

IGB Scripting Commands List

Commands	Arguments	Description	Examples
bringToFront	none	Make IGB the top window on the Desktop.	bringToFront
genome	<version>	Load a genome version. Accepts IGB-friendly genome version names (e.g., H_sapiens_Feb_2014) and synonyms.	genome H_sapiens_Mar_2006
goto	<region>	Go to a region. Any format that's accepted by IGB is accepted here. Commas are optional.	goto chr1:13,640,211-13,643,760 goto chr1:13640211-13643760
hidetrack	<file or URL>	Hide the track. Accepts one or more comma separated files identified by full path or URL.	hidetrack http://igbquickload.org/H_sapiens_Dec_2013/H_sapiens_Dec_2013_all_mrna.psl.gz
homescreen	none	Return to the IGB Start Screen.	homescreen
load	<file or URL>	Load the specified file (identified by full path) or URL into IGB. The data set will appear in the Data Management table upon completion.	load http://igbquickload.org/D_melanogaster_Jul_2014/D_melanogaster_Jul_2014.bed.gz
loadmode	<NO_LOAD REGION_IN_VIEW GENOME> <file or URL>	Change the load mode for a data set. Note: The loadmode command will work for any loaded track. Make sure to load your desired track before calling the loadmode command.	loadmode GENOME http://igbquickload.org/M_musculus_Dec_2011/M_musculus_Dec_2011_refGene.bed.gz
loadsequence	none	This is equivalent to clicking the Load Sequence button in IGB. This triggers loading of the reference sequence for the region in view.	loadsequence
refresh	none	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.	refresh
select	<geneids>	Selects the given gene IDs, which are passed in as a comma-separated list. If the command contains a single gene ID then IGB will select and jump-zoom to the given gene.	select AT1G36280.2,AT1G36240.1,AT1G36340.1
selectfeature	<geneids>	Selects the given gene IDs, which are passed in as a comma-separated list.	selectfeature
showtrack	<file or URL>	Unhide the specified track. Accepts one or more comma separated files identified by full path or URL.	showtrack http://igbquickload.org/O_sativa_japonica_Oct_2011/O_sativa_japonica_Oct_2011.bed.gz
sleep	<milliseconds>	Sleep the application for x milliseconds.	sleep 6000
snapshot	<filename> Note: specify the full path to file.	Create an image showing the entire IGB window. the entire frame an image file. The filename extension determines the format. Supported formats are .png, .jpeg, and .svg. Note: This command only works on Mac and Linux if attempting to export an SVG file.	snapshot alternativesplicing1.png
snapshotmain View	<filename>	Same as snapshot but only makes an image showing the main IGB data display.	snapshotmainView testimage.jpeg
snapshotmain ViewWithLabels	<filename>	Export the main view with labels an image file. The filename extension determines the format. Supported formats are .png, .jpeg, and .svg.	snapshotmainViewWithLabels imageexport1.svg
snapshotsliced ViewWithLabels	<filename>	Export the sliced view an image file. The filename extension determines the format. Supported formats are .png, .jpeg, and .svg.	snapshotslicedViewWithLabels April_1_2015.png
snapshotwhole Frame	<filename>	Export the entire frame to an image file. The filename extension determines the format. Supported formats are .png, .jpeg, and .svg. Note: This command only works on Mac and Linux if attempting to export an SVG file.	snapshotwholeFrame GeneAT1G36280wholeframe.jpeg
unload	<file or URL>	If a matching track is found for the specified URL/path it will be deleted. Accepts one or more comma separated files identified by full path or URL.	unload http://www.igbquickload.org/rnaseq/A_thaliana_Jun_2009/auxin_arf19/Col.C.1.bam , http://www.igbquickload.org/rnaseq/A_thaliana_Jun_2009/auxin_arf19/Col.C.2.bam