



IGV Documentation

Description: Launches the Integrative Genomics Viewer (IGV) with the provided file and input parameters.

Author: Marc-Danie Nazaire, Barbara Hill, Peter Carr, and Jim Robinson.
gp-help@broadinstitute.org

Summary

This module launches IGV on a specified data file or IGV session file. For full documentation and more information about IGV, please visit [the IGV website](http://broadinstitute.org/igv). (<http://broadinstitute.org/igv>).

Each run of the module creates a Java WebStart file named `igv_job_<gp_job_id>.jnlp`. A corresponding launch button is also displayed on the IGV job status page. Click on this button to launch IGV. Note that in some Web browsers you must download the file, and then directly launch it from your client computer. The launcher automatically installs or updates to the latest released version of IGV.

IGV will prompt you for your GenePattern username and password before it opens the data or session file.

Once you have IGV running, you can also directly open GenePattern files by selecting *File>Load from URL...* from the IGV menu and entering the URL of the GenePattern file. Right-click (CTRL-click on the Mac) on a filename in GenePattern to copy the URL link address and then paste it into the IGV URL entry box. Note that accessing your GenePattern files from IGV will only work with GenePattern Server versions 3.3.2 or later.

Parameters

Name	Description
input.file (required)	Data file or session file to open in IGV. It can be in any format accepted by IGV. See the IGV website for accepted file formats (http://www.broadinstitute.org/igv/FileFormats.html).
index.file (optional)	An index file that corresponds to an input BAM file. This does not need to be specified when the index file is in the same directory as the BAM file and follows the IGV naming conventions for index files. See the IGV website for details (http://www.broadinstitute.org/igv/BAM).
genomeld (optional)	A genome identifier (e.g., hg18). Choose from the drop-down list.

GenePattern

locus (optional)	Locus to display initially. Use any syntax that is valid in the IGV search box, for example, chromosomal coordinates (e.g., chr5:90,339,000-90,349,000), or a gene symbol or other feature identifier (e.g., DPYD or NM_1000000)
---------------------	--

Input Files

1. input.file

The input file can be in any format accepted by IGV. See the IGV website for [accepted file formats](http://broadinstitute.org/igv/FileFormats). (<http://broadinstitute.org/igv/FileFormats>)

2. index.file

BAM index file, created by running the SAMtools *index* command on a BAM file (see <http://samtools.sourceforge.net>).

Module type:	IGV
CPU type:	Any
OS:	Any
Language:	Java 1.6 or greater