Integrative Genomics Viewer (IGV) Quick Start

Quick Start

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This 10-minute tutorial introduces you to the Integrative Genomics Viewer (IGV) by providing step-by-step instructions for loading and visualizing gene expression and SNP (single nucleotide polymorphism) copy number data.

Download GISTIC Data Files

The tutorial uses segmented copy-number and gene expression data from Beroukhim et al. (2007). The paper describes a method, Genomic Identification of Significant Targets in Cancer (GISTIC), for identifying significant chromosomal aberrations and applies that method to a collection of 141 glioma samples.

Download the GISTIC data files: GISTIC.zip.
The GISTIC data files are also available on the IGV home page (http://broad.mit.edu/igv/).

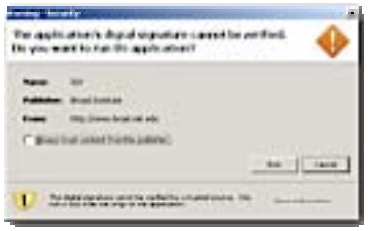
Start IGV

To start IGV:

1. Go to the IGV downloads page: http://www.broad.mit.edu/igv/downloads/downloads.html.
2. Register as instructed.
3. Click the launch icon:

The browser displays the web start launch window (the file name will match the version number):

4. Select Open with Java™ Web Start Launcher and click *OK*. The launcher downloads and starts the application.
5. If the security message appears, click *Run* to continue:



IGV starts. By default, IGV displays chromosome 1 of the human (hg18) genome or the chromosome and genome that you were viewing when you last exited IGV.

6. For the tutorial:
   - Click the Genome link in the toolbar and select hg16 (the genome on which the GISTIC data was processed).
   - If you have another chromosome selected, click chr1 in the chromosome drop-down box in the toolbar (the chromosome on which the tutorial begins).

Load Data

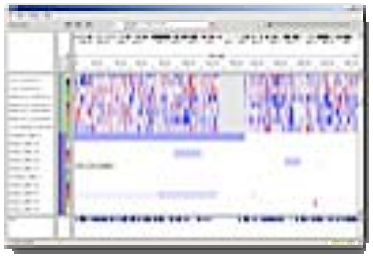
To display data, load data files:

1. Select *File>Load*. IGV displays the Select Files window.
2. Select one or more data files. For this tutorial, ctrl-click to select two files (on a Mac, command-click):
   - PrimaryGBMs.43.centered_and_normalized.gct (gene expression data)
   - segmented_data_080520.seg (SNP copy number data)

3. Click *OK*. IGV displays the data in horizontal rows called tracks. Typically, each track represents one sample or experiment. For each track, IGV displays the track identifier, one or more attributes, and the data.

Above the track data, the chromosome ideogram represents the whole chromosome and the ruler reflects the visible portion of the chromosome. In the Attributes panel, attributes with the same value have the same color. The colors may differ from those shown here.

4. Scroll through the tracks until you can see both gene expression and copy number data:



5. Hover over the attributes to display the file name and data type of the data you have loaded. You are displaying gene expression data from PrimaryGBMs.43.centered_and_normalized.gct and copy number data from segmented_data_080520.seg.

Load Attributes

To display additional attributes, load an attribute file (also called a sample information file):

1. Select *File>Load*. IGV displays the Select Files window.
2. For this tutorial, select Sample_info_tutorial.txt.
3. Click *OK*. IGV displays the attributes. Attribute values are color-coded; where the values are the same, the color is the same. The colors may differ from those shown here. Hover over a colored attribute box to see its value.

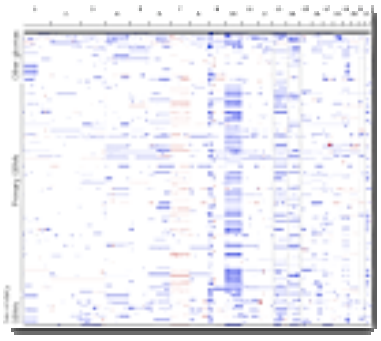
You can hide/show all attributes or selected attributes, as described in the IGV User Guide.

Change Display Options

IGV offers several display options for tracks. As an example, the tutorial modifies the display of the copy number data to match the visualization shown in Figure 2a of Beroukhim et al. (2007):

Figure 2a from the paper:

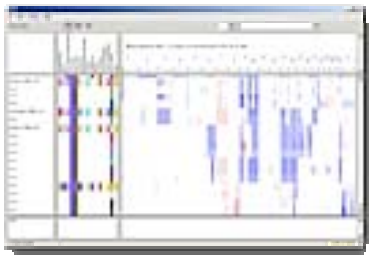
Displayed in IGV:



To modify the IGV display:

Zoom out to the whole genome

1. Click the  *whole genome view* icon to view the whole genome:



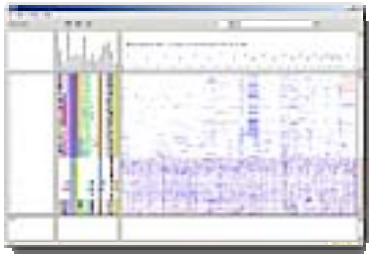
Modify the track height

2. Select *Tracks>Set Default Track Height*. IGV prompts you for the new track height.
3. Enter 4 and click *OK*.

Sort the tracks by data type (expression vs copy number) and diagnosis (primary vs secondary vs other gliomas)

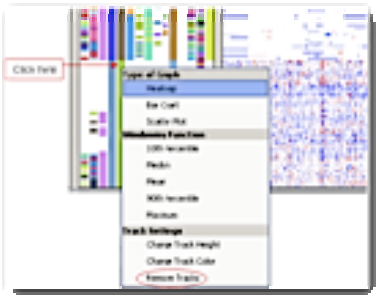
4. Select *Tracks>Sort Tracks*. IGV displays the Sort window.
5. Sort by Data Type and then Diagnosis by selecting those attributes:

6. Click *OK* to sort the tracks:



Remove the gene expression data

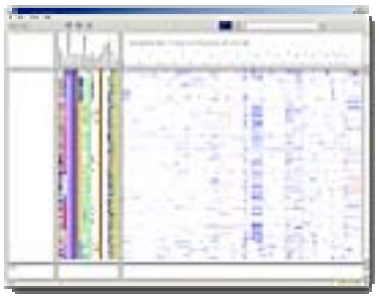
7. Click the Data Type attribute of any gene expression data track to display a context menu.
8. Click *Remove Tracks*. IGV displays a list of all tracks that have that attribute value.
9. Click *Yes* to remove the tracks.



Apply a filter that displays only the gliomas (Type = Glioma) hiding the normals (Ploidy(Numeric) ≠ 2)

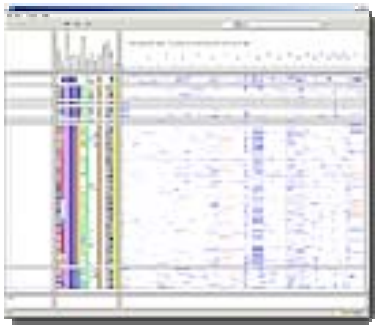
10. Click *Tracks>Filter Tracks*. IGV displays the Filter Tracks window.
11. Define a filter that displays the gliomas (Type is equal to Glioma):
    1. Select `Type` from the first drop-down list.
    2. Select `is equal to` from the second drop-down list.
    3. Enter: `glioma`.
12. Click the plus (+) button to add a second filter.
13. Define a filter that hides normals (Ploidy(Numeric) is not equal to 2).
14. Select the check box *Match all of the following* at the top of the window to combine the filter criteria using a logical AND (Type is equal to Glioma AND Ploidy(Numeric) is not equal to 2):

15. Click *OK* to apply the filter.
16. If necessary, increase the size of the window to see the whole display:



The tracks are sorted by diagnosis; that is, they are sorted by the value of the DIAGNOSIS attribute. Grouping the tracks by attribute makes it easier to see the tracks associated with each attribute value. As an example, group the tracks by diagnosis:

1. Select *Tracks>Group Tracks*. IGV displays a drop-down list of attributes.
2. Select DIAGNOSIS and click OK. IGV groups the tracks by diagnosis.



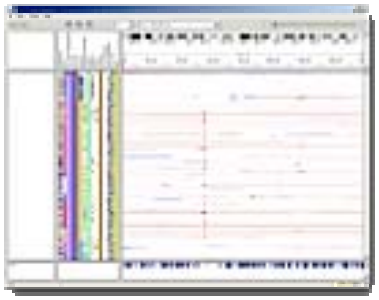
3. To ungroup the tracks, click *Tracks>Group Tracks* and select 'None' from the attribute list.

For more information about setting display options, filtering data, or sorting and grouping data, see the IGV User Guide.

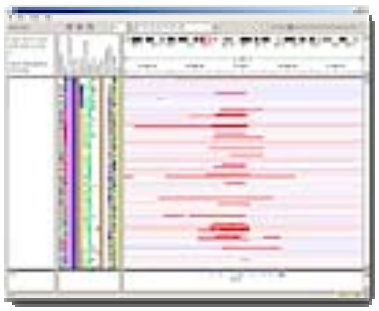
Zoom and Scroll

IGV supports zooming and scrolling from full genome to base pair resolution. As an example, the tutorial explores chromosome 7:

1. Jump to chromosome 7 by clicking 7 at the top of the whole genome view or by selecting chr7 from the drop-down list in the toolbar. The heat map display of chromosome 7 makes it easy to see the amplifications between 53,000,000 and 54,000,000, but the resolution is not fine enough to read the gene names.



2. Zoom in until the gene names are legible by double-clicking on the amplified area of data tracks:



3. To see the track names, hover over a track. Alternatively, select *Tracks>Set Default Track Height* and increase the track size until the track names are legible.

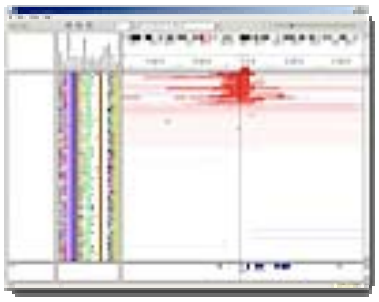
For more information about zooming and scrolling, see the IGV User Guide.

Sort Tracks

In this tutorial, you have sorted and grouped tracks by attribute. In IGV, you can also define a *region of interest* on the genome and sort tracks based on the data in that region. As an example, define a region of interest around the EGFR gene and sort the tracks based on the data in that region:

1. Click the *Define a region of interest* icon in the tool bar.
2. Click a point in the data panel to define the start of this region.
3. Click a second point in the data panel to define the end of the region. IGV draws a red annotation bar above the data panel to indicate the region of region.
4. Click the red annotation bar for the region. IGV displays a menu.

5. Select a menu option. For the tutorial, select *Sort by amplification*, which sorts tracks based on copy number values in this region, from highest to lowest.



To return to the previous view:

1. Delete the region of interest by clicking the red annotation bar for the region and selecting *Delete*.
2. Sort the tracks (*Tracks>Sort Tracks*) by TRACK NAME and DIAGNOSIS attributes.

For More Information

Thank you for taking the time to learn about IGV. For more information, please see the IGV User Guide.

Document History

Version	Release date	Comments
1.0	July 2008	Documentation for IGV release 1.0.