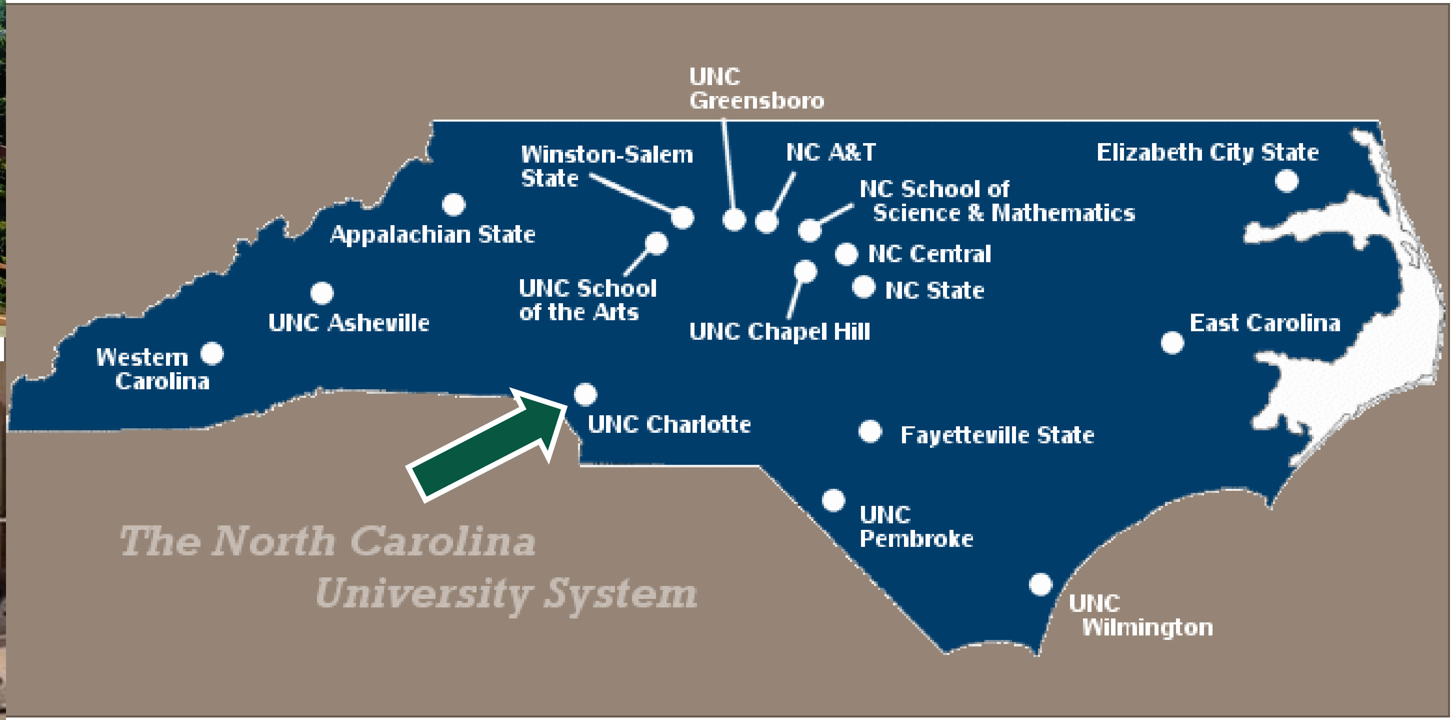
Toward Sustainable Genomic Data Accessibility and Visualization with the Integrated Genome Browser

AgBioData Webinar – October 1st, 2025

Paige Kulzer


UNC Greensboro
Winston-Salem State
NC A&T
Elizabeth City State
NC School of Science & Mathematics
Appalachian State
NC Central
NC State
UNC School of the Arts
UNC Chapel Hill
UNC Asheville
East Carolina
Western Carolina
UNC Charlotte
Fayetteville State
UNC Pembroke
UNC Wilmington
The North Carolina University System

Loraine Lab

Dr. Ann Loraine
Professor

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Research Assistant Professor

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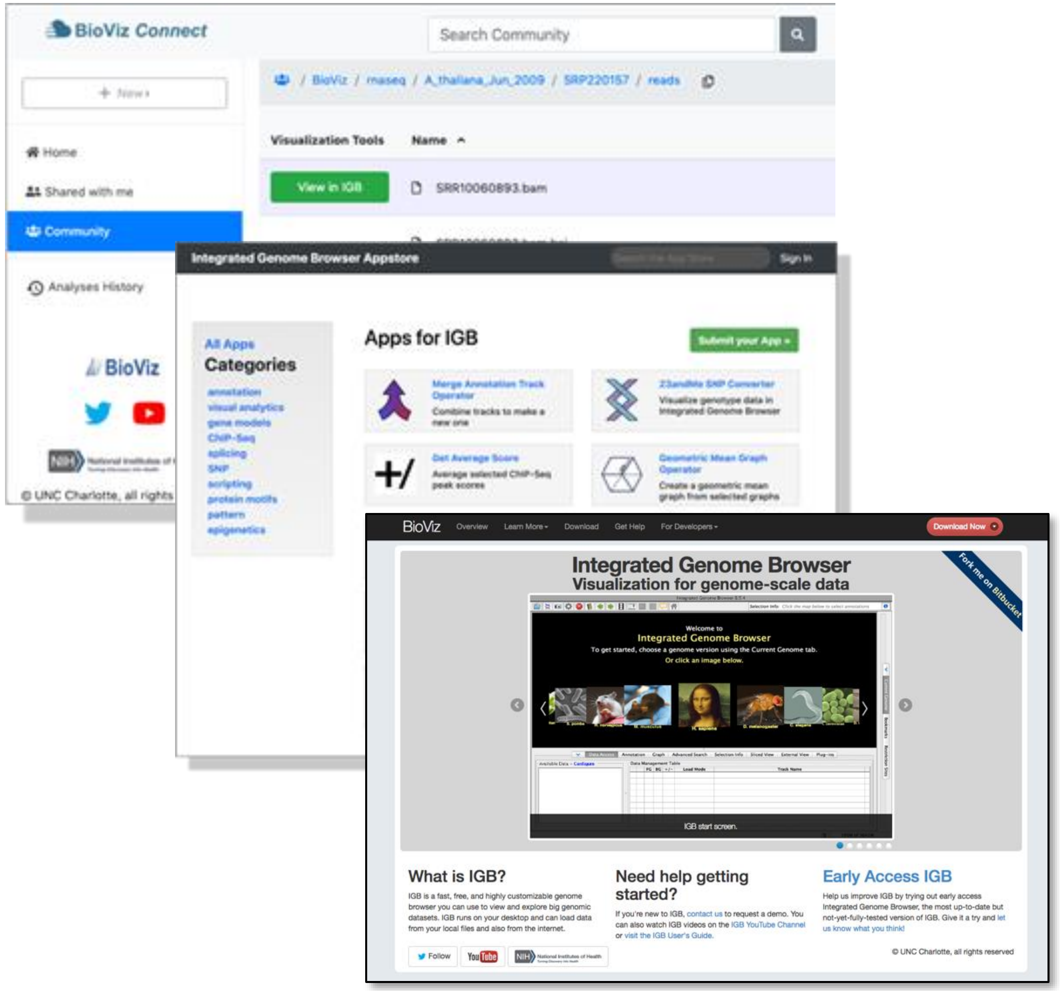
Bioinformatics Data Manager and Trainer

Karthik Raveendran
Computer Science PhD Candidate

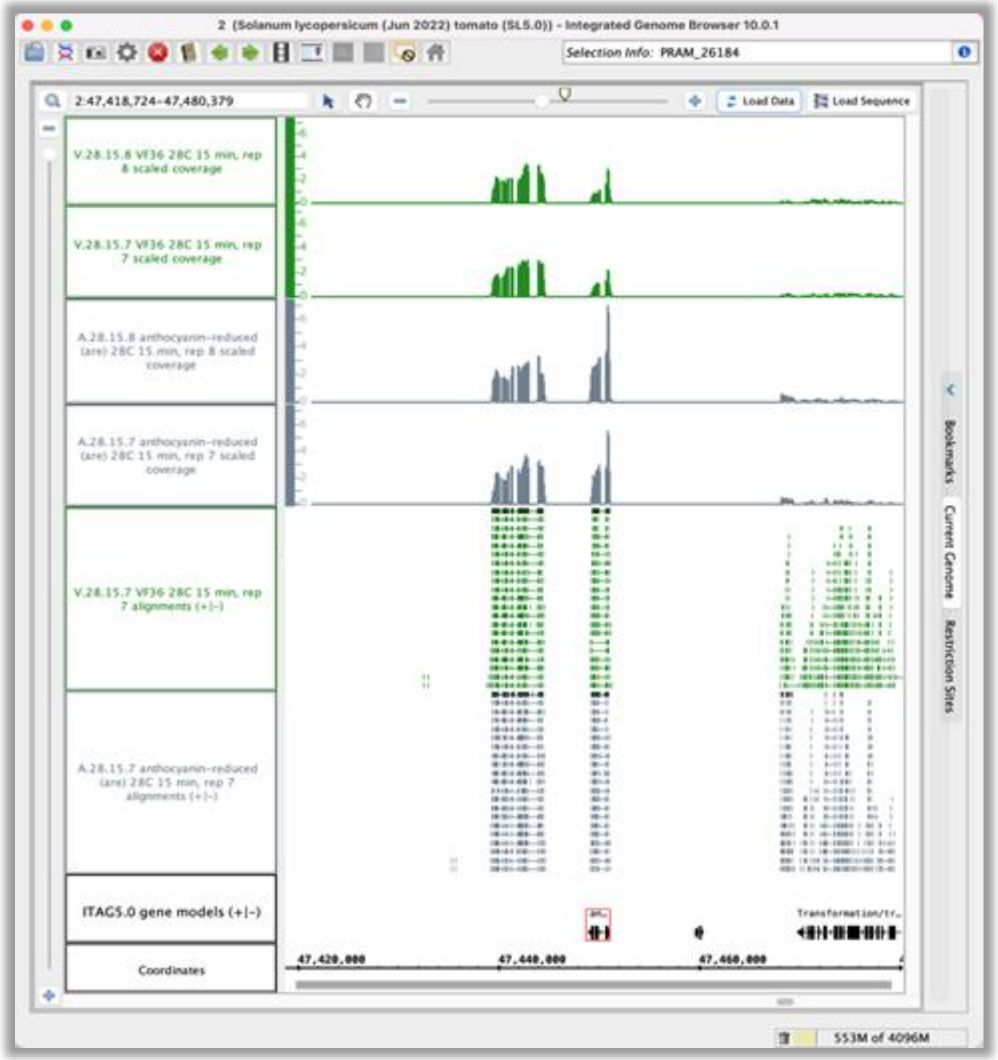
Udaya Chinta
Master's Student

Saideepthi Jagarapu
Master's Student

The Loraine Lab Mission



BioViz.org



We write software for scientists to visualize and understand data better.

UNIVERSITY OF NORTH CAROLINA
CHARLOTTE

There are many great genome browsers!

UCSC Genome Browser

JBrowse

NCBI Genome Data Viewer

WashU Epigenome Browser

Ensembl

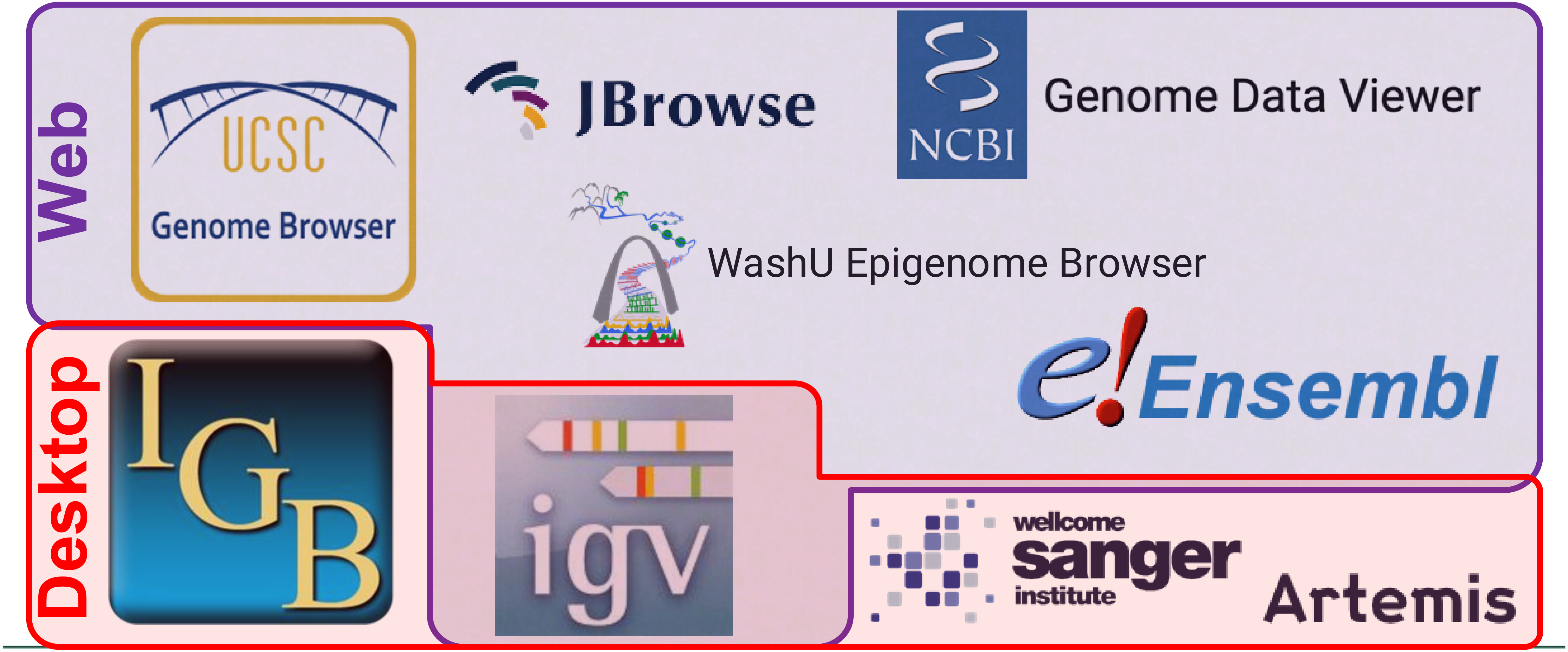
IGB

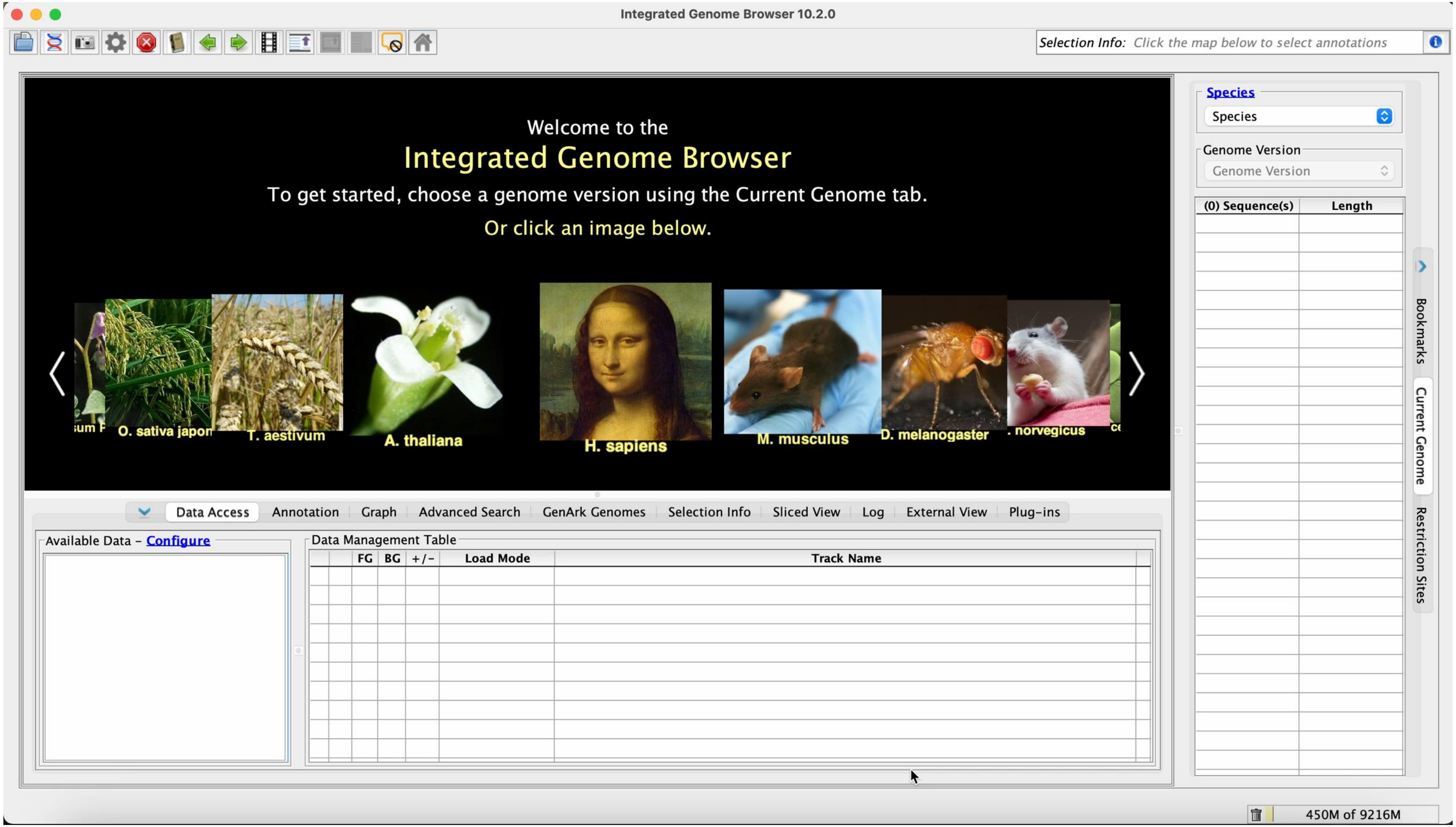
igv

wellcome sanger institute Artemis

There are many great genome browsers!

There are many great genome browsers!





Integrated Genome Browser 10.2.0

Selection Info: *Click the map below to select annotations*

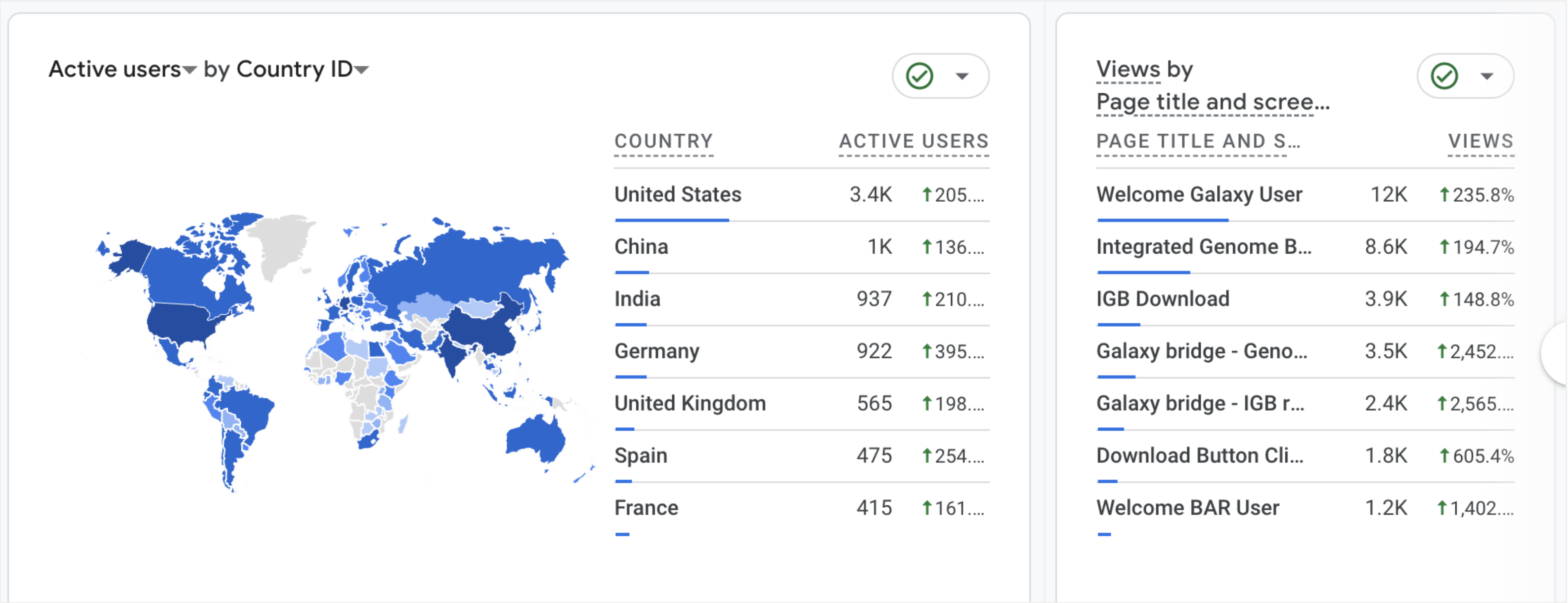
Welcome to the

Integrated Genome Browser

To get started, choose a genome version using the Current Genome tab.

Or click an image below.

The people using IGB



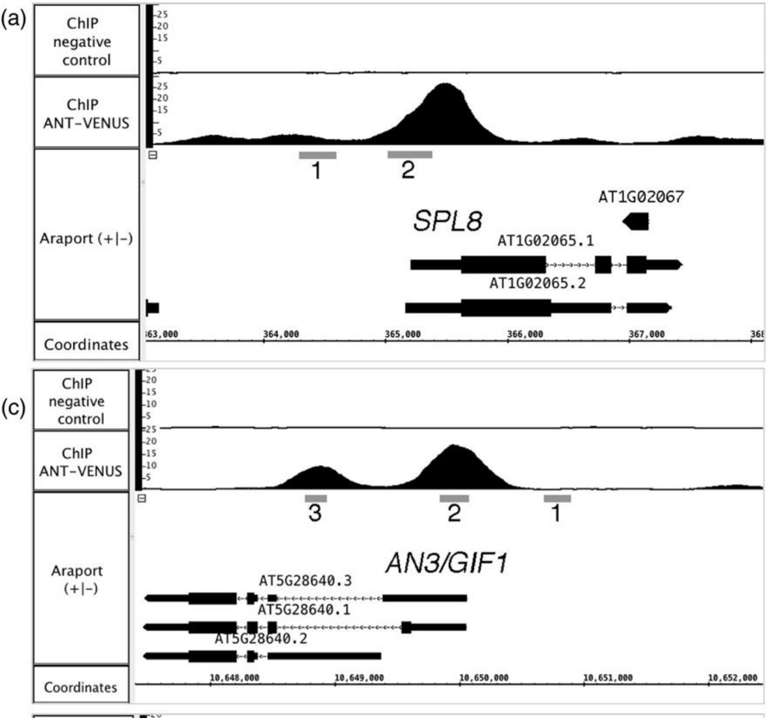
Active users by Country ID

COUNTRY	ACTIVE USERS	
United States	3.4K	↑205....
China	1K	↑136....
India	937	↑210....
Germany	922	↑395....
United Kingdom	565	↑198....
Spain	475	↑254....
France	415	↑161....

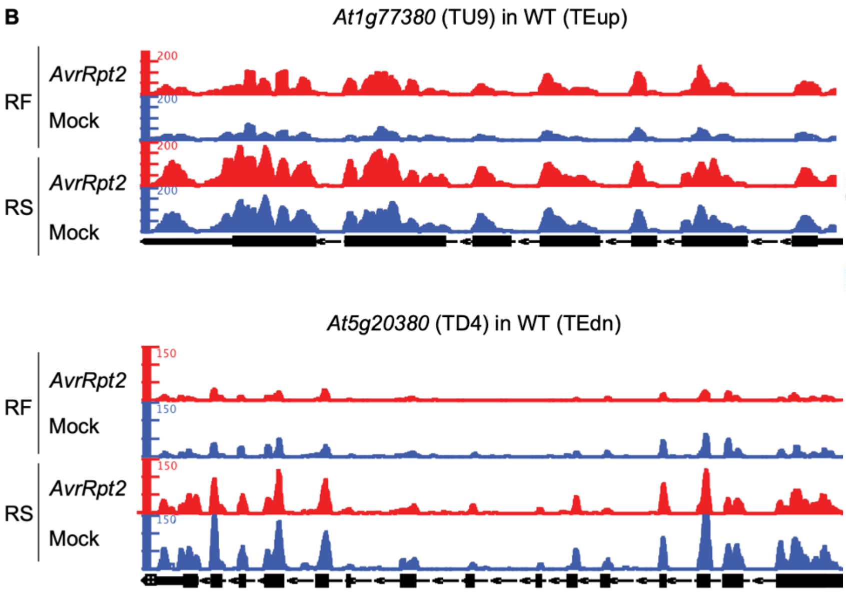
Views by
Page title and scree...

PAGE TITLE AND S...	VIEWS	
Welcome Galaxy User	12K	↑235.8%
Integrated Genome B...	8.6K	↑194.7%
IGB Download	3.9K	↑148.8%
Galaxy bridge - Geno...	3.5K	↑2,452....
Galaxy bridge - IGB r...	2.4K	↑2,565....
Download Button Cli...	1.8K	↑605.4%
Welcome BAR User	1.2K	↑1,402....

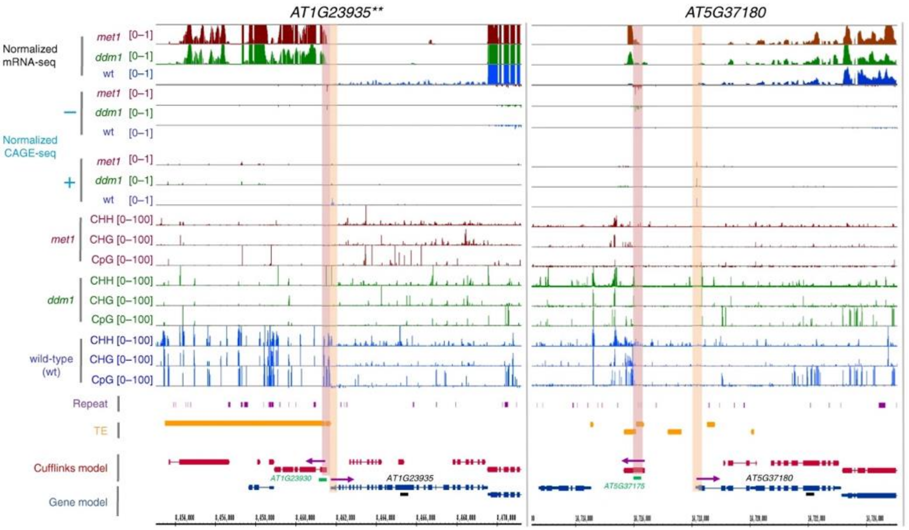
Make publication quality figures of your data in IGB



Krizek et al., 2020
https://doi.org/10.1111/tpj.14769



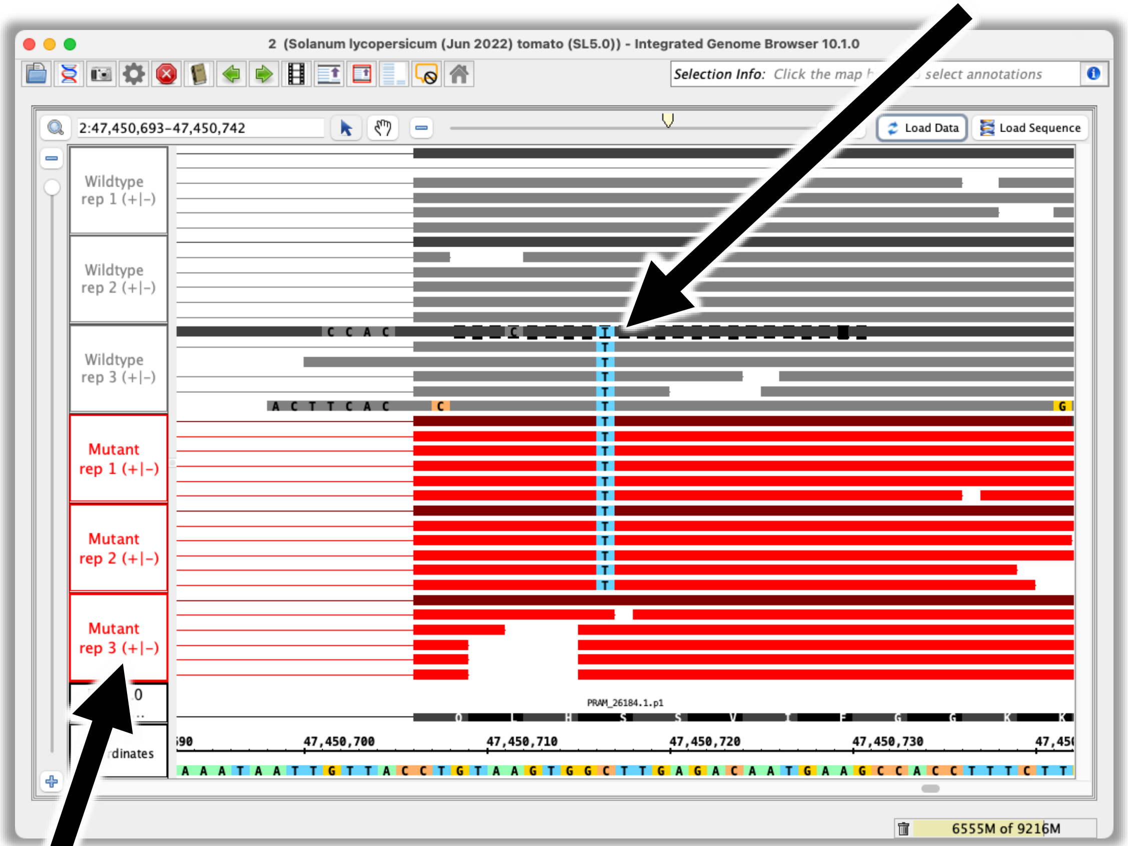
Heejin Yoo et al., 2020
pubmed.ncbi.nlm.nih.gov/31568832/



Ngoc Tu Le et al., 2020
pubmed.ncbi.nlm.nih.gov/32591528/

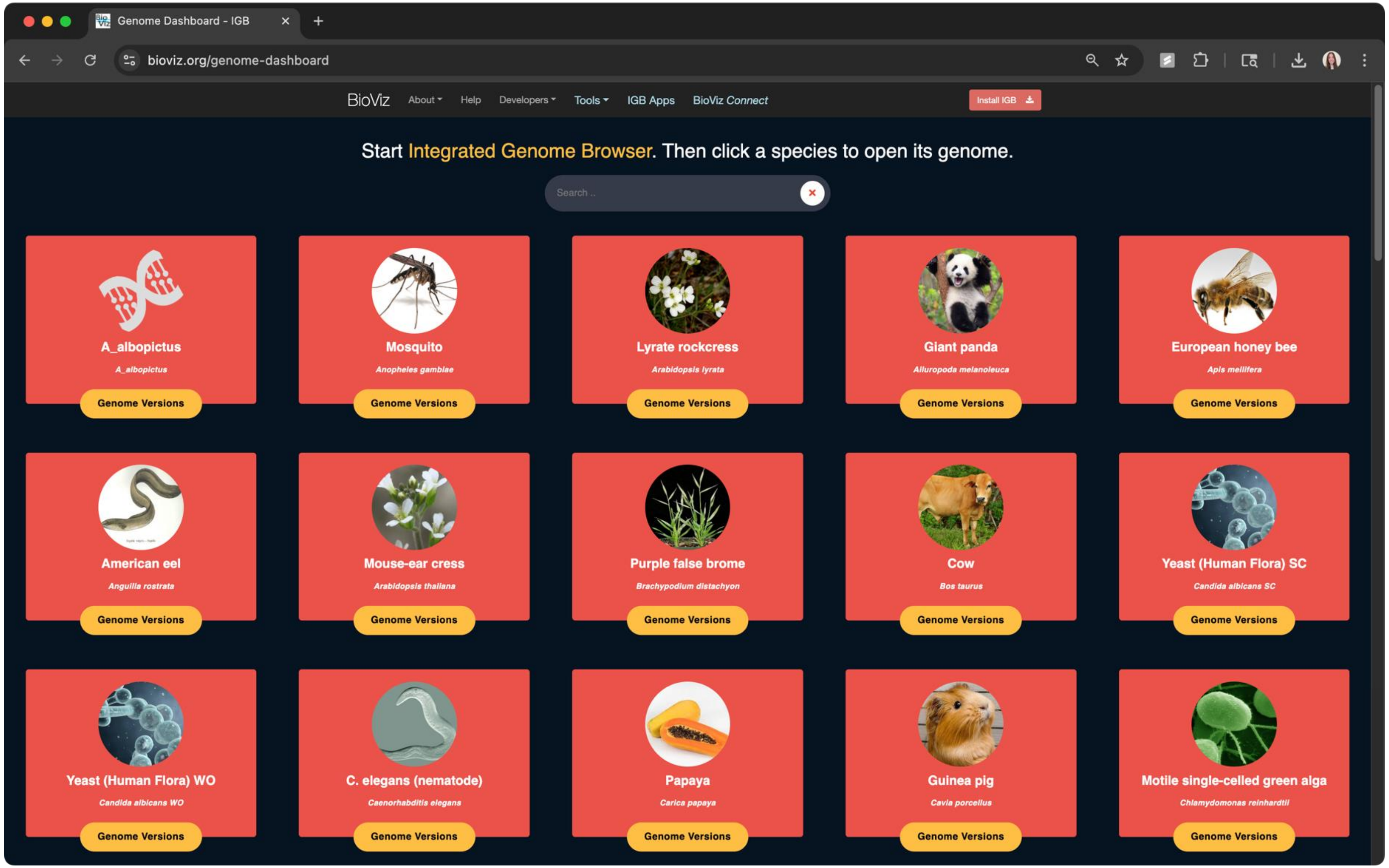
Identify issues such as sample switching

Wildtype samples should not have this **SNP**.



This **mutant** sample is really a **wildtype**, as it is missing the **SNP**.

IGB hosts 70+ genomes and genome annotations



Start Integrated Genome Browser. Then click a species to open its genome.

A_albopictus
A_albopictus

Mosquito
Anopheles gambiae

Lyrate rockcress
Arabidopsis lyrata

Giant panda
Ailuropoda melanoleuca

European honey bee
Apis mellifera

American eel
Anguilla rostrata

Mouse-ear cress
Arabidopsis thaliana

Purple false brome
Brachypodium distachyon

Cow
Bos taurus

Yeast (Human Flora) SC
Candida albicans SC

Yeast (Human Flora) WO
Candida albicans WO

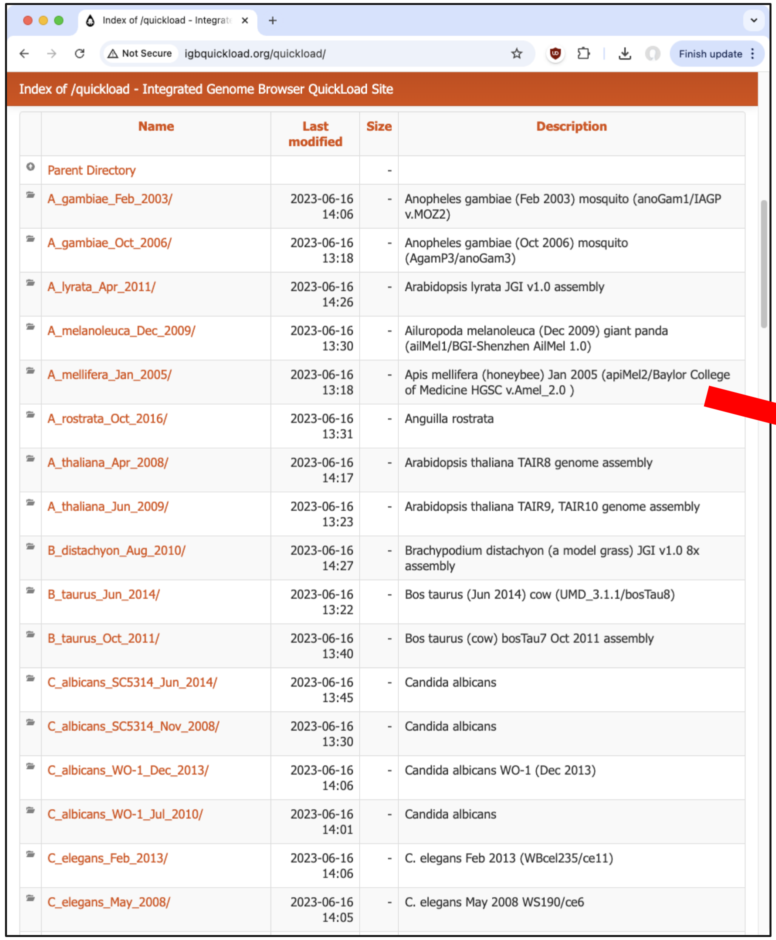
C. elegans (nematode)
Caenorhabditis elegans

Papaya
Carica papaya

Guinea pig
Cavia porcellus

Motile single-celled green alga
Chlamydomonas reinhardtii

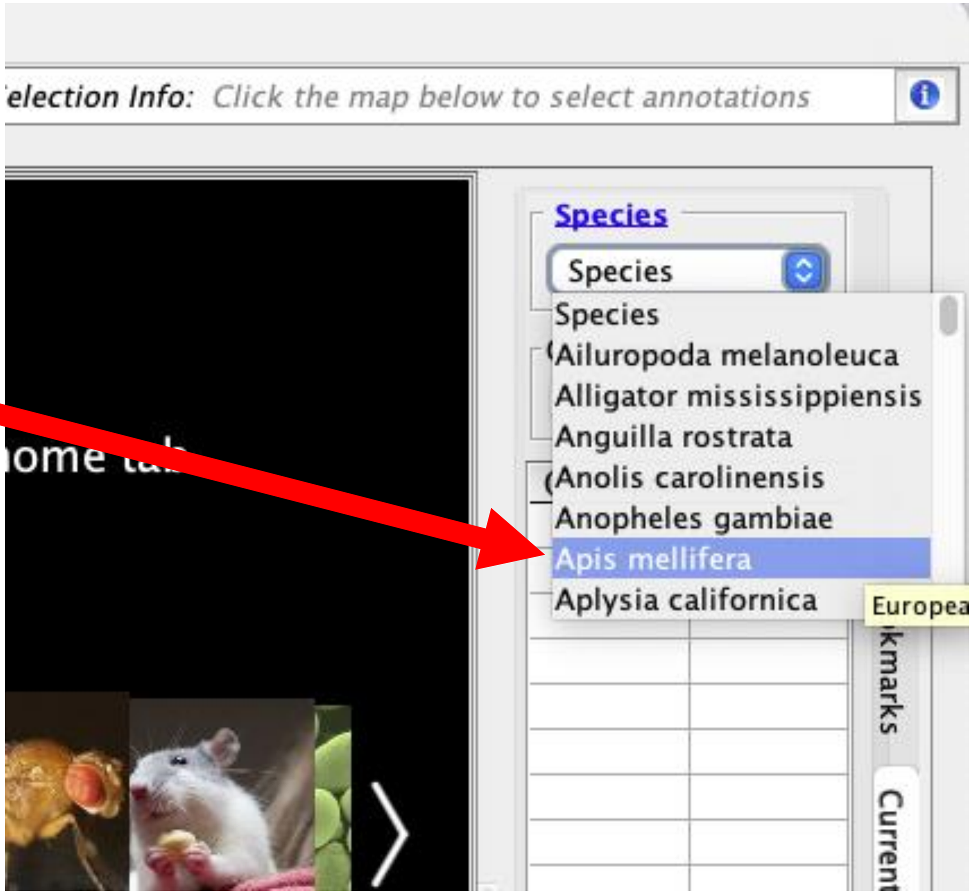
We were manually adding genomes and annotations...



Index of /quickload - Integrated Genome Browser QuickLoad Site

Name	Last modified	Size	Description
Parent Directory		-	
A_gambiae_Feb_2003/	2023-06-16 14:06	-	Anopheles gambiae (Feb 2003) mosquito (anoGam1/IAGP v.MOZ2)
A_gambiae_Oct_2006/	2023-06-16 13:18	-	Anopheles gambiae (Oct 2006) mosquito (AgamP3/anoGam3)
A_lyrata_Apr_2011/	2023-06-16 14:26	-	Arabidopsis lyrata JGI v1.0 assembly
A_melanoleuca_Dec_2009/	2023-06-16 13:30	-	Ailuropoda melanoleuca (Dec 2009) giant panda (ailMel1/BGI-Shenzhen AilMel 1.0)
A_mellifera_Jan_2005/	2023-06-16 13:18	-	Apis mellifera (honeybee) Jan 2005 (apiMel2/Baylor College of Medicine HGSC v.Amel_2.0)
A_rostrata_Oct_2016/	2023-06-16 13:31	-	Anguilla rostrata
A_thaliana_Apr_2008/	2023-06-16 14:17	-	Arabidopsis thaliana TAIR8 genome assembly
A_thaliana_Jun_2009/	2023-06-16 13:23	-	Arabidopsis thaliana TAIR9, TAIR10 genome assembly
B_distachyon_Aug_2010/	2023-06-16 14:27	-	Brachypodium distachyon (a model grass) JGI v1.0 8x assembly
B_taurus_Jun_2014/	2023-06-16 13:22	-	Bos taurus (Jun 2014) cow (UMD_3.1.1/bosTau8)
B_taurus_Oct_2011/	2023-06-16 13:40	-	Bos taurus (cow) bosTau7 Oct 2011 assembly
C_albicans_SC5314_Jun_2014/	2023-06-16 13:45	-	Candida albicans
C_albicans_SC5314_Nov_2008/	2023-06-16 13:30	-	Candida albicans
C_albicans_WO-1_Dec_2013/	2023-06-16 14:06	-	Candida albicans WO-1 (Dec 2013)
C_albicans_WO-1_Jul_2010/	2023-06-16 14:01	-	Candida albicans
C_elegans_Feb_2013/	2023-06-16 14:06	-	C. elegans Feb 2013 (WBcel235/ce11)
C_elegans_May_2008/	2023-06-16 14:05	-	C. elegans May 2008 WS190/ce6

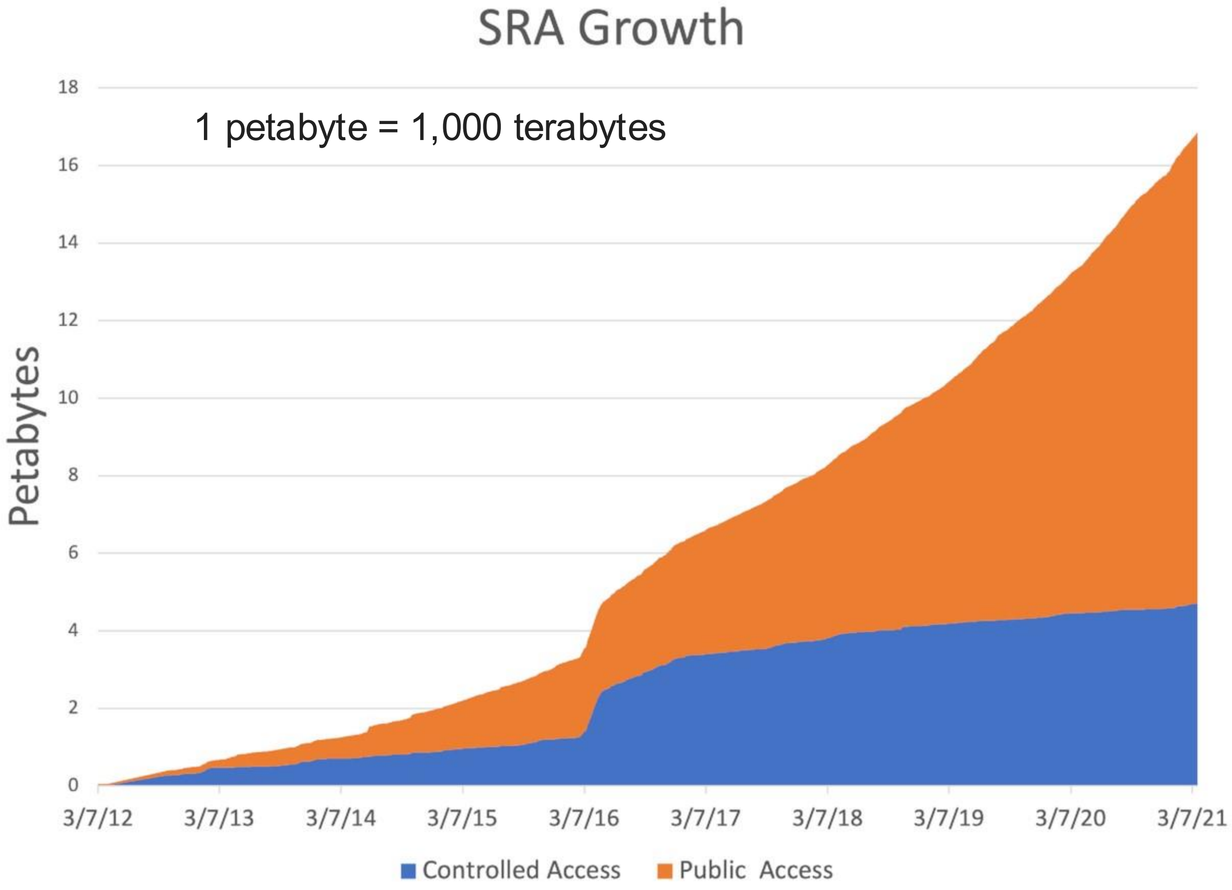
igbquickload.org/quickload



tair

maizeGDB
MAIZE GENETICS AND GENOMICS DATABASE

...but genomic data repositories are growing exponentially



1 petabyte = 1,000 terabytes

Katz et al., 2021
https://doi.org/10.1093/nar/gkab1053


SHORT REPORT **Open Access**

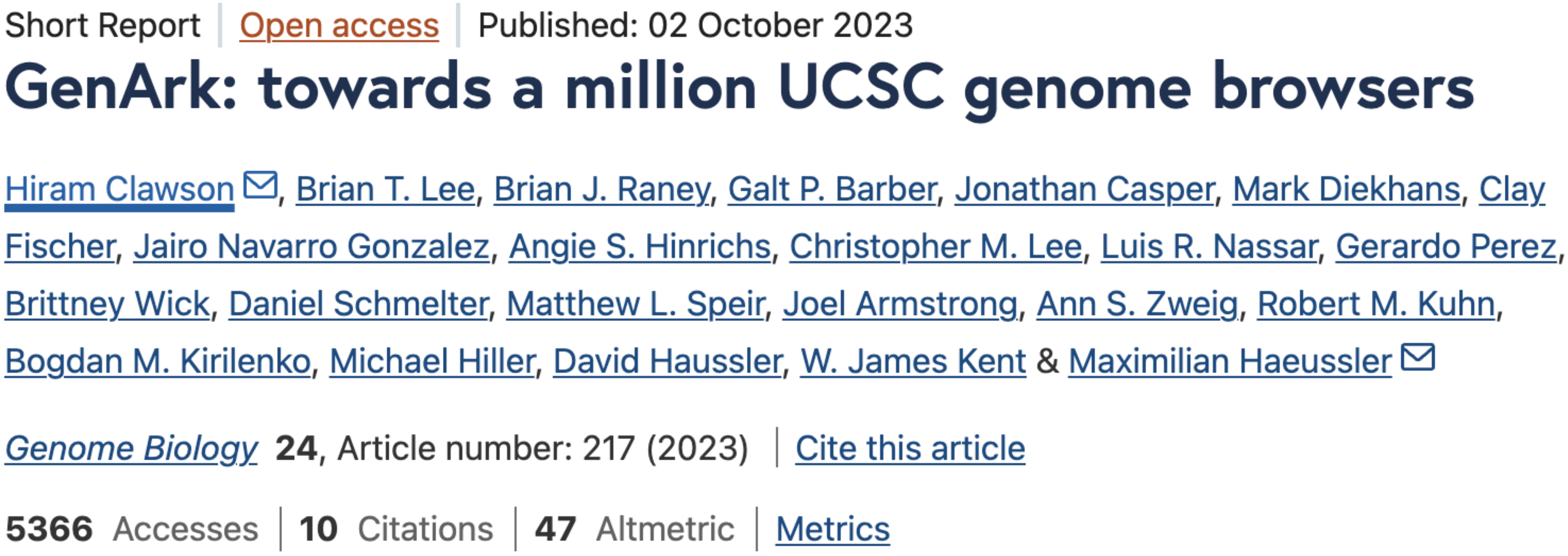
GenArk: towards a million UCSC genome browsers

“Gone are the days when a new genome for an organism made White House press briefings and news headlines. Instead, several dozen are completed every day and silently submitted to data archives.”

IGB Integrations

Data providers

IGB integrations – UCSC GenArk



Short Report | Open access | Published: 02 October 2023

GenArk: towards a million UCSC genome browsers

Hiram Clawson, Brian T. Lee, Brian J. Raney, Galt P. Barber, Jonathan Casper, Mark Diekhans, Clay Fischer, Jairo Navarro Gonzalez, Angie S. Hinrichs, Christopher M. Lee, Luis R. Nassar, Gerardo Perez, Brittney Wick, Daniel Schmelter, Matthew L. Speir, Joel Armstrong, Ann S. Zweig, Robert M. Kuhn, Bogdan M. Kirilenko, Michael Hiller, David Haussler, W. James Kent & Maximilian Haeussler

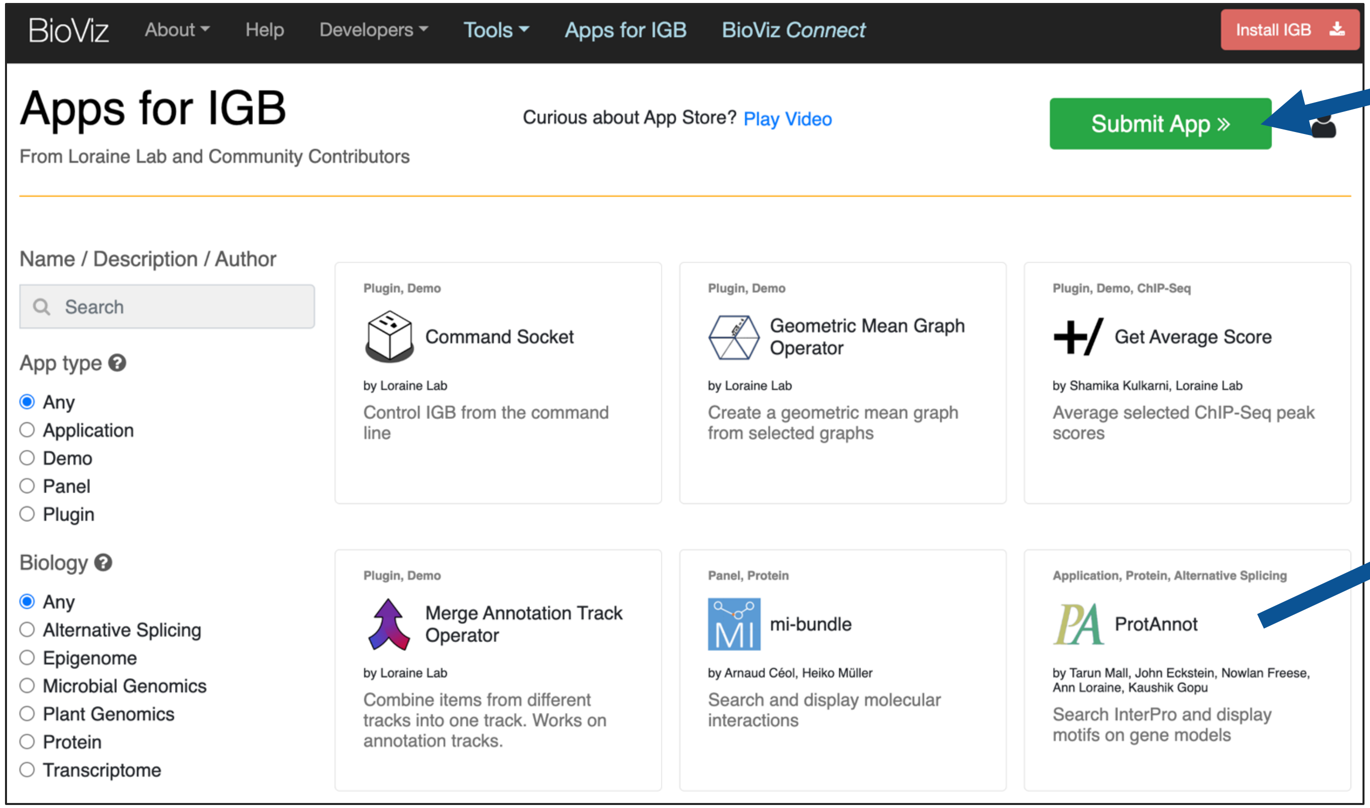
Genome Biology **24**, Article number: 217 (2023) | Cite this article

5366 Accesses | **10** Citations | **47** Altmetric | Metrics

Jaya Sravani Sirigineedi

Add new features using IGB Apps

Loraine lab students create new apps as part of their projects!



Apps for IGB

From Loraine Lab and Community Contributors

Curious about App Store? Play Video

Name / Description / Author

App type

- ● Any
- ○ Application
- ○ Demo
- ○ Panel
- ○ Plugin

Biology

- ● Any
- ○ Alternative Splicing
- ○ Epigenome
- ○ Microbial Genomics
- ○ Plant Genomics
- ○ Protein
- ○ Transcriptome

Plugin, Demo
Command Socket
by Loraine Lab
Control IGB from the command line

Plugin, Demo
Geometric Mean Graph Operator
by Loraine Lab
Create a geometric mean graph from selected graphs

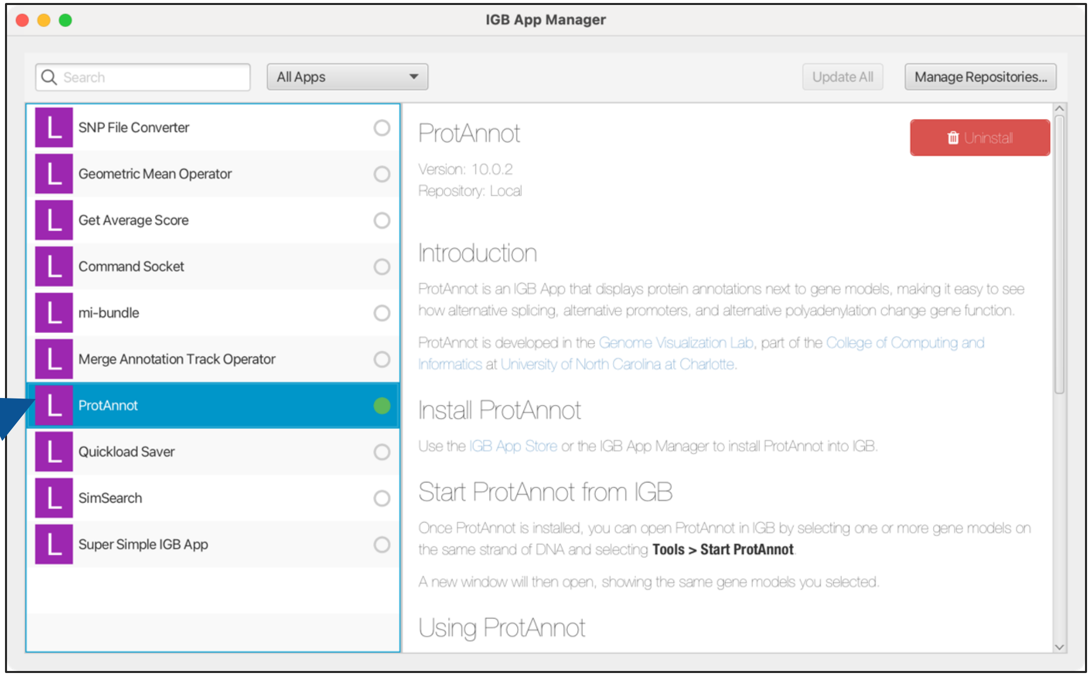
Plugin, Demo, ChIP-Seq
Get Average Score
by Shamika Kulkarni, Loraine Lab
Average selected ChIP-Seq peak scores

Plugin, Demo
Merge Annotation Track Operator
by Loraine Lab
Combine items from different tracks into one track. Works on annotation tracks.

Panel, Protein
mi-bundle
by Arnaud Céol, Heiko Müller
Search and display molecular interactions

Application, Protein, Alternative Splicing
ProtAnnot
by Tarun Mall, John Eckstein, Nowlan Freese, Ann Loraine, Kaushik Gopu
Search InterPro and display motifs on gene models

apps.bioviz.org



ProtAnnot

Version: 10.0.2
Repository: Local

Introduction

ProtAnnot is an IGB App that displays protein annotations next to gene models, making it easy to see how alternative splicing, alternative promoters, and alternative polyadenylation change gene function.

ProtAnnot is developed in the Genome Visualization Lab, part of the College of Computing and Informatics at University of North Carolina at Charlotte.

Install ProtAnnot

Use the IGB App Store or the IGB App Manager to install ProtAnnot into IGB.

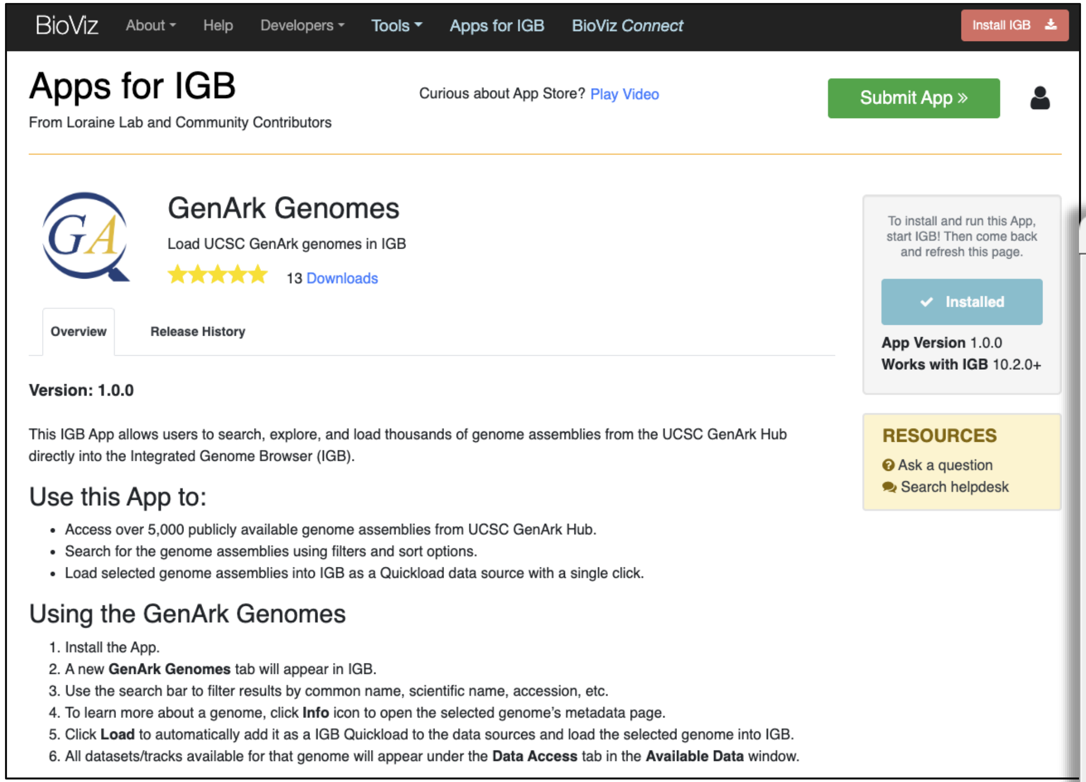
Start ProtAnnot from IGB

Once ProtAnnot is installed, you can open ProtAnnot in IGB by selecting one or more gene models on the same strand of DNA and selecting **Tools > Start ProtAnnot**.

A new window will then open, showing the same gene models you selected.

Using ProtAnnot

UCSC GenArk adds thousands of new genomes to IGB



Apps for IGB

From Loraine Lab and Community Contributors

Curious about App Store? Play Video

GenArk Genomes

Load UCSC GenArk genomes in IGB

★★★★★ 13 Downloads

To install and run this App, start IGB! Then come back and refresh this page.

App Version 1.0.0
Works with IGB 10.2.0+

RESOURCES
Ask a question
Search helpdesk

Version: 1.0.0

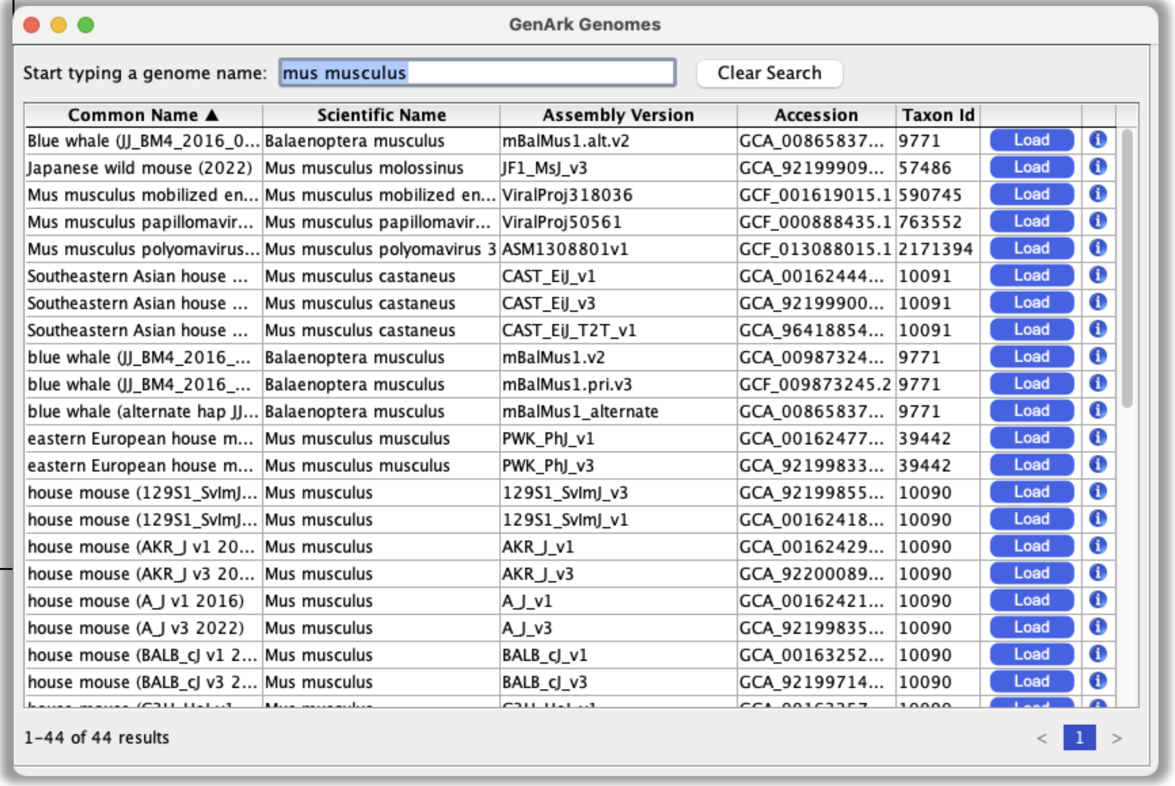
This IGB App allows users to search, explore, and load thousands of genome assemblies from the UCSC GenArk Hub directly into the Integrated Genome Browser (IGB).

Use this App to:

- Access over 5,000 publicly available genome assemblies from UCSC GenArk Hub.
- Search for the genome assemblies using filters and sort options.
- Load selected genome assemblies into IGB as a Quickload data source with a single click.

Using the GenArk Genomes

1. Install the App.
2. A new **GenArk Genomes** tab will appear in IGB.
3. Use the search bar to filter results by common name, scientific name, accession, etc.
4. To learn more about a genome, click **Info** icon to open the selected genome's metadata page.
5. Click **Load** to automatically add it as a IGB Quickload to the data sources and load the selected genome into IGB.
6. All datasets/tracks available for that genome will appear under the **Data Access** tab in the **Available Data** window.



Start typing a genome name: mus musculus

Common Name ▲	Scientific Name	Assembly Version	Accession	Taxon Id		
Blue whale (JJ_BM4_2016_0...	Balaenoptera musculus	mBalMus1.alt.v2	GCA_00865837...	9771	Load	ⓘ
Japanese wild mouse (2022)	Mus musculus molossinus	JF1_MsJ_v3	GCA_92199909...	57486	Load	ⓘ
Mus musculus mobilized en...	Mus musculus mobilized en...	ViralProj318036	GCF_001619015.1	590745	Load	ⓘ
Mus musculus papillomavir...	Mus musculus papillomavir...	ViralProj50561	GCF_000888435.1	763552	Load	ⓘ
Mus musculus polyomavirus...	Mus musculus polyomavirus 3	ASM1308801v1	GCF_013088015.1	2171394	Load	ⓘ
Southeastern Asian house ...	Mus musculus castaneus	CAST_EiJ_v1	GCA_00162444...	10091	Load	ⓘ
Southeastern Asian house ...	Mus musculus castaneus	CAST_EiJ_v3	GCA_92199900...	10091	Load	ⓘ
Southeastern Asian house ...	Mus musculus castaneus	CAST_EiJ_T2T_v1	GCA_96418854...	10091	Load	ⓘ
blue whale (JJ_BM4_2016_...	Balaenoptera musculus	mBalMus1.v2	GCA_00987324...	9771	Load	ⓘ
blue whale (JJ_BM4_2016_...	Balaenoptera musculus	mBalMus1.pri.v3	GCF_009873245.2	9771	Load	ⓘ
blue whale (alternate hap JJ...	Balaenoptera musculus	mBalMus1_alternate	GCA_00865837...	9771	Load	ⓘ
eastern European house m...	Mus musculus musculus	PWK_PhJ_v1	GCA_00162477...	39442	Load	ⓘ
eastern European house m...	Mus musculus musculus	PWK_PhJ_v3	GCA_92199833...	39442	Load	ⓘ
house mouse (129S1_SvImJ...	Mus musculus	129S1_SvImJ_v3	GCA_92199855...	10090	Load	ⓘ
house mouse (129S1_SvImJ...	Mus musculus	129S1_SvImJ_v1	GCA_00162418...	10090	Load	ⓘ
house mouse (AKR_J v1 20...	Mus musculus	AKR_J_v1	GCA_00162429...	10090	Load	ⓘ
house mouse (AKR_J v3 20...	Mus musculus	AKR_J_v3	GCA_92200089...	10090	Load	ⓘ
house mouse (A_J v1 2016)	Mus musculus	A_J_v1	GCA_00162421...	10090	Load	ⓘ
house mouse (A_J v3 2022)	Mus musculus	A_J_v3	GCA_92199835...	10090	Load	ⓘ
house mouse (BALB_cJ v1 2...	Mus musculus	BALB_cJ_v1	GCA_00163252...	10090	Load	ⓘ
house mouse (BALB_cJ v3 2...	Mus musculus	BALB_cJ_v3	GCA_92199714...	10090	Load	ⓘ

1-44 of 44 results

4,000+ genome assemblies, thousands of data tracks available for some species

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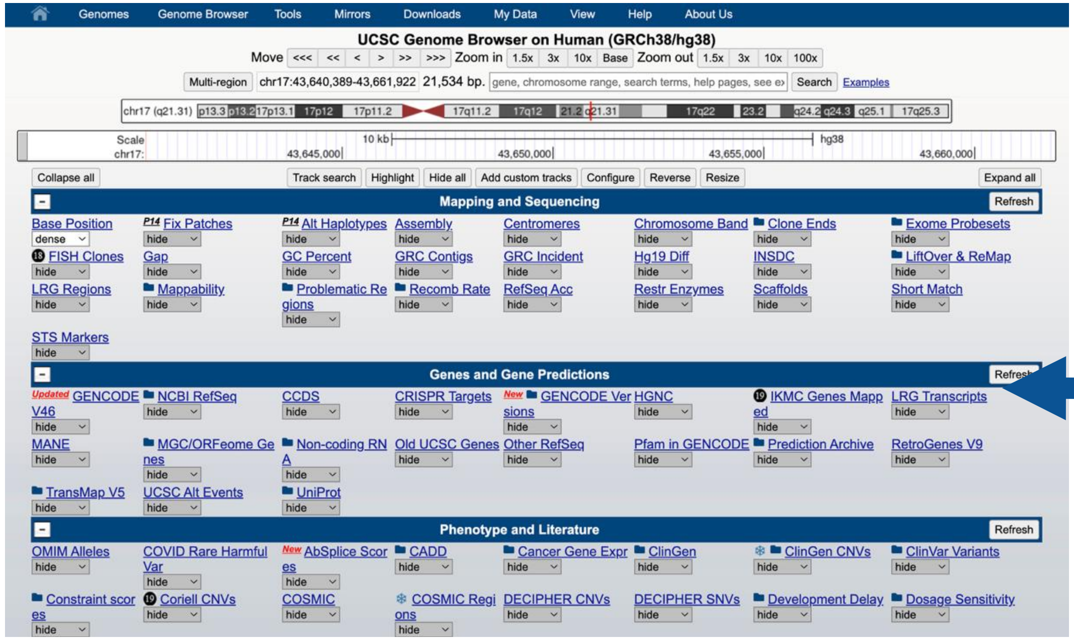
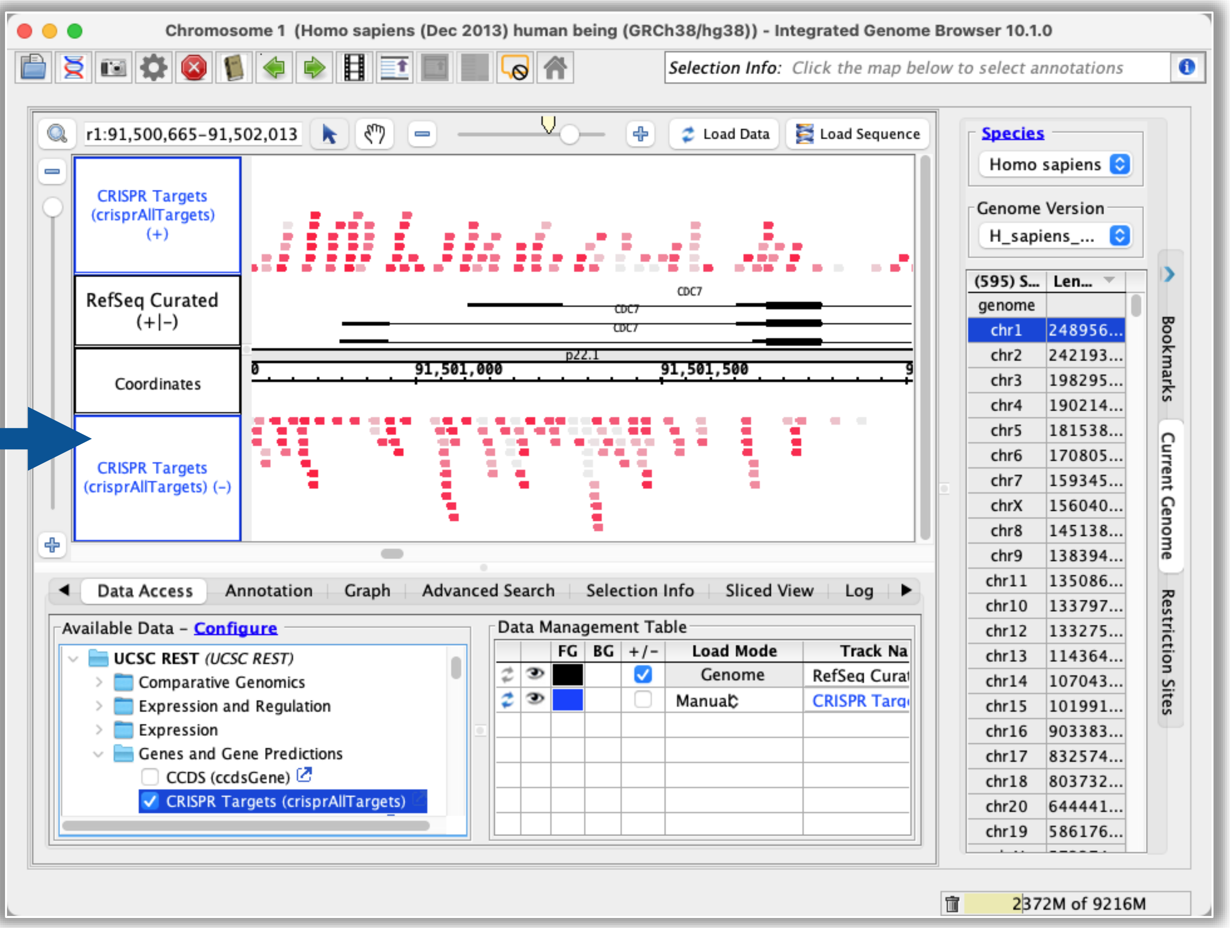
IGB integrations – UCSC Genome Browser

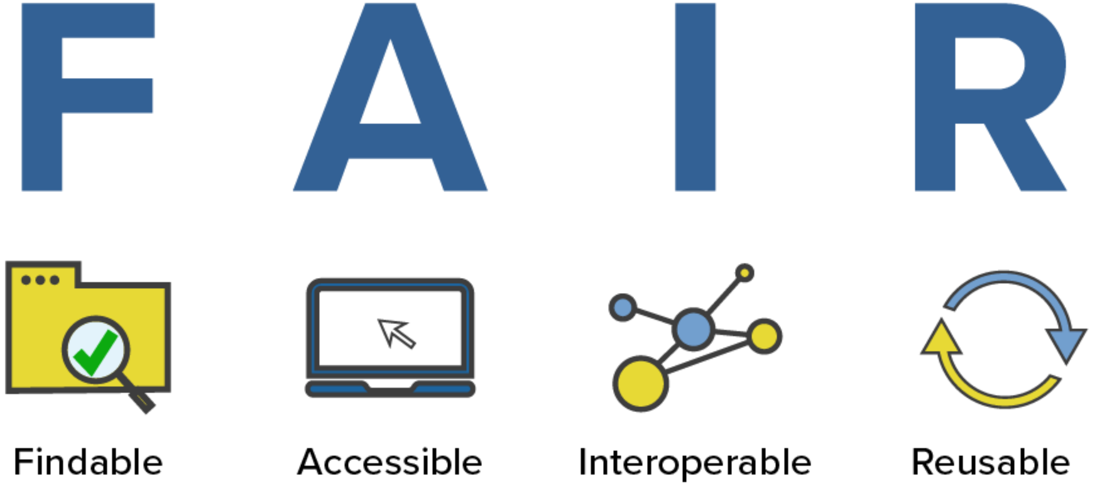
Computational access via REST API

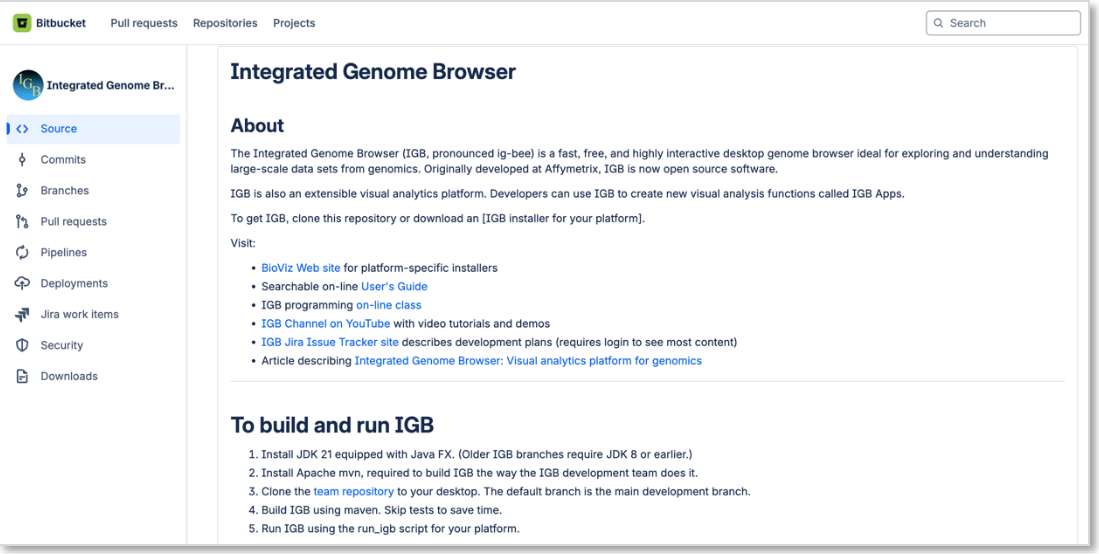




What other data sources can we integrate with?

APIs and FAIR Data Principles





Integrated Genome Browser

About

The Integrated Genome Browser (IGB, pronounced ig-bee) is a fast, free, and highly interactive desktop genome browser ideal for exploring and understanding large-scale data sets from genomics. Originally developed at Affymetrix, IGB is now open source software.

IGB is also an extensible visual analytics platform. Developers can use IGB to create new visual analysis functions called IGB Apps.

To get IGB, clone this repository or download an [IGB installer for your platform].

Visit:

- BioViz Web site for platform-specific installers
- Searchable on-line User's Guide
- IGB programming on-line class
- IGB Channel on YouTube with video tutorials and demos
- IGB Jira Issue Tracker site describes development plans (requires login to see most content)
- Article describing Integrated Genome Browser: Visual analytics platform for genomics

To build and run IGB

1. Install JDK 21 equipped with Java FX. (Older IGB branches require JDK 8 or earlier.)
2. Install Apache mvn, required to build IGB the way the IGB development team does it.
3. Clone the team repository to your desktop. The default branch is the main development branch.
4. Build IGB using maven. Skip tests to save time.
5. Run IGB using the run_igb script for your platform.

Bitbucket

IGB integrations – BAR

the plant journal

SEB
SOCIETY FOR EXPERIMENTAL BIOLOGY

Resource | Open Access

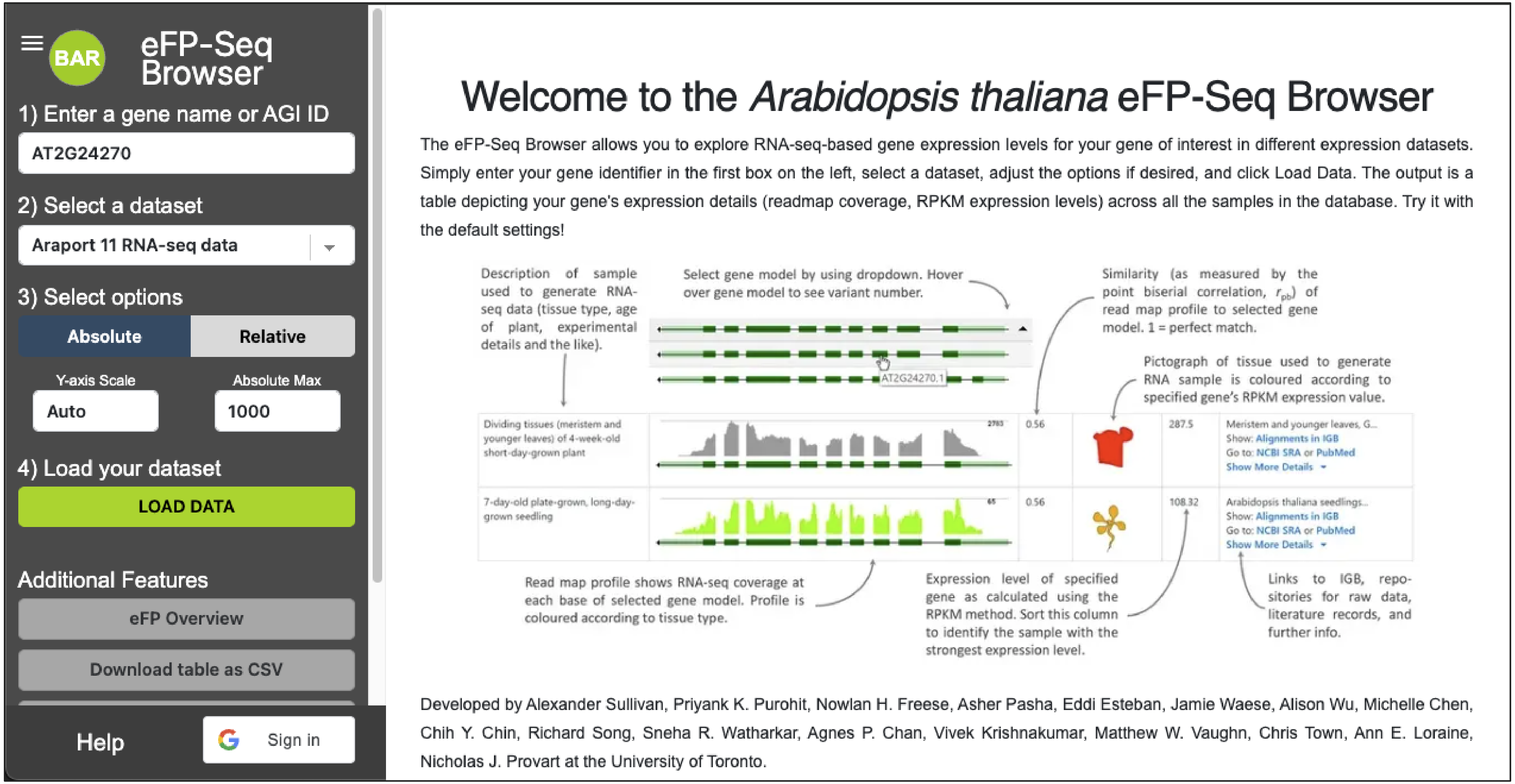
An ‘eFP-Seq Browser’ for visualizing and exploring RNA sequencing data

Alexander Sullivan, Priyank K. Purohit, Nowlan H. Freese, Asher Pasha, Eddi Esteban, Jamie Waese, Alison Wu, Michelle Chen, Chih Y. Chin, Richard Song, Sneha R. Watharkar, Agnes P. Chan, Vivek Krishnakumar, Matthew W. Vaughn, Chris Town, Ann E. Loraine ✉, Nicholas J. Provart ✉

... See fewer authors ^

First published: 26 July 2019 | https://doi.org/10.1111/tpj.14468 | Citations: 38

IGB integrations – BAR



1) Enter a gene name or AGI ID

AT2G24270

2) Select a dataset

Araport 11 RNA-seq data

3) Select options

Y-axis Scale: Auto

Absolute Max: 1000

4) Load your dataset

Welcome to the *Arabidopsis thaliana* eFP-Seq Browser

The eFP-Seq Browser allows you to explore RNA-seq-based gene expression levels for your gene of interest in different expression datasets. Simply enter your gene identifier in the first box on the left, select a dataset, adjust the options if desired, and click Load Data. The output is a table depicting your gene's expression details (readmap coverage, RPKM expression levels) across all the samples in the database. Try it with the default settings!

Description of sample used to generate RNA-seq data (tissue type, age of plant, experimental details and the like).

Select gene model by using dropdown. Hover over gene model to see variant number.

Similarity (as measured by the point biserial correlation, r_{pb}) of read map profile to selected gene model. 1 = perfect match.

Pictograph of tissue used to generate RNA sample is coloured according to specified gene's RPKM expression value.

Dividing tissues (meristem and younger leaves) of 4-week-old short-day-grown plant		0.56		287.5	Meristem and younger leaves, G... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
7-day-old plate-grown, long-day-grown seedling		0.56		108.32	Arabidopsis thaliana seedlings... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details

Read map profile shows RNA-seq coverage at each base of selected gene model. Profile is coloured according to tissue type.

Expression level of specified gene as calculated using the RPKM method. Sort this column to identify the sample with the strongest expression level.

Links to IGB, repositories for raw data, literature records, and further info.

Developed by Alexander Sullivan, Priyank K. Purohit, Nowlan H. Freese, Asher Pasha, Eddi Esteban, Jamie Waese, Alison Wu, Michelle Chen, Chih Y. Chin, Richard Song, Sneha R. Watharkar, Agnes P. Chan, Vivek Krishnakumar, Matthew W. Vaughn, Chris Town, Ann E. Loraine, Nicholas J. Provart at the University of Toronto.

(a)

Title	RNA-Seq Coverage	r_{pb}	eFP (RPKM)	RPKM	Details
!treat		Filter	0 Max	Filter	leaf
Arabidopsis thaliana Leaf Lamina of the young leaf		0.70		26.34	L.LAM.y, Leaf blade of the thi... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Arabidopsis thaliana Leaf, mature		0.69		36.4	L.lg, Whole third leaf. Sample... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Arabidopsis thaliana Leaf, mature		0.70		41.81	L.lg, Whole third leaf. Sample... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Arabidopsis thaliana Leaf Lamina of the mature leaf		0.71		34.93	L.LAM.lg, Parts of the leaf bl... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Arabidopsis thaliana Leaf Lamina, intermediate 2		0.66		23.78	L.LAM.i2, Parts of the leaf bl... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Arabidopsis thaliana Leaf Lamina, intermediate 1		0.67		31.97	L.LAM.i1, Leaf blade of the th... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Arabidopsis thaliana Leaf Lamina, intermediate 1		0.69		26.75	L.LAM.i1, Leaf blade of the th... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Arabidopsis thaliana Leaf Lamina of the mature leaf		0.66		38.24	L.LAM.lg, Parts of the leaf bl... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Arabidopsis thaliana Leaf Lamina of the young leaf		0.63		24.33	L.LAM.y, Leaf blade of the thi... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Arabidopsis thaliana Leaf Lamina, intermediate 2		0.65		29.04	L.LAM.i2, Parts of the leaf bl... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details

(b)

Title	RNA-Seq Coverage	r_{pb}	eFP (RPKM)	RPKM	Details
heat		Filter	0 Max	Filter	leaf
Arabidopsis thaliana Heat Treatment 24 hours Replicate 1		0.72		619.82	Third leaf was collected from ... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Arabidopsis thaliana Heat Treatment 12 hours Replicate 1		0.71		277.82	Third leaf was collected from ... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Arabidopsis thaliana Heat Treatment 3 hours Replicate 2		0.66		615.55	Third leaf was collected from ... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Arabidopsis thaliana Heat Treatment 6 hours Replicate 1		0.66		341.11	Third leaf was collected from ... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Arabidopsis thaliana Heat Treatment 12 hours Replicate 2		0.66		485.21	Third leaf was collected from ... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Arabidopsis thaliana Heat Treatment 24 hours Replicate 2		0.64		555.26	Third leaf was collected from ... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Arabidopsis thaliana Heat Treatment 6 hours Replicate 2		0.63		479.66	Third leaf was collected from ... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Arabidopsis thaliana Heat Treatment 1 hour Replicate 2		0.59		1048.54	Third leaf was collected from ... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Arabidopsis thaliana Heat Treatment 3 hours Replicate 1		0.59		235.15	Third leaf was collected from ... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Arabidopsis thaliana Heat Treatment 1 hour Replicate 1		0.59		775.81	Third leaf was collected from ... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details

Fig. 5: Comparison of exon skipping in *SR45a* (*At1g07350*) in untreated and heat-treated leaf samples in the Klepikova *et al*. (2016) data set.

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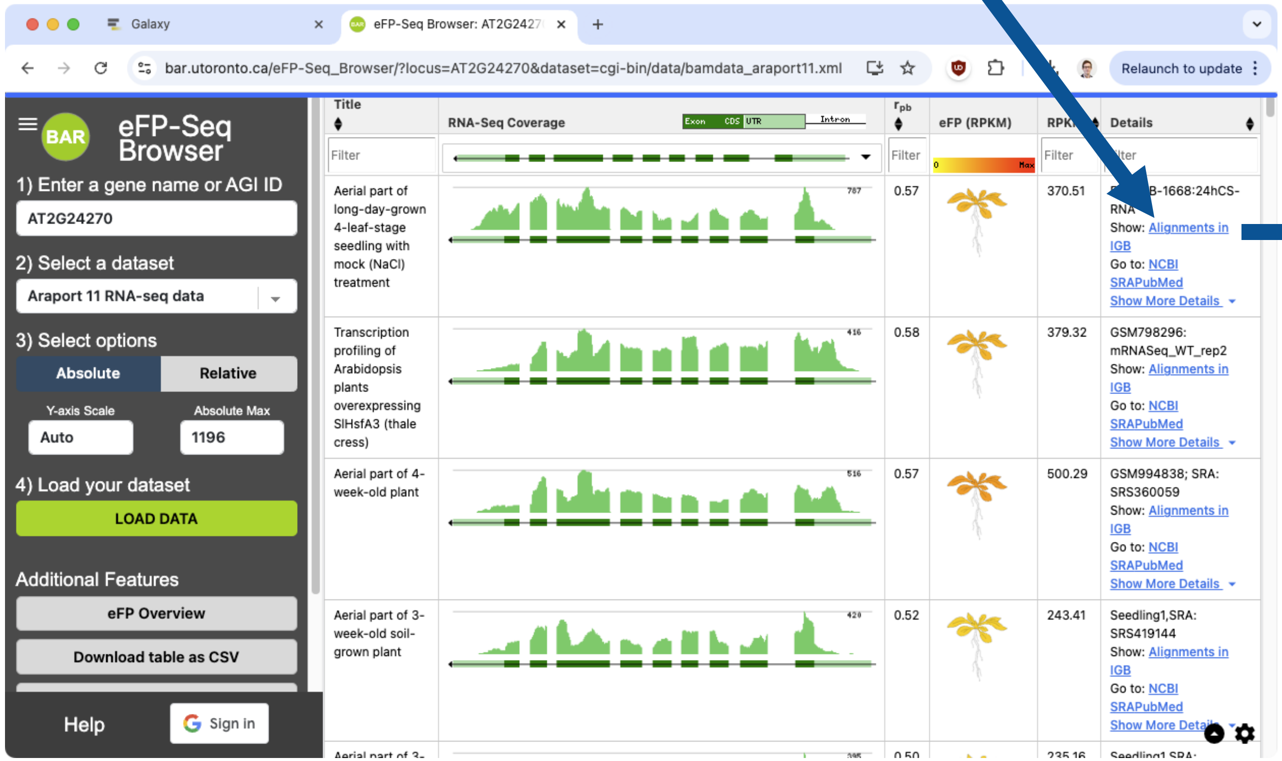
Click Alignments in IGB



1) Enter a gene name or AGI ID: AT2G24270

2) Select a dataset: Araport 11 RNA-seq data

3) Select options: **Absolute** | Relative

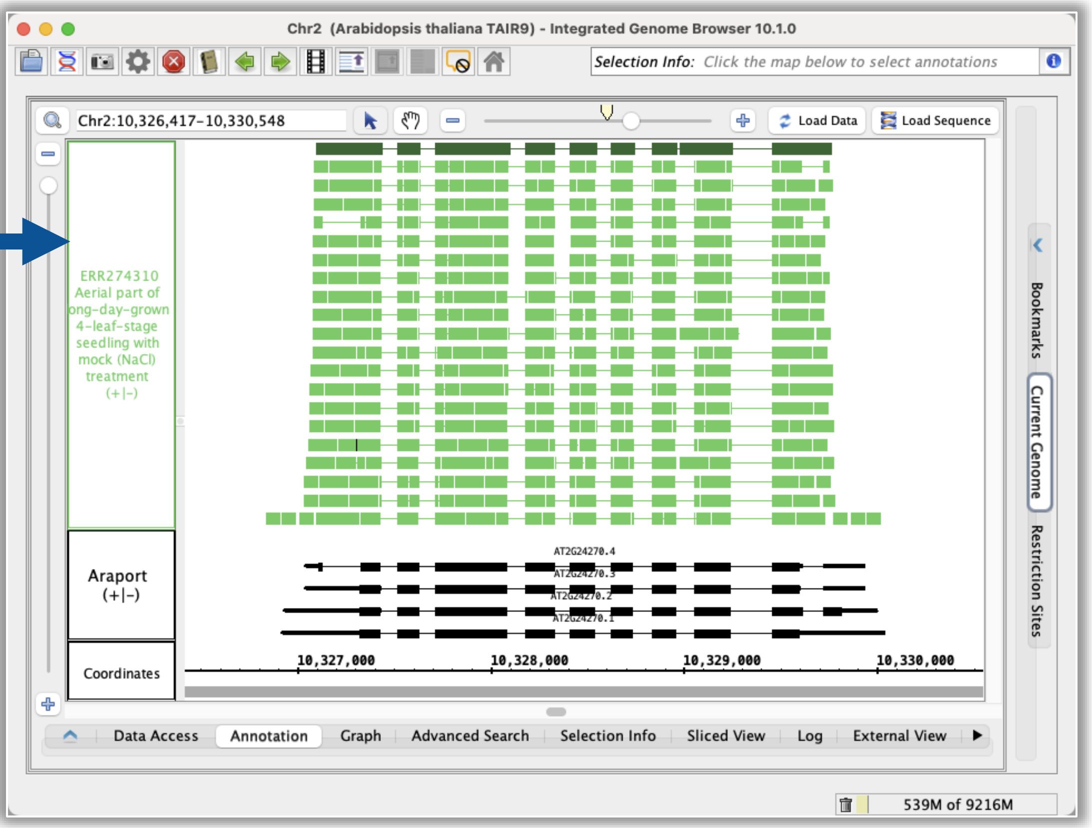
Y-axis Scale: Auto

Absolute Max: 1196

4) Load your dataset

Title	RNA-Seq Coverage	r_{pb}	eFP (RPKM)	RPKM	Details
Filter		Filter		Filter	Filter
Aerial part of long-day-grown 4-leaf-stage seedling with mock (NaCl) treatment		0.57		370.51	B-1668:24hCS-RNA Show: Alignments in IGB Go to: NCBI SRAPubMed Show More Details
Transcription profiling of Arabidopsis plants overexpressing SlHsfA3 (thale cress)		0.58		379.32	GSM798296: mRNASeq_WT_rep2 Show: Alignments in IGB Go to: NCBI SRAPubMed Show More Details
Aerial part of 4-week-old plant		0.57		500.29	GSM994838; SRA: SRS360059 Show: Alignments in IGB Go to: NCBI SRAPubMed Show More Details
Aerial part of 3-week-old soil-grown plant		0.52		243.41	Seedling1,SRA: SRS419144 Show: Alignments in IGB Go to: NCBI SRAPubMed Show More Details
Aerial part of 3-		0.50		235.16	Seedling1,SRA:

bar.utoronto.ca/eFP-Seq_Browser



Chr2 (Arabidopsis thaliana TAIR9) - Integrated Genome Browser 10.1.0

Selection Info: *Click the map below to select annotations*

Chr2:10,326,417-10,330,548

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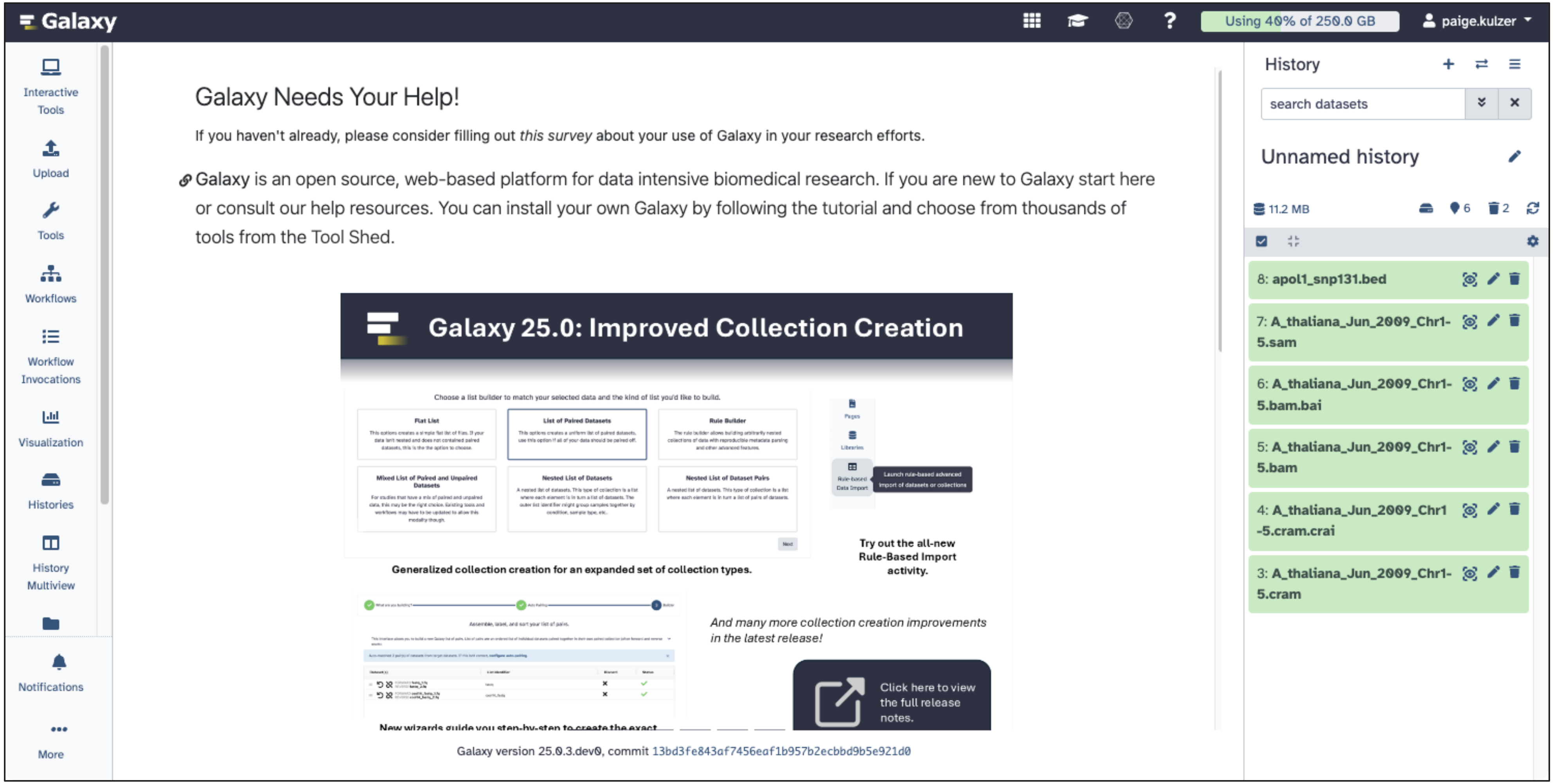
IGB integrations – Galaxy



Galaxy Needs Your Help!

If you haven't already, please consider filling out *this survey* about your use of Galaxy in your research efforts.

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. You can install your own Galaxy by following the tutorial and choose from thousands of tools from the Tool Shed.

Galaxy 25.0: Improved Collection Creation

Choose a list builder to match your selected data and the kind of list you'd like to build.

Generalized collection creation for an expanded set of collection types.

Try out the all-new Rule-Based Import activity.

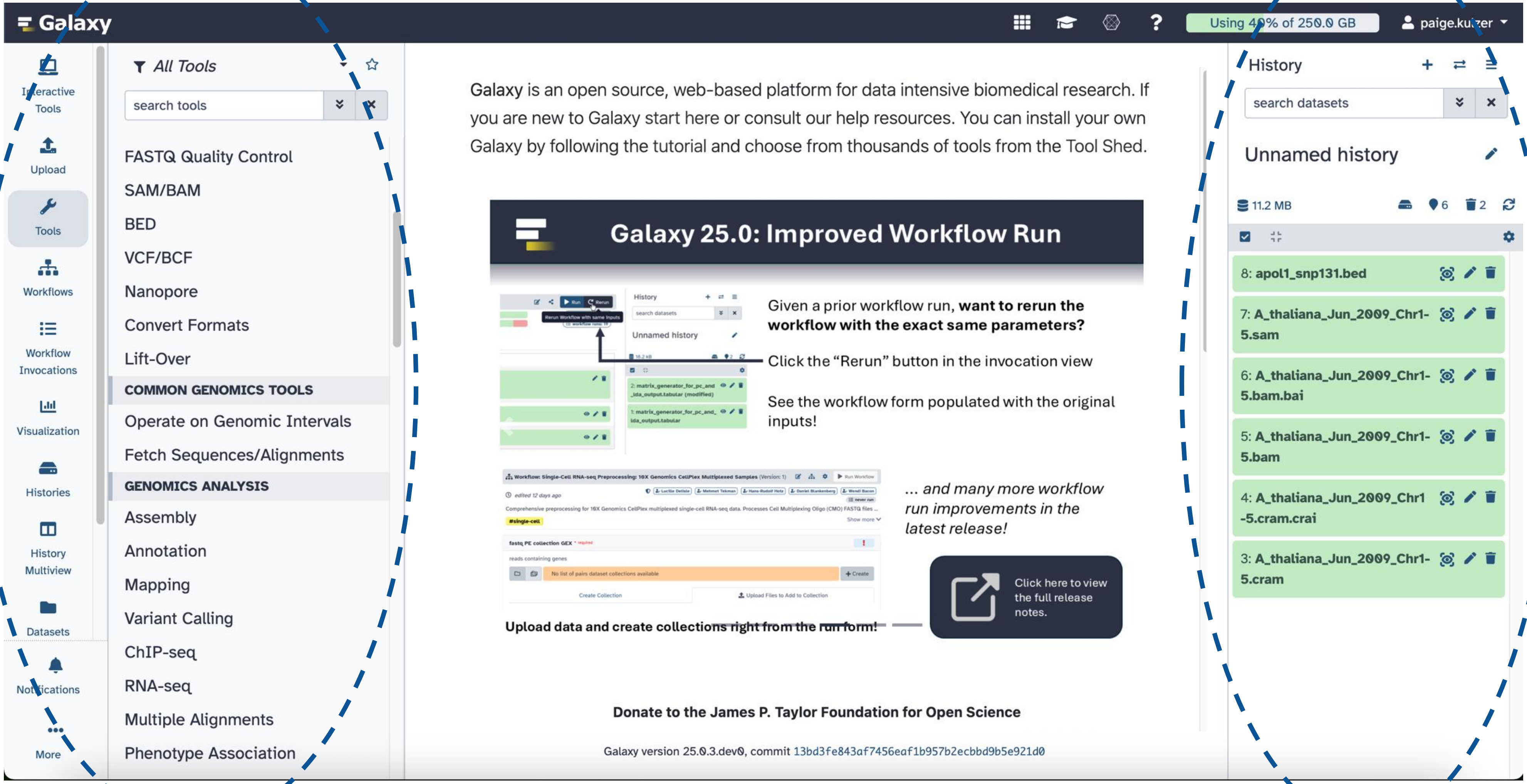
And many more collection creation improvements in the latest release!

New wizards guide you step-by-step to create the exact

Galaxy version 25.0.3.dev0, commit 13bd3fe843af7456eaf1b957b2ecbbd9b5e921d0

8: apol1_snp131.bed
7: A_thaliana_Jun_2009_Chr1-5.sam
6: A_thaliana_Jun_2009_Chr1-5.bam.bai
5: A_thaliana_Jun_2009_Chr1-5.bam
4: A_thaliana_Jun_2009_Chr1-5.cram.crai
3: A_thaliana_Jun_2009_Chr1-5.cram

IGB integrations – Galaxy



FASTQ Quality Control
SAM/BAM
BED
VCF/BCF
Nanopore
Convert Formats
Lift-Over
COMMON GENOMICS TOOLS
Operate on Genomic Intervals
Fetch Sequences/Alignments
GENOMICS ANALYSIS
Assembly
Annotation
Mapping
Variant Calling
ChIP-seq
RNA-seq
Multiple Alignments
Phenotype Association

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Galaxy 25.0: Improved Workflow Run

Given a prior workflow run, **want to rerun the workflow with the exact same parameters?**

Click the "Rerun" button in the invocation view

See the workflow form populated with the original inputs!

... and many more workflow run improvements in the latest release!

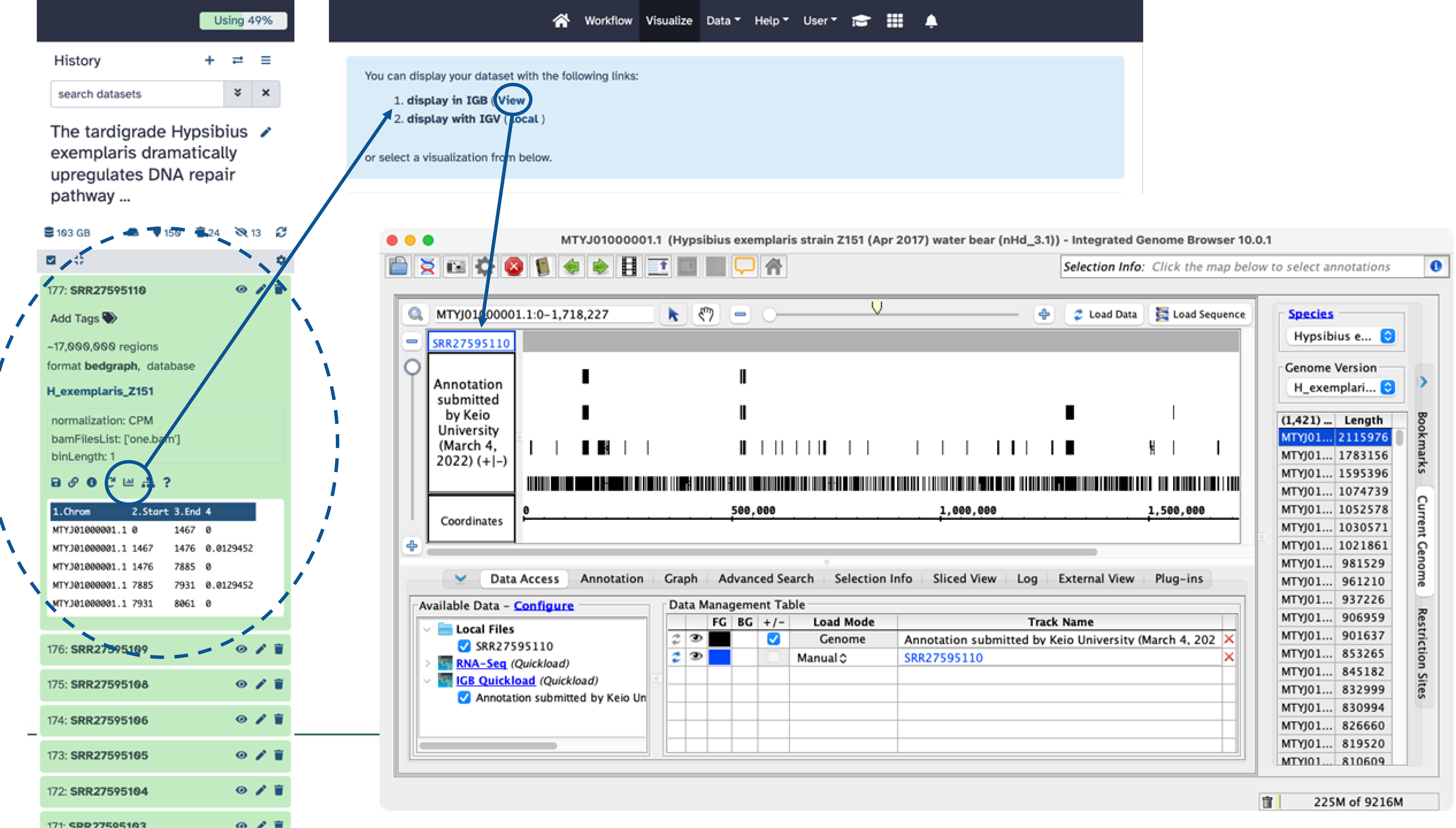
Upload data and create collections right from the run form!

Click here to view the full release notes.

Donate to the James P. Taylor Foundation for Open Science

Galaxy version 25.0.3.dev0, commit `13bd3fe843af7456eaf1b957b2ecbbd9b5e921d0`

8: apol1_snp131.bed
7: A_thaliana_Jun_2009_Chr1-5.sam
6: A_thaliana_Jun_2009_Chr1-5.bam.bai
5: A_thaliana_Jun_2009_Chr1-5.bam
4: A_thaliana_Jun_2009_Chr1-5.cram.crai
3: A_thaliana_Jun_2009_Chr1-5.cram



The tardigrade Hypsibius exemplaris dramatically upregulates DNA repair pathway ...

177: SRR27595110

~17,000,000 regions

format **bedgraph**, database **H_exemplaris_Z151**

normalization: CPM

bamFilesList: ['one.bam']

binLength: 1

```
1.Chrom           2.Start 3.End 4
MTYJ01000001.1 0       1467  0
MTYJ01000001.1 1467    1476  0.0129452
MTYJ01000001.1 1476    7885  0
MTYJ01000001.1 7885    7931  0.0129452
MTYJ01000001.1 7931    8061  0
```

176: SRR27595109

175: SRR27595108

174: SRR27595106

173: SRR27595105

172: SRR27595104

171: SRR27595103

You can display your dataset with the following links:

1. **display in IGB** (**View**)
2. **display with IGV** (**local**)

or select a visualization from below.

MTYJ01000001.1 (Hypsibius exemplaris strain Z151 (Apr 2017) water bear (nHd_3.1)) - Integrated Genome Browser 10.0.1

Selection Info: *Click the map below to select annotations*

MTYJ01000001.1:0-1,718,227

SRR27595110

Annotation submitted by Keio University (March 4, 2022) (+|-)

Species: Hypsibius e...

Genome Version: H_exemplari...

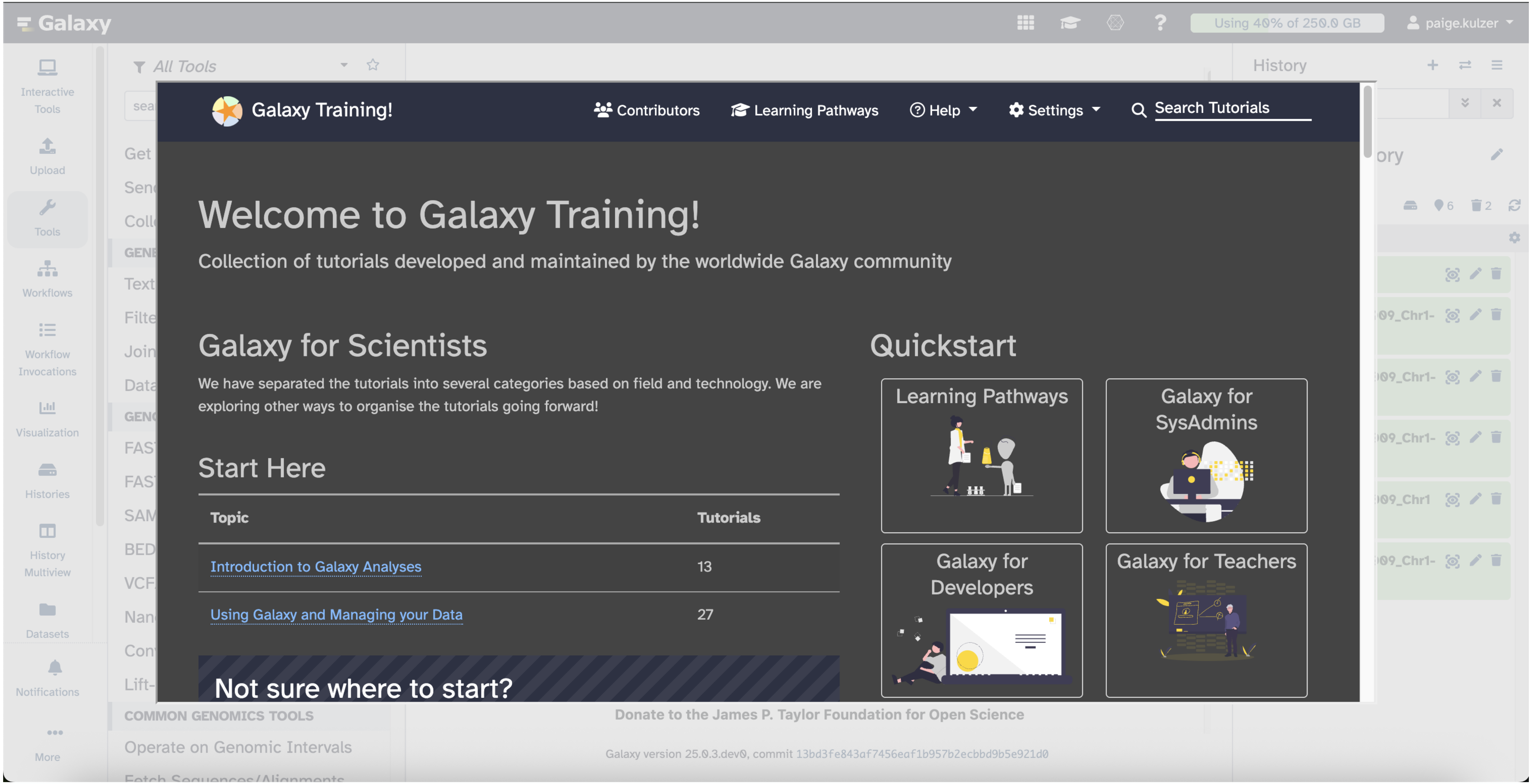
(1,421) ...	Length
MTYJ01...	2115976
MTYJ01...	1783156
MTYJ01...	1595396
MTYJ01...	1074739
MTYJ01...	1052578
MTYJ01...	1030571
MTYJ01...	1021861
MTYJ01...	981529
MTYJ01...	961210
MTYJ01...	937226
MTYJ01...	906959
MTYJ01...	901637
MTYJ01...	853265
MTYJ01...	845182
MTYJ01...	832999
MTYJ01...	830994
MTYJ01...	826660
MTYJ01...	819520
MTYJ01...	810609

Available Data – Configure

- Local Files
  - ☑ SRR27595110
- RNA-Seq *(Quickload)*
- IGB Quickload *(Quickload)*
  - ☑ Annotation submitted by Keio Un

Data Management Table

FG	BG	+/-	Load Mode	Track Name
■		☑	Genome	Annotation submitted by Keio University (March 4, 202
🟦		☐	Manual	SRR27595110



Welcome to Galaxy Training!

Collection of tutorials developed and maintained by the worldwide Galaxy community

Galaxy for Scientists

We have separated the tutorials into several categories based on field and technology. We are exploring other ways to organise the tutorials going forward!

Start Here

Topic	Tutorials
Introduction to Galaxy Analyses	13
Using Galaxy and Managing your Data	27

Not sure where to start?

Quickstart

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Galaxy version 25.0.3.dev0, commit 13bd3fe843af7456eaf1b957b2ecbbd9b5e921d0

https://usegalaxy.org/

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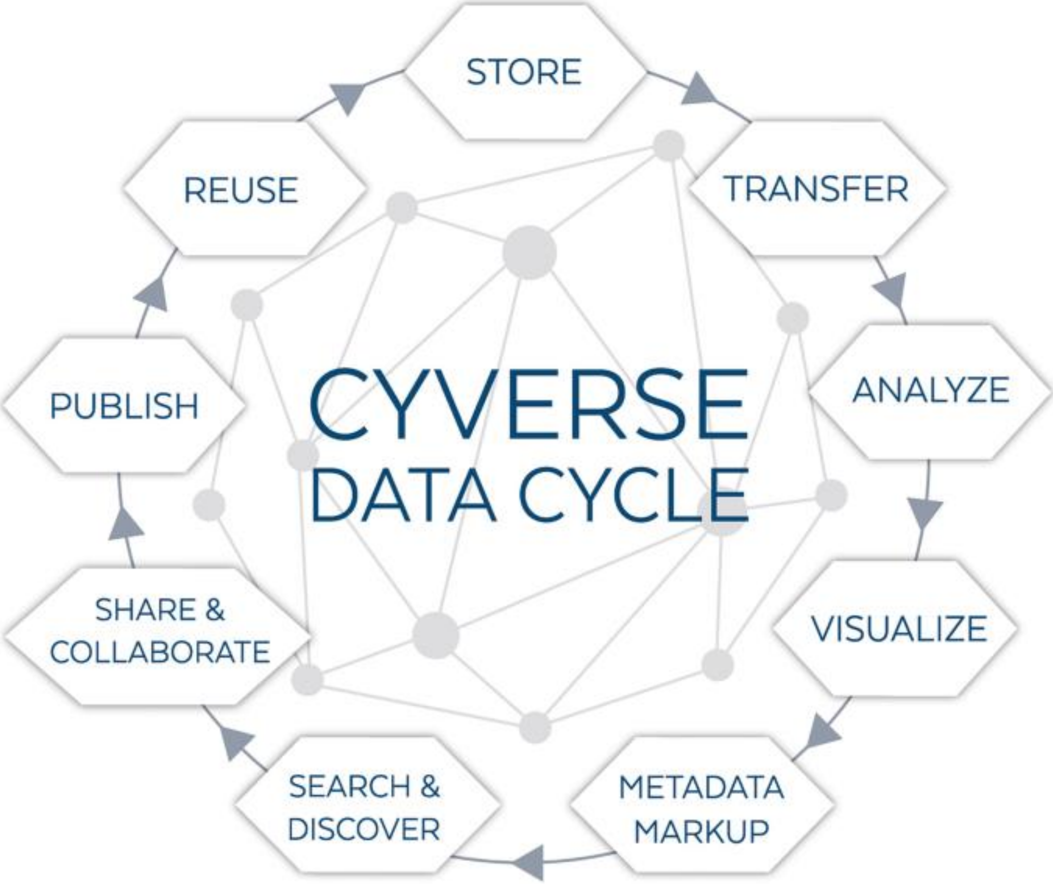
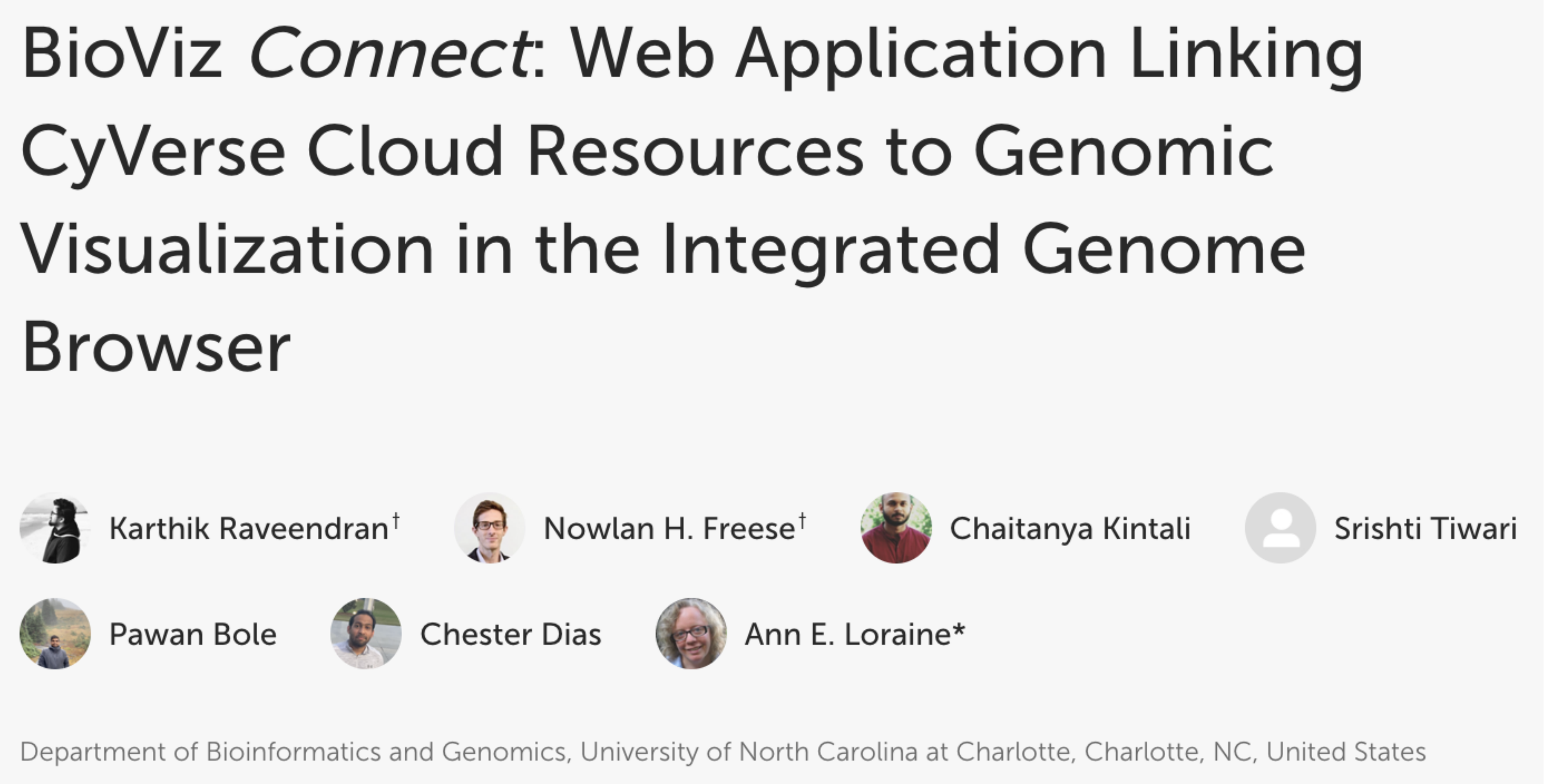
IGB integrations – CYVERSE

CyVerse is powerful cyberinfrastructure geared towards reproducible research with a simple web interface for managing, sharing, running, and visualizing your data



We developed BioViz *Connect* to link CyVerse with IGB



BioViz *Connect*: Web Application Linking CyVerse Cloud Resources to Genomic Visualization in the Integrated Genome Browser

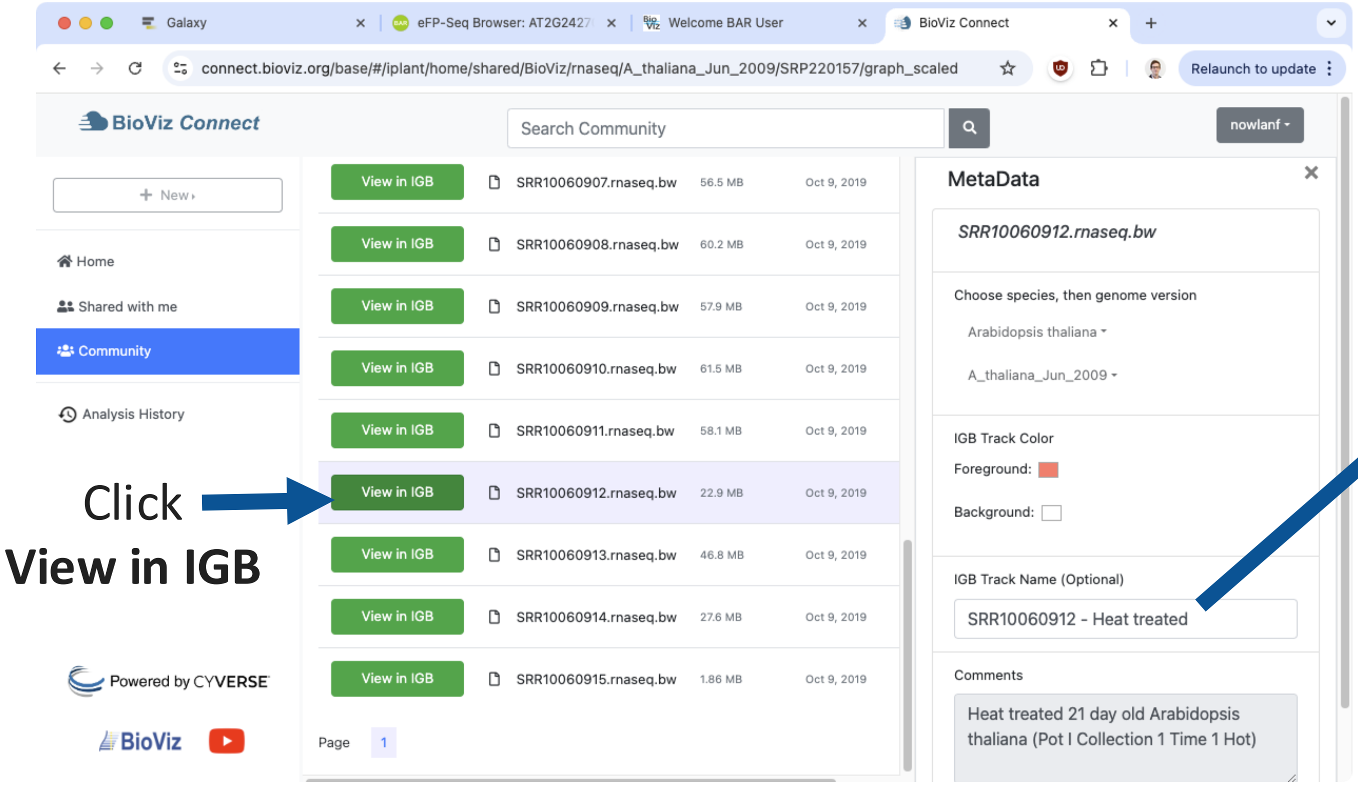
Karthik Raveendran[†] Nowlan H. Freese[†] Chaitanya Kintali Srishti Tiwari Pawan Bole Chester Dias Ann E. Loraine*

Department of Bioinformatics and Genomics, University of North Carolina at Charlotte, Charlotte, NC, United States

https://doi.org/10.3389/fbinf.2022.764619

Karthik Raveendran
Computer Science
PhD Candidate

We developed BioViz *Connect* to link CyVerse with IGB



View in IGB	SRR10060907.rnaseq.bw	56.5 MB	Oct 9, 2019
View in IGB	SRR10060908.rnaseq.bw	60.2 MB	Oct 9, 2019
View in IGB	SRR10060909.rnaseq.bw	57.9 MB	Oct 9, 2019
View in IGB	SRR10060910.rnaseq.bw	61.5 MB	Oct 9, 2019
View in IGB	SRR10060911.rnaseq.bw	58.1 MB	Oct 9, 2019
View in IGB	SRR10060912.rnaseq.bw	22.9 MB	Oct 9, 2019
View in IGB	SRR10060913.rnaseq.bw	46.8 MB	Oct 9, 2019
View in IGB	SRR10060914.rnaseq.bw	27.6 MB	Oct 9, 2019
View in IGB	SRR10060915.rnaseq.bw	1.86 MB	Oct 9, 2019

Page 1

MetaData

SRR10060912.rnaseq.bw

Choose species, then genome version

Arabidopsis thaliana

A_thaliana_Jun_2009

IGB Track Color

Foreground: 🟥

Background: ☐

IGB Track Name (Optional)

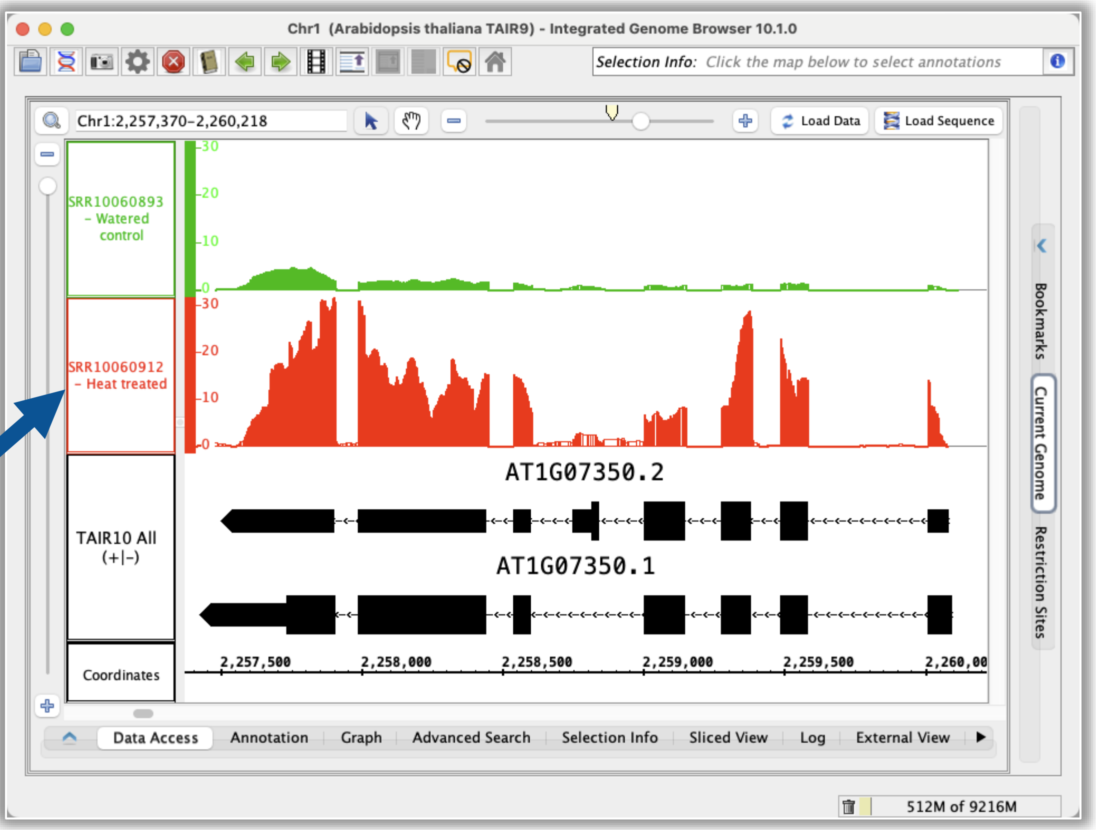
SRR10060912 - Heat treated

Comments

Heat treated 21 day old Arabidopsis thaliana (Pot I Collection 1 Time 1 Hot)

Click
View in IGB

connect.bioviz.org



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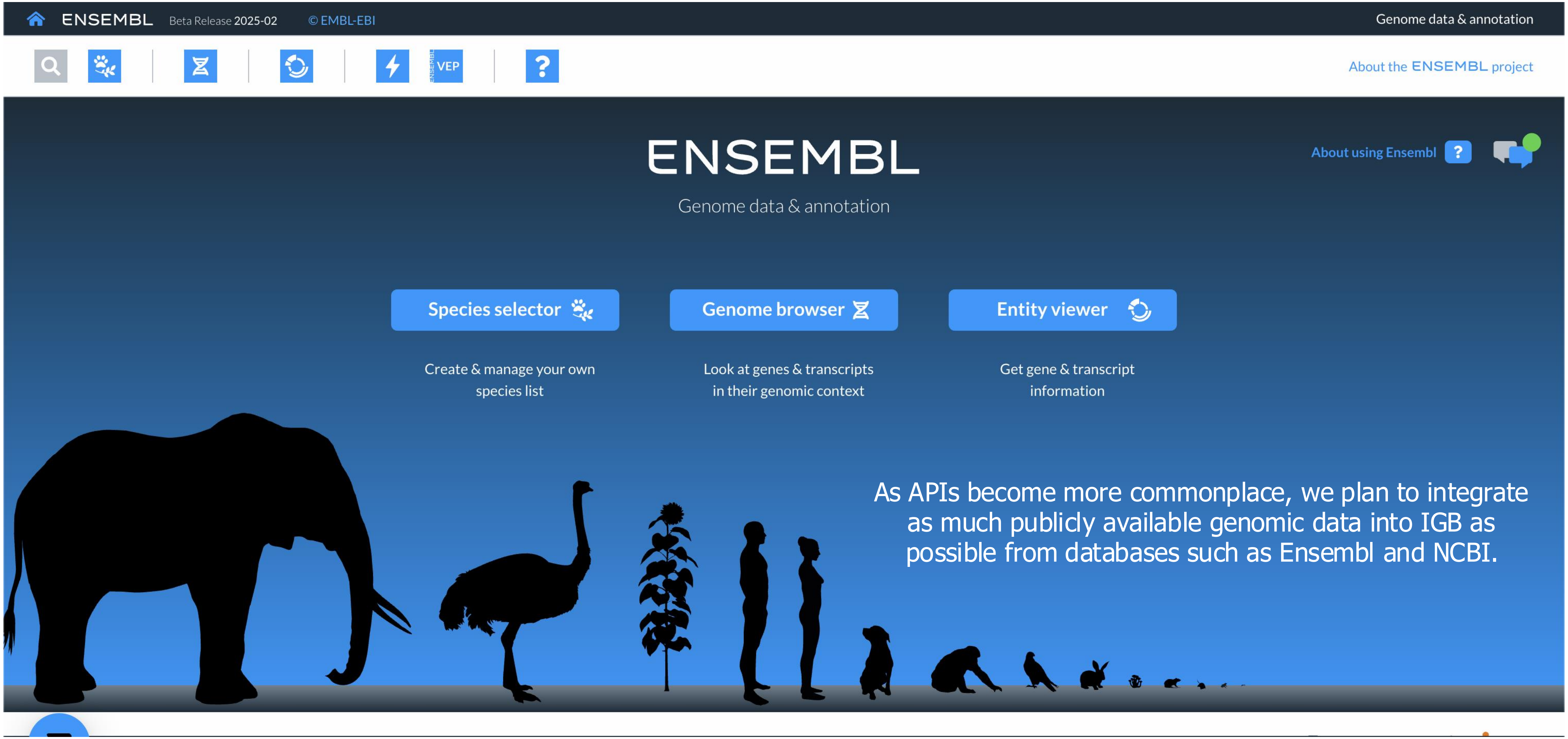
IGB integrations - Ensembl



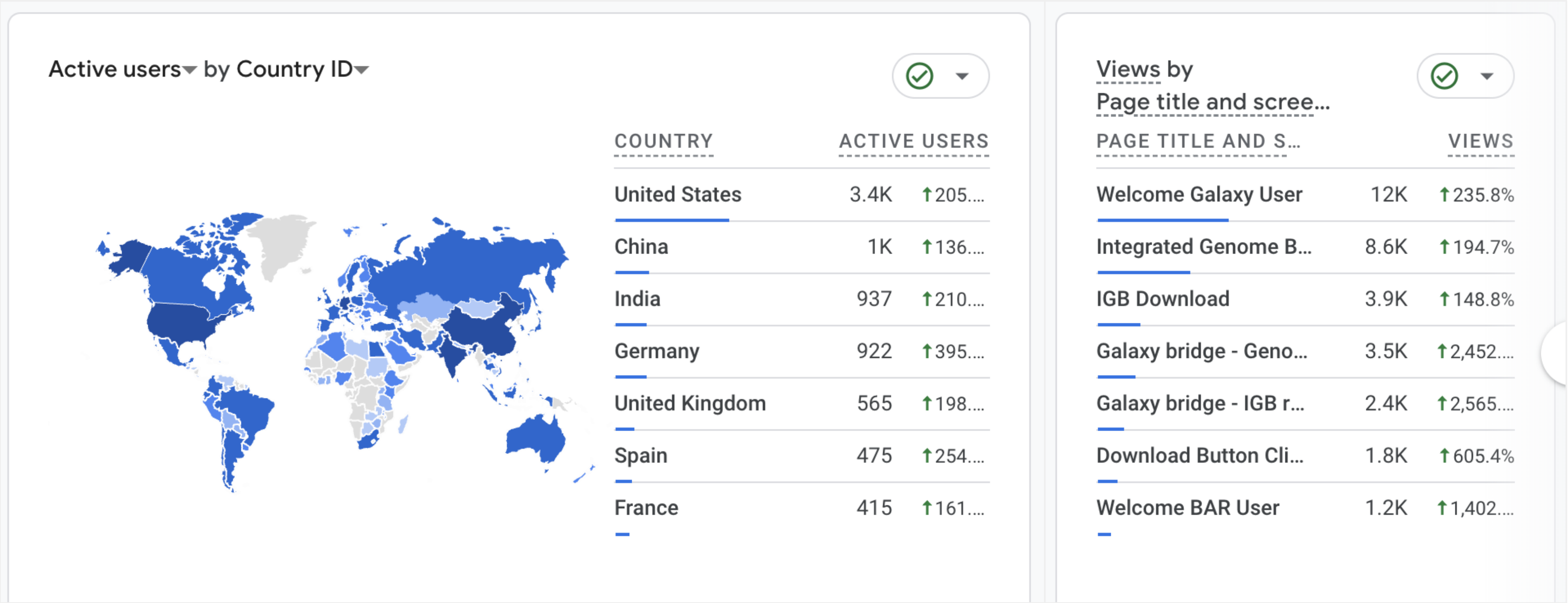
Create & manage your own species list

Look at genes & transcripts in their genomic context

Get gene & transcript information

As APIs become more commonplace, we plan to integrate as much publicly available genomic data into IGB as possible from databases such as Ensembl and NCBI.

The people using IGB



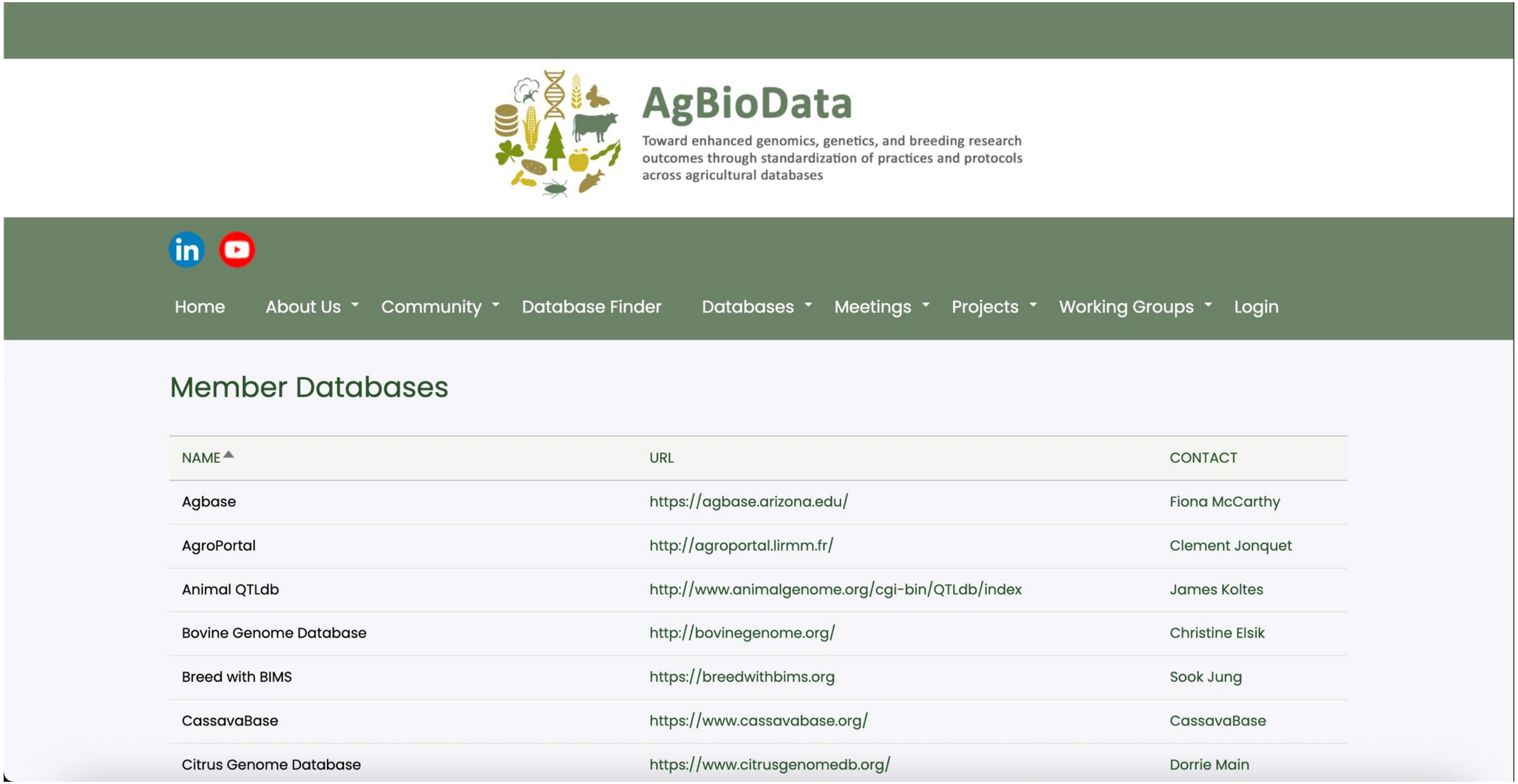
Active users by Country ID

COUNTRY	ACTIVE USERS	
United States	3.4K	↑205....
China	1K	↑136....
India	937	↑210....
Germany	922	↑395....
United Kingdom	565	↑198....
Spain	475	↑254....
France	415	↑161....

Views by
Page title and scree...

PAGE TITLE AND S...	VIEWS	
Welcome Galaxy User	12K	↑235.8%
Integrated Genome B...	8.6K	↑194.7%
IGB Download	3.9K	↑148.8%
Galaxy bridge - Geno...	3.5K	↑2,452....
Galaxy bridge - IGB r...	2.4K	↑2,565....
Download Button Cli...	1.8K	↑605.4%
Welcome BAR User	1.2K	↑1,402....

IGB integrations - Future directions



Member Databases

NAME	URL	CONTACT
Agbase	https://agbase.arizona.edu/	Fiona McCarthy
AgroPortal	http://agroportal.lirmm.fr/	Clement Jonquet
Animal QTLdb	http://www.animalgenome.org/cgi-bin/QTLdb/index	James Koltes
Bovine Genome Database	http://bovinegenome.org/	Christine Elsik
Breed with BIMS	https://breedwithbims.org	Sook Jung
CassavaBase	https://www.cassavabase.org/	CassavaBase
Citrus Genome Database	https://www.citrusgenomedb.org/	Dorrie Main

Get in touch!

Contact me at

pkulzer@charlotte.edu

I host weekly help sessions every Tuesday 1-2PM ET
Scan the QR code or follow the link below for more details:

https://bioviz.org/helpSessions.html

Acknowledgements

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Anton Nekrutenko
Gareth Price
Galaxy

Stefano Giorgetti
Arne Becker
Jorge Batista da Rocha
e!Ensembl

Rasha Alawieh
Mark Johnson
BROWN

Maximilian Haeussler
Luis Nassar
UCSC
Genome Browser

This work was supported by NIH NIGMS (R35GM139609)
NIH

Resources

Access

- Download Integrated Genome Browser: bioviz.org
- Sign in to BioViz *Connect*: connect.bioviz.org
- IGB App Store: apps.bioviz.org

Code

- BioViz *Connect* source code: bitbucket.org/nfreese/bioviz-connect
- UCSC GenArk source code: bitbucket.org/lorainelab/ucsc-genark-data-provider
- Integrated Genome Browser source code: bitbucket.org/lorainelab/integrated-genome-browser

Guides

- IGB User’s Guide: wiki.bioviz.org/confluence
- Videos on using IGB: youtube.com/c/integratedgenomebrowser
- BioViz *Connect* webinar: https://cyverse.org/webinar-BioVizConnect
- BioViz *Connect* paper: https://doi.org/10.3389/fbinf.2022.764619
- eFP-Seq Browser paper: https://doi.org/10.1111/tpj.14468
- IGB App Store paper: https://doi.org/10.1093/bioinformatics/btac109