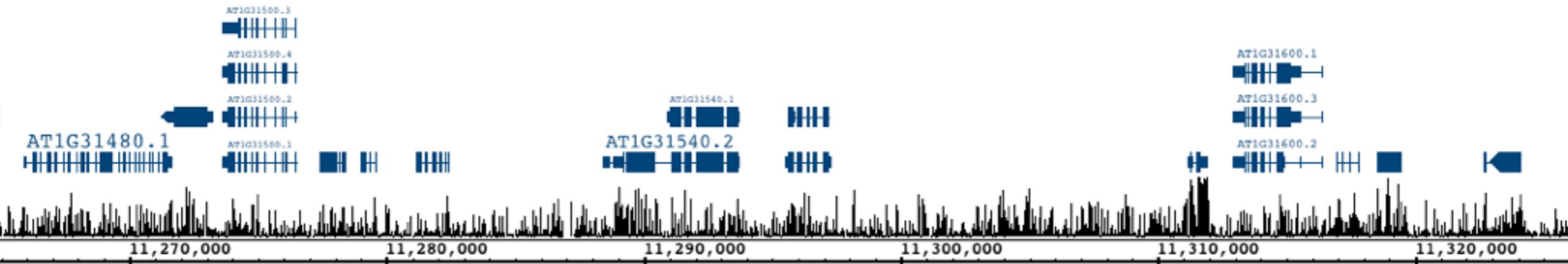




Integrated Genome Browser

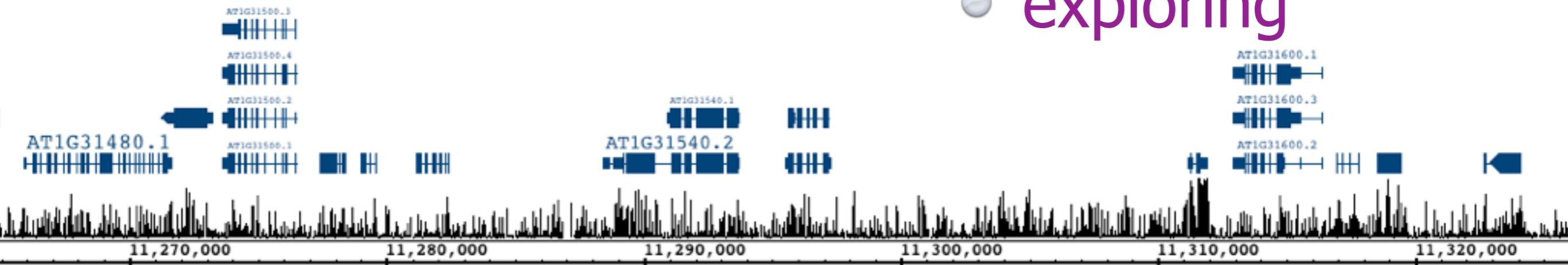
Analyze, Visualize, Share

Fast Flexible Free

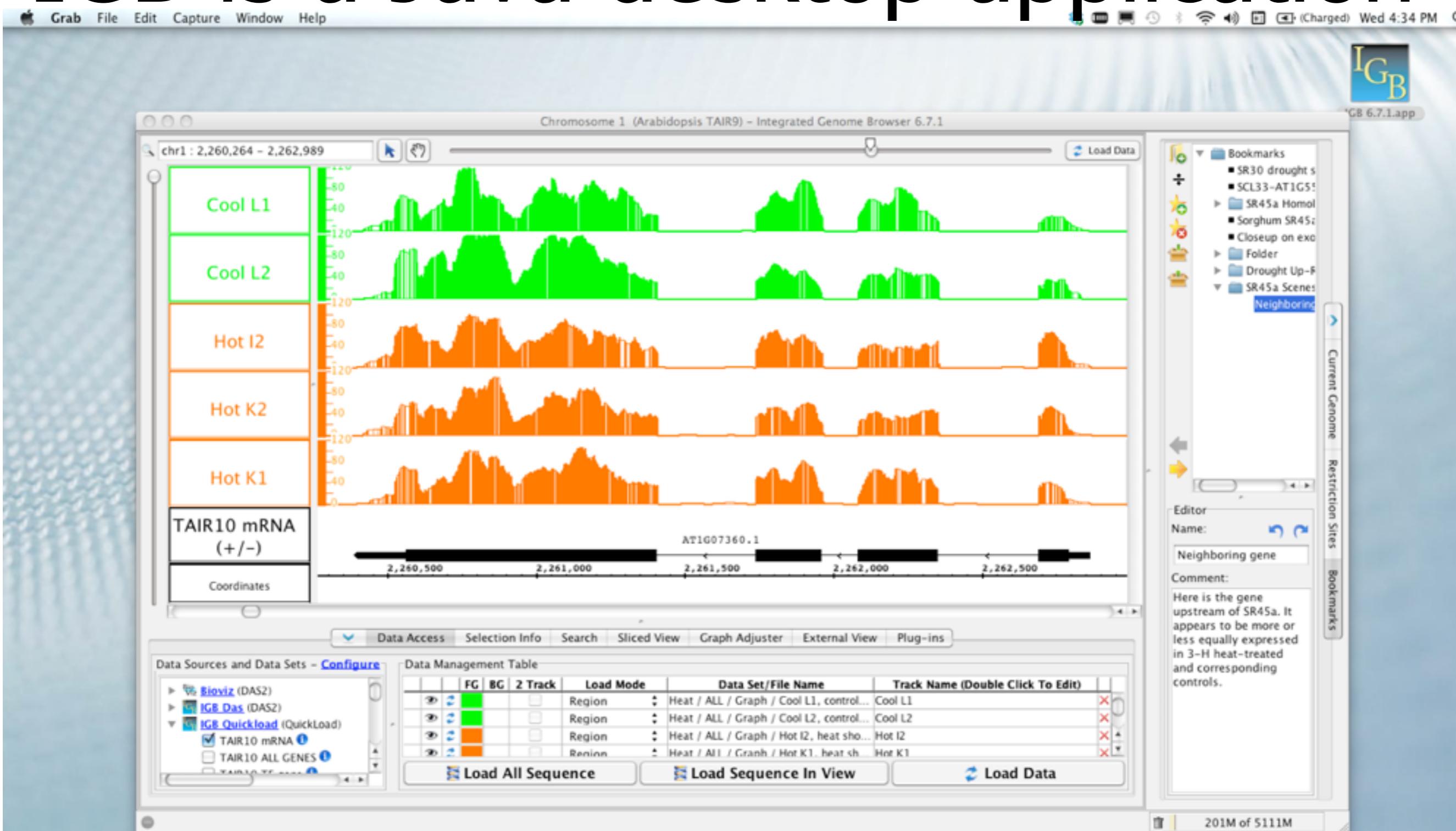


Goals

- Stimulate insight, creativity
- Support all aspects of scientific process
 - taking notes
 - making images
 - publishing data
 - exploring



IGB is a Java desktop application



Download & run locally

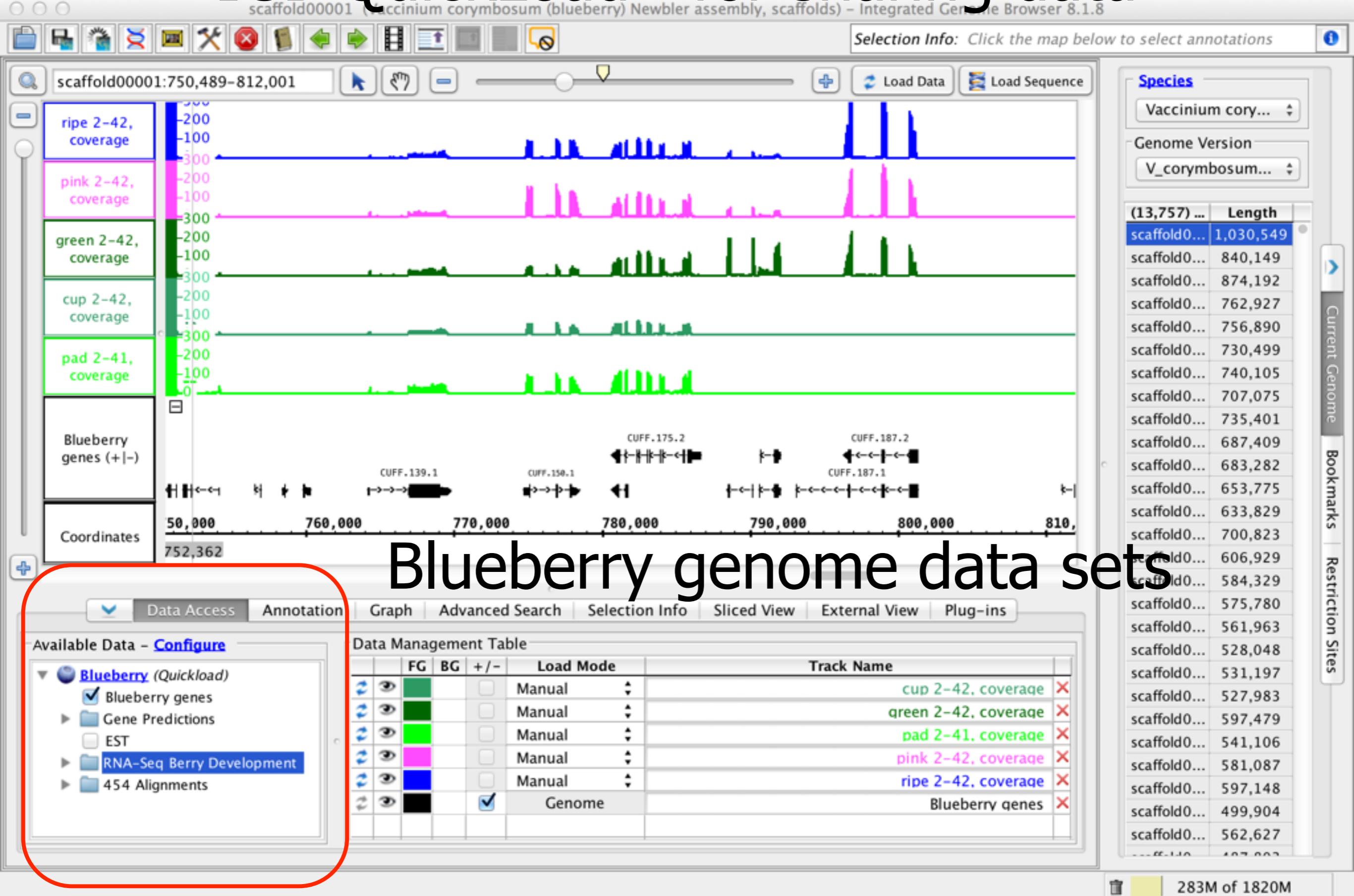
Benefits: Simple. Install it. Open files.



Pick a file

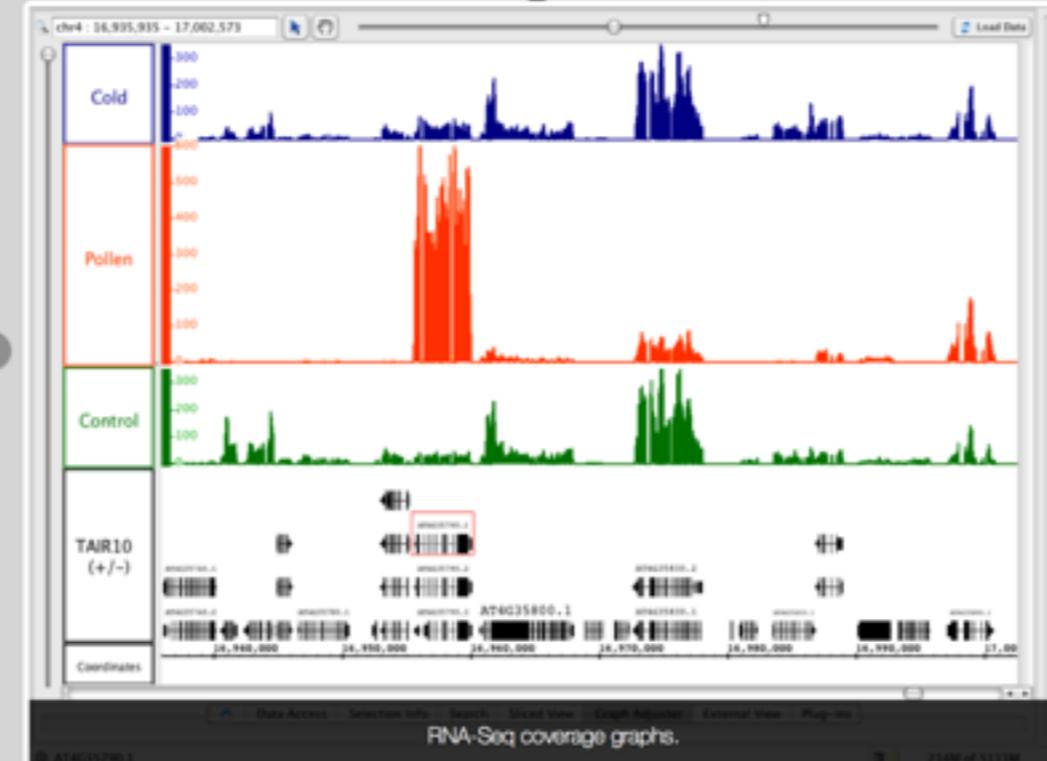
Open it

IGB QuickLoad - for sharing data



Free from BioViz.org

Integrated Genome Browser Visualization for genome-scale data



What is IGB?

Integrated Genome Browser is an easy-to-use, highly customizable genome browser you can use to view and explore genomic data and annotations, especially RNA-Seq and ChIP-Seq data sets.

[Learn More >](#)

Where can I get IGB?

IGB is free and runs on Windows, Mac, and Unix computers. Visit the IGB [download page](#) to install and run IGB. The source code is hosted in a [git repository](#) at [BitBucket](#).

[Visit BioViz Download Page >](#)

Questions?

To get help, post questions to the [GenoViz Help Forum](#). Also try searching the [IGB User's Guide](#). For help with advanced features and programming IGB, visit the [IGB Developer's Guide](#).

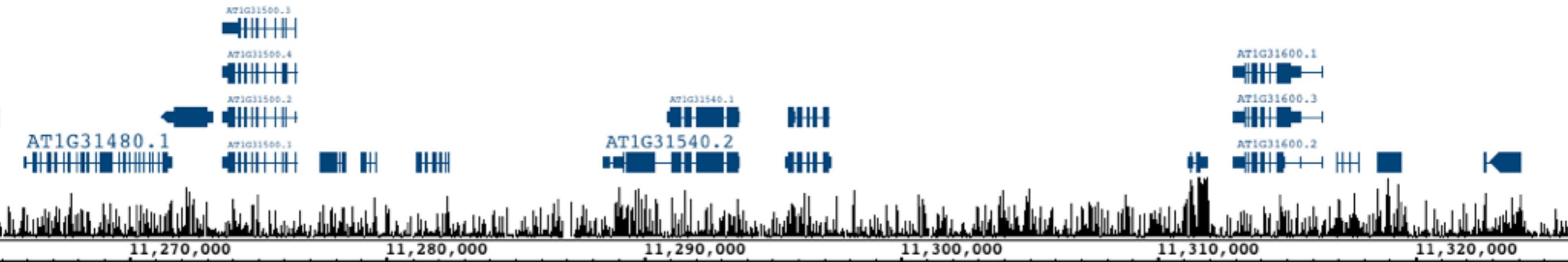
[Visit IGB User's Guide >](#)

© UNC Charlotte, all rights reserved
Genoviz is a [sourceforge](#) project

- git repository hosted on bitbucket
- public issue tracking at jira.transvar.org

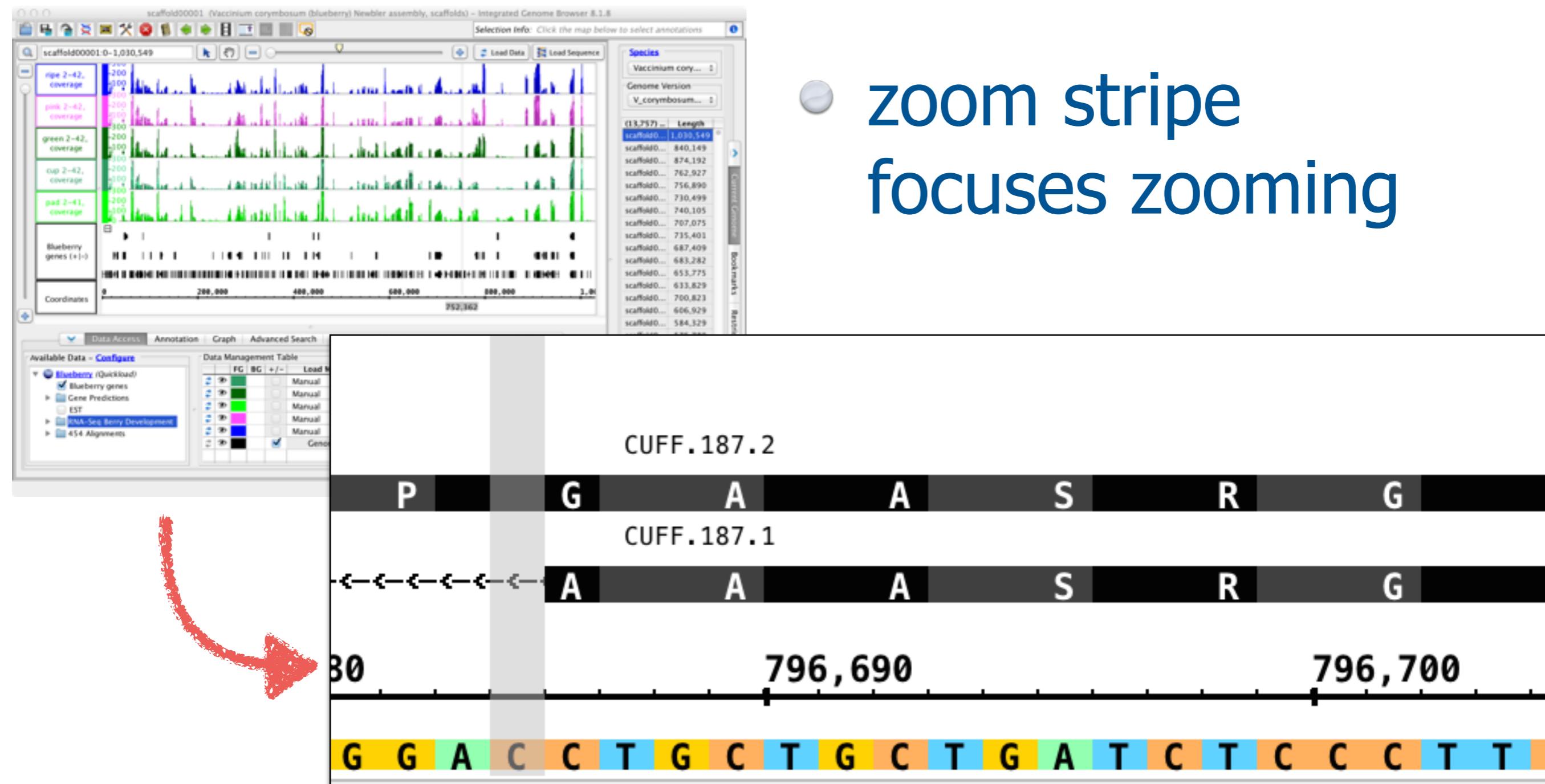
What makes IGB unique?

- fast, fluid animated zooming
- highly interactive
- dozens of features, alternative views, analytical functions, and more

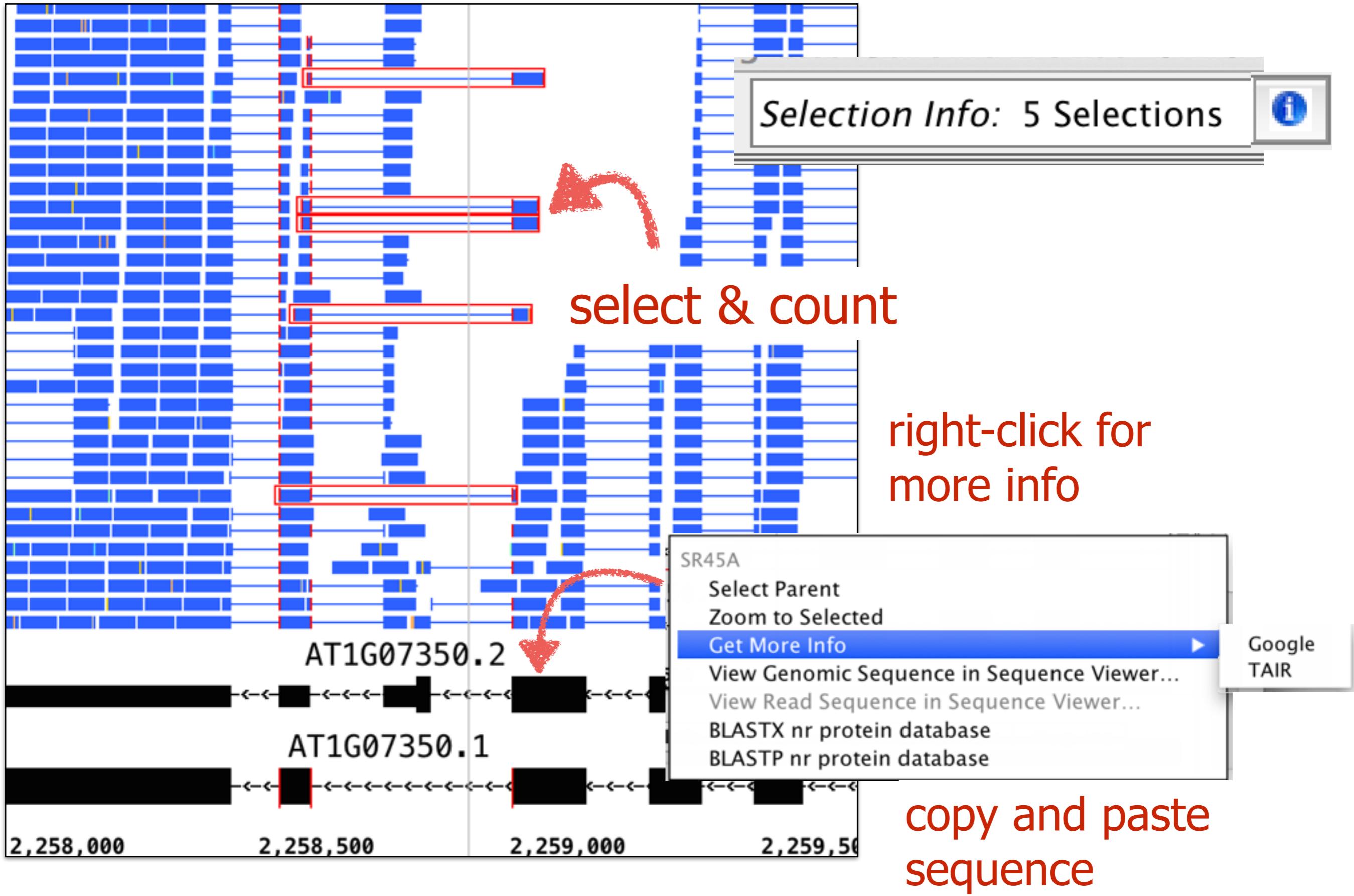


Fast, fluid animated zooming

- zoom stripe focuses zooming



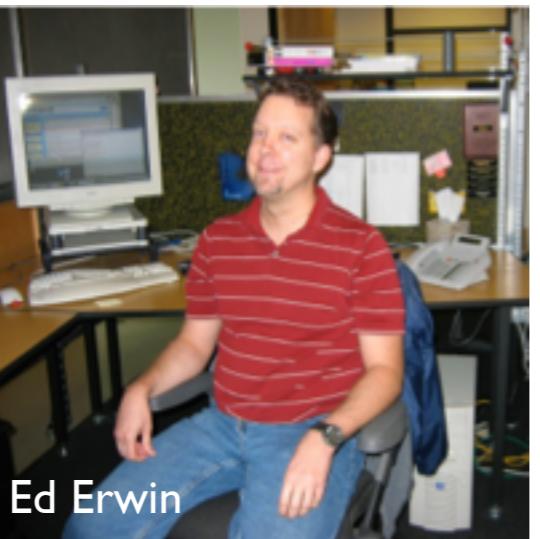
You interact with data



Many features, many contributors: 2002 - 2014



Gregg Helt



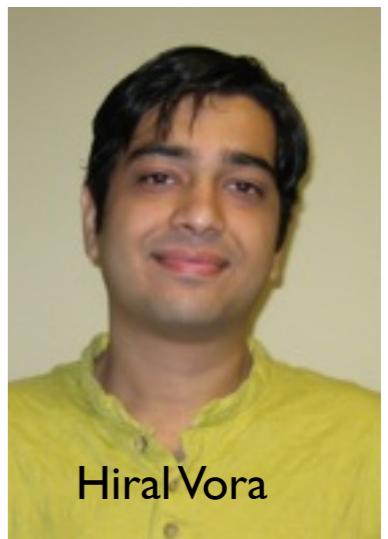
Ed Erwin



John Nicol



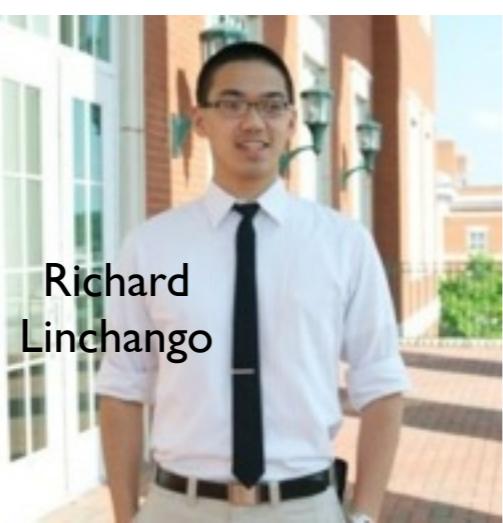
Stephen
Blanchard



Hiral Vora



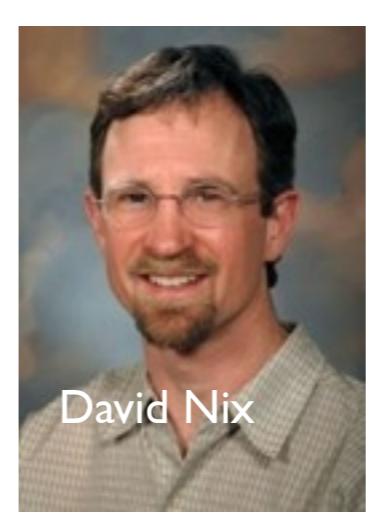
Archana Raja



Richard
Linchango



Vikram
Bishnoi



David Nix



Nick Ren



David
Norris



Neomorphic
Software



Alyssa
Guledge



Ehsan Tabari



Ivory
Blakley



Mason
Meyer

Michael
Lawrence

Lance
Frohman

Katie
Kubiak

Ido
Tamir

Fuquan
Wang

Anuj
Puram

Nate
Watson

Shira
Stav

Max Li

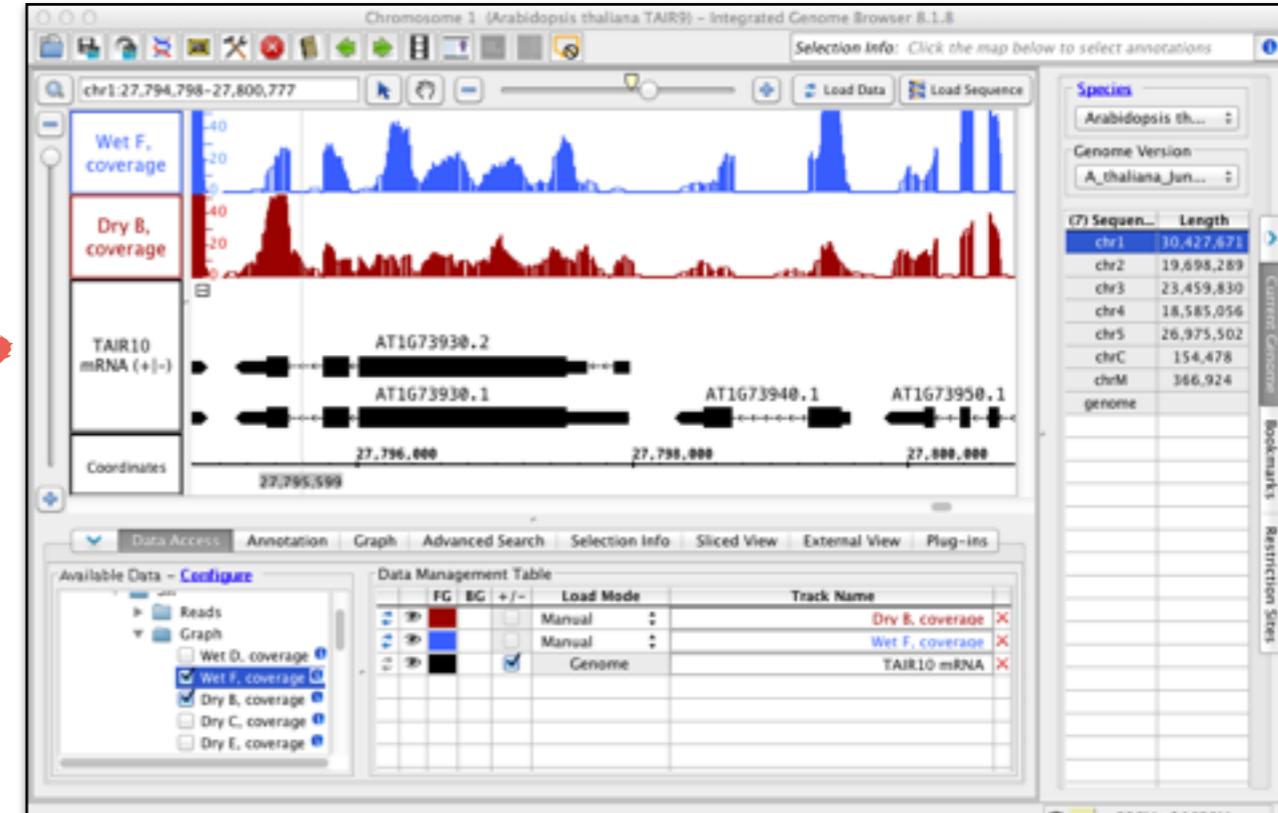
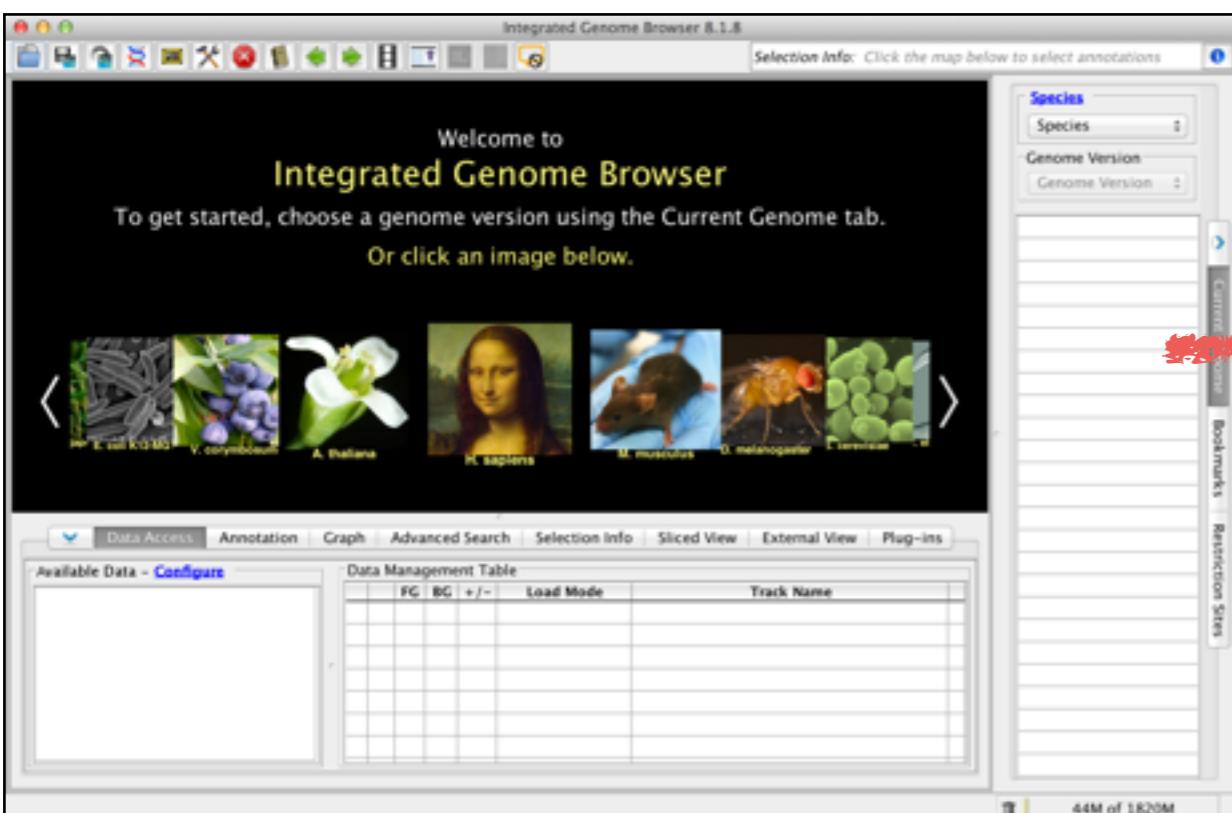
Tarun
Kanaparthi

Kyle
Suttlemyre

IGB ReST-style API

[http://localhost:7085/\[parameters\]](http://localhost:7085/[parameters])

IGB zooms to new location



for
parameters,
google
“IGB links”

Controlling IGB using IGB Links - Dashboard
<https://wiki.transvar.org/.../igbman/Controlling+IGB+using+IGB+Links> ▾
Jan 20, 2013 - Introduction. You can control IGB by embedding IGB links in Web pages.
This is useful when you need to manually inspect a large number of ...

Controlling IGB using IGB ...
IGB recognizes commonly-used
synonyms for a variety of ...
[More results from transvar.org »](#)

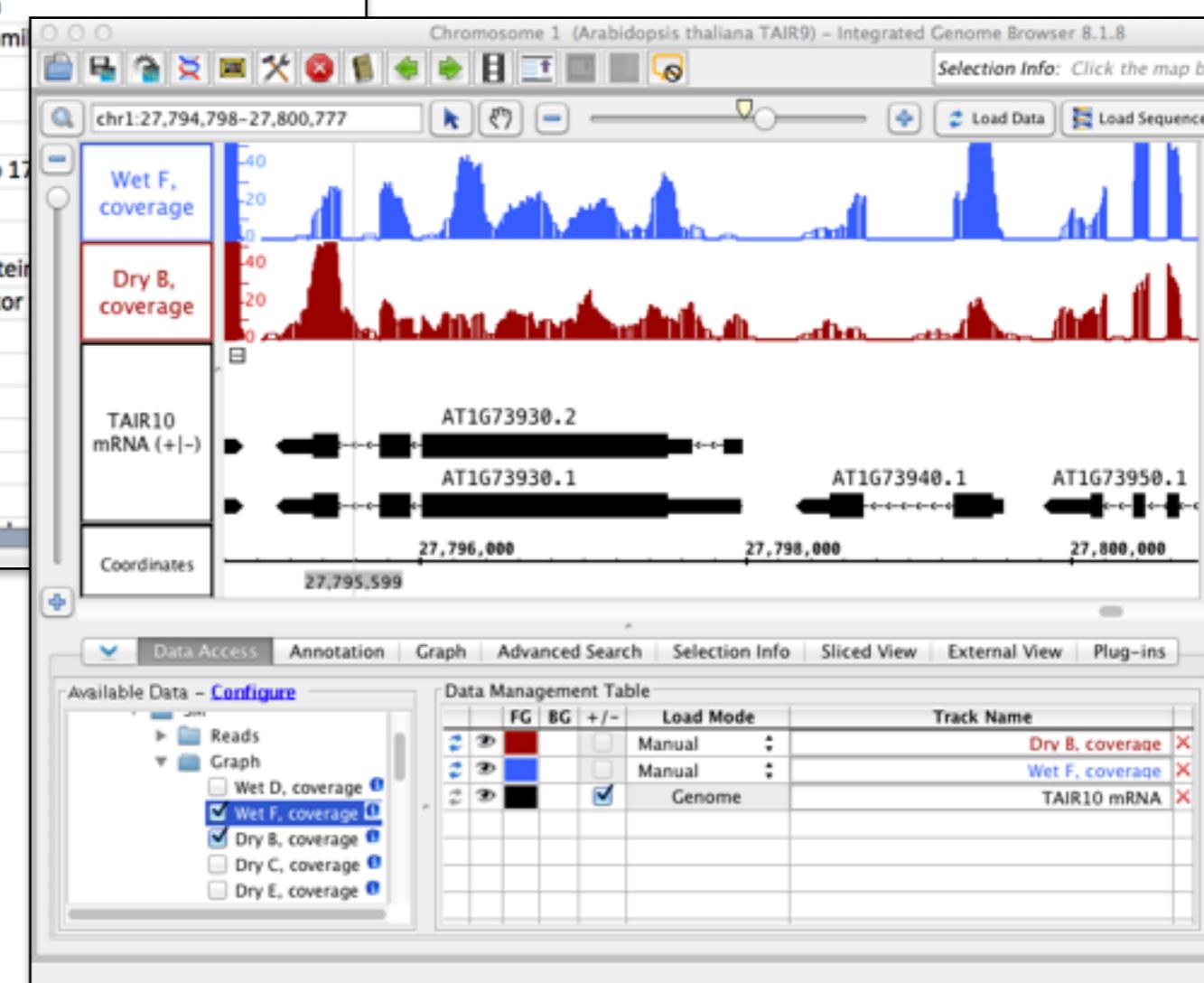
Spreadsheet with IGB links

A	I	J		
1	IGB link	fdr	gene	description
2	chr1:-1:27797680:27797863:RI	1.26E-05	AT1G73930	unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function
3	chr1:-1:2943226:2943564:AS	2.07E-04	At-SR30	RNA-binding SR protein At-SR30 subfamily SR
4	chr1:-1:182135:182252:RI	1.51E-03	AT1G01490	Heavy metal transport/detoxification superfamily protein
5	chr4:-1:13787373:13788083:RI	1.51E-03	AT4G27610	unknown protein; FUNCTIONS IN: molecular_function unknown
6	chr5:-1:9285615:9285618:AS	1.55E-03	emb1138	DEAD box RNA helicase (RH3)
7	chr1:-1:3525119:3525209:RI	1.68E-03	AT1G10650	SBP (S-ribonuclease binding protein) family protein
8	chr2:1:12872819:12872822:AS	1.68E-03	AT2G30140	UDP-Glycosyltransferase superfamily protein
9	chr3:-1:5072959:5073040:DS/ES	4.49E-03	AT3G15070	RING/U-box superfamily protein
10	chr5:-1:26413838:26414154:RI	4.56E-03	AT5G66050	Wound-responsive family protein
11	chr2:-1:11702387:11702526:AS	4.71E-03	AT2G27350	OTU-like cysteine protease family protein
12	chr2:-1:11702449:11702526:AS			protein
13	chr4:1:609857:609955:DS			inter family
14	chr4:-1:13574622:135747:AS			
15	chr4:-1:14535882:145360:DS			
16	chr4:-1:13574622:135746:DS			
17	chr1:1:30411680:30411748:RI	3.57E-03	AT1G80940	unknown protein; Has 30201 blast hits to 17
18	chr4:-1:10455011:10455020:AS	5.84E-03	AT4G19110	Protein kinase superfamily protein
19	chr4:1:11461341:11461364:DS	6.79E-03	SPHK1	sphingosine kinase 1
20	chr5:-1:26275685:26275722:DS/ES	6.89E-03	AT5G65685	UDP-Glycosyltransferase superfamily protein
21	chr1:1:9668904:9669096:RI	6.90E-03	AT5AT32 SAT32	interferon-related developmental regulator
22	chr4:-1:10455008:10455020:AS	6.90E-03	AT4G19110	Protein kinase superfamily protein
23	chr5:-1:1251501:1251564:AS	6.90E-03	R1 BTR1L BTR	binding to TOMV RNA 1L (long form)
24	chr5:1:1548221:1548221:DS			protein
25	chr5:-1:251501:251501:DS			subunit A
26	chr1:1:29660:29660:DS			
27	chr1:1:21979:21979:DS			

1. Start IGB

2. Click link

IGB scrolls and zooms,
loads data



Made in R using xlsx
library

IGB linked to Galaxy

1. Click Galaxy History file

2. Click link

3. Click Again

New Galaxy track in IGB

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.

Running Your Own
Understanding how Galaxy

display in IGB View

Cold_Treatment_assembled_transcripts (+)

TAIR10 mRNA (+|-)

Coordinates

Cold_Treatment_assembled_transcripts (-)

Integrated Genome Browser
Visualization for genome-scale data

Welcome Galaxy User

Thank you for using IGB!

display in IGB View

Binary bam alignments

Follow YouTube

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Genoviz is a sourceforge project

0 10,000,000 20,000,000 30,000,000

Save track, choose format

Chromosome 1 (Arabidopsis thaliana TAIR9) – Integrated Genome Browser 8.1.8

Selection Info: Cold_Treatment_assembled_transcripts.gtf

chr1:11,176,644-14,363,900

Cold_Treatment_assembled_transcripts (+)

TAIR10 mRNA (+|-)

Coordinates

Cold_Treatment_assembled_transcripts (-)

Data Access

Available Data – Configure

- Reads
- Graph
 - Wet D, c
 - Wet F, c
 - Dry B, c
 - Dry C, c
 - Dry E, c
- IGB-Bookmarks

File Format: BED (*.bed)

New Folder Cancel Save

Species: Arabidopsis thaliana

Genome Version: A_thaliana_Jun...

(7) Sequen... Length

Sequence	Length
chr1	30,427,671
chr2	19,698,289
chr3	23,459,830
chr4	18,585,056
chr5	26,975,502
chrC	154,478
chrM	366,924

Current Genome Bookmarks Restriction Sites

Save As: AssembledTranscripts.bed

pi

Name Date Modified

Name	Date Modified
Applications	Tuesday, June 10, 2014 5:00 PM
bin	Friday, June 20, 2014 2:05 PM
blast2go	Monday, December 30, 2013 12:36 AM
Coursera	Wednesday, April 9, 2014 3:03 PM
Desktop	Wednesday, July 9, 2014 4:22 PM
Documents	Wednesday, April 2, 2014 11:02 PM
Downloads	Wednesday, July 9, 2014 1:32 PM
Dropbox	Thursday, July 3, 2014 11:58 AM
hs_err_pid31465.log	Sunday, May 11, 2014 11:23 AM
IGB-Bookmarks	Sunday, January 27, 2013 9:50 PM

AssembledTranscripts

TAIR10 mRNA

345M of 1820M

The screenshot shows the Integrated Genome Browser (IGB) interface for Chromosome 1 of Arabidopsis thaliana TAIR9. A context menu is open over a blue transcript track labeled 'Cold_Treatment_assembled_transcripts (+)'. The menu includes options like 'Save' and 'Copy'. A 'Save' dialog box is displayed, prompting the user to 'Save As:' 'AssembledTranscripts.bed'. The 'File Format:' dropdown is set to 'BED (*.bed)'. The 'Save' dialog also lists the current directory as 'pi'. In the background, the genome browser displays other tracks such as 'TAIR10 mRNA (+|-)' and 'Coordinates'. To the right, a sidebar shows genome statistics for chromosomes chr1 through chrM and the genome. A file browser window is also visible in the foreground, showing a list of files in the 'pi' directory, including various application and document folders.

User's Guide

Home – IGB User's Guide – Confluence

Home – IGB User's Guide – Confl... +

wiki.transvar.org/confluence/display/igbman/Home

Google

Dashboard > IGB User's Guide > Home

Browse Log In Search Confluence

Search

New in IGB 6.7

Quick Start

Introduction

IGB Anatomy

IGB Preferences

Loading Data

Data Sources

- Adding and Managing Data Sources
- Creating QuickLoad Sites

File Formats

- Converting FASTA to BNIB
- Making BAM Files for IGB (RNA-Seq)
- Working with .wig files

Removing data from a current session

Creating your own genome version

Personal Synonyms

Species currently recognized by IGB

Saving and sharing data

Bookmarks

IGB Home

1 Added by Ann Loraine, last edited by Ann Loraine on Apr 29, 2012 (view change)

About IGB

New sequencing technologies are making it much easier for labs to produce huge volumes of short- and long-read sequencing data. At the same time, more labs are using DNA microarrays to study expression patterns, identify sites bound by transcriptional factors, and explore the epigenome. To understand these new data sets, researchers need to view their data alongside other known features of the genomic landscape.

The Integrated Genome Browser (IGB, pronounced Ig-Bee) aims to meet this need. First developed at Affymetrix in 2003 for their tiling array products, IGB provides an advanced, highly customizable environment for exploring and analyzing large-scale genomic data sets.

Using IGB, you can:

- View your RNA-Seq, ChIP-chip or ChIP-seq data alongside genome annotations and sequence.
- Investigate alternative splicing, regulation of gene expression, epigenetic modifications of DNA, and other genome-scale questions.
- View results from aligning short-read sequences onto a target genome, identify SNPs, and check alignment quality.
- Copy and paste genomic sequences for further analysis into other tools, such as primer design and promoter analysis tools.
- Create high-quality images for publication in a variety of formats.

Tools

https://wiki.transvar.org

IGB Gallery

IGB 6.7.1 running in iPlant Atmosphere – IGB User's Guide – Confluence

IGB 6.7.1 running in iPlant Atmosphere transvar.org https://wiki.transvar.org/confluence/display/igbman/IGB+6.7.1+running+in+iPlant+Atmosphere Google Search Confluence

Dashboard > IGB User's Guide > ... > IGB Gallery > IGB 6.7.1 running in iPlant Atmosphere

Printing and Exporting Images
Navigation
Working with Sequence Data
Working with Annotation Tracks
Working with Graph Tracks
Visualizing probe sets
Interactive tutorials
Advanced Features
Troubleshooting
Who uses IGB
IGB License
New in IGB 6.5
New in IGB 6.6
IGB Gallery
Color-coding read alignments by strand
A new gene induced by cold in *Arabidopsis thaliana*?
Edge matching ESTs to assess alternative splicing
Counting reads with selection tool
Alternative splicing in GRP7 (AT2G21660)
Using IGB to view effects of kmer on assembly quality
Comparing new and old annotation releases
Viewing RNA-Seq and expression tiling array data in the same view
Visualizing output from TopHat and BowTie
Visualizing RNA-Seq reads aligned onto a genome
IGB 6.7.1 running in iPlant Atmosphere
Tutorials
IGB Demos and Screencasts
Holding page for outdated materials

RNASeq experiment from the Loraine lab that we deployed the publicly-accessible IGBQuickLoad site at UNC Charlotte.

vm142-21.iplantcollaborative.org:1 (loraine) – VNC Viewer

Applications Places System

Chromosome 1 (*Arabidopsis TAIR9*) - Integrated Genome Browser 6.7.1

File Edit View Tools Bookmarks Help

chr1 : 2,942,203 - 2,946,533

Cold (bedgraph) (0, 181.42)

Control (bedgraph) (0, 181.42)

TAIR10 mRNA (+ / -)

Coordinates

AT1009140.1

AT1009140.2

AT1009150.1

2,942,373 2,943,000 2,944,000 2,945,000 2,946,000

Data Access Selection Info Search Sliced View Graph Adjuster External View Plug-ins

Data Sources and Data Sets – Configure

RNA-Seq

- Lorraine Lab
- Mixed Cold
- SM
 - Reads
 - Graph
 - Control, coverage
 - Cold, coverage
- MM
- Juncs

Data Management Table

	FG	BG	2 Track	Load Mode	Data Set/File Name	Track Name (Double ...)	
①	●	●	●	Region	RNA-Seq / Lorraine...	Cold (bedgraph)	X
②	●	●	●	Region	RNA-Seq / Lorraine...	Control (bedgraph)	X
③	●	●	●	Genome	TAIR10 mRNA	TAIR10 mRNA	X

Load All Sequence Load Sequence In View Load Data

316M of 910M

<http://wiki.transvar.org>

Lorraine Lab Agile Board

QUICK FILTERS: David Ivory Mason Tarun Ann Tiffany Only My Issues Recently Updated

VERSIONS

EPICS

All issues

Technical Debt Reduction

Integration with SNpedia

Paired End Visualization

Needs Clarification or blocked

Issues without epics

Sprint 1 15 issues

Start Sprint

- ↑ IGBF-87 Dragging and dropping an arrow from the toolbar causes constant scrolling. 1
- ✘ IGBF-103 Save all the data, not just the current chromosome 2
- ↑ IGBF-27 Improve right-click menu when users right-click a feature or sequence in IGB display 1
- ↑ IGBF-67 External Viewer does not work. 2
- ↑ IGBF-93 Help menu improvements - new link to BioStars, rewording 0.5
- ↑ IGBF-59 Create a Deprecated server list that IGB applies to older user server lists 1.5
- ↑ IGBF-104 Update Jira Configuration with similar "promotion" based au Technical Debt Red... 1
- ↑ IGBF-62 User can not delete a track that does not contain data via context menu 1
- ↑ IGBF-58 IGB gives confusing message when adding a duplicate data source and duplicates dat 1
- ↑ IGBF-49 Creating a "Not" track with the coordinates track. (should this be allowed?) When dele 1
- ↓ IGBF-81 Zoom in and load data message appears even when file can't be loaded 1
- ↓ IGBF-47 Add context menu "copy" to bookmarks right click 0.5
- ↓ IGBF-30 file choosers should recall the last directory user navigated to 0.5
- ↓ IGBF-56 Update circle info icon to have a clear background instead of white background 0.25
- ↓ IGBF-43 Remove RELEASES.txt from igb.zip 0.1

15 issues Estimate 14.35

Backlog 47 issues

Create Sprint

jira.transvar.org

IGB 8.2 / IGBF-32

Don't replace spaces with underscore characters when viewing files from Galaxy.

Estimate: 1

Details

Status: OPEN

Component/s: None

Labels: None

Affects Version/s: None

Fix Version/s: None

Epic: Galaxy Server galaxy.transvar.org

People

Reporter: Ann Loraine

Assignee: David Norris

Dates

Created: 13/Apr/14 10:34 AM

Updated: 10/Jul/14 1:18 PM



agile development



3 week sprints

sprints, stories public
technical debt reduction