

# JBrowse – 1.9.0 and beyond

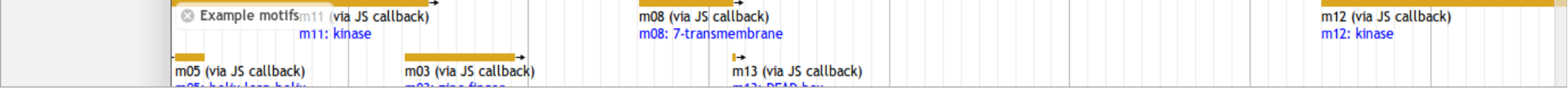
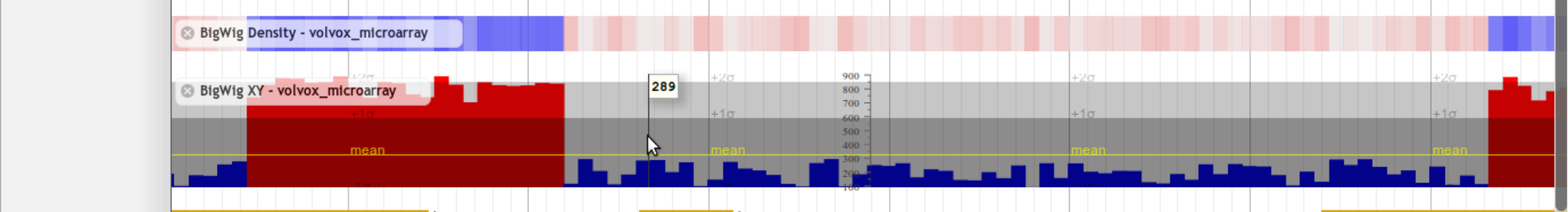
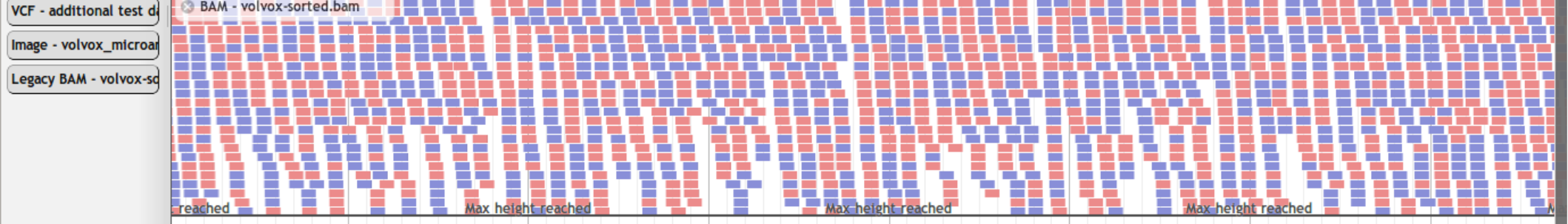
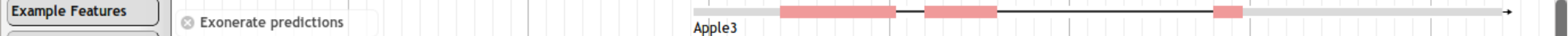
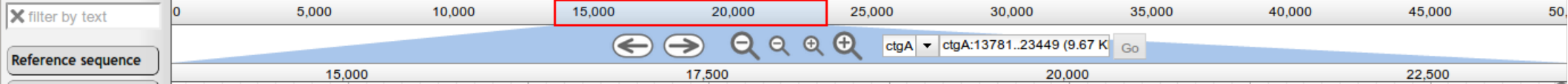
Robert Buels  
Bio-IT World 2013  
April 11, 2013



University of California, Berkeley

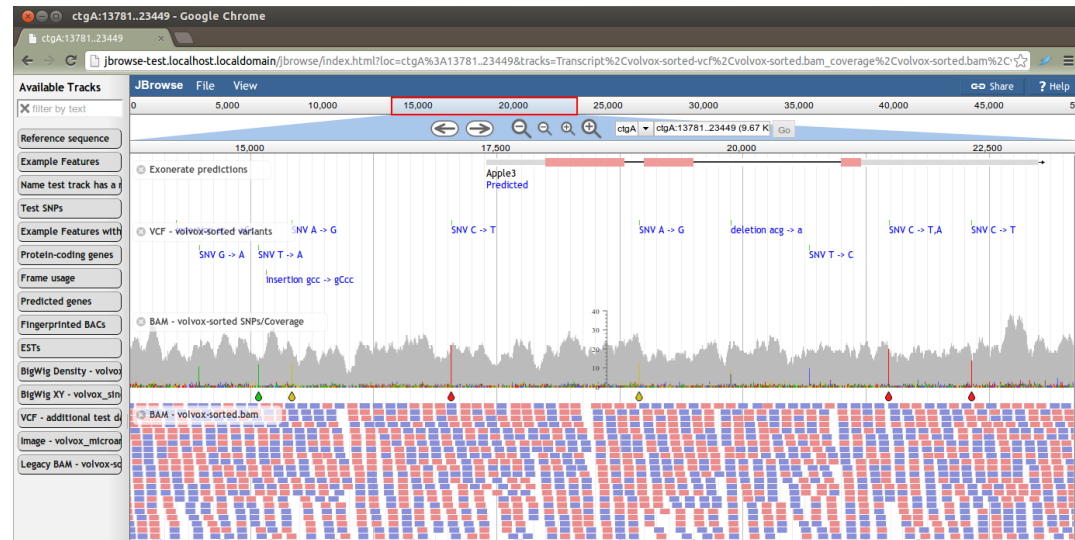


(JBrowse 1.9.0 will be released Any Day Now)



# 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.

# The JBrowse Project

- free and open source (license: LGPL / Artistic)
- a **GMOD** project  
<http://gmod.org>
- developed using `git`, hosted on GitHub  
<http://github.com/GMOD/jbrowse>
- PIs most involved: Ian Holmes, Lincoln Stein, Suzi Lewis

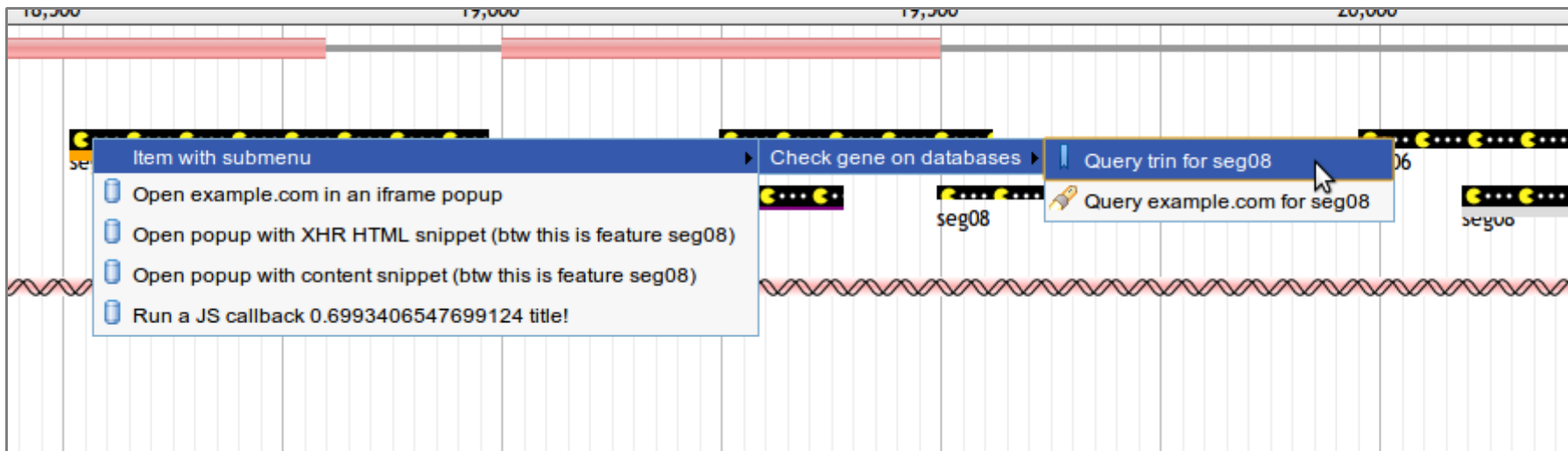




- Umbrella organization of open source bioinformatics (mostly genomics) projects.
- All try to be interoperable.
- Holds satellite meetings, summer schools, etc.

# Feature Tracks

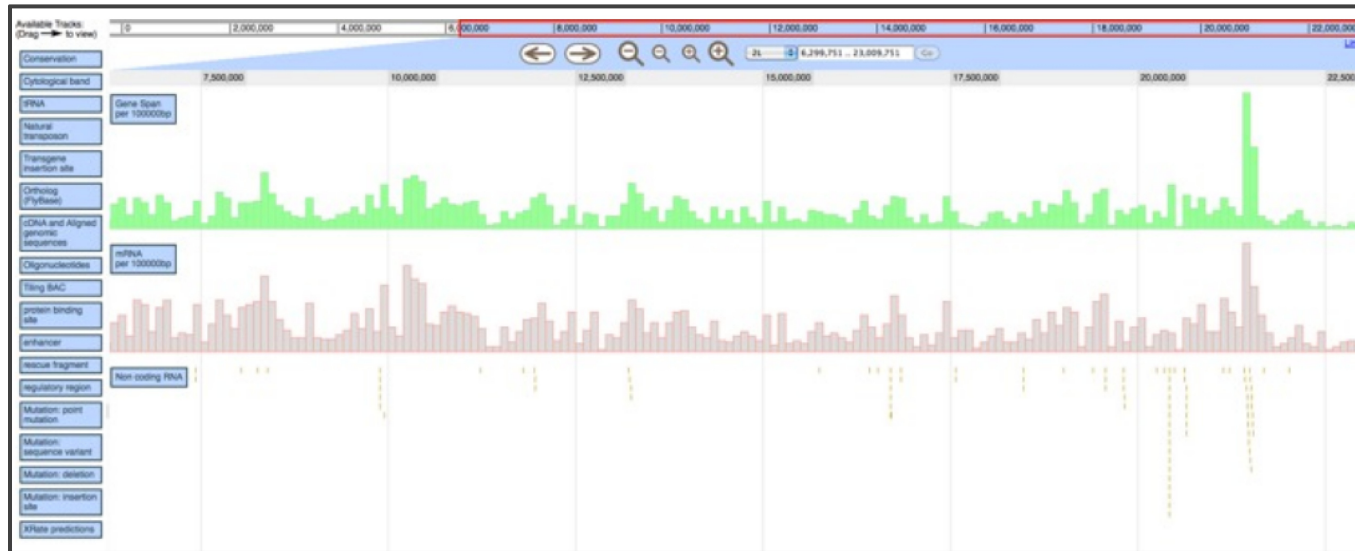
- rectangles (<div>s) with various fills and heights to represent the feature spans
- Super-configurable left clicking and right-click menus.



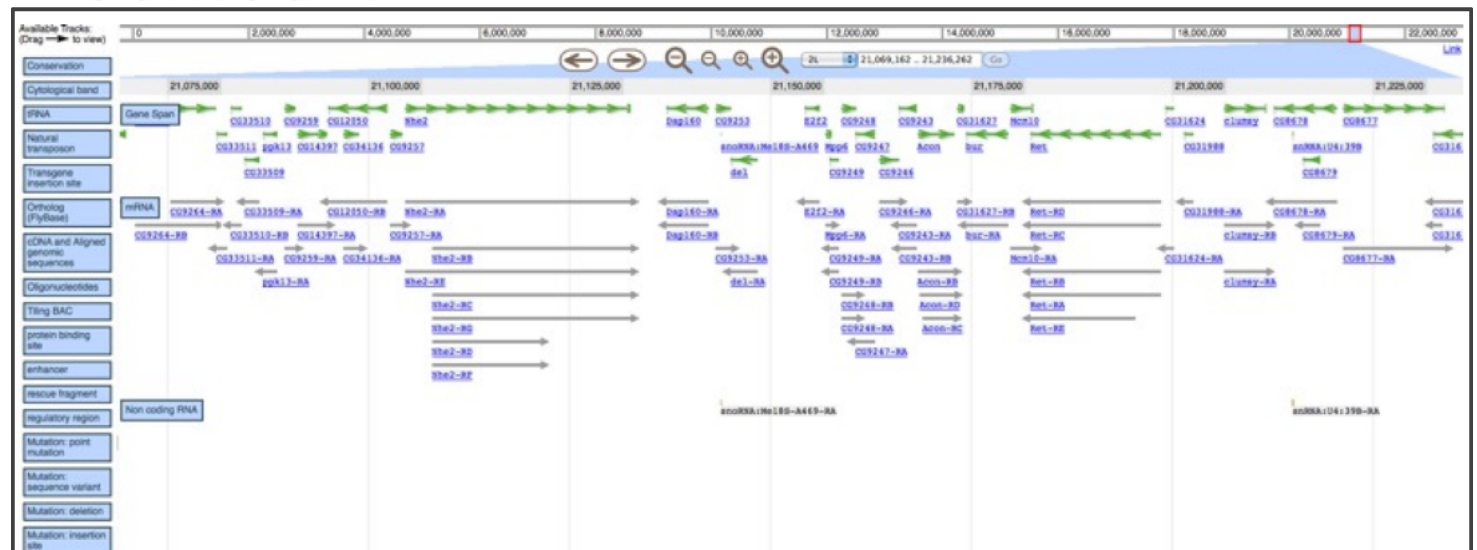


# Feature Density Plots

Zoomed out

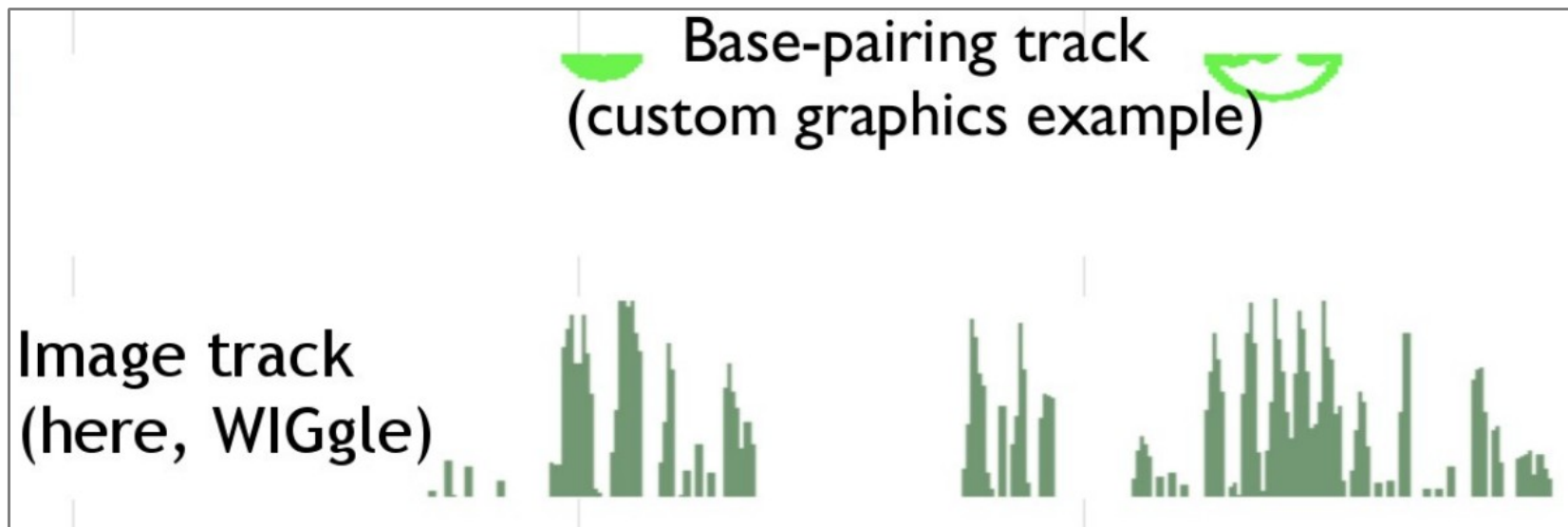


Zoomed in



# Image Tracks

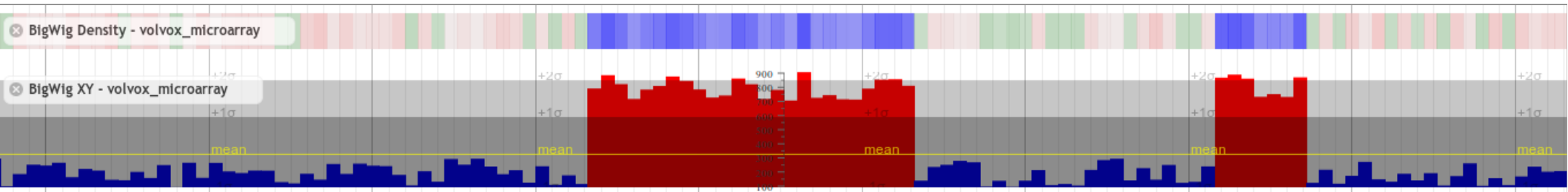
- any pre-generated images that cover the genome
  - RNA base-pairing
  - Images from other genome browsers
  - Legacy JBrowse .wig formatter used this also



# Wiggle/BigWig Tracks

<http://goo.gl/4kWFP>

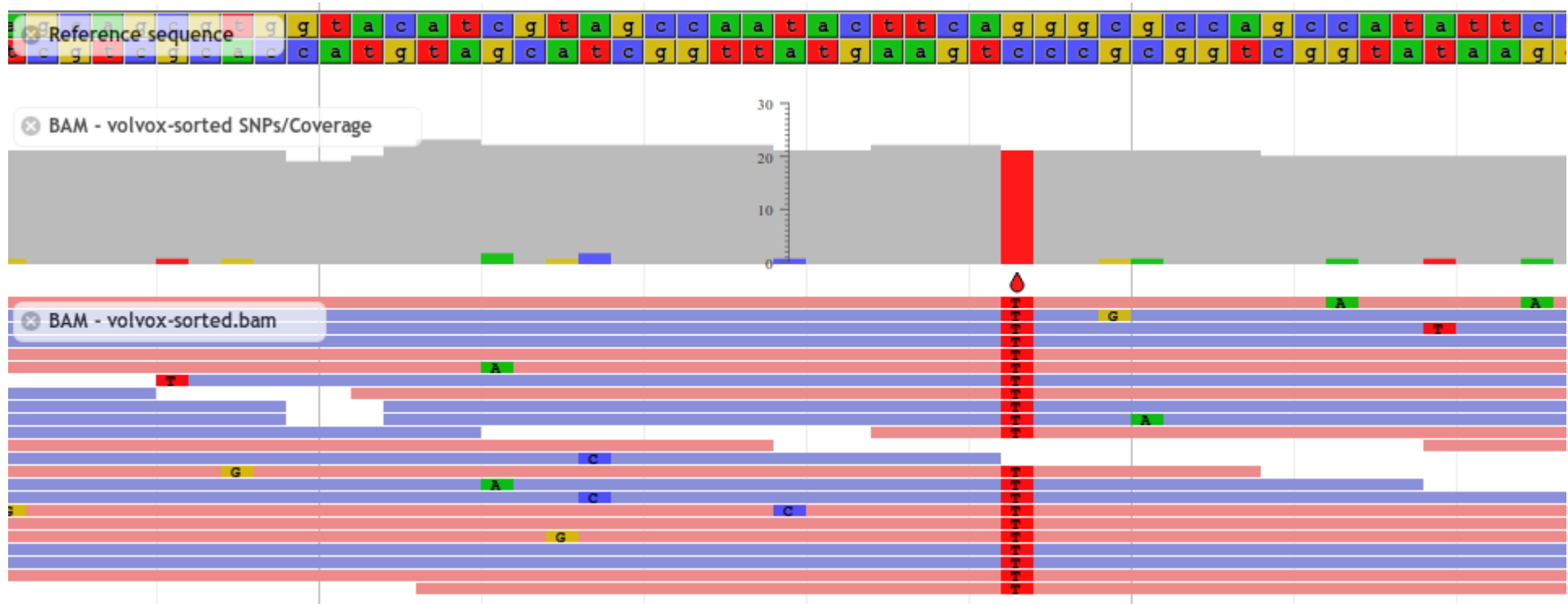
<http://jbrowse.org/genomes/tomato/>



- Reads small chunks directly from BigWig file.
- Needs only a not-super-old (< 4 yrs) browser, except for Internet Explorer.
- IE requires version 10.

# BAM Alignment Tracks

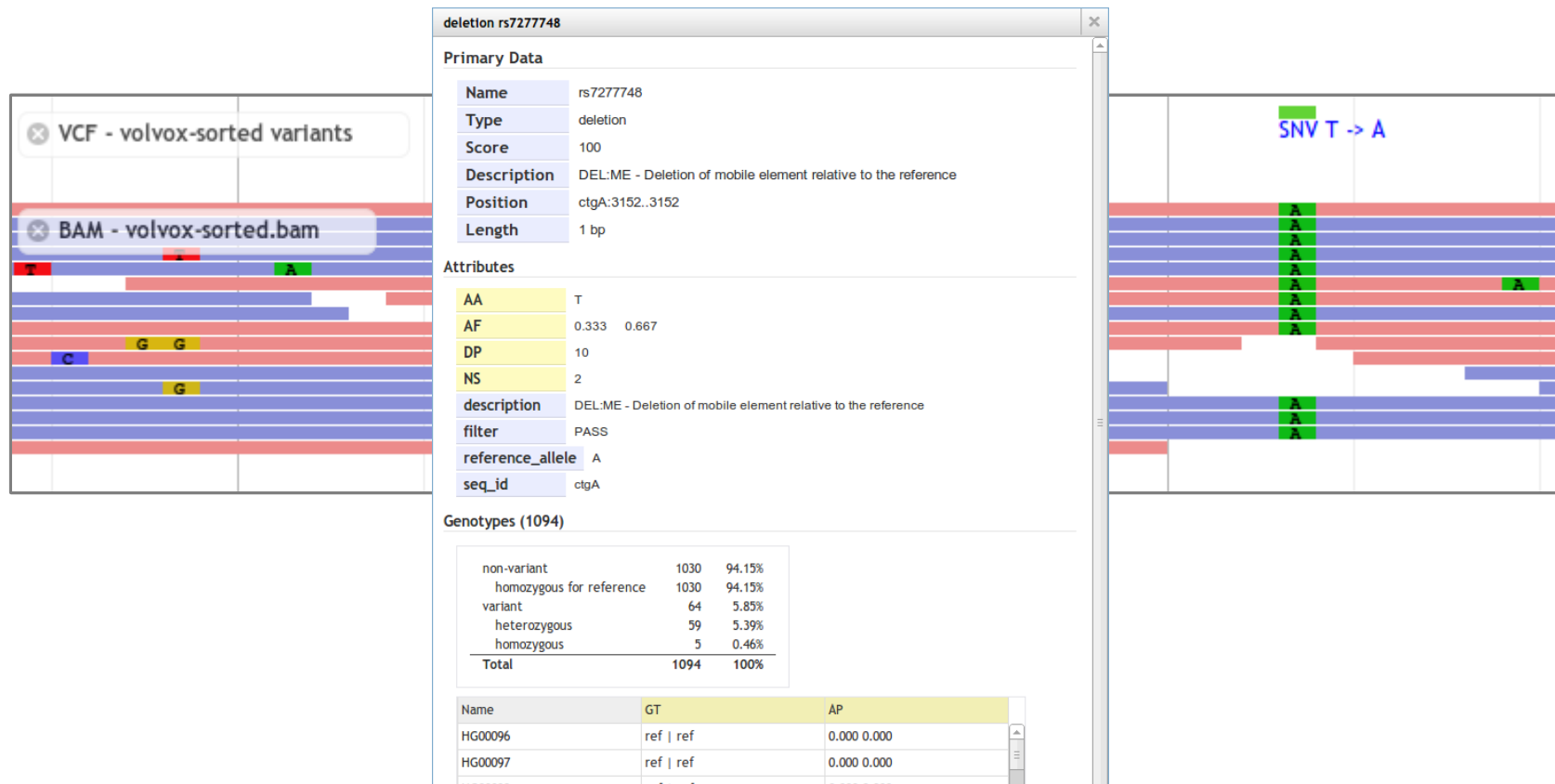
<http://goo.gl/XSVN2>



- Reads small chunks directly from BAM file.
- Coverage and mismatches.

# VCF Tracks

- Reads directly from VCF files compressed and indexed with `bgzip` and `tabix`.
- Shows all VCF data: alleles, genotypes, quality, etc.



# ++ Particular Strengths ++

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

# ++ Particular Strengths ++

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

# Faceted Track Selection

- make a CSV file of as much track metadata, and/or put track metadata in JSON config files

[http://jbrowse.org/code/JBrowse-1.4.0-full/index.html?data=sample\\_data/json/modencode](http://jbrowse.org/code/JBrowse-1.4.0-full/index.html?data=sample_data/json/modencode)

The screenshot shows the 'Select Tracks' interface in a web browser. The browser title is 'ctgA:20002..30055 - Google Chrome'. The address bar shows the URL: [jbrowse.org/code/JBrowse-1.4.0-full/index.html?data=sample\\_data/json/modencode](http://jbrowse.org/code/JBrowse-1.4.0-full/index.html?data=sample_data/json/modencode). The interface has a blue header with 'Select Tracks' and 'Help' (50). Below the header, there are controls: 'My Tracks', 'Back to browser', 'Clear All Filters', and a search box containing 'dauer' with '5 matching tracks'. The main area is a table with columns: Name, Organism, Technique, Target, Factor, Conditions, Principal investigator, and Submission ID. The table lists several tracks, with one track selected (checked). The selected track is: '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' for 'C. elegans' using 'integrated-gene-model' technique, targeting 'mRNA' as a 'total-RNA' factor, under conditions 'Dauer exit daf-2(e1370) 91 hrs 15dC 12 hrs post-L1 stage larvae', by 'Waterston, R.', with submission ID '2950'. Other tracks are listed but not selected.

Name	Organism	Technique	Target	Factor	Conditions	Principal investigator	Submission ID
<input type="checkbox"/> 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
<input checked="" type="checkbox"/> 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
<input type="checkbox"/> 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
<input type="checkbox"/> 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



# Open Local Files

- Select multiple files
- Paste multiple URLs
- Blurring the line between “desktop” and “web”

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

Open immediately  Add to tracks

✗ Cancel Open

# Integrating JBrowse

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

# WebApollo

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

- based on JBrowse, using plugin system
- next generation of the popular Apollo annotation editor
- online annotation editing and curation!



# WebApollo

- clients receive updates in real time (like Google Docs)
- saves edits to a central Chado database
- client side is a **JBrowse plugin**
- extensive server-side Java

¡Maybe Live Demo!

<http://genomearchitect.org/WebApolloDemo/>



# 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 at all.
- WebApollo client is a JBrowse plugin

# Coming Soon

- **More:** data types, sorting options, speed
- Graphical configuration
- Tiled, linked views
- Data uploading, track sharing
- Circular genome support

# 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)

# Robert Buels

[rbuels@gmail.com](mailto: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

# Releases

## 1.3.0 – April 13

Rubberbanding, y-axis scales, embedded mode, many other small fixes

## 1.4.0 – June 14

Faceted track selector, name autocompletion

## 1.5.0 – August 13

Direct BigWig, wiggle XY plot tracks, detail popups, context menus

## 1.6.0 – August 25

Feature descriptions, bugfixes for GMOD summer school

## 1.7.0 – November 5

Direct BAM, alignment tracks, data export, coverage tracks, wiggle density

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2012

2013

## 1.8.0 – January 31

Open local BAM, BigWig, and GFF3 files, faster BAM.

## 1.9.0 – April 1

**today**

Direct VCF, faster BAM, more configurability, wiggle track autoscaling

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## 2.0.0 – June 2013?

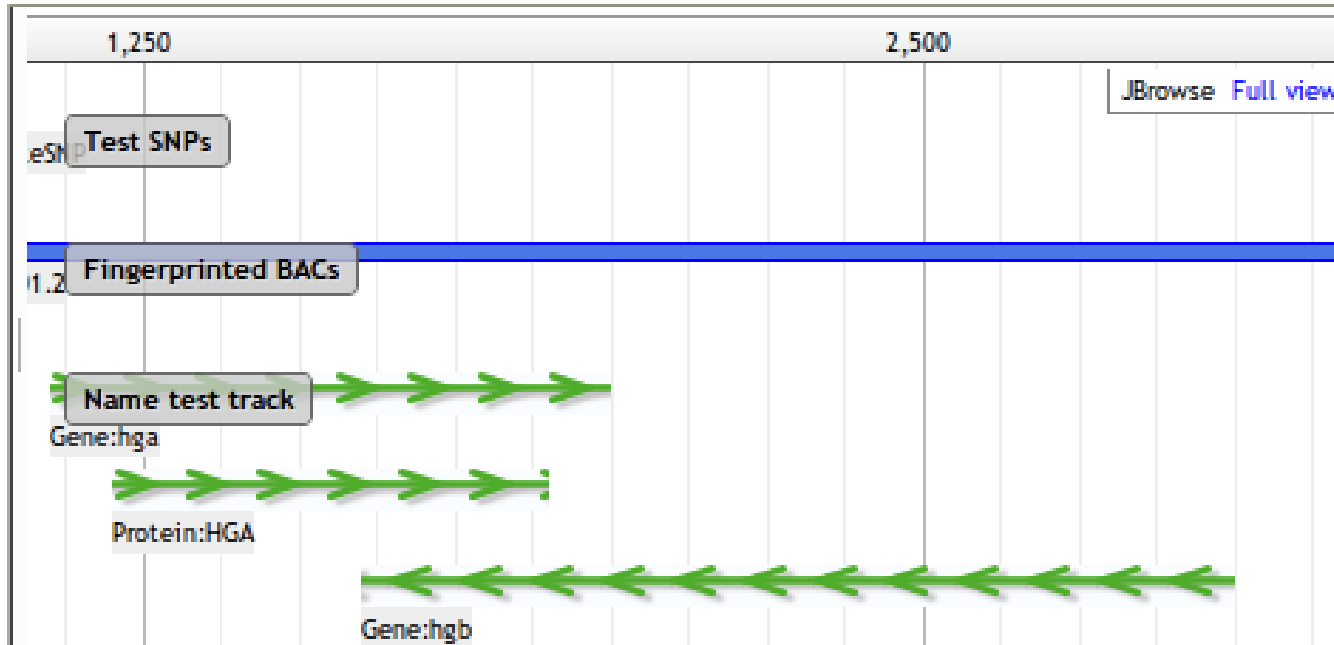
Graphical configuration, multiple independent views, more GBrowse compatibility.

# FeatureTrack Hooks

```
"hooks": {
  "modify": "function(track, feat, elem) {
    var fType = feat.get('Type');
    if (fType) {
      elem.className = 'basic';
      switch (fType) {
        case 'CDS':
        case 'thick':
          elem.style.height = "10px";
          elem.style.marginTop = '-3px';
          break;
        case "UTR":
        case "thin":
          elem.style.height = '6px';
          elem.style.marginTop = '-1px';
          break;
      }
      elem.style.backgroundColor = 'red';
    }
  }"
```

have to edit data/trackList.json to use these >:-{

# Embedded Mode



**Julie Moon, OICR co-op student**

```
http://localhost/jbrowse/index.html  
?loc=ctgA:1386..6057  
&tracks=<list of tracks>  
&data=sample_data/json/volvox  
&nav=0  
&overview=0  
&tracklist=0
```

# Publish / Subscribe Example

- JBrowse publishes

```
/jbrowse/v1/v/region/highlighted chrI:12345..67890
```

- Some **other code** has subscribed to this, and
  - calls a web service to launch an analysis on that region
  - pops up a notification saying it has done so
- When the analysis is done, it publishes

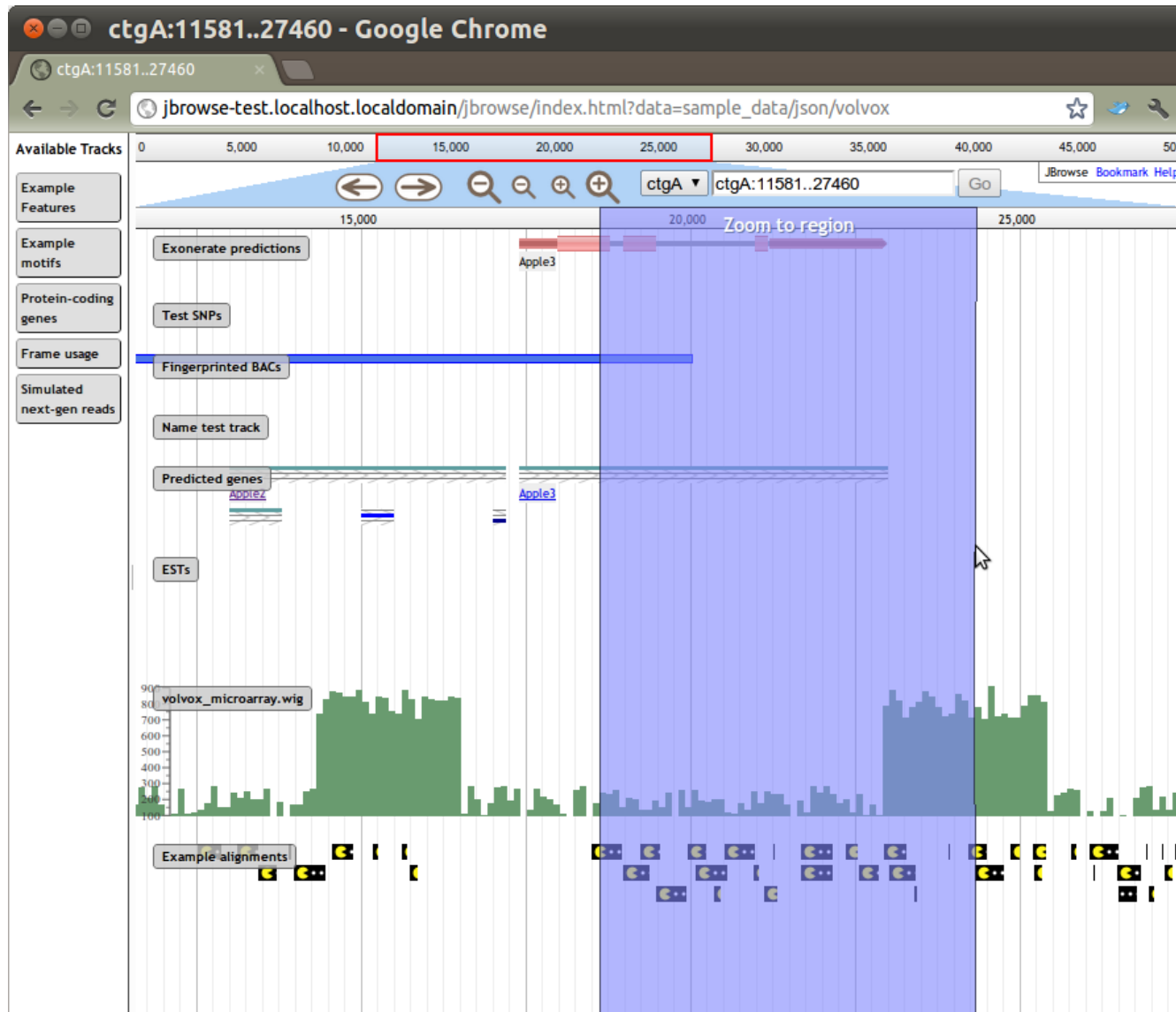
```
/jbrowse/v1/c/track/add {track config JSON}
```

- Track with the analysis results appears in the browser!

# Pre-Compression

- gzips static data files on disk
- shrinks data directories by **about 60%**
  - takes GRCh37 from 19GB to 7.6GB.
- needs some webserver configuration for headers
  - Apache: AllowOverride FileInfo (.htaccess files)
  - nginx: add a smallish config snippet

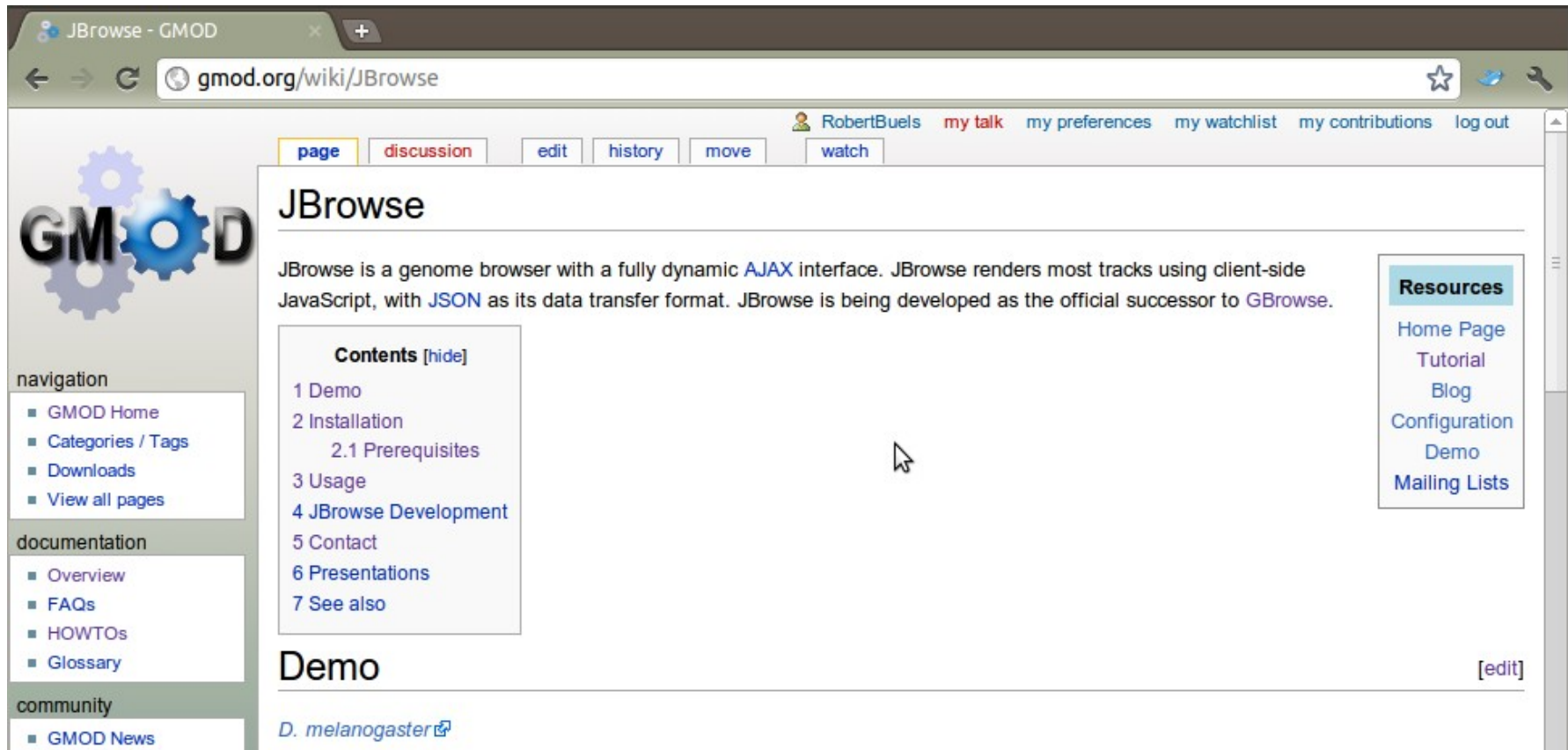
# Rubber-band Zooming





# JBrowse Documentation

The GMOD wiki is the documentation hub  
<http://gmod.org/wiki/JBrowse>



The screenshot shows a web browser window with the address bar displaying `gmod.org/wiki/JBrowse`. The page title is "JBrowse" and the user is logged in as "RobertBuels". The page content includes a description of JBrowse as a genome browser with a fully dynamic AJAX interface, rendered using client-side JavaScript and JSON. A table of contents is visible, listing sections from 1 Demo to 7 See also. The page also features a navigation sidebar on the left and a resources sidebar on the right.

JBrowse - GMOD

gmod.org/wiki/JBrowse

RobertBuels my talk my preferences my watchlist my contributions log out

page discussion edit history move watch

## JBrowse

JBrowse is a genome browser with a fully dynamic [AJAX](#) interface. JBrowse renders most tracks using client-side JavaScript, with [JSON](#) as its data transfer format. JBrowse is being developed as the official successor to [GBrowse](#).

**Contents** [hide]

- 1 Demo
- 2 Installation
  - 2.1 Prerequisites
- 3 Usage
- 4 JBrowse Development
- 5 Contact
- 6 Presentations
- 7 See also

## Demo

[D. melanogaster](#)

[edit]

**Resources**

- Home Page
- Tutorial
- Blog
- Configuration
- Demo
- Mailing Lists

**navigation**

- GMOD Home
- Categories / Tags
- Downloads
- View all pages

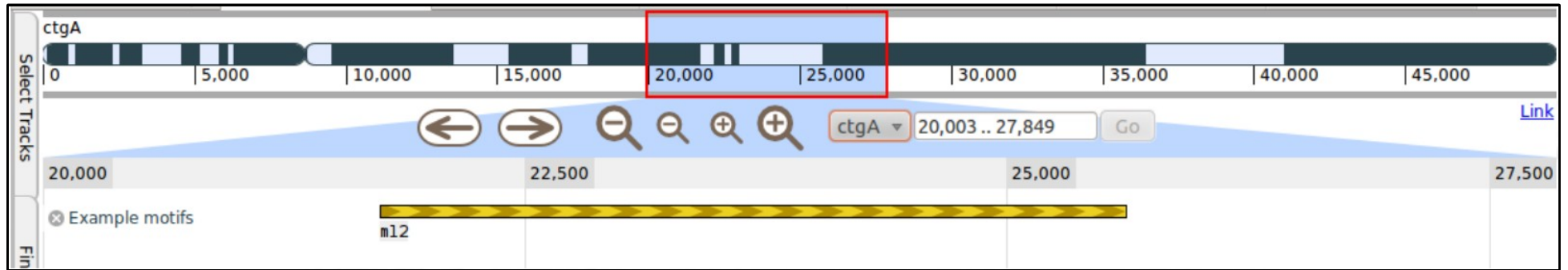
**documentation**

- Overview
- FAQs
- HOWTOs
- Glossary

**community**

- GMOD News

# Coming: Overview Images



Can have a karyotype, or any other image.

# Migrating: GBrowse to JBrowse

- JBrowse does not yet have all the features of GBrowse
- Configuration and data formats are different
- Adam Wright, intern at OICR, has worked on automated migration tools to help
- Another thing I need to merge into master ;-)

