Downloading and starting IGV (Integrative Genomics Viewer)

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Downloading IGV

IGV is one of several platforms that you can use to visualize short read and genomics data. It's available from the Broad Institute: <u>https://software.broadinstitute.org/software/igv/download</u>

IGV is built in Java and therefore requires a recent install of Java. If you know that you have Java 11 on your machine already, you can install IGV separately, otherwise download the IGV/Java bundle for your operating system.



Command line IGV and igvtools for all platforms Separate Java 11 required

Start the installer, accept the license agreement and install it.

Starting IGV (different memory allocation)

Just click on the IGV icon to run it with default options.

The default memory allocation for IGV is 4Gb. Depending on your computer specs, this may be too much or too little. If you have 8+ Gb memory on your system, this is a good starting point. If you only have 4Gb memory, you may want to decrease IGV's memory allocation to 2Gb.

If IGV uses too much memory on your system, the whole system will slow to a crawl. If it uses too little, and you're trying to work with large or many files, IGV may slow to a crawl.

When using the installer, IGV automatically places a file called java_arguments in a hidden directory within your home directory named .igv/



The path looks something like this using Bash on Windows for Windows machines. For Mac and Linux users, the path should be ~/.igv/

Opening the java_arguments file looks something like this:



Uncomment the –Xmx8G line and input whatever memory limit you need (-Xmx2G for 2Gb).

If you are starting IGV from a JAR file on the command line (such as on a super computer), you can also enter the memory allocation each time you initialize the program:

<java -Xmx8G -jar igv.jar>