

Introduction

The Integrated Genome Browser (IGB - pronounced ig-bee) helps researchers view, analyze, and share genome-scale data sets. An easy-to-install, easy-to-use desktop program, IGB enables dynamic, real-time zooming and panning through chromosome or genome assemblies. IGB already features 18 plant genomes, and the IGB team can easily add more upon request. You can also open and view your own custom genomes in IGB.

File Formats and Data Sources

IGB can display data from many different data sources, all merged into the same view. These include data sets loaded from your computer, from Web sites, or from public (and private) DAS and Quickload servers. IGB can open and display data from many file types, such as BAM, BED, and WIG files. See the IGB User's Guide for a comprehensive list of supported formats.

Questions?

Visit the IGB user's guide for more information on using IGB, including information on advanced features and troubleshooting (<https://wiki.transvar.org/display/igbman/Home>).

Or contact the IGB team: Ann Loraine - ann.loraine@uncc.edu or Nowlan Freese - nfreese@uncc.edu

Downloading IGB

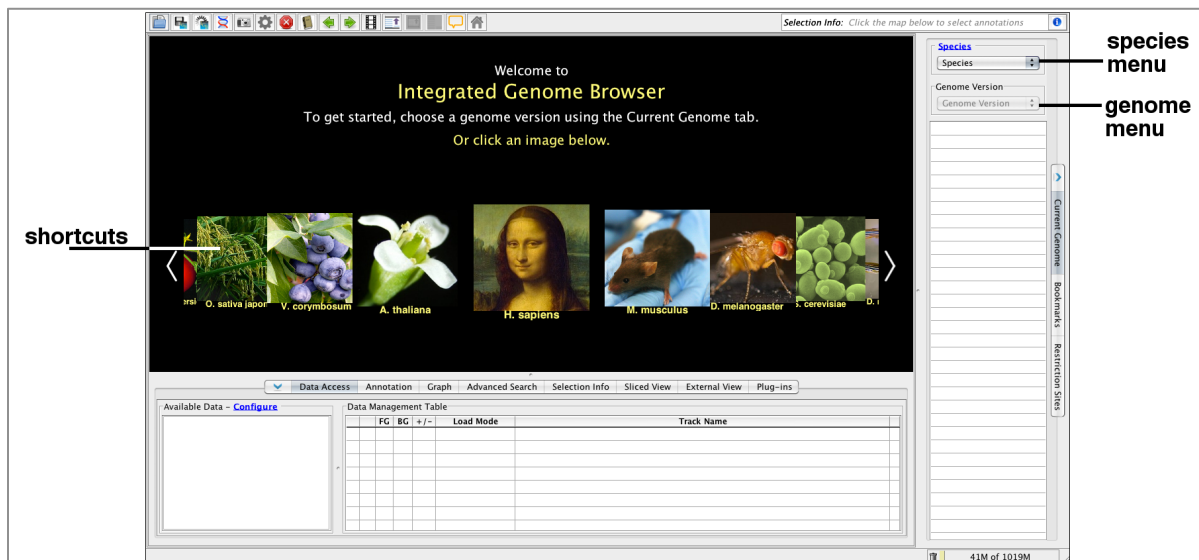
Downloading and installing IGB is free and easy!

1. Go to <http://bioviz.org>, select Downloads and download the IGB installer.
2. Double-click the installer to install IGB. A shortcut will appear on your desktop.
3. Double-click on the desktop shortcut (IGB icon) to launch IGB.

Getting Started with IGB

To select a genome:

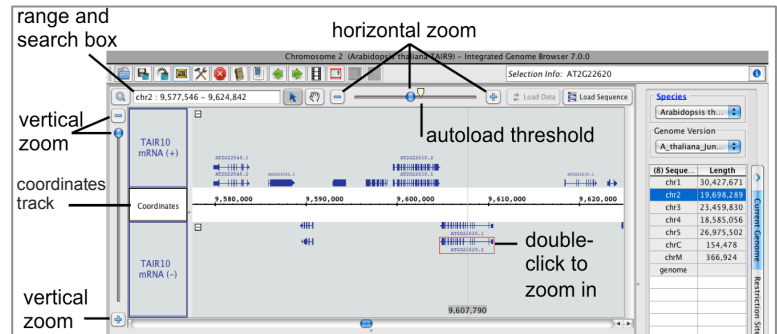
- Click on an image (**shortcut**) to load the most recent genome (not all supported genomes have shortcut).
- Or, use the **Species** menu (top-right) to select from available **Genomes** (includes all supported genomes).



Navigating in IGB

To navigate through the genome:

- Use the **horizontal zoom** slider, or highlight an area of interest in the **Coordinates** track.
- To zoom in on a gene, enter its name in the **Search Box**, or double click on the gene.
- Use the **Vertical Zoom** to expand gene models.



Loading Your Data

- Open a file by dragging it directly into IGB. Or select it using **File > Open File...**
- Access files available from a website by entering the URL. Select **File > Open URL...**
- Many genomes also include publicly available data, found in **Available Data** under the **Data Access** tab.

IGB loads data into tracks. Tracks will appear grayed out at first, as they do not load automatically.

To load data into tracks or to load sequence:

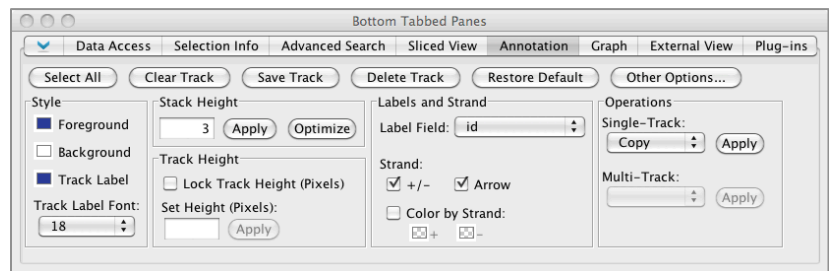
1. Zoom in to a region or gene of interest.
2. Click the **Load Data** button in the upper right corner to load data.
3. Click on **Load Sequence** to load genomic sequence.



Customizing Track Appearance

Use the **Annotation** tab to change annotation and track appearance, including:

- Color and font size.
- **Track and Stack Height.**
- Whether to merge +/- strand features into a single track.



Saving Images

1. Click on the **Camera** tool, or select **File > Save Image...**
2. Select the **Image Format** - PNG, JPEG, or SVG.
3. Change the **Image Size** and **Resolution** as desired.
4. Select **Whole Frame**, **Main View**, **Main View with Labels**, or **Sliced View with Labels**.
5. Select a save location, then click **OK** to save.

