

Get IGB

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Get IGB using native installer for your platform

Get the latest version of IGB from Bioviz.org. Follow the downloads link to get an IGB installer for your platform.

Get compiled IGB (not using native installer)

You can get a "zip" file with compiled IGB from this link: <http://www.bioviz.org/igb/releases/current/igb.zip>

Unpack the "zip" file and launch IGB using the IGB run script for your platform: run_igb.bat for Windows, run_igb.command for Mac, and run_igb.sh for Linux.

Installing on Linux

Download the Linux installer and run it using:

```
sh IGB_unix_current.sh
```

How to get older versions of IGB

Installers with older versions of IGB are available from: <http://sourceforge.net/projects/genoviz/files/>

How to change IGB memory usage

If you used the IGB installer, then when IGB starts, it will use 25% of your system's memory. This means that when IGB runs on a machine with 4 GB of memory (RAM), it will use 1 GB. Or if IGB starts on a machine with 16 GB of RAM, it will use around 4 GB of memory. You can see how much memory IGB is using by looking at the lower right corner of the IGB window.

The only exception is when you run IGB on a 32-bit Windows computer. In that case, IGB will use 1GB of RAM.

You can change how much memory IGB can use.

There is a "vmoptions" file in your IGB installation directory which contains a commented-out jvm argument that sets the max heap size, which is the amount of memory IGB uses.

To change the heap size, un-comment the jvm argument line and modify to suit your needs.

The vmoptions file on Mac is located in /Applications/Integrated Genome Browser/IntegratedGenomeBrowser.app/Contents/vmoptions.txt

On Linux/Windows, the vmoptions file is in `${IGB_INSTALLATION_DIR}/IntegratedGenomeBrowser.vmoptions`, where `$IGB_INSTALLATION_DIR` is the folder where IGB resides.

IGB License

Source code for IGB is released under the [Common Public License version 1.0](#).