

## IGB

The Integrated Genome Browser (IGB) is a freely available program that enables dynamic, real-time zooming through genomes. IGB has access to the majority of model genomes, and can load data from short and long read aligned sequences (SAM/BAM), annotations (BED, GFF3, GTF), variant calls (VCF), and tiling arrays (WIG).

## Questions?

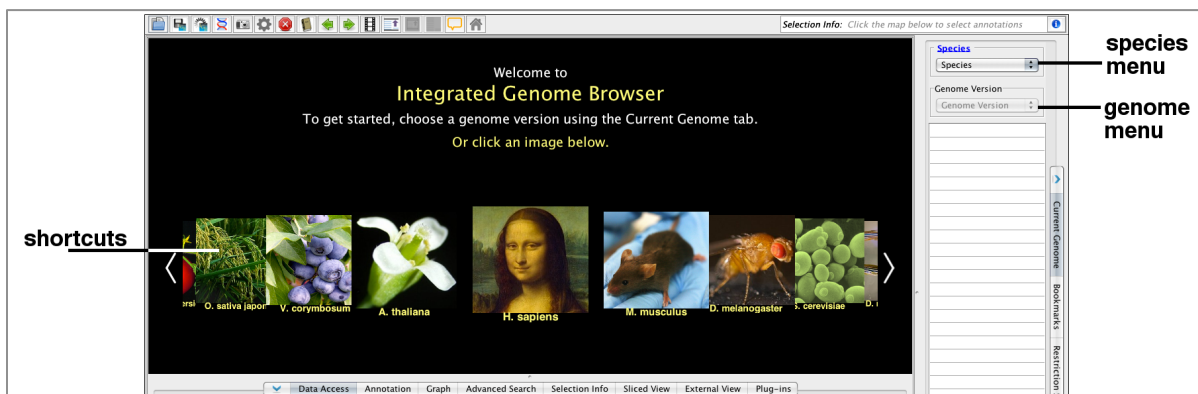
Visit the IGB user's guide for more information on using IGB (<https://wiki.transvar.org/display/igbman/Home>). Or contact the IGB team: Ann Loraine - [ann.loraine@uncc.edu](mailto:ann.loraine@uncc.edu) or Nowlan Freese - [nfreese@uncc.edu](mailto:nfreese@uncc.edu)

## Downloading IGB

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.

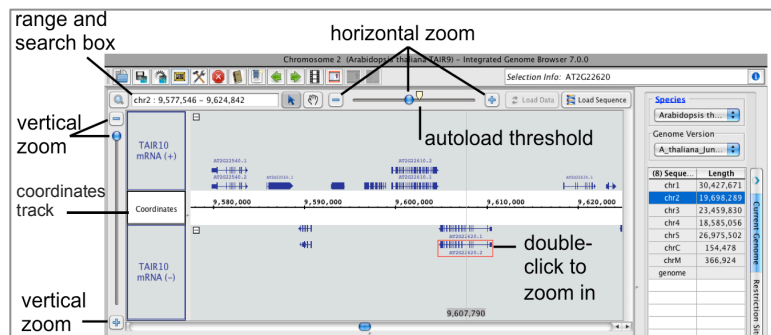
## Getting Started with IGB

- Click on an image (**shortcut**) to load the most recent genome version.
- Or, use the **Species** menu (top-right) to select from all available **Genomes**.



## Navigating in IGB

- 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.



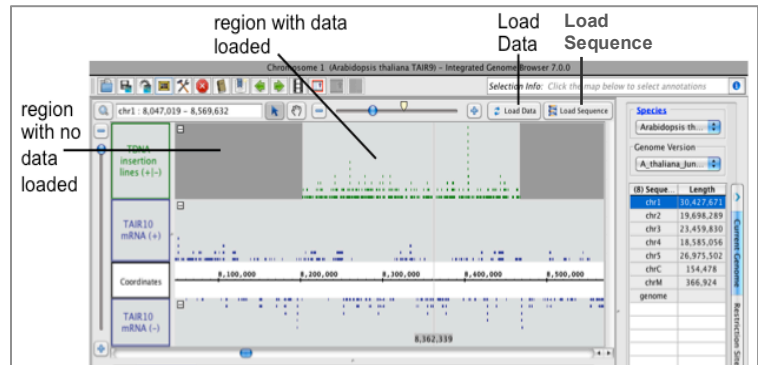
## Loading Your Data

- 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...**

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.



## Galaxy

Galaxy is an open source, web-based platform for data intensive biomedical research. Signing up for Galaxy is free, and gives you access to 200 GB of online storage as well as cloud based computing.

## Creating an Account

- Go to <https://usegalaxy.org/>, click on **User** at the top, and select **Register**.

## Importing Example Data

1. Click on **Shared Data**, and select **Published Histories**.
2. Search for SESDB, and select SESDB Workshop 2015.
3. Click on **Import history** to import the data into your Galaxy.

Tools

Primary screen

History

Galaxy

Analyze Data Workflow Shared Data Visualization Cloud Help User

Using 55%

We are experiencing intermittent filesystem errors that are causing job failures and are working on the problem. If your job fails, please try it again.

Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy [start here](#) or consult our [help resources](#).

060+ Public Galaxy Servers and still counting

Tweets

PyPI Recent Updates @pypi\_updates 1h  
pulsar-app 0.5.0: Distributed job execution application built for Galaxy (galaxyproject.org). bit.ly/1dStHs

iPlant Collaborative @iPlantCollab 7 May  
Registration open for Applied Knowledge Exchange Sessions of the International Society for Computational Biology: bit.ly/1Ee6yMU

NIH R02PK @NIH\_R02PK 22h  
Tweet to @galaxyproject

History

search datasets

SESDB Workshop 2015  
21 shown  
36.7 GB

- 21: TopHat: Splice Junctions - KO
- 20: TopHat: Deletions - KO
- 19: TopHat: Insertions - KO
- 18: TopHat: Accepted Hits - KO
- 17: TopHat: Alignment Summary - KO
- 16: TopHat: Splice Junctions - WT
- 15: TopHat: Deletions - WT
- 14: TopHat: Insertions - WT
- 13: TopHat: Accepted Hits - WT
- 12: TopHat: Alignment Summary - WT
- 11: FASTA danRer7/Zv9 Genome
- 10: FastQC after Trim - KO
- 9: FastQC after Trim - WT
- 8: FASTQ Trimmer - KO
- 7: FASTQ Trimmer - WT
- 6: FASTQ Groomed - KO
- 5: FASTQ Groomed - WT
- 4: FastQC - KO

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iPlant Collaborative

The Galaxy Team is a part of the Center for Comparative Genomics and Bioinformatics at Penn State, and the Department of Biology and at Johns Hopkins University.

This instance of Galaxy is utilizing infrastructure generously provided by the iPlant Collaborative at the Texas Advanced Computing Center, with support from the National Science Foundation.