Forward (Pane History)

Displays the next pane in your browsing history.

Information and Attributes

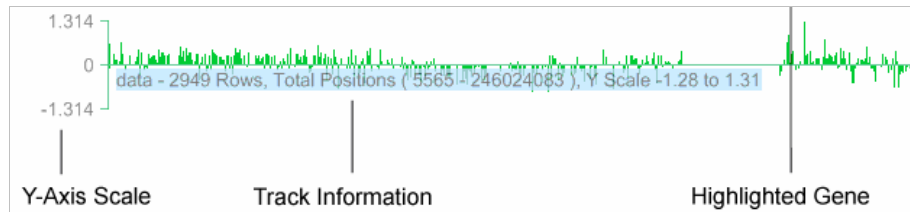
Displays information about the dataset and attributes for the specific data point under the pointer. Each line is optional:

- ◆ Displays the names of imported GFF files and the time taken to import the data.
- ◆ Displays the number of loaded rows, positions displayed, and total positions.
- ◆ Displays the information that corresponds to the data under the pointer.
Score: The score for the data point.
Start and End Position: The first and last position for the data point.
Attribute information: The contents of an optional column in the GFF file. Attribute information could include web site links and annotation.
- ◆ Displays the information that corresponds to the gray cursor selection.

Position Scale

Displays the x-axis scale for all tracks in the pane. This scale corresponds to the start and end column in the GFF file.

Tracks



Each track displays data for different types of features in the GFF file.

- ◆ *Y-Axis Scale:* Displays the y-axis scale information.
- ◆ *Track Information:* Displays the feature, number of rows, and other information about the track.
- ◆ *Highlighted Gene:* A transparent gray bar is displayed over the track at the location of the selected gene.

Status Bar

Caps Lock

Displays CAPS when the Caps Lock key is set on your keyboard.

Num Lock

Displays NUM when the Num Lock key is set on your keyboard.

Scroll Lock

Displays SCRL when the Scroll Lock key is set on your keyboard.

GFF Files

SignalMap can import and export GFF files with either GFF or TXT filename extensions. For more information about GFF files, see www.sanger.ac.uk/Software/formats/GFF/GFF_Spec.shtml or see “Understanding GFF File Format” in Appendix A, GFF Files.

Importing Your Data



To import data into a new SignalMap document, choose File -> New or click the New button on the toolbar. The Import GFF Files dialog box automatically appears. Use this dialog box to open the GFF file(s) to load. You can also import GFF files by dragging and dropping them into an existing document.

For more information, see “Importing Data” in Chapter 2, Importing Your Data.

Printing Your Data

SignalMap prints your data based on the magnification of the display. That is, the Print command prints exactly what you see on your screen. Therefore, zoom in to the region before using the Print command. (See “Magnifying Regions of Data” in Chapter 3 for details.) Data always print to a single page.

Note: Before you print your data, check your print settings. You may need to change the print orientation from portrait to landscape.

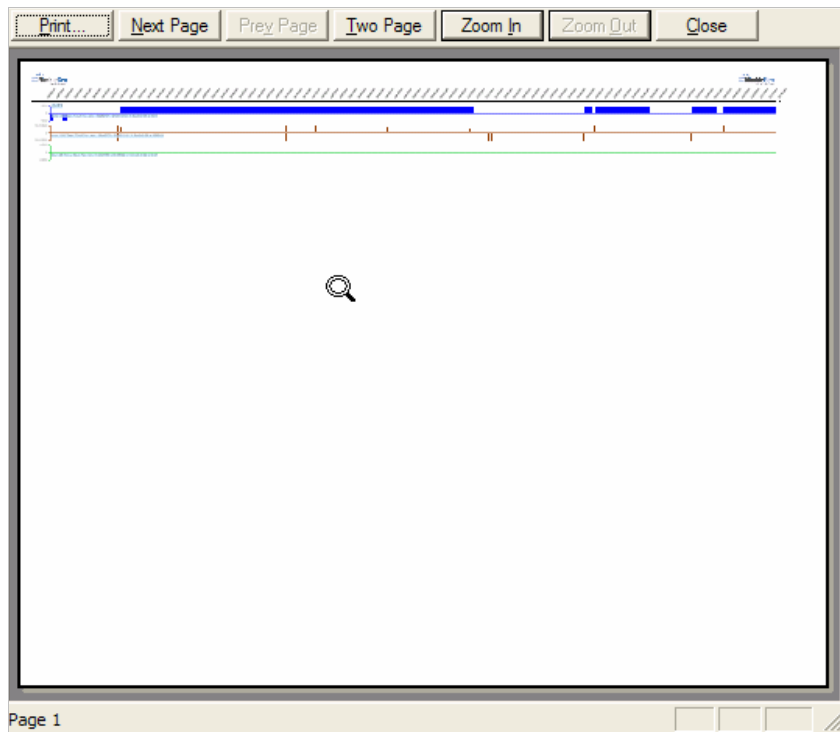
To view or change your print settings:

1. Choose File -> Print Setup.
The Print Setup dialog box appears.
2. Select your printer and print properties.
For example, you may want to change the Orientation from Portrait to Landscape.
3. Click OK to print.
Your data prints onto one page.



To preview your data before you print:

1. Choose File -> Print Preview or click the Print Preview button on the toolbar.
A preview of what will print displays in the window, as shown in the following image.



2. Click Print... at the top of the preview window to print the data.

To print your data as shown on the screen:



1. Choose File -> Print or click the Print button on the toolbar.
The Print dialog box appears.
2. Select your printing preferences.
3. Click OK.
Your data prints onto one page.

Chapter 2. Importing Your Data

SignalMap can quickly import large GFF (General Feature Format) files, importing more than one million rows of data in less than 40 seconds with a Pentium IV computer.

SignalMap performs best when other memory-intensive software, such as graphics software, are not running simultaneously. Close any Windows software you do not need before importing your data files.

! **CAUTION:** *Although SignalMap easily imports very large files, it requires significant amounts of memory to do so. NimbleGen recommends you close other memory-intensive software, such as graphics programs, when working with SignalMap to avoid losing information should those programs stop responding. If SignalMap stops responding, report the problem to NimbleGen as described in "Appendix B. Reporting Bugs."*

SignalMap organizes GFF data is by seqname, one per pane, then by feature, one per track, and then by position.

In this chapter, you learn to:

- ◆ Import data
- ◆ Import annotation
- ◆ Include hyperlinks

Importing Data

You can import any GFF file with a GFF or TXT filename extension into SignalMap.

To import data:

1. Choose between the following:

- ◆ To import data into your current document, choose File -> Import or click the Import GFF Files button on the toolbar.
- ◆ To import data into a new document, choose File -> New or click the New button on the toolbar.

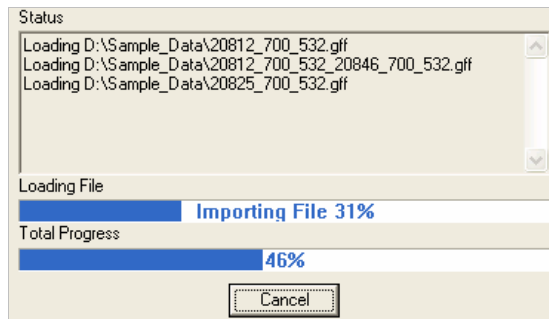
A new document window opens, and the Import GFF Files dialog box appears.

Tip: *Drag and drop GFF files into the current document to import them.*

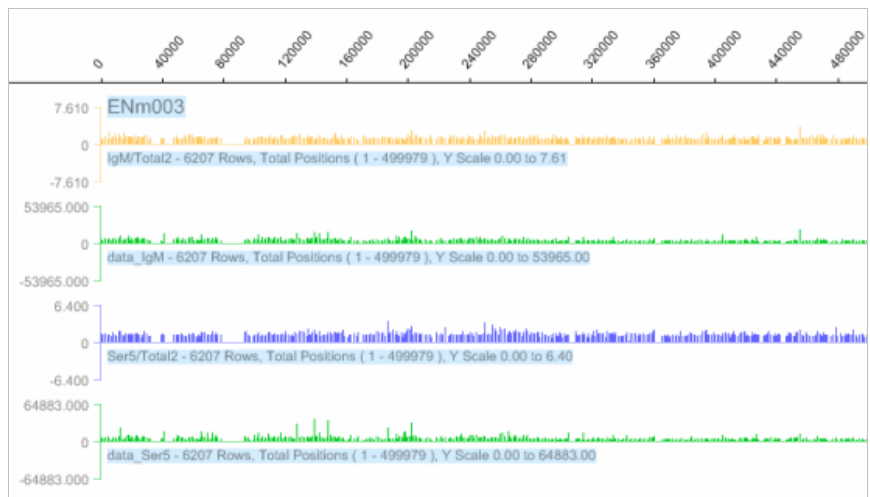


2. Select the GFF files to import. Hold down the Ctrl key while clicking to select multiple files.
3. Click Open.
SignalMap imports the files into the document.

The Import Files window, shown in the following image, provides status information that shows the progress of the import. In this example, SignalMap has loaded 31% of the third file, representing 46% progress towards the time required to import all files.



The following image shows an example of data-only GFF files.



You will notice some data tracks are displayed in a green color, while other data tracks are shown in other colors.

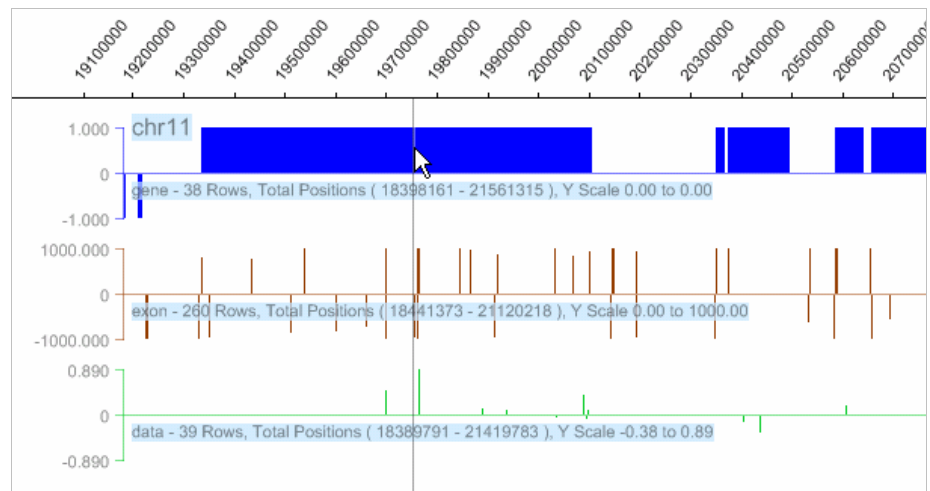
When data tracks contain the word “data” in the feature field of the GFF file, SignalMap displays the track with a green color. However, data tracks frequently are named according to sample ratios (e.g. AcK9H3/Total1) or other naming schemes preferred by the researcher and will thus display with various colors.

Annotation

SignalMap imports annotation (*any* feature other than data) in the same way as any other GFF file.

Note: To display the track with the colors designated below, the GFF file must specify the name of the track in the feature field. If it does not, SignalMap displays the track in a different standard color.

When possible, SignalMap displays certain tracks with specific colors to enable you to more easily identify them in the pane. The following image provides a typical example.



Track color assignments for annotation:

- ◆ *gene*: This track contains information about the start and end of genes. You can click a gene to highlight all data in the same position as that gene. If web hyperlinks were specified in the GFF file, you can double-click their location on the gene track to open your computer's default web browser and access the specified web site. Usually displays with a blue color.
- ◆ *exon*: This track contains exon data. Usually displays with a brown color.
- ◆ *CDS*: This track contains CDS data. Usually displays with a turquoise color.
- ◆ *start_codon*: This track contains the start codon position. Usually displays with a red color.

Hyperlinks

SignalMap treats any http hyperlink in the GFF file's attribute field as a hyperlink. URLs can also be specified using the GFF3 tag format `url=someurl`. You can separate multiple items in the attribute field with a semicolon (;).

Placing the pointer over a data point containing a hyperlink allows you to view the web address. Double-clicking data with a hyperlink opens your computer's default web browser and accesses the specified web site.

A common use for hyperlinks is to link to web site information about specific genes. This would be accomplished by adding URL links in the attribute fields for gene feature records. The following lines provide acceptable hyperlinks.

Chr1	NGS	track1	20	30	30.0	.	.	chr info; http://www.nimblegen.com
Chr1	NGS	track1	30	40	40.0	.	.	url='http://www.nimblegen.com'
ChrX	NGS	track1	10	15	20.0	.	.	http://www.gene.gov/N_001412

Chapter 3. Browsing Your Data

SignalMap allows you to quickly browse your GFF (General Feature Format) data. In this chapter, you learn to:

- ◆ View panes and tracks
- ◆ Reorganize tracks
- ◆ Detect peaks
- ◆ Search data
- ◆ Magnify regions of data
- ◆ Change the track height
- ◆ Change the y-axis scale
- ◆ Change the track style
- ◆ Change the color
- ◆ Highlight track data
- ◆ Use hyperlinks

Viewing Panes and Tracks

SignalMap organizes GFF data into *panes* and *tracks*. Each SignalMap document can contain up to 32,768 panes.

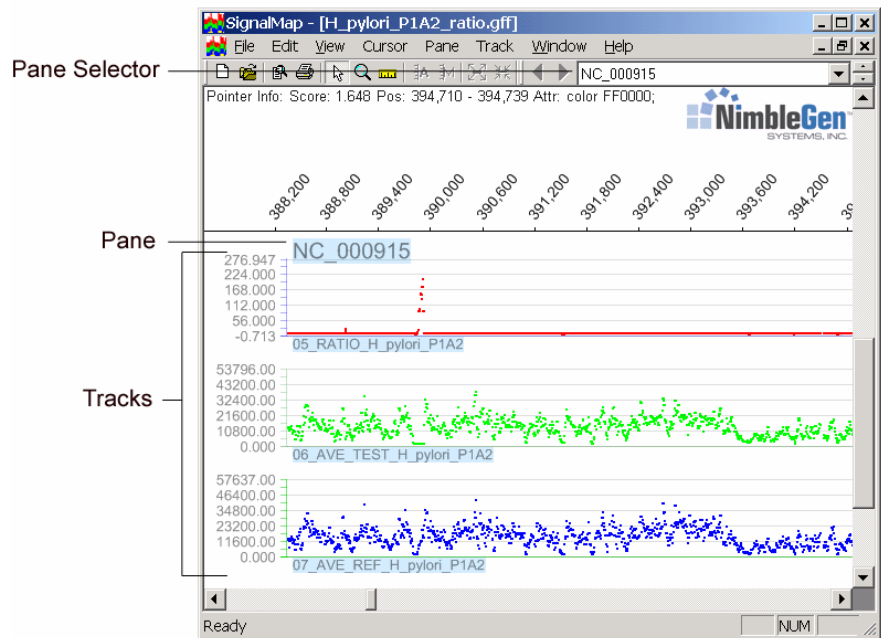
Each *pane* can contain an unlimited number of tracks. A pane contains data tracks corresponding to one seqname. NimbleGen-supplied GFF data will usually be organized to display one chromosome or region per pane. The name of the pane (seqname) appears above the first track shown, as marked on the image shown on the following page.

Typically, each individual *track* contains only one data or annotation *feature*. The feature name and other details are printed below the graphical representation of the data on the track.

When a new GFF file is imported, the first pane is selected by default.

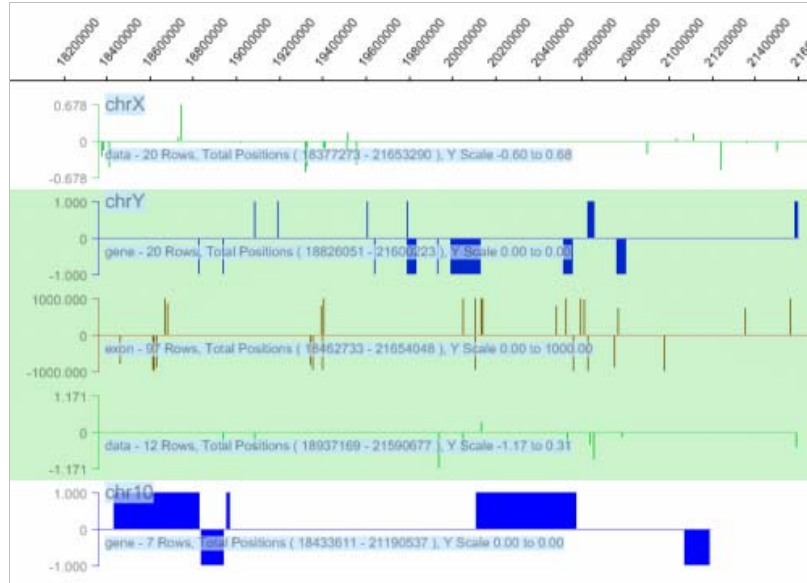
To view tracks on a particular pane:

1. Use the pane selector to select to a pane of interest or browse through panes using the history buttons and the up/down buttons. SignalMap displays the data tracks for the selected pane (seqname), as shown in the following image.



To view all tracks:

1. Select All Tracks (the top selection in the pane selector drop-down list). All tracks appear in the pane, as shown in the following image.

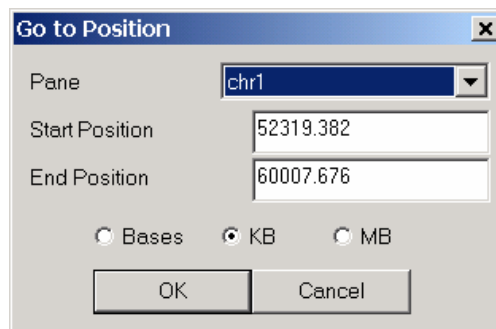


The tracks for each seqname appear with alternating color backgrounds (white and lime green) to separate the seqname data visually.

2. Use the window's vertical scroll bar keys to scroll to the tracks to view in this pane.

To go to a specific location:

1. Choose View -> Go to Position or press Ctrl + G. The Go to Position dialog box appears, as shown below:



2. Select the pane and position and click OK. SignalMap displays the pane and positions selected.

Reorganizing Panes

SignalMap sorts newly imported panes in the order that they were in the file. You can change the sort preference in the Pane menu. You can also delete panes you do not want.

To reorder panes:

1. Choose Pane -> Sort.
2. Choose from the following options.
 - ◆ *Unsorted*: Panes are displayed in the order they were loaded.
 - ◆ *Alphanumeric*: Panes are sorted alphabetically (case-insensitive). If the pane starts with "chr", the pane is sorted numerically using the number following "chr".

To delete panes:

1. Select the pane to delete.
2. Choose Pane -> Delete.
SignalMap deletes the pane.

Reorganizing Tracks

SignalMap sorts newly imported tracks in alphabetic order. You can select and move tracks up or down to suit your needs. You can also delete tracks you do not want.

To select tracks:

1. Using the Pointer tool, select tracks by clicking to the left of the y-axis scale of the track. Hold down the Ctrl key and click to select multiple tracks.
The tracks are selected and a blue bar appears over the y-axis scale.

Note: You can select all tracks by choosing *Track -> Select All* or pressing *Ctrl + Alt + A*.

To move tracks:

1. Select the tracks to move.
2. Click one of the selected tracks and move them to a new location in the pane.
The selected tracks are moved to the designated location.

To delete tracks:

1. Select the tracks to delete.
2. Choose between the following:
 - ◆ Right-click one of the selected tracks and choose delete.
 - ◆ Choose Track -> Delete.

SignalMap deletes the selected tracks.

Detecting Peaks

SignalMap can detect peaks in your data and display the location of these peaks in a separate track. You can then use the peak track to highlight your data. SignalMap can use one of the following procedures to detect peaks.

Windowed Threshold Detection

1. Looks for at least 4 data points within a window that are above a threshold value.
2. Groups these points and adds them to the peak track with a score of the maximum value.
3. Tags isolated data points above the threshold as peaks but displays them in a gray color.

You have the option to change the following parameters.

- ◆ *Peak Window Size*: This is the width of the window in base pairs.
- ◆ *Peak Threshold*: This can be specified as a percentage of the maximum data or as a score.

Second Derivative Peak Detection

1. Averages the data over the range of the track to create a smooth data set. The negative values are discarded. In addition, an optional \log_2 to linear conversion is applied to detect peaks in \log_2 data.
2. Calculates the negative 2nd derivative of the smoothed data. The negative values are discarded.
3. Multiplies the smooth data and the 2nd derivative data.
4. Detects peaks from this data by searching for all points above a percentage of the maximum data.

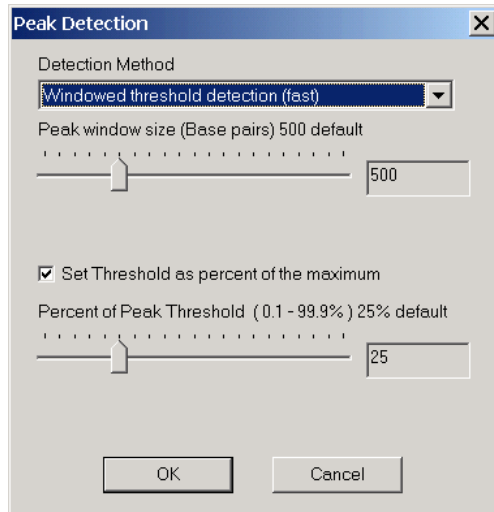
You have the option to change the following parameters:

- ◆ *Peak Window Size*: The approximate width of your peaks in base pairs. This is used for the smoothing width and for the derivative kernel width.
- ◆ *Smooth Step*: The number of bases between each smoothing position. Smaller values will detect more peaks but will take longer to process.
- ◆ *Peak Threshold*: The percentage of the maximum value that should be called as a peak.

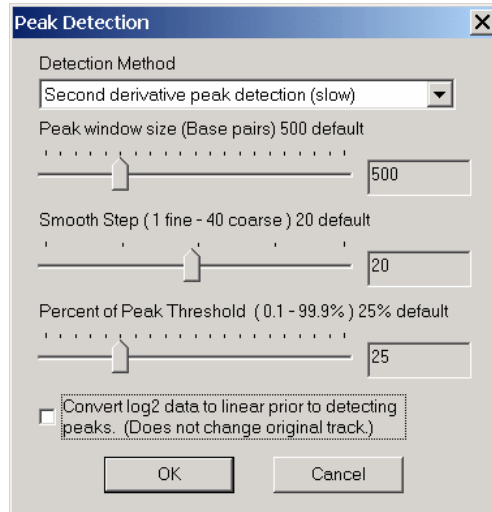
To detect peaks:

1. Select the tracks in which to detect peaks.
2. Right-click one of the selected tracks and choose Find Peaks, or choose Track -> Find Peaks.
3. Select the detection method.

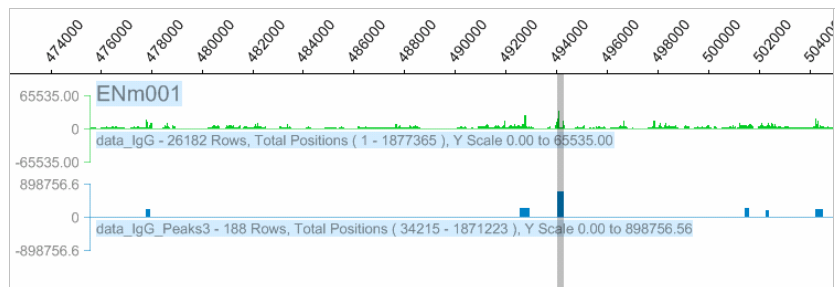
Windowed Threshold Peak Detection Parameters



Second Derivative Peak Detection Parameters



- Adjust the parameters and click OK.
A new track displays under each selected track.



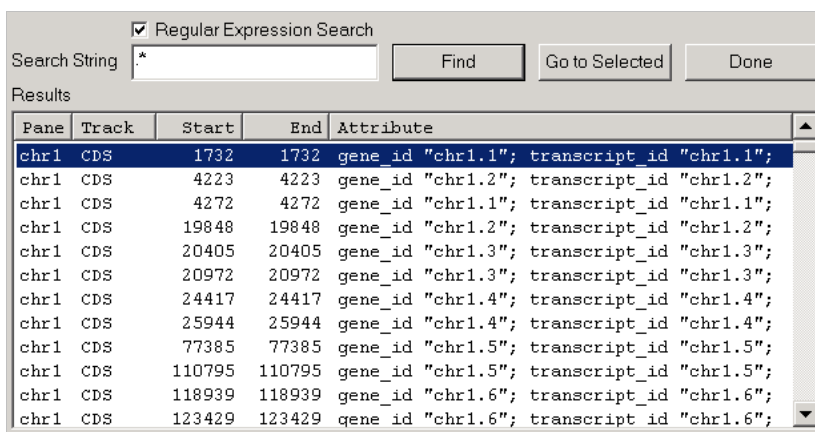
- To highlight the peaks in the track, select the new peak track, and then right-click and choose Attach Cursor.
SignalMap highlights the detected peaks. You can now select peaks with the mouse or by using the arrow keys.

Searching

SignalMap can search for keywords or do regular expression searches in the attribute column of your data.

To search your data:

1. Choose Edit -> Search or press Ctrl + F.
SignalMap displays the Search dialog box.



2. Select the Regular Expression check box if appropriate.
3. Type the search keyword or regular expression and click Find.
SignalMap searches for your keyword or regular expression in the attribute column of your data. The results are displayed in the dialog box.
4. Double-click the item you are interested in.
SignalMap displays the item and highlights it with a selection bar.

Magnifying Regions of Data

SignalMap maintains magnification and scroll position for each pane independently. Use the Zoom tools described below to magnify areas of interest in your data and annotation tracks. For example, you may want to magnify areas where spikes in your experiment data track correspond to gene and/or exon annotation.

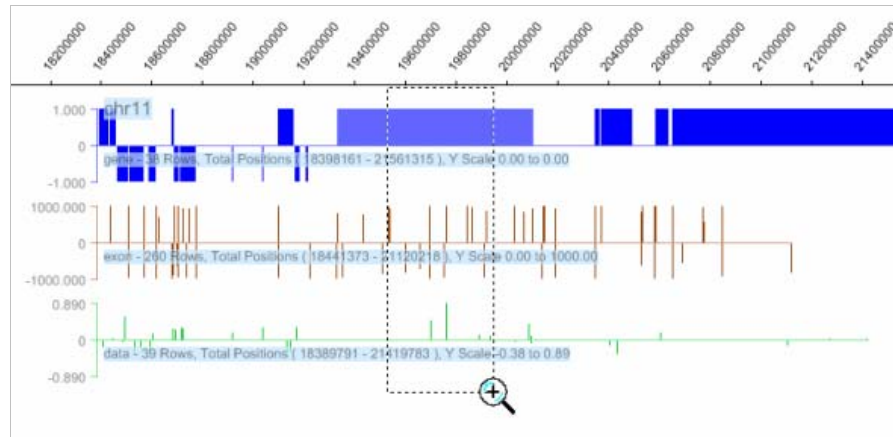
To zoom in (increase magnification):



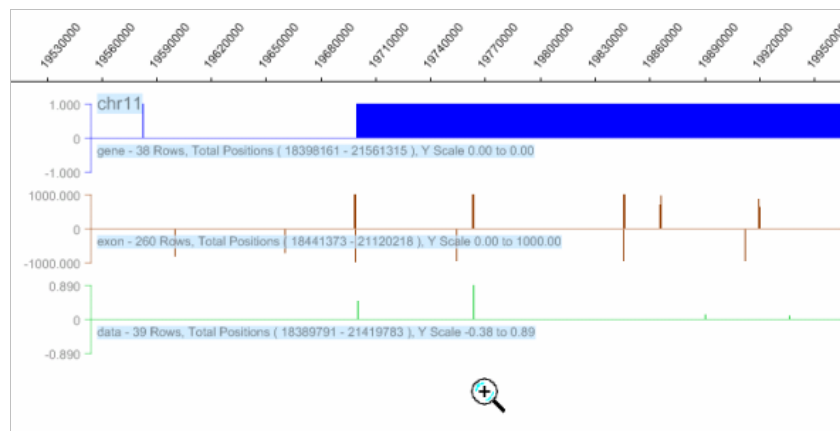
1. Choose View -> Zoom In or click the Zoom button on the toolbar.
The cursor becomes a magnifying glass.

2. Choose between the following:

- ◆ Click the track in the position to magnify. The magnification is doubled around the center of the click. Click again to zoom in further.
- ◆ Click and drag a bounding box around the region of interest to magnify, as shown below.



SignalMap changes the position scale to center the selected region in the document window, as shown below.





To zoom out (decrease magnification):

1. Click the Zoom button on the toolbar.
The cursor becomes a magnifying glass.
2. Choose between the following:
 - ◆ Hold down the Ctrl key and click the position at which to decrease the magnification.
The magnification is halved around the center of the click. Repeat as needed to zoom out to your desired view.
 - ◆ Choose View -> Zoom Out.
 - ◆ Press Ctrl + -.

Tip: To zoom out completely, choose View -> Full Zoom Out or press Ctrl + 0.

Tip: You can also use the right mouse button to zoom in or out.

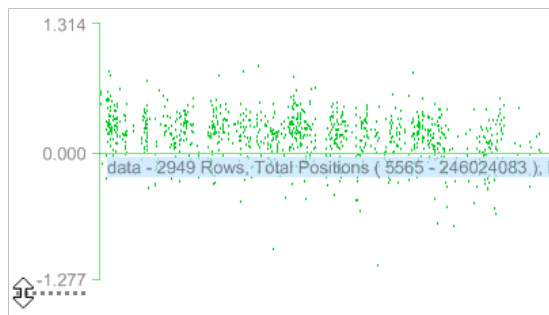
Changing the Track Height

The track height can be adjusted to show more detail.

To change the track height:

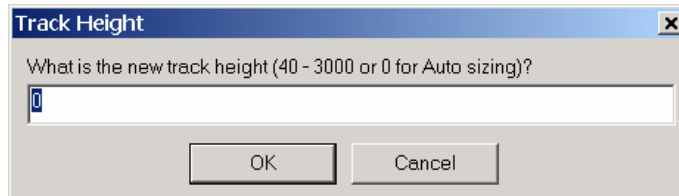
Choose between the following:

- ◆ Place the mouse over the region under the track's y-axis scale.
A track separator displays and the cursor changes to a resize cursor as shown below.



Then click and drag the separator to the new track height.

- ◆ Select a track and choose Track -> Set Height. The Track Height dialog box appears.



Enter the new pixel height for the track. Then click OK.

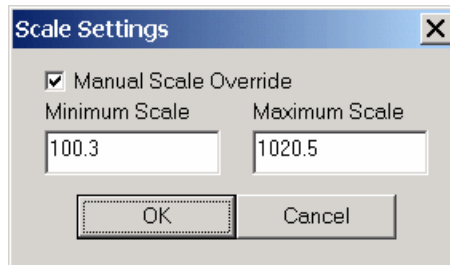
Changing the Y Axis

The y axis is automatically scaled from the minimum to the maximum data within each track, while ensuring that zero is also displayed. You can manually adjust the *extent* of any y-axis scale.



To manually set the y-axis scale:

1. Select the tracks to adjust.
2. Choose View -> Manual Scale or click the Set Manual Scale button on the toolbar. SignalMap displays the Scale Settings dialog box, shown below.



3. Enter the minimum and maximum value for the y-axis scale. SignalMap sets all selected tracks to display with a manual y-axis scale.

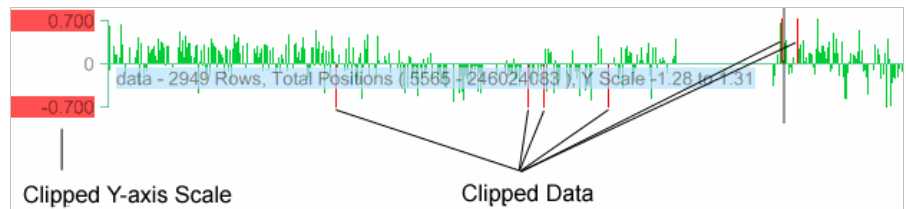
Note: Annotation does not have scale data, and its scale does not change.



To automatically set the y-axis scale:

1. Select the tracks to adjust.
2. Choose View -> Auto Scale or click the Set Auto Scale button on the toolbar. SignalMap sets all selected tracks to display with an automatic y-axis scale.

Note: If you manually set a y-axis scale, it is possible that data will fall outside of the track. This data will be clipped and colored red as shown in the example below.



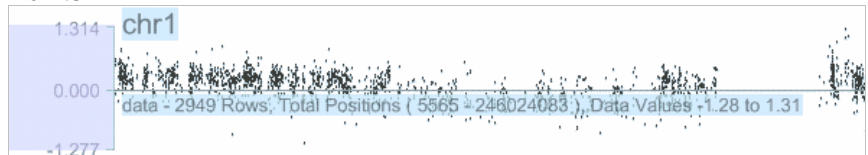
Changing the Track Style

SignalMap displays track data in different ways depending on the data type and the number of data points. Annotation displays as vertical bars while experiment data displays as points when possible. When SignalMap is drawing a track with more than 24,576 points, it always draws the data as bars for performance reasons. When drawing points, SignalMap displays data as horizontal lines spanning from the start to end position.

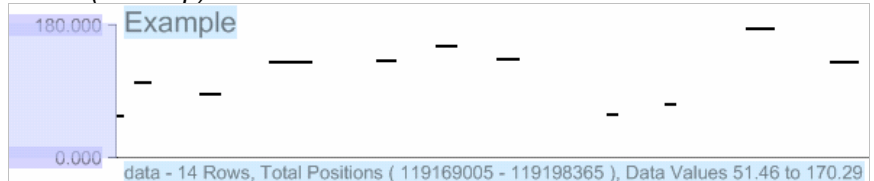
To change the track style:

1. Select the track.
2. Choose Track -> Style and select a new style.
SignalMap displays the data in the new style:

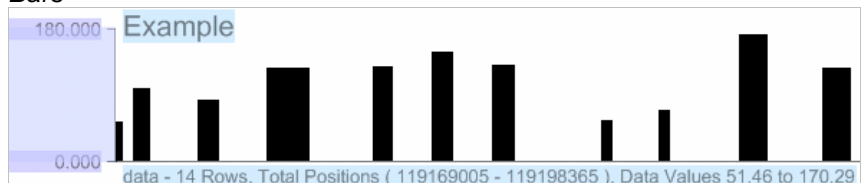
Points



Points (close up)



Bars



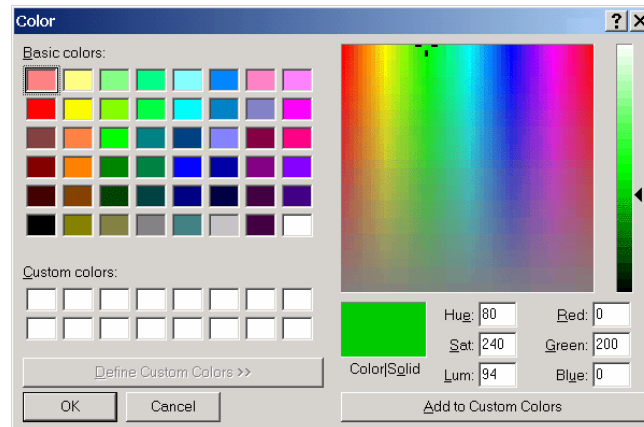
Changing the Track Color

The color used for each track is dependent on the type of data. In addition, the data source may have color annotation that overrides the track color. You cannot override the data source color if it exists in the GFF file.

To change the track color:

1. Select a track.
2. Choose Track -> Set Color, or right-click the selected track and choose Set Color.

SignalMap displays the Color dialog box.

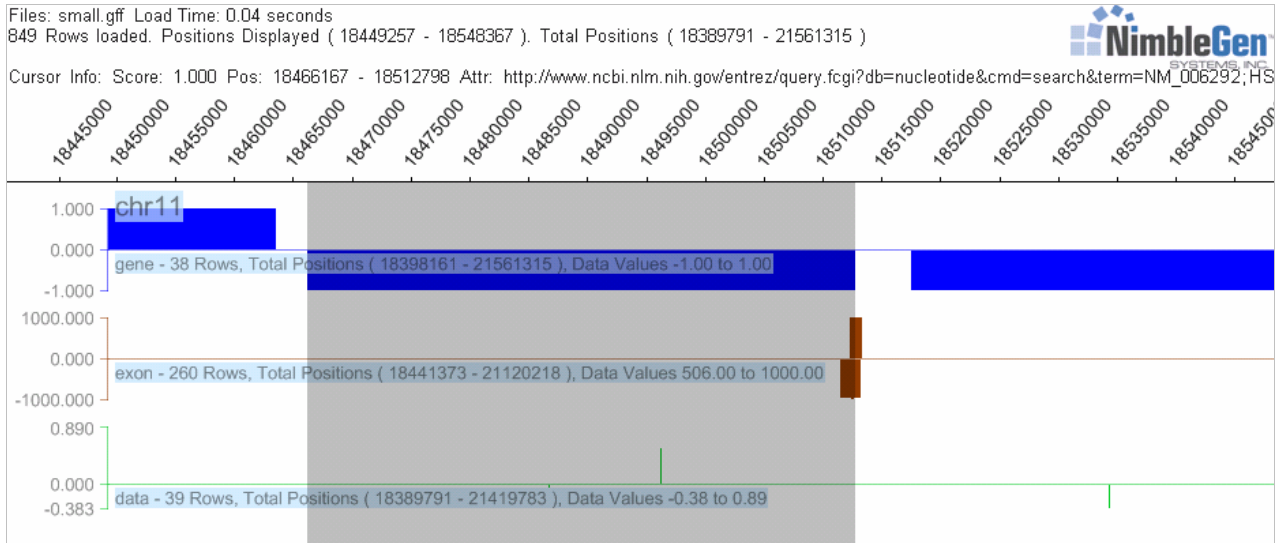


3. Choose the new track color.
4. Click OK.

Highlighting Tracks

SignalMap can use one track as a cursor track. When you click on a data point in this track, SignalMap displays a transparent gray bar over *all tracks* at the position of the data in the cursor track. In addition, information about the data point appears on the fourth line in the Information area.

In the example below, a positive data point on the gene track and an exon value on the reverse strand share position with the selected data point.



Note: More than one data point can be located on the same position on a track. Use the arrow keys to move the cursor to another data point on the track.

To select a cursor track:

1. Using the Pointer tool, select a track by clicking to the left of the y scale of the track.
The track is selected and a blue bar overlays the y scale.
2. Choose Track -> Attach Cursor or right-click the track and choose Attach Cursor or press Alt + A.
The data in the track is associated with the cursor.
3. To detach the cursor from a previously selected track, choose Track -> Detach Cursor or press Alt + A.

To highlight a data point:

1. Using the Pointer tool, click near the data point to highlight.
SignalMap displays a transparent gray bar over all tracks at the position of the selected data point.
2. View attribute information about the selected data point in the Cursor Info line of the document window.
This information may include hyperlinks, described on the next page

To jump to the next or previous data point:

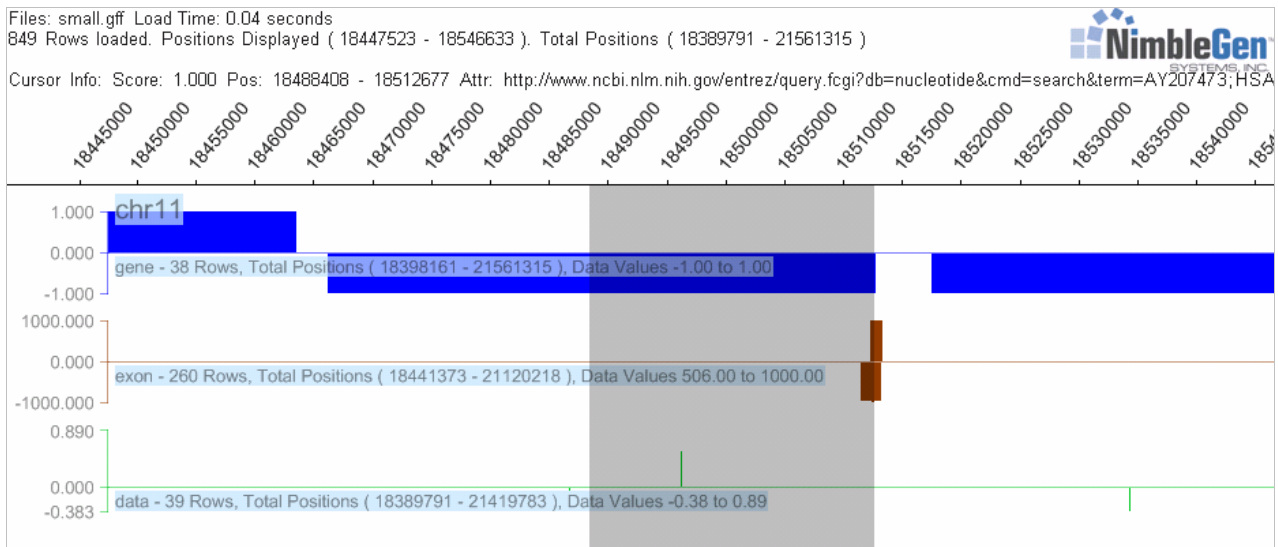
1. Press the *right arrow* key on your keyboard or choose Cursor -> Next Item to jump to the next data point on the track.

To jump to the previous data point, press the *left arrow* key or choose Cursor -> Previous Item.

SignalMap displays a transparent gray bar over all tracks at the position of the selected data point.

2. To view attribute information about other tracks in the region, place your mouse over the selected area on the track. You do not need to click a point, simply hover over the area of interest on the track.

The following image shows what happens when the Next Item command goes to a data point located within the data region already selected. The right half of the previously selected region is now highlighted.



Using Hyperlinks

SignalMap allows you to activate hyperlinks included in the attributes field of the GFF file. Typically, attributes will be placed on gene data so you can link to web sites describing specific genes.

To activate a hyperlink:

1. Put your mouse over a data point of interest.
The attribute information displays. The data point displays with a light blue transparent shade if there is an available hyperlink.
2. Double-click the data point.
SignalMap opens your default browser to the hyperlink, as shown in the following image.

Chapter 4. Exporting Your Data

SignalMap allows you to export a selection of your data to a GFF file. In this chapter, you learn to:

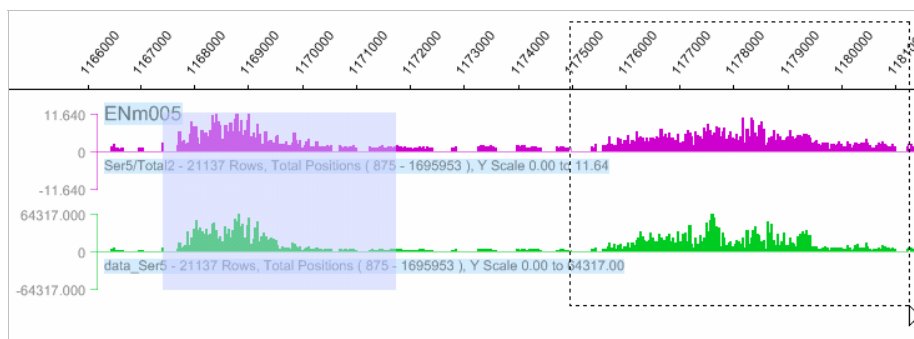
- ◆ Select data
- ◆ Export selections to a GFF file
- ◆ Export a screen capture

Selecting Data

You can select data in each pane based on position. If you do *not* use the Control key while selecting a region of data, SignalMap maintains the selection for each pane independently.

To select one region of data for export:

1. Click the Pointer tool.
2. Use the left mouse button to click and drag around the data of interest, as shown at right in the following image.
A transparent blue rectangle displays over the selected data, as shown at left in the following image.



To select multiple regions of data for export:

1. Click the Pointer button on the toolbar.
2. Click and drag around the data of interest.
A transparent blue rectangle displays over the selected data, as shown on the left side of the previous image.



3. Press the Ctrl key and click to select additional areas.

Tip: Multiple selections will be maintained between panes if you hold down the Ctrl key. This will allow you to export selections in multiple panes as GFF files. However, you may not export selected areas as images.

A transparent blue rectangle appears over all selected data regions, as shown in the following image.



Tip: Choose Edit -> Select All to select all data in the pane.

Exporting Selections to a GFF File

SignalMap exports selected data in the order that it was selected. It does not attempt to remove duplicate data. If you used the Control key to select multiple regions from different panes, all your selected data will be exported to the GFF file.

To export selected data:

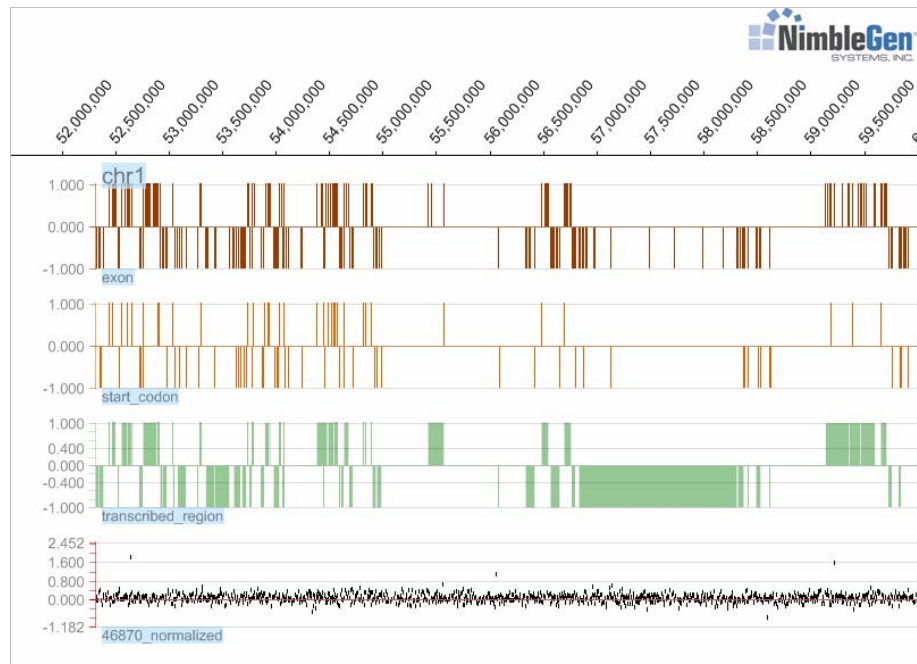
1. Select File -> Export -> Selections from the menu. A File dialog box appears.
2. Enter the filename and select the type (GFF or TXT).
3. Click Save to save your selections. SignalMap saves the selected data from all panes into the file. You may now open this GFF file in SignalMap as you would any other GFF file.

Exporting a Screen Capture

SignalMap can export a screen capture (an image of the currently displayed screen) as any of the following image file types:

- ◆ *WMF* (Windows Metafile): This format can be imported into Microsoft Office products or any software that can read WMF files. This file type is useful for large presentations since the resolution scales with the size.
- ◆ *BMP* (Bitmap file): This is a standard Windows bitmap file. It is not compressed and can take up a lot of disk space.
- ◆ *GIF* (Graphics Interchange Format): A standard lossy compressed image format used widely for graphics on the web.
- ◆ *PNG* (Portable Network Graphics): A standard lossless image format for web and image editing purposes. This format works well for large pixel widths. PNG files give the best results.
- ◆ *TIFF* (Tagged Image File Format): A standard image format often used for high-quality print applications. Most image editing software can open this format.

Note: *The exported image contains all tracks after the first displayed track in the pane. This makes it possible to export all tracks on a pane, even if the vertical image size would be larger than your display. This is likely if you export the screen in the All Tracks pane, as shown in the following image.*

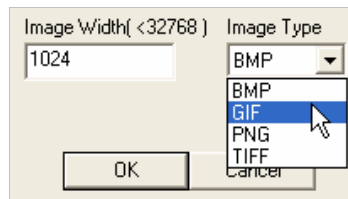


To export a screen capture as a Windows metafile:

1. Scroll to and magnify the area of interest.
Remember SignalMap will export any tracks that appear *below* those shown on your screen.
2. Choose File -> Export -> Metafile Capture.
The Save As dialog box appears.
3. Type in the file name and click Save.
The image saves to the selected file. You may then open it in any application that supports the WMF file type.

To export a screen capture as a BMP, GIF, PNG, or TIFF:

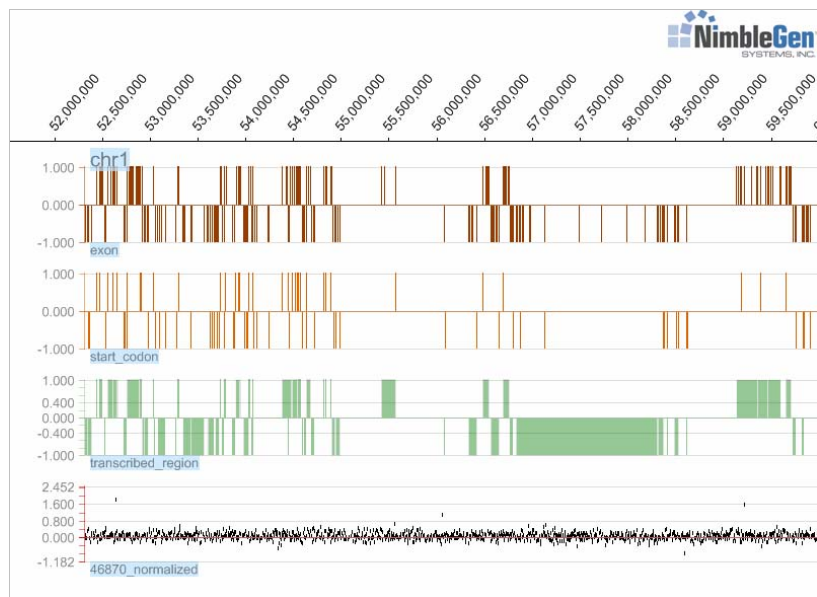
1. Scroll to and magnify the area of interest.
Remember SignalMap will export any tracks that appear *below* those shown on your screen.
2. Choose File -> Export -> Image Capture.
The Export Image dialog box appears.



3. Enter your desired image width (in pixels).
The default setting is 1,024 pixels, and the maximum width is 32,768 pixels. When you save the file, SignalMap resizes the screen shot to fit the width you selected. This feature allows you to create images of set widths for your publications.
4. Select a file type from the Image Type drop-down menu.
See the description of file types on page 37 if you are not sure which file type to choose.
5. Click OK.
The Save As dialog box appears.

6. Type your file name and click Save.
Your image is saved.

You can now open your image in image editing software. In the following example, the image was saved with a width of 800 pixels, causing a resizing of the original image as well as a change to the x-axis scale from that displayed on the SignalMap screen.



Note: The exported image may display a different position scale than that shown on the SignalMap screen; however, the position range will be the same.

Appendix A. GFF Files

GFF (General Feature Format) is a standard file format to describe genome data. The Sanger Institute defines the file format; see www.sanger.ac.uk/Software/formats/GFF/. Below is a summary of the format.

Understanding GFF Files

SignalMap imports and exports GFF files. There is no header in a GFF file. However, you can add a comment line that describes the file's contents by using a pound sign (#) at the beginning of the line.

Each line of data is tab delimited and has the following information in the order specified. For a complete description of the format, see www.sanger.ac.uk/Software/formats/GFF/.

```
<seqname> <source> <feature> <start> <end> <score> <strand> <frame>  
[attributes] [comments]
```

SignalMap does not use some of these fields; however, all fields are maintained in memory.

seqname

The sequence name used by SignalMap to separate the data into panes. This is limited to 32,768 panes. SignalMap can handle more than this, but having more than this number makes it difficult to browse for panes in the Pane Selector.

source

SignalMap does not use this.

feature

The feature type name used by SignalMap to separate the data into tracks.

start

This is used by SignalMap to display the start position.

end

This is used by SignalMap to display the end position.

score

This is used by SignalMap to display the data value (magnitude). It is ignored for the gene tracks. In some cases (such as exon data), the score refers to the confidence level of the prediction. For data tracks, the score either refers to a data value or the ratio of two data values (sample over the total).

strand

This is used by SignalMap to place gene, exon, or other relevant data above or below the track line.

Data tracks do not contain strand information: a plus sign is placed in this field in all data tracks. The score (see above) determines whether data on a "data track" is placed above or below the track line.

frame

SignalMap does not use this.

attributes

This is used by SignalMap to display extra information about the data. Hyperlinks can be included in the attribute, separated by semicolons (;), and URLs can be specified using the GFF3 tag format, url=urlpath. Color can be specified for the data point by placing color RRGGBB, where RRGGBB are the red, green and blue components of the color in web color format. For example, color xFF0000 will change the data point to red.

comments

SignalMap does not use this.

Examples in Text File Format

seqname	source	feature	start	end	score	strand	frame	attributes
chrX	UW	data	1950	3077	-0.28	+	.	HSAP0307S00028922
chrX	UW	gene	4099	6290	1.00	-	.	http://www.gene.com;H7898
chrX	UT	exon	7800	9068	670	-	.	gene_id "exon(1044-)"
ENm001	UT	data_IgG	1	51	1225	+	.	ENm000P0000000001

Appendix B. Reporting Bugs

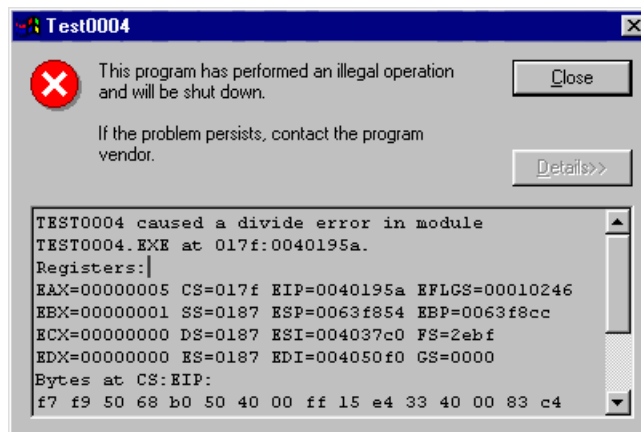
You can send information regarding the nature of a SignalMap problem to NimbleGen. Send the email to bugreports@NimbleGen.com and include as much of the following information as possible.

To report unexpected or undesired operations:

1. Attempt to repeat the sequence of events that led you to the problem, and try to determine the smallest number of steps that will cause the problem. Describe each step in your bug report.
2. Describe in as much detail as possible the nature of the problem and the steps that you took to solve to the problem.
3. If possible, save and attach the GFF file that is related to the problem.
4. Email this information to bugreports@NimbleGen.com.

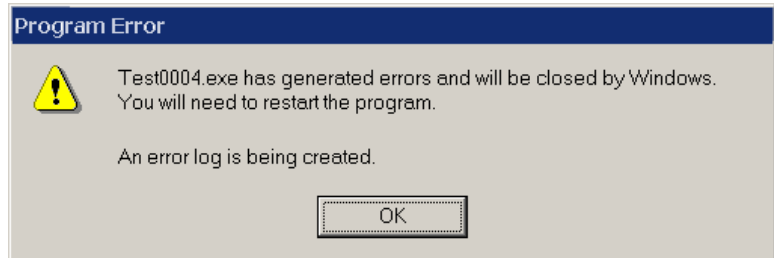
To report an unexpected application termination or crash:

1. Gather the information described in the “To report unexpected or undesired operations” task above. Type it into a new email message.
2. Capture the information regarding the state of the system. This information is found in different places depending on your operating system:
 - ◆ Windows 98 or Windows ME: An error dialog box appears.



1. Click the Details button.
2. Copy and paste the text information from this dialog box into the email message you began earlier. Send to bugreports@NimbleGen.com.

- ◆ Windows 2000 or Windows XP: A Program Error dialog box appears.



1. Search your computer for the DrWtsn32.log file. The default location is C:\Documents and Settings\All Users\Documents\DrWatson\DrWtsn32.log.
2. Attach this file to your email, or copy and paste the last part of the file relating to SignalMap into your email and send to bugreports@NimbleGen.com.