

### 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



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#### 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?

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#### **The JBrowse Project**

<u>2006</u> First prototype (pre-rendered Gbrowse tiles).
 NHGRI funds 3yr development of project.
 Mitch Skinner joins as lead developer.

- <u>2007</u> CSHL Biology of Genomes: scaling.
- <u>2008</u> 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.

<u>2011</u> Mitch Skinner moves on.

NHGRI renews for 3yrs.

2012 Robert Buels joins as lead developer.

Aggressive development on NGS formats, scalability, configurability.

- <u>2013</u> WebApollo first public release.
- <u>2014</u> 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

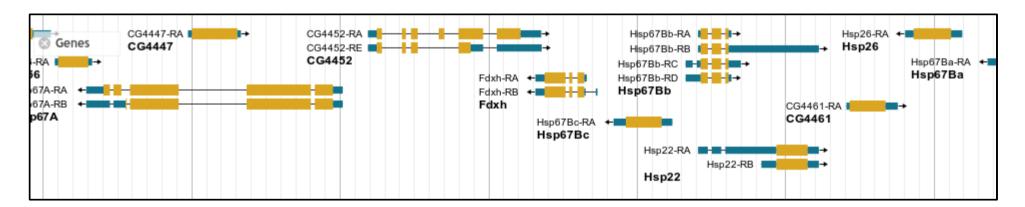
XYPlot

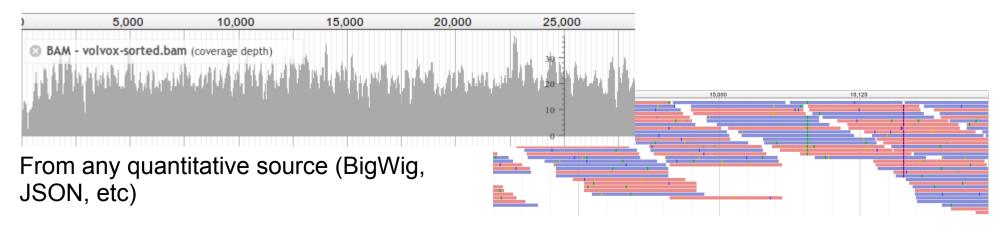
Color density

SNPCoverage

#### **Feature Tracks**

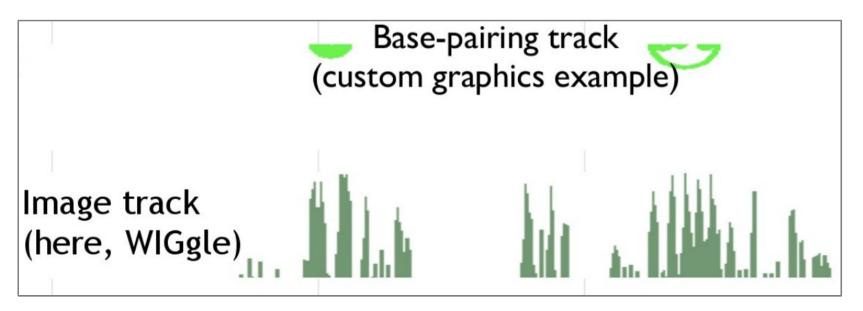
 Clicks on features and menu items can open URLs in popup dialogs or new windows, or can run any JavaScript code.



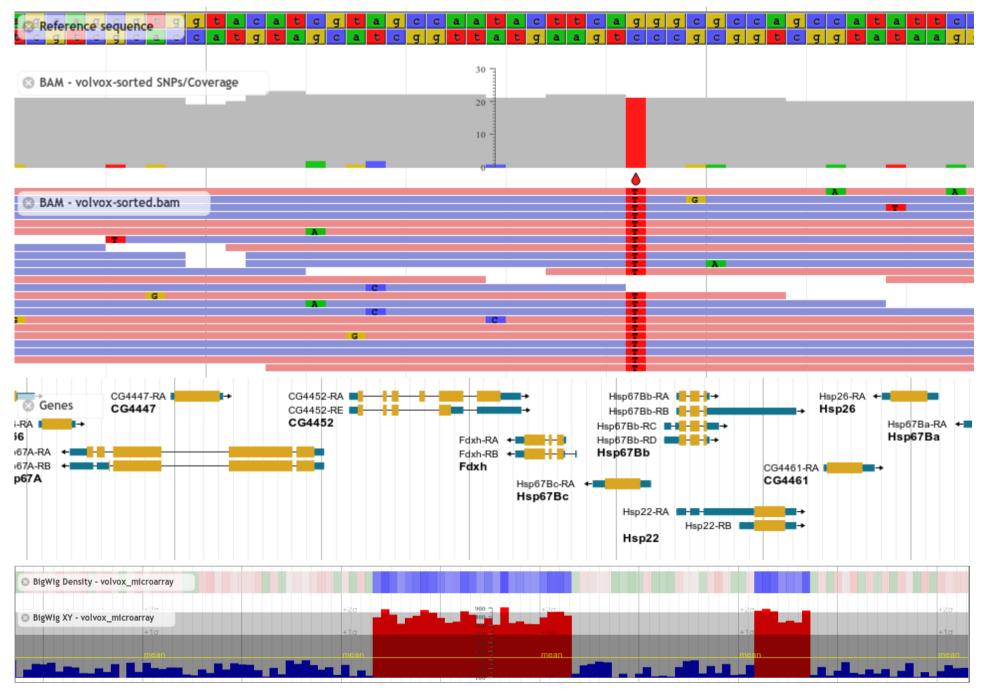


#### Image Tracks

- 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

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#### **Combination Tracks**

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

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#### 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.

ocal files	Remote URLs - one per line					
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Open immediately						

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# ¡Live Demos!

http://jbrowse.org/demos





All query and display runs on the server computer. Send images.	All browsing code runs in the user's web browser. Servers send only data.
Bottleneck: server CPU and mem	Bottleneck: client network, client CPU and mem
Local files must be sent to the server.	Local files are <b>opened in-place</b> .
15-year development history.	6-year development history (but only 2 years of Rob, heh).
Few demands on web browsers, compatible with <b>very old browsers</b> .	Browsers <b>newer than 4 years old</b> 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

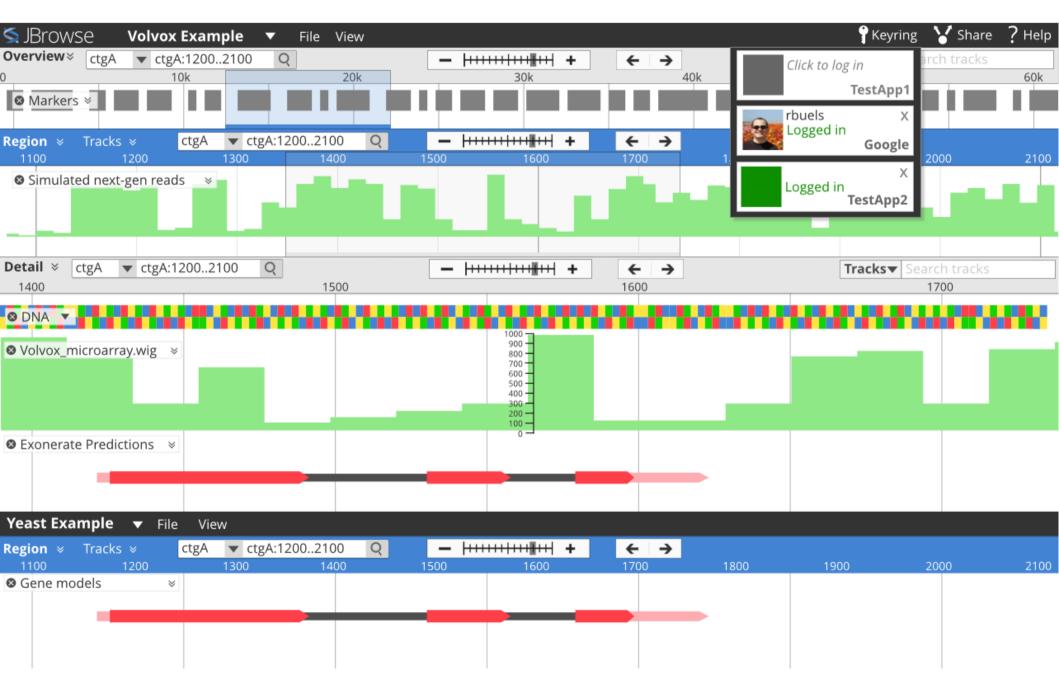
• Not vaporware! But very delayed!

- 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

# NHGRI

Ian Holmes (UC) Amelia Ireland Mitch Skinner



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



#### The End

## http://jbrowse.org



# github http://github.com/GMOD/jbrowse

(yes, jbrowse needs a logo)

#### **Robert Buels**

rbuels@gmail.com

**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