

Scripting and the IGB command language

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Introduction

You can control IGB from scripts, which are text files containing simple commands for navigation, loading data, and making snapshots.

To run an IGB script:

- Open a script file using **File > Open**. Script files should end with .igb.
- Click an IGB script link. See: [Controlling IGB using IGB Links](#)
- Drag and drop a script file into an open IGB window.

Syntax

The script file has a simple, space-delimited syntax. Each command should occupy a separate line.

Commands

Bring IGB to front

```
bringToFront
```

Bring the IGB window to the front of the user's desktop.

Open a genome version

```
genome <version>
```

Open genome version (e.g., H_sapiens_Mar_2006). Any genome version or synonym that's accepted by IGB is accepted here.

Go back to the IGB start screen.

```
homescreen
```

Return to the IGB start screen.

Go to a region

```
goto <region>
```

Go to a region of a chromosome (e.g., "chr1:40000-60000" or "chr1:40,000-60,000"). Commas are optional. Any region format accepted by the IGB quick search text entry (top left corner) is acceptable.

Hide a track

```
hidetrack <file or URL>
```

Hide the track. Accepts one or more comma separated files identified by full path or URL.

Add a new data set to IGB's list of active data sets

```
load <file or URL>
```

Load the specified file (identified by full path) or URL into IGB. The data set will appear in the user's **Data Management** table upon completion.

Remove a data set from IGB's list of active data sets

```
unload <file or URL>
```

Change the load mode for an active (opened) data set

```
loadmode <NO_LOAD | REGION_IN_VIEW | CHROMOSOME | GENOME> <file or URL>
```

Change the load mode for the specified data set or file, identified by full path.



The **loadmode** command will work for any loaded track. Make sure to load your desired track before calling the **loadmode** command.

Load data from currently active data sets

```
refresh
```

This is equivalent to clicking the **Load Data** button in IGB. This triggers loading of data from the active data sets available in IGB, as specified in the load command.

Make images

```
snapshot <filename>
```

```
snapshotwholeFrame <filename>
```

```
snapshotmainView <filename>
```

```
snapshotmainViewWithLabels <filename>
```

```
snapshotslicedViewWithLabels <absolute path to file>
```

Export the entire frame, main view, main view with labels, or sliced view, respectively, to a PNG format file. You must include the full path to the file or IGB will write the file to the location from where you launched IGB.

The filename defaults to "<genome_version><timestamp>.png" if not specified.



The **snapshot** and **snapshotwholeFrame** commands only work on Mac and Linux if attempting to export an SVG file.

Select genes

```
select <geneids>
```

Selects the given gene IDs, which are passed in as a comma-separated list.

Wait (sleep) for commands to finish

```
sleep <milliseconds>
```

Sleep the application for x milliseconds.



IGB is multi-threaded, which means that the user may be able to operate IGB while data are being loaded. If your IGB script includes loading data from remote sites (e.g. RNASeq data from the IGBQuickLoad.org site) then you should include a sleep command to give IGB time to load the data.

Comments

Lines starting with the IGB script comment character '#' are ignored.

Examples

Loading a BAM file

```
# select genome
genome A_thaliana_Jun_2009
# go to a region in chr4
# commas are optional
goto chr4:8,860,484-8,872,096
# load a file
load http://igbquickload.org/rnaseq/A_thaliana_Jun_2009/SRP029896/ColdControl.bam
# load the data
refresh
```

Exporting images

<https://gist.github.com/Hillrunner2008/25976458488b65a3a25b>

