



and WebApollo!

JBrowse: Robert Buels, Mitchell Skinner, Lincoln Stein, Ian Holmes

WebApollo: Ed Lee, Gregg Helt, Justin Reese, Monica Munoz-Torres, Chris Childers, Robert Buels, Lincoln Stein, Ian Holmes, Christine Elsik, Suzanna Lewis

2014 GMOD Community Meeting
January 16, 2014



University of California, Berkeley



Talk outline

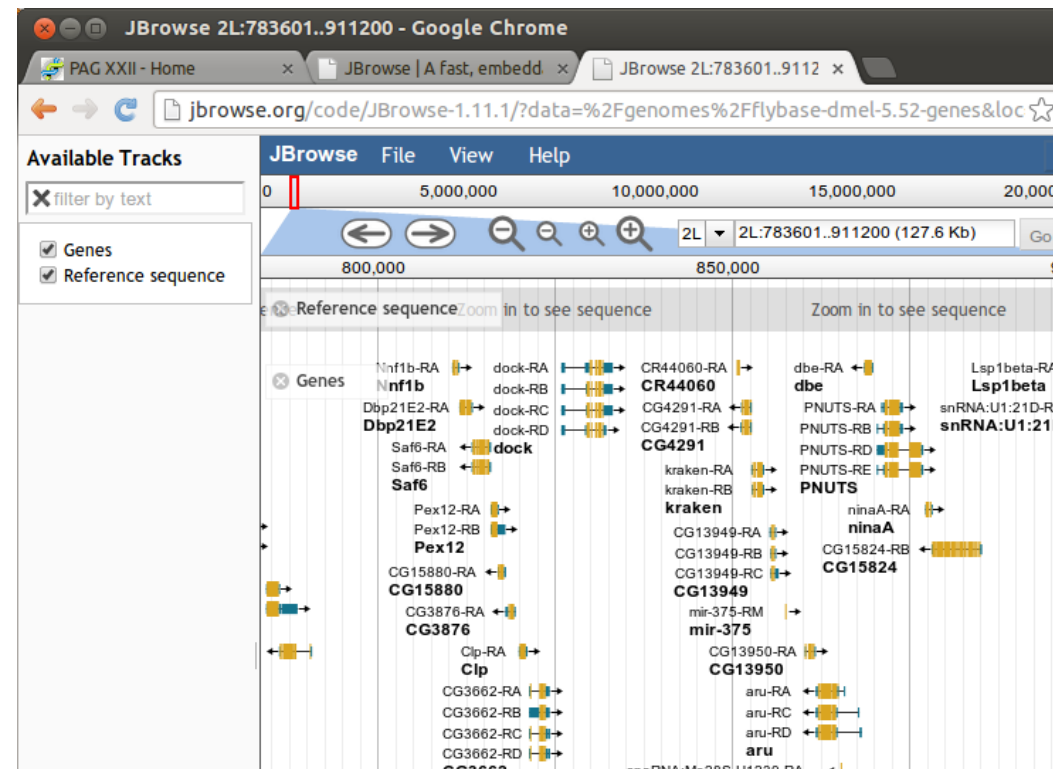
1. JBrowse quick tour
2. Comparison to GBrowse
3. Integrating it
4. Extending it
5. JBrowse 2! The next-next browser





JBrowse

- Do everything possible on the client side, in JavaScript.
- **Fast**, smooth navigation.
- Supports GFF3, BED, Bio::DB::*, Chado, WIG, BAM, BigWig, VCF, and UCSC import (*intron/exon structure, name lookups, quantitative plots*).
- Is stably funded by NHGRI.
- Is open source, of course.
- Did I mention it's fast?



The JBrowse Project

- 2006 First prototype (pre-rendered Gbrowse tiles).
NHGRI funds 3yr development of project.
Mitch Skinner joins as lead developer.
- 2007 CSHL Biology of Genomes: scaling.
- 2008 All-JavaScript rendering on the client.
- 2009 Paper in Genome Research.
- 2010 WebApollo funded for development based on JBrowse.
NHGRI renews for 6mo.
JBrowse dubbed “official” successor of GBrowse.
- 2011 Mitch Skinner moves on.
NHGRI renews for 3yrs.
- 2012 Robert Buels joins as lead developer.
Aggressive development on NGS formats, scalability, configurability.
- 2013 WebApollo first public release.
- 2014 JBrowse 2 release! Really! Need to write a paper!

Stores and Tracks

Stores

BAM

SNPCoverage

BigWig

NCList

GFF3

SequenceChunks

SPARQL

VCF

Tracks

Reference Sequence

Features

Alignments

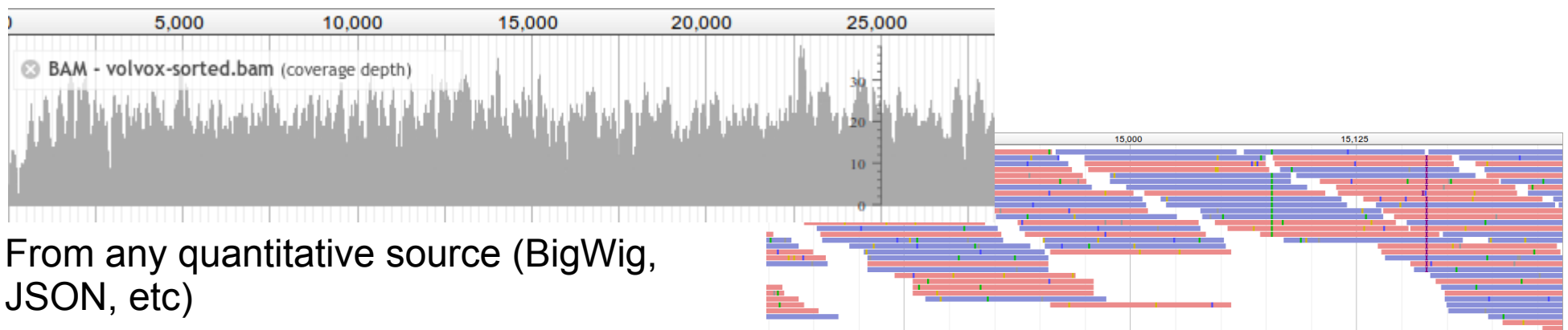
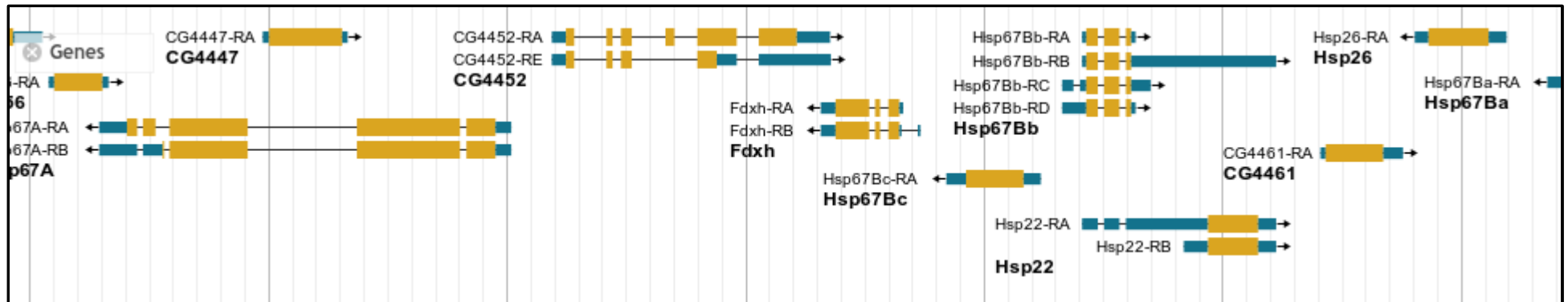
XYPlot

Color density

SNPCoverage

Feature Tracks

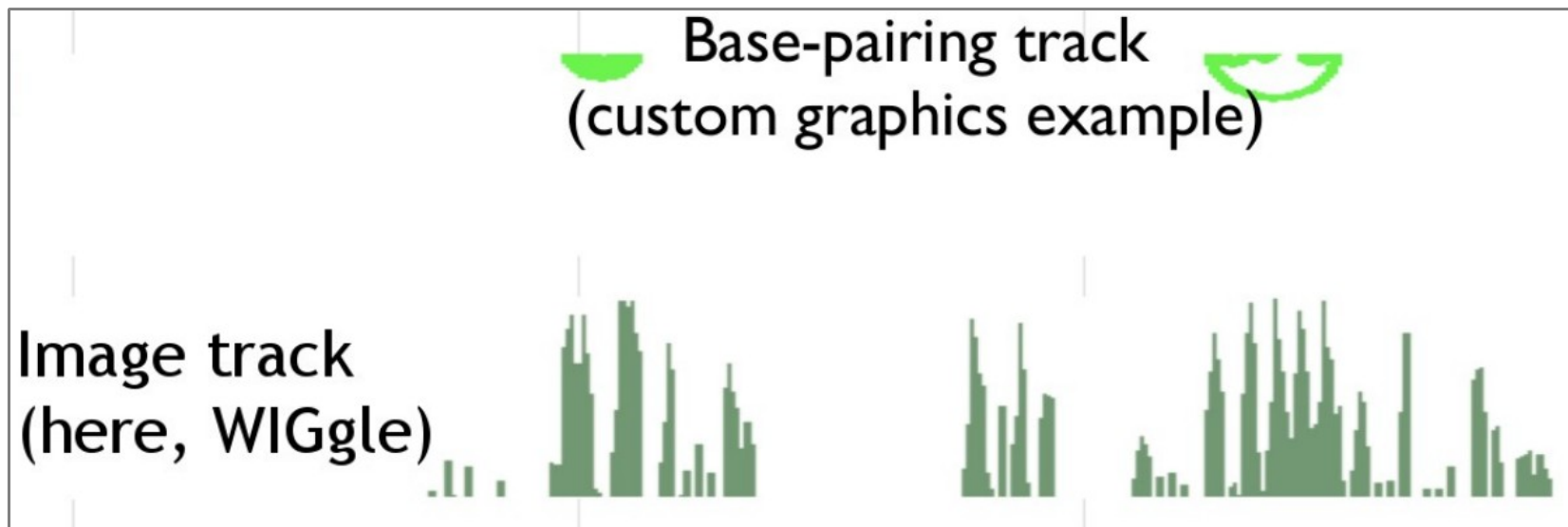
- Clicks on features and menu items can open URLs in popup dialogs or new windows, or can run any JavaScript code.



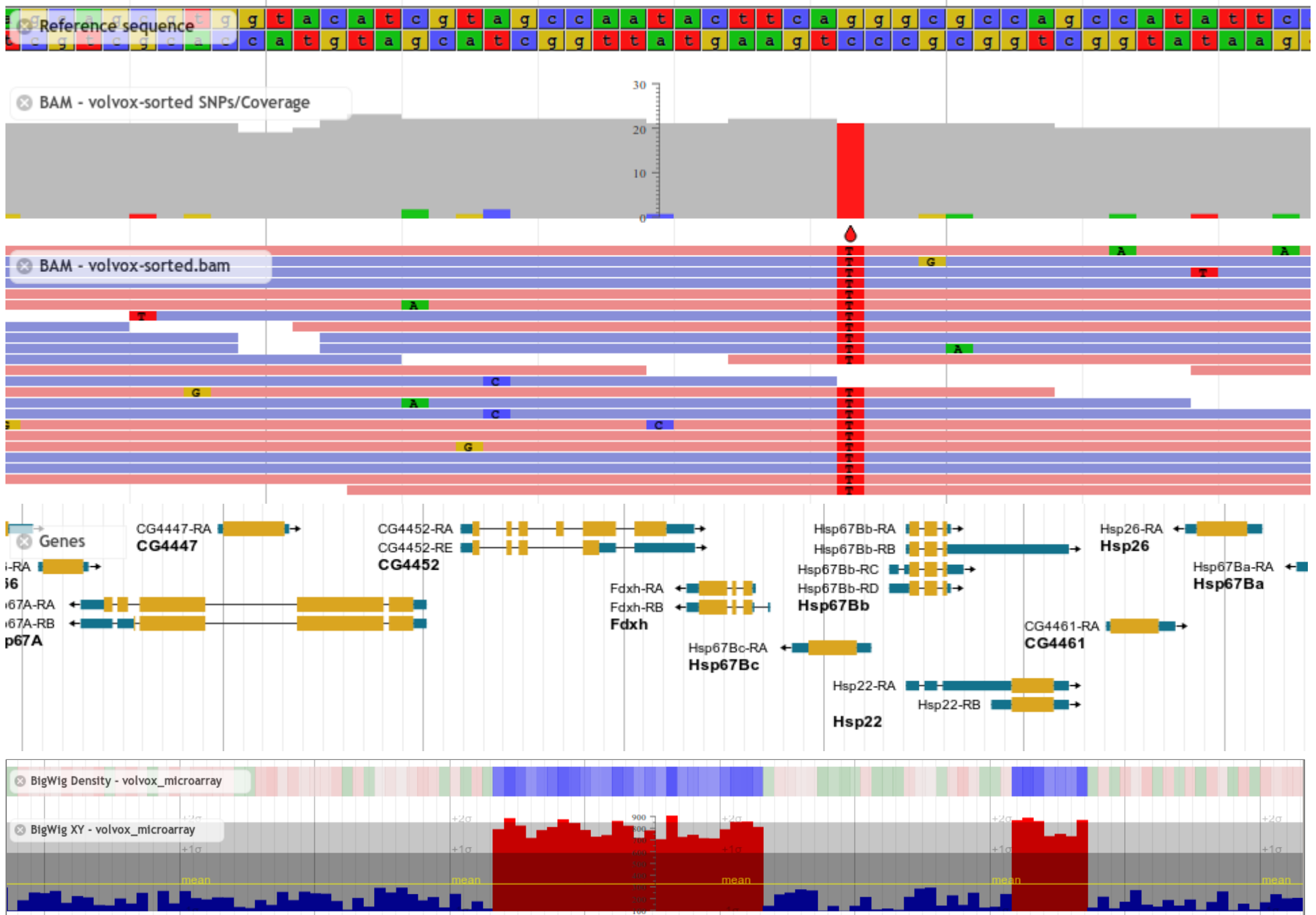
From any quantitative source (BigWig, JSON, etc)

Image Tracks

- any pre-generated images that cover the genome
 - RNA base-pairing
 - Images from other genome browsers
 - Legacy JBrowse .wig formatter uses this



Track Visualizations



++ Particular Strengths ++

- online, but fast and smooth
- easy to administer
- compressed NGS data: direct-to-browser BAM, BigWig, and VCF
- optional faceted track selector - efficiently search thousands of tracks

++ Particular Strengths ++

- combination tracks
- open local files directly on client, no data transfer required
- highly customizable, embeddable, integratable, programmable

Faceted Track Selection

- make CSV file(s) of track metadata, and/or put track metadata in JSON config files

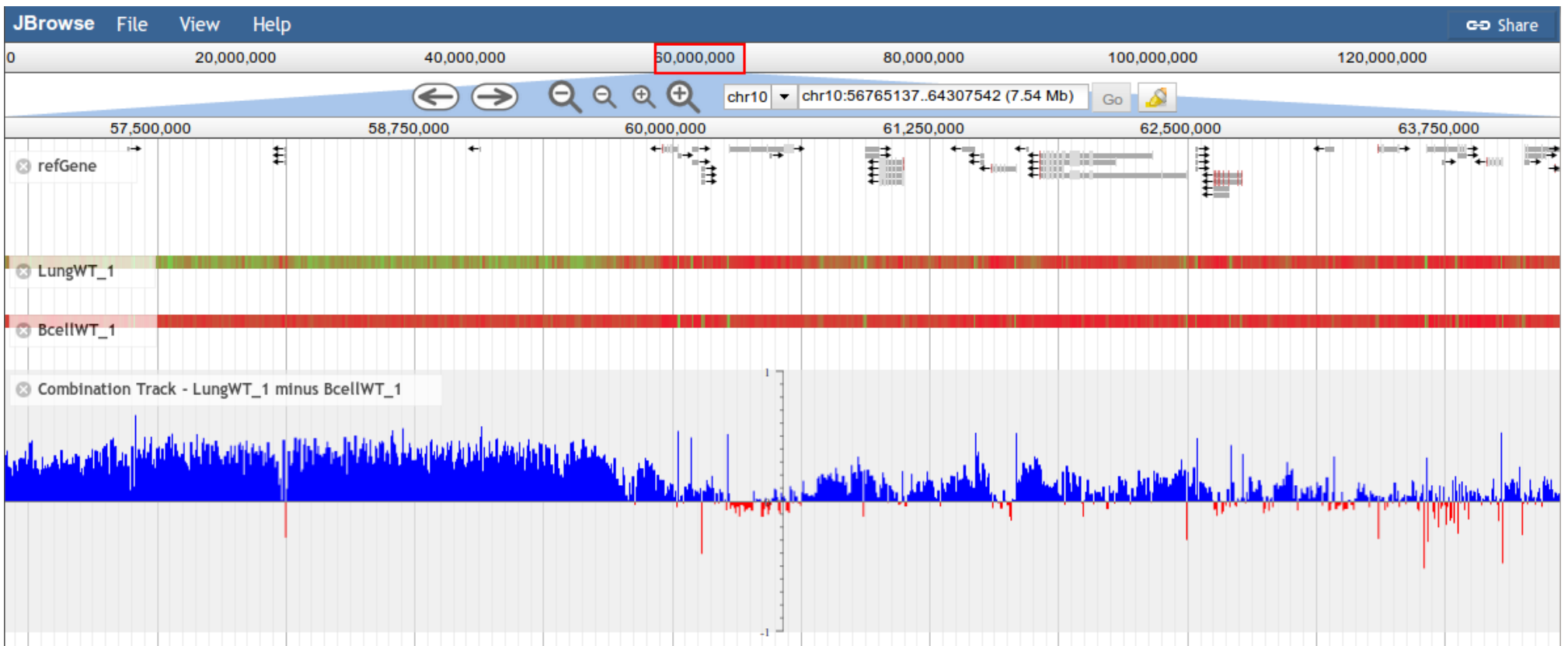
http://jbrowse.org/code/latest-release/index.html?data=sample_data/json/modencode

The screenshot shows the JBrowse 'Select Tracks' interface. The browser address bar displays the URL: http://jbrowse.org/code/latest-release/index.html?data=sample_data/json/modencode. The page title is 'ctgA:20002..30055 - Google Chrome'. The main content area is titled 'Select Tracks' and includes a search bar with the text 'dauer' and a result count of '5 matching tracks'. Below the search bar, there are buttons for 'Back to browser' and 'Clear All Filters'. The main table lists tracks with columns for Name, Organism, Technique, Target, Factor, Conditions, Principal investigator, and Submission ID. The table is filtered to show tracks related to 'dauer' in C. elegans. The second track in the list is selected with a checkmark in the checkbox column.

Category	Name	Organism	Technique	Target	Factor	Conditions	Principal investigator	Submission ID
Conditions	total-RNA;25 degree celsius;daf-2(e1370);Dauer exit daf-2(e1370) 91 hrs 15dC 12 hrs post-L1 stage larvae;integrated-gene-model	C. elegans	integrated-gene-model	mRNA	total-RNA	Dauer exit daf-2(e1370) 91 hrs 15dC 12 hrs post-L1 stage larvae	Waterston, R.	2950
Conditions	total-RNA;25 degree celsius;daf-2(e1370);Dauer exit daf-2(e1370) 91 hrs 15dC 12 hrs post-L1 stage larvae;integrated-gene-model	C. elegans	integrated-gene-model	mRNA	total-RNA	Dauer exit daf-2(e1370) 91 hrs 15dC 12 hrs post-L1 stage larvae	Waterston, R.	2950
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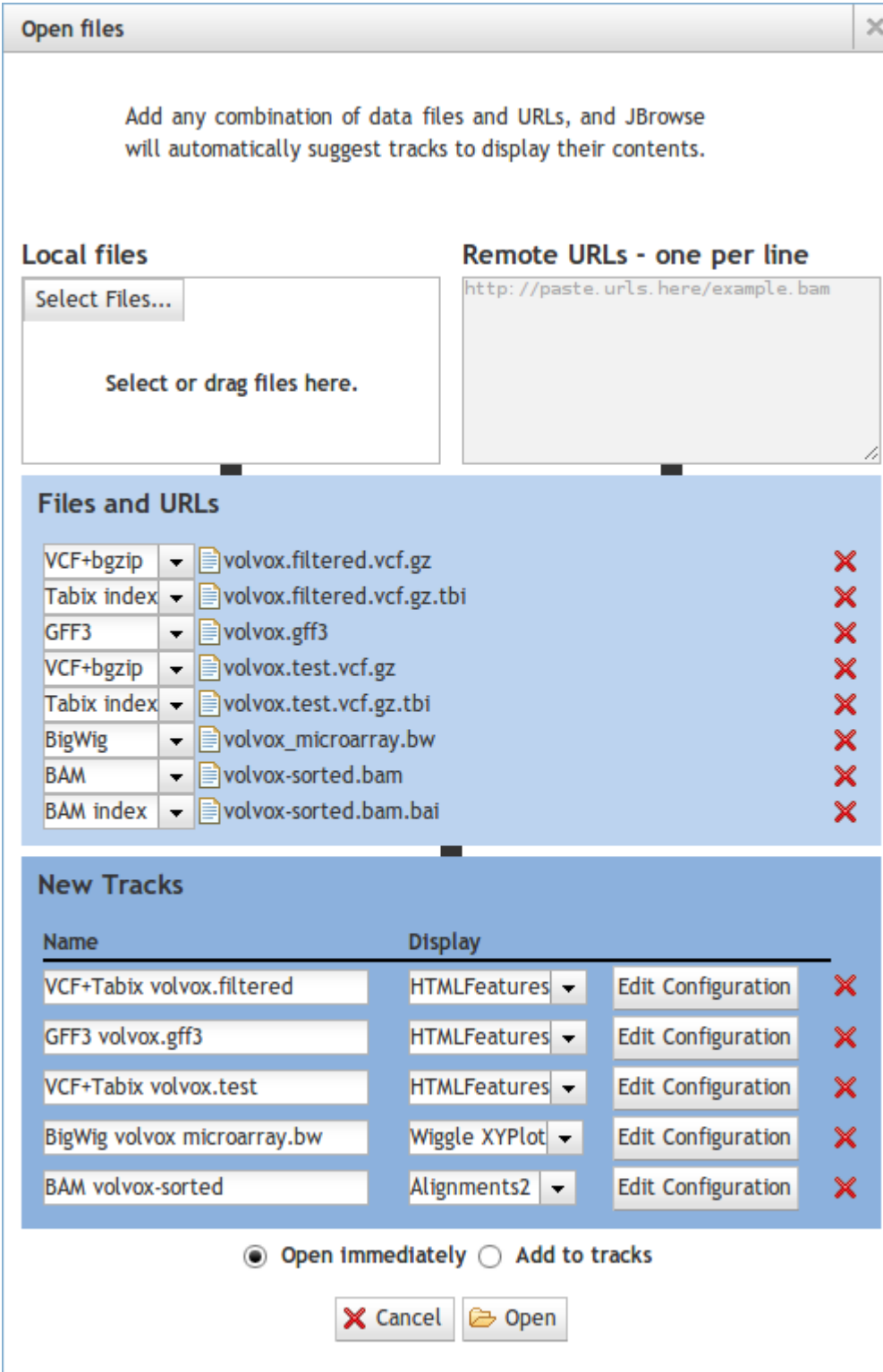
Combination Tracks

- Combine spans: set ops
- Combine quantitative: arithmetic ops
- “Mask” one track with spans from another



Open Local Files

- Select lots of files
- Paste lots of URLs
- Files are never transferred anywhere.
- More like a desktop app than an old-style web app.



Open files

Add any combination of data files and URLs, and JBrowse will automatically suggest tracks to display their contents.

Local files

Select Files...

Select or drag files here.

Remote URLs - one per line

http://paste.urls.here/example.bam

Files and URLs

VCF+bgzip	volvox.filtered.vcf.gz	✗
Tabix index	volvox.filtered.vcf.gz.tbi	✗
GFF3	volvox.gff3	✗
VCF+bgzip	volvox.test.vcf.gz	✗
Tabix index	volvox.test.vcf.gz.tbi	✗
BigWig	volvox_microarray.bw	✗
BAM	volvox-sorted.bam	✗
BAM index	volvox-sorted.bam.bai	✗

New Tracks

Name	Display	Edit Configuration
VCF+Tabix volvox.filtered	HTMLFeatures	✗
GFF3 volvox.gff3	HTMLFeatures	✗
VCF+Tabix volvox.test	HTMLFeatures	✗
BigWig volvox_microarray.bw	Wiggle XYPlot	✗
BAM volvox-sorted	Alignments2	✗

Open immediately Add to tracks

✗ Cancel Open

iLive Demos!

<http://jbrowse.org/demos>



All query and display runs on the server computer. Send images.

Bottleneck: server CPU and mem

All browsing code runs in the user's web browser. Servers send only data.

Bottleneck: client network, client CPU and mem

Local files must be **sent to the server**.

Local files are **opened in-place**.

15-year development history.

6-year development history (but only 2 years of Rob, heh).

Few demands on web browsers, compatible with **very old browsers**.

Browsers **newer than 4 years old** are all fine. For IE, version 9 is minimum (Windows 7).

- Lincoln would like everyone to please hurry up and move to JBrowse, thanks.
- JBrowse is ready for **most** users to move.
- Some users need more things. Please help me!

WebApollo

<http://www.gmod.org/wiki/WebApollo>

- next generation of the popular Apollo annotation editor
- UI built on top of JBrowse as a plugin
- realtime annotation editing and curation on the web!



Integrating JBrowse

- Your systems can directly drive JBrowse by emitting JSON
 - JSON Configuration
 - Data (JBrowse/Store/SeqFeature/REST)
 - Name searches and completions (Jbrowse/Store/Names/REST)
- JBrowse is static and self-contained, can **go to the data**
 - e.g. put it on the end of your cloud-based SNP-calling pipeline to visually validate SNPs
- Plugin system: can build on top of JBrowse!

Web Apollo

- Users see updates in real time (like Google Docs)
- saves edits to a central Chado database
- front-end is a **JBrowse plugin** (Gregg Helt)
- back-end is extensive server-side Java (Ed Lee)



JBrowse Plugins

- Extend JBrowse with your own JavaScript code
- Can do pretty much anything
 - Add your own track visualizations
 - Add your own data backends
 - Add menu items
 - Subscribe to event notifications (pub/sub system)
 - Reach deep into the guts of JBrowse and (carefully!) change anything.
- WebApollo front-end is a JBrowse plugin

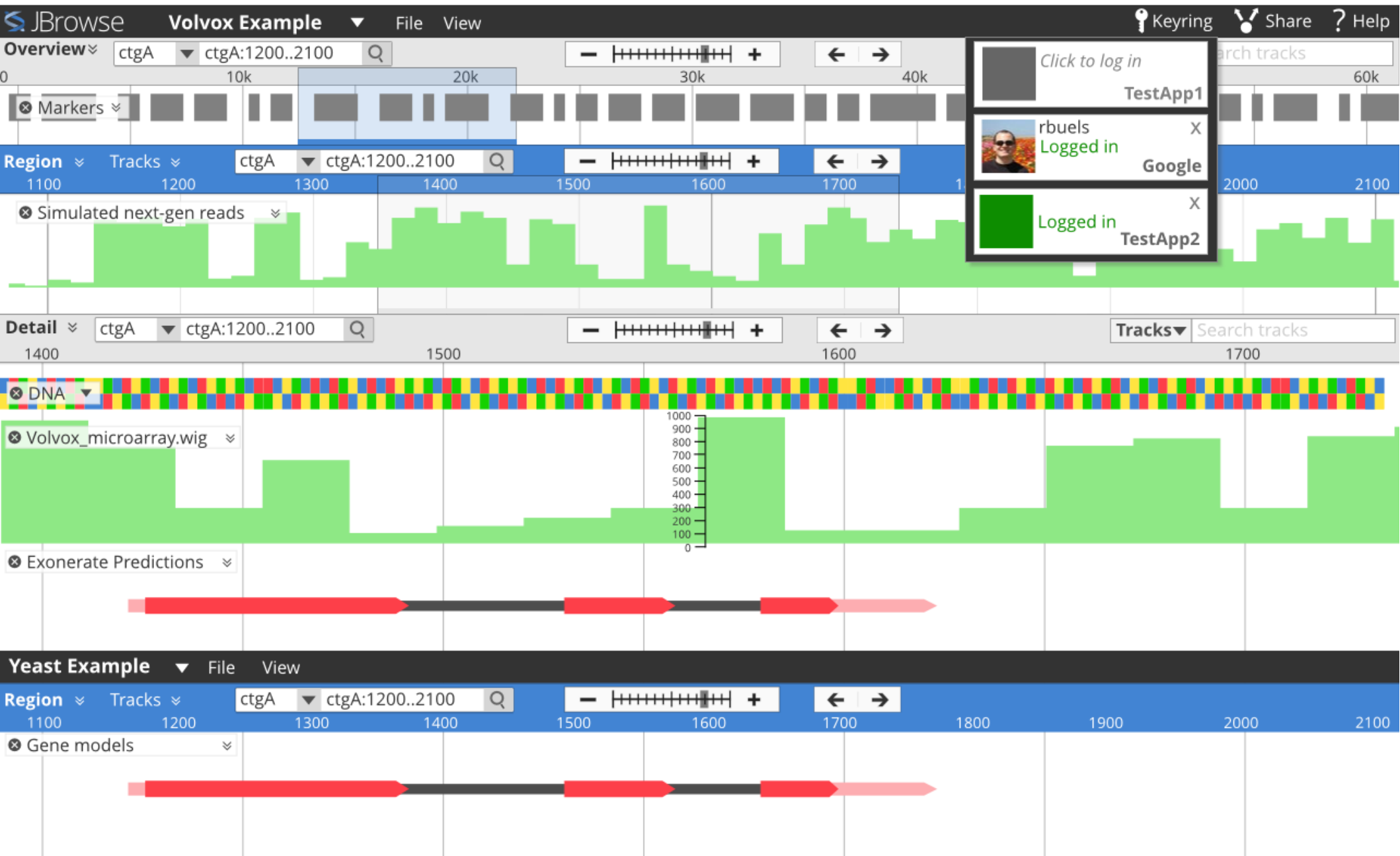
JBrowse 2

- Not vaporware! But very delayed!
- Because I prioritized caring for existing users.
- They needed a lot of things very badly that I could still do in 1.x (JBrowse 1.10 and 1.11)

JBrowse 2 Plans

- Even more of a desktop-web hybrid
 - go to <http://jbrow.se> and just open your local or network files
- Tiled, related views of one or many genomes
- Show only regions of interest (e.g. collapse introns)
- Advanced authentication - OAuth2, Google, Dropbox, iPlant?
- Graphical conf - both admins and users

JBrowse 2 UI Mockup



Beyond JBrowse 2

- JBrowse 2 architecture lays solid groundwork for advanced features
- Multiple views lays foundation for
 - Synteny views
 - Circular views
 - Whole-genome vertical views
 - Network views
- Juxtaposing regions lays foundations for
 - List of interesting regions
 - Showing gene fusions (e.g. in cancer)

It's an Open Source Project

- If you are interested in seeing all this happen sooner
 - Can you spare your time?
 - Some of your developers' time?
- My door is always open

Big Thanks

Suzi Lewis (LBNL)
Gregg Helt
Ed Lee



Ian Holmes (UC)
Amelia Ireland
Mitch Skinner



Lincoln Stein (OICR)
Julien Smith-Roberge
Erik Derohanian
Julie Moon
Natalie Fox
Adam Wright



NHGRI



The End

<http://jbrowse.org>



<http://gmod.org/wiki/JBrowse>

github

<http://github.com/GMOD/jbrowse>

(yes, jbrowse needs a logo)

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(#bioperl, #gmod)



- Was Engineering Lead at Sol Genomics Network <http://solgenomics.net>, at BTI with Lukas Mueller
- Jan. 2012, became new JBrowse Lead Developer at UC Berkeley with Ian Holmes, also at OICR with Lincoln Stein