JBrowse and WebApollo!

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 ctgA:14701..25630 - Google Chrome

PAG XXII - Home | JBrowse | A fast, embedd | JBrowse ctgA:14701..256

jbrowse.org/code/JBrowse-1.11.1/?loc=ctgA%3A14701..25630&tracks=DNA%2CTranscript%2Cvolvox_microarray_bw_density%2Cvolvox_microarray_bw_xyplot%2Cvolvox-sorted-vcf%2

Volvox Example | File | View | Help | Share

ctgA | ctgA:14701..25630 (10.93 k | Go

0 5,000 10,000 15,000 20,000 25,000 30,000 35,000 40,000 45,000 50,

15,000 17,500 20,000 22,500 25,000

Reference sequence | Zoom in to see sequence | Zoom in to see sequence | Zoom in to see sequence

CanvasFeatures - transcripts

Apple3

mRNA with both CDSs and UTRs

BigWig Density - volvox_microarray

BigWig XY - volvox_microarray

mean

VCF - volvox-sorted variants

BAM - volvox-sorted SNPs/Coverage

BAM - volvox-sorted.bam

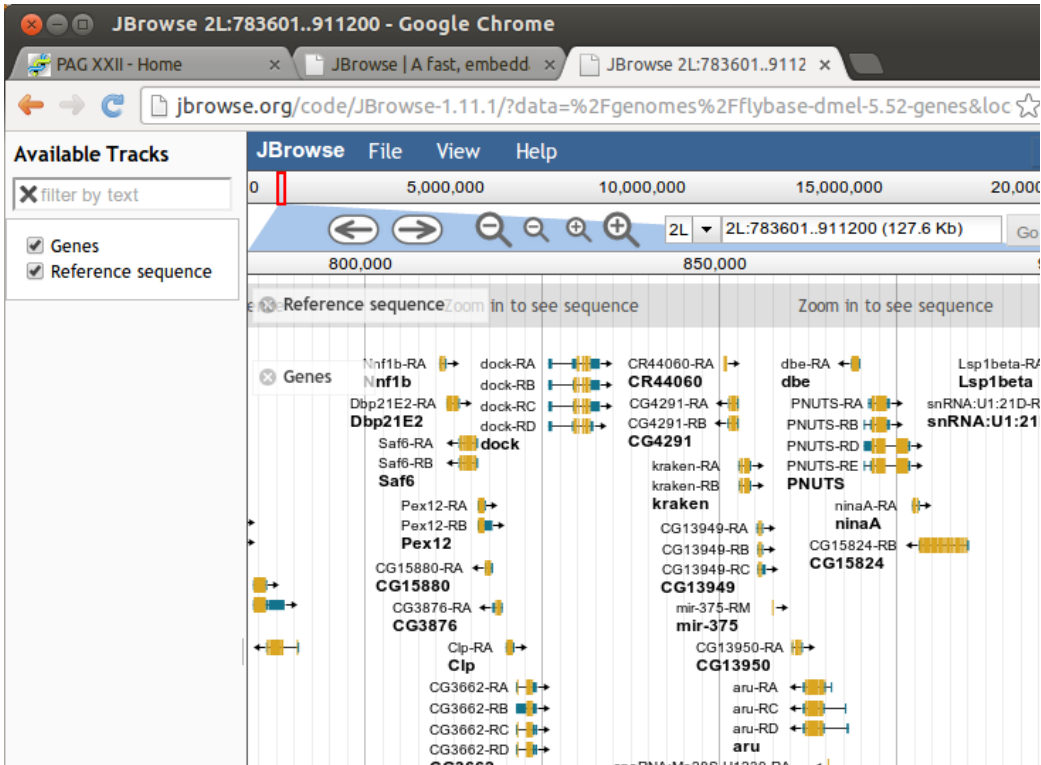
Available Tracks

filter by text

- BAM 3
  - BAM - volvox-sorted SNPs/Coverage
  - BAM - volvox-sorted.bam
  - Legacy BAM - volvox-sorted.bam
- Miscellaneous 9
  - FromConfig - Features in Configuration
  - GFF3 - volvox.gff3 in-memory adaptor
  - HTMLFeatures - ESTs
  - HTMLFeatures - Example Features
  - HTMLFeatures - Example motifs
  - HTMLFeatures - Features with right-click menus
  - HTMLFeatures - Fingerprinted BACs
  - HTMLFeatures - Name test track has a really long track label
  - HTMLFeatures - SNPs
- Pre-generated images 1
  - Image - volvox_microarray.wig
- Quantitative 4
  - Density 2
    - BigWig Density - volvox_microarray
    - BigWig Density - volvox_sine
  - XY Plot 2
    - BigWig XY - volvox_microarray
    - BigWig XY - volvox_sine
- Reference sequence 1
  - Reference sequence
- Transcripts 4
  - CanvasFeatures - Protein-coding genes
  - CanvasFeatures - mixed mRNAs and CDSs
  - CanvasFeatures - transcripts
  - HTMLFeatures - mRNAs
- VCF 2
  - VCF - additional test data
  - VCF - volvox-sorted variants

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

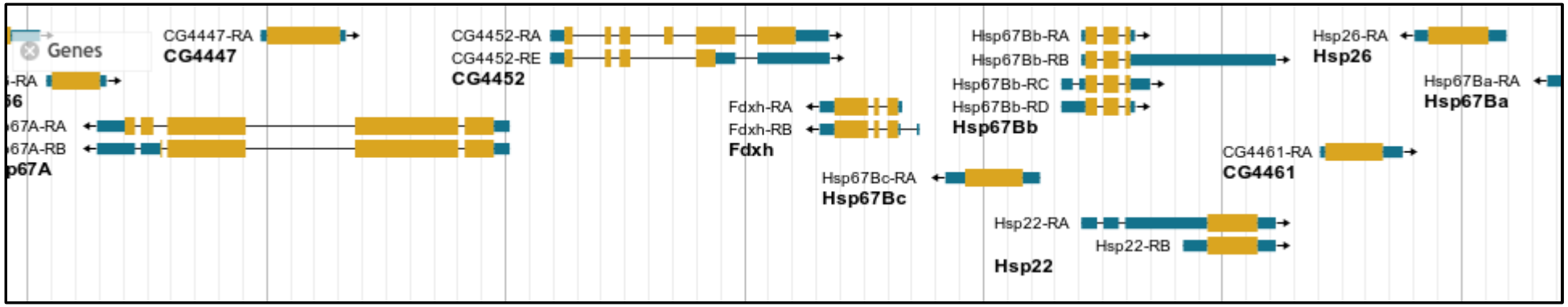
XYPlot

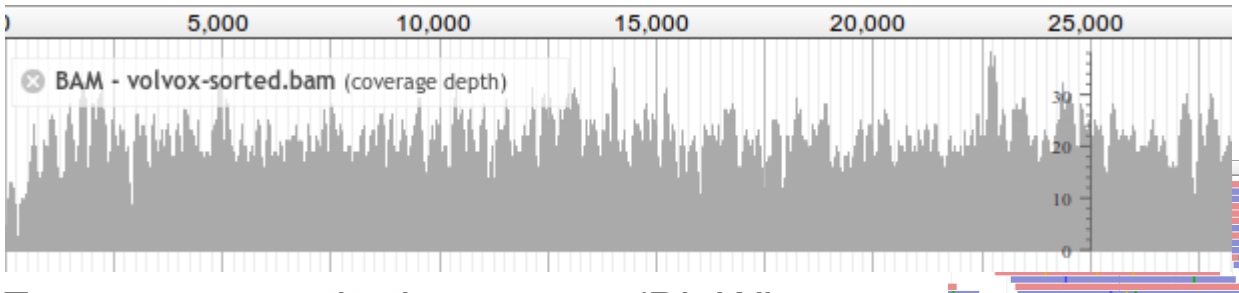
Color density

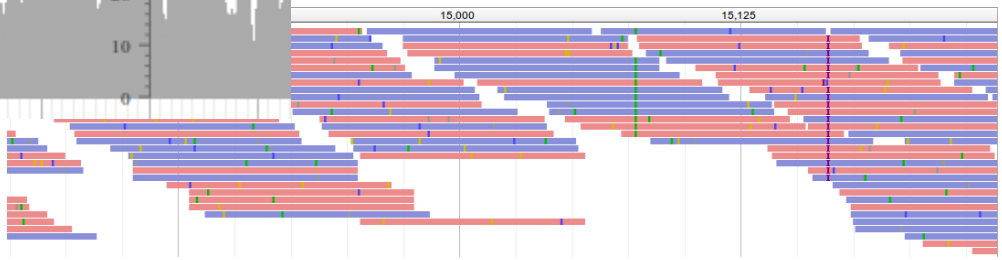
SNPCoverage

Feature Tracks

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



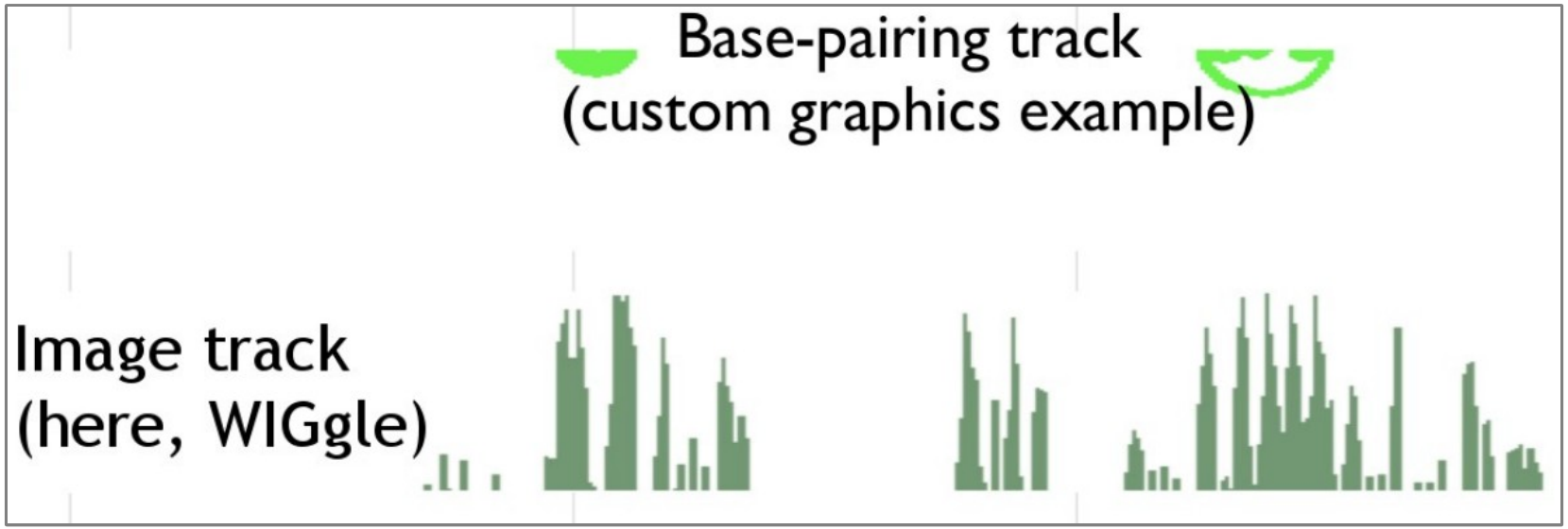




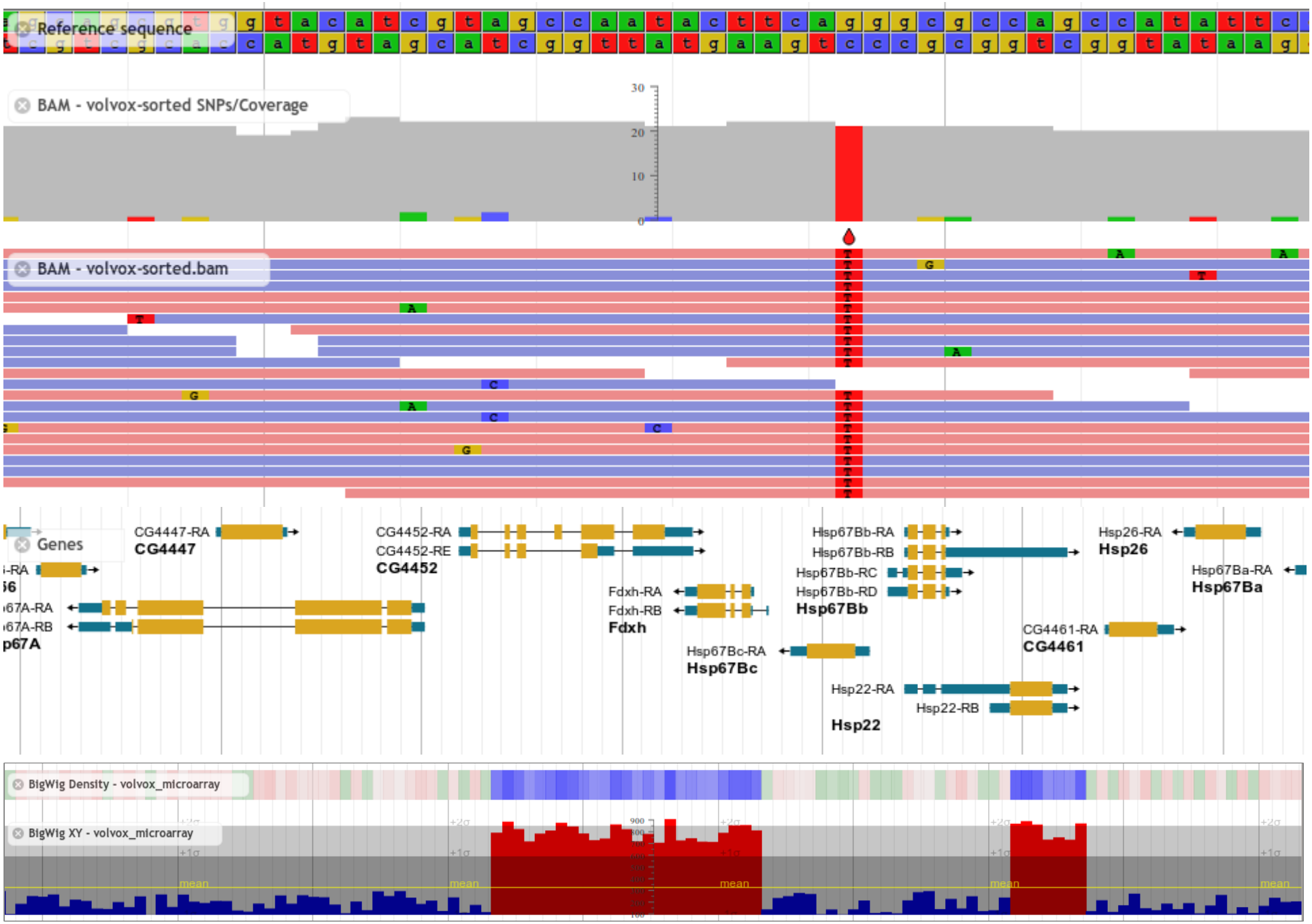
From any quantitative source (BigWig, JSON, etc)

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

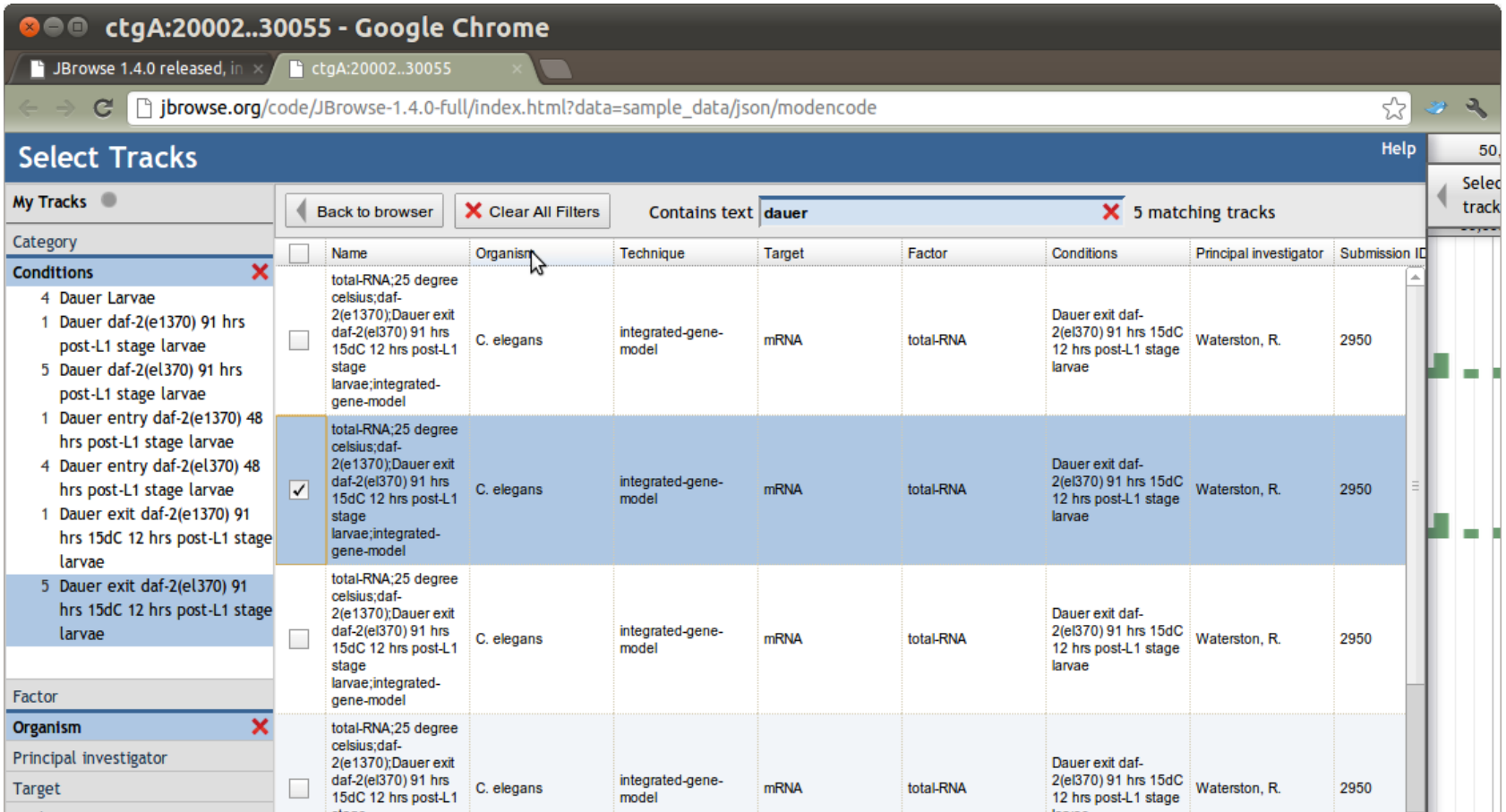
++ Particular Strengths ++

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

Faceted Track Selection

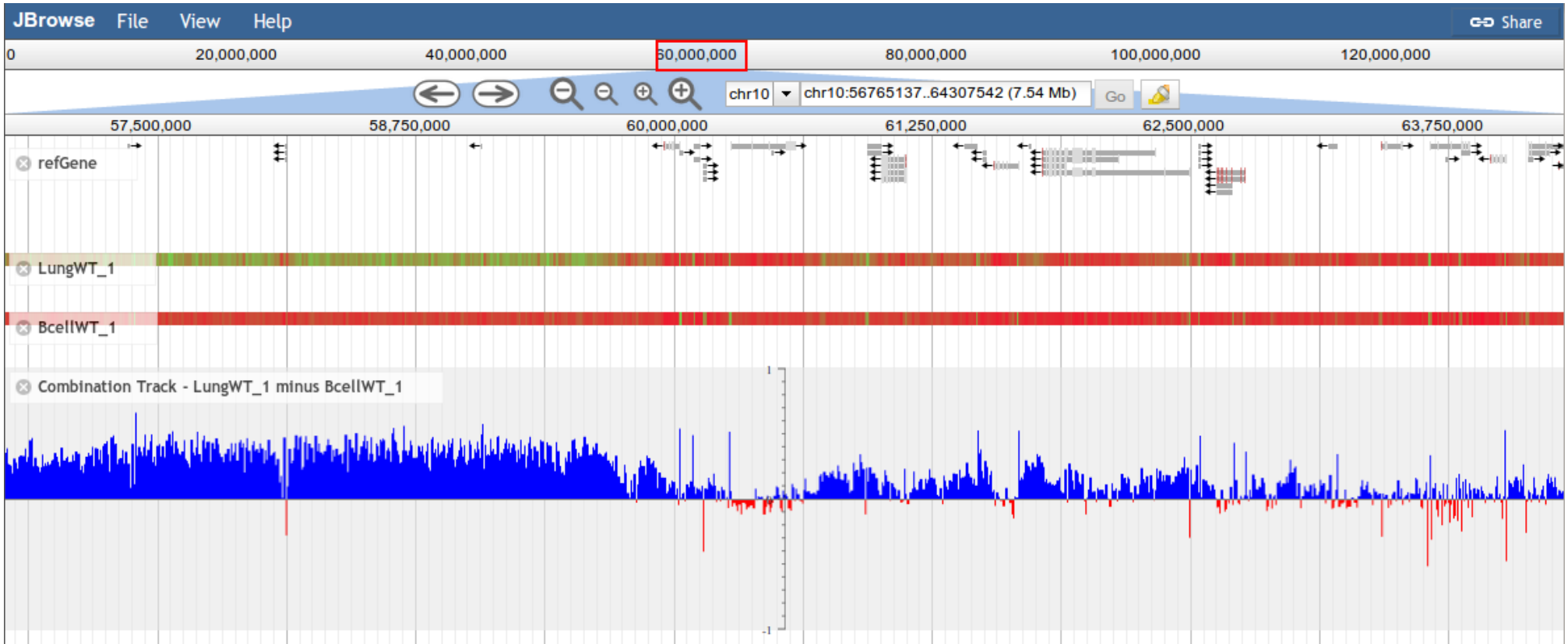
- make CSV file(s) of track metadata, and/or put track metadata in JSON config files

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



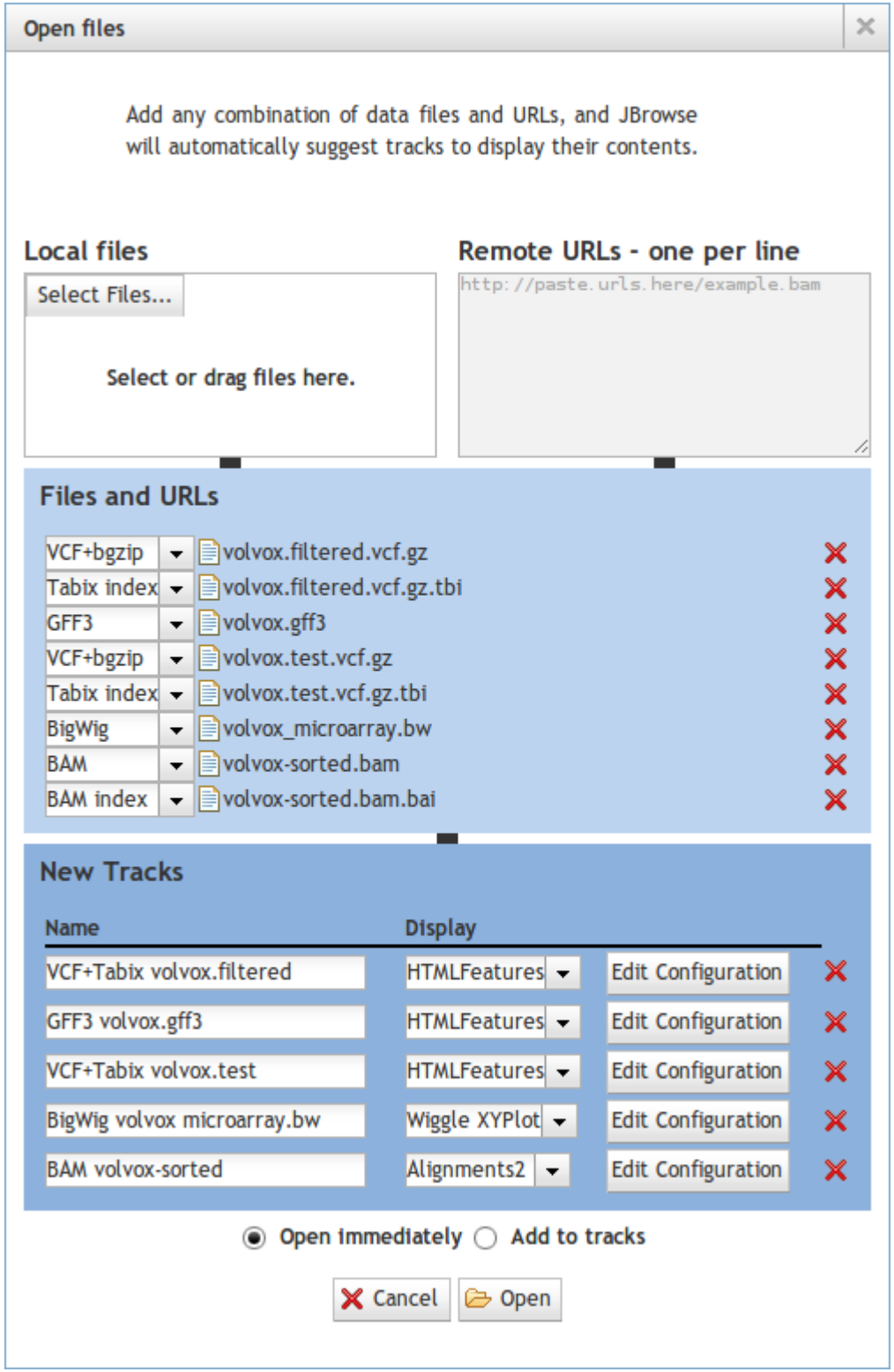
Combination Tracks

- 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.



¡Live Demos!

http://jbrowse.org/demos

GBrowse	JBrowse
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)

Apollo

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

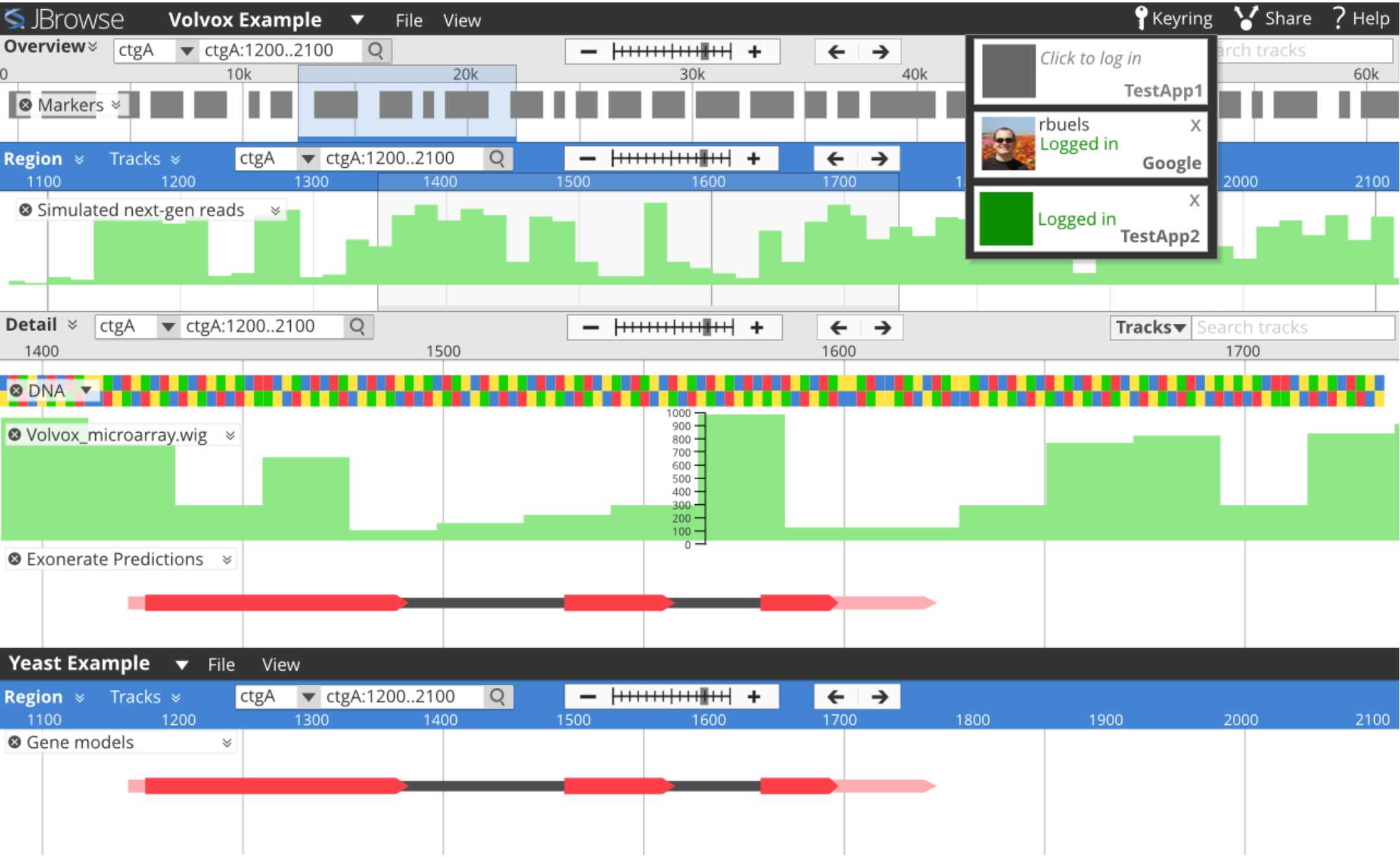
JBrowse 2

- 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
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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

http://github.com/GMOD/jbrowse

(yes, jbrowse needs a logo)

Robert Buels

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rbuels on freenode IRC
(#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