

JBrowse – 1.10.0 and beyond

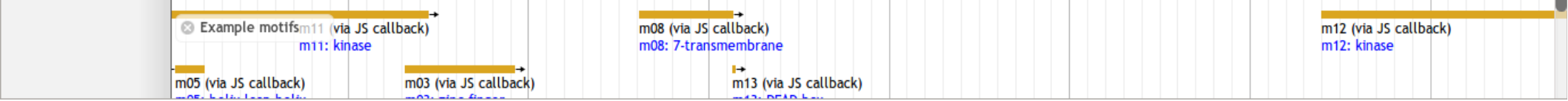
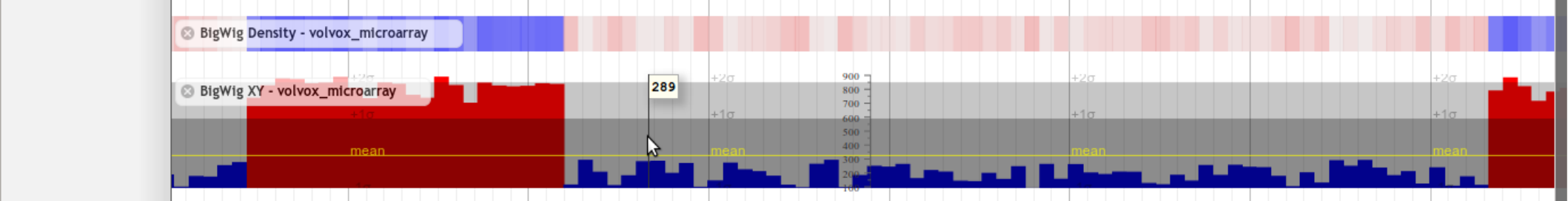
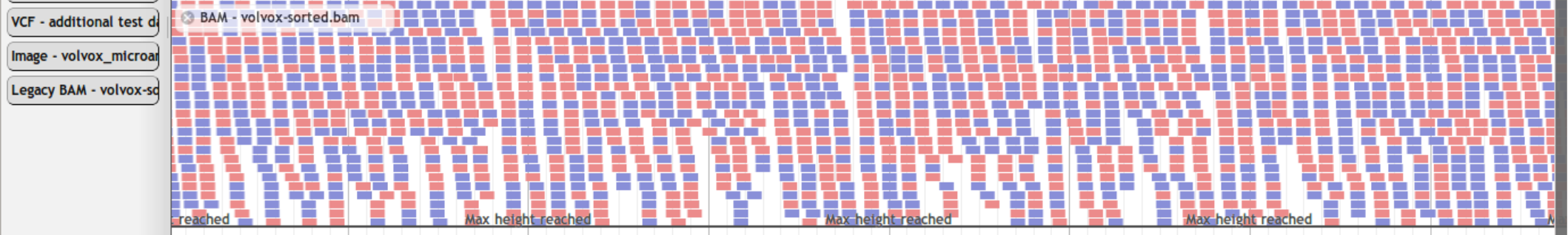
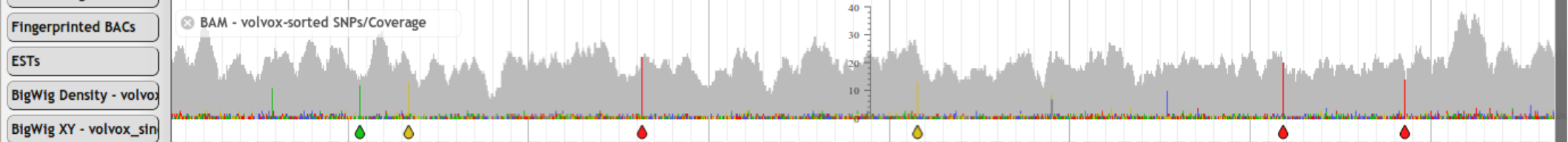
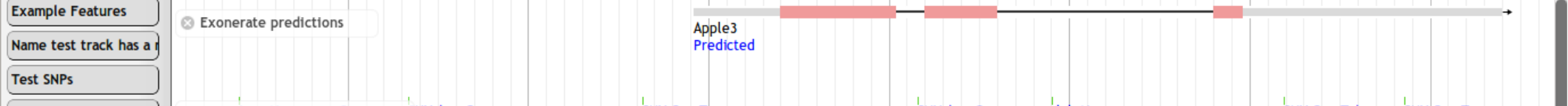
Robert Buels
GMOD Summer School 2013
July 21, 2013



University of California, Berkeley

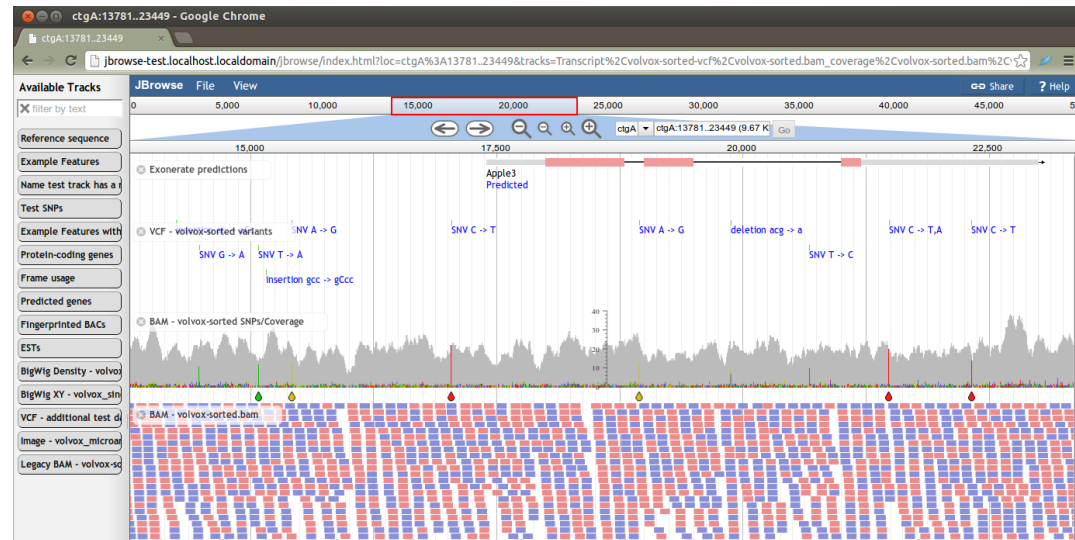


(JBrowse 1.10.0 will be released Any Day Now)



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.

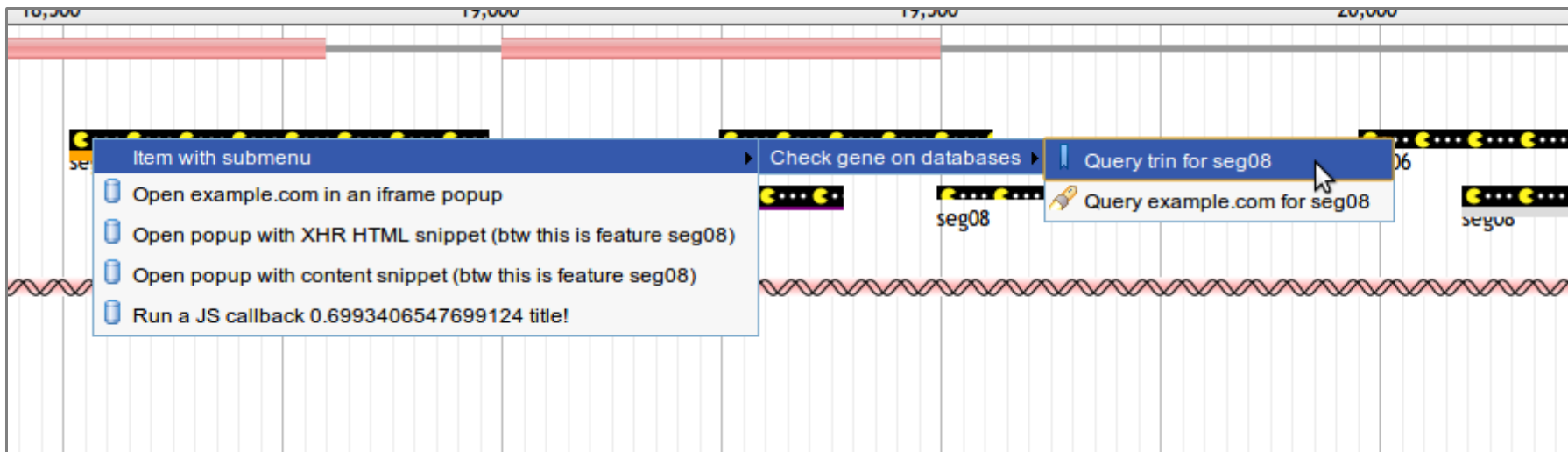
The JBrowse Project

- 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



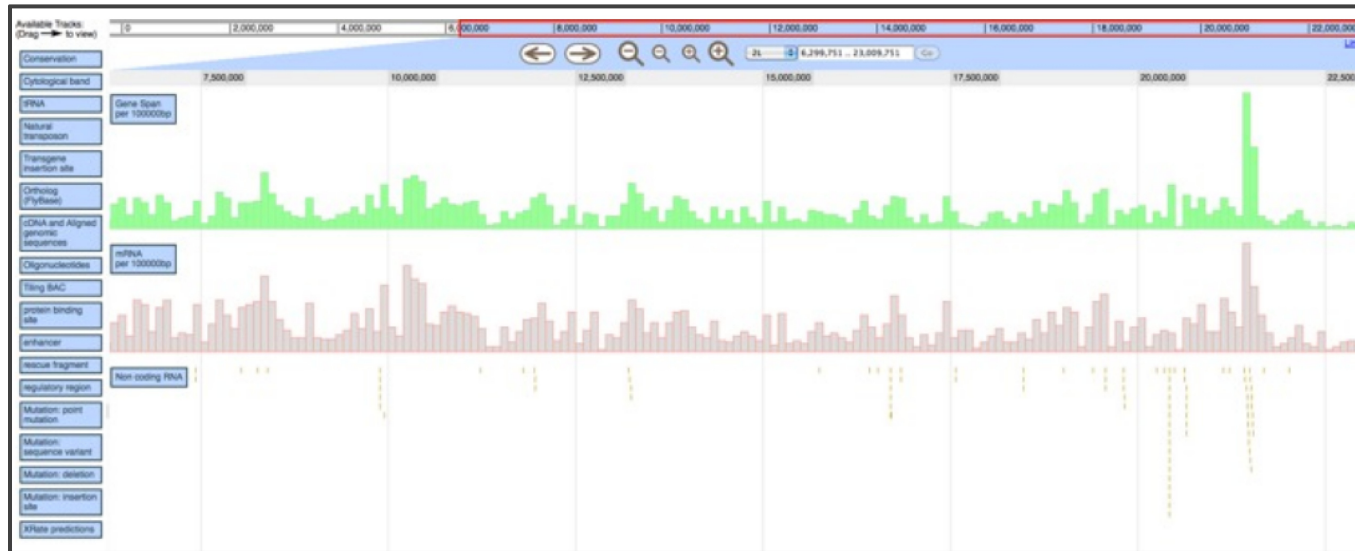
Feature Tracks

- 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

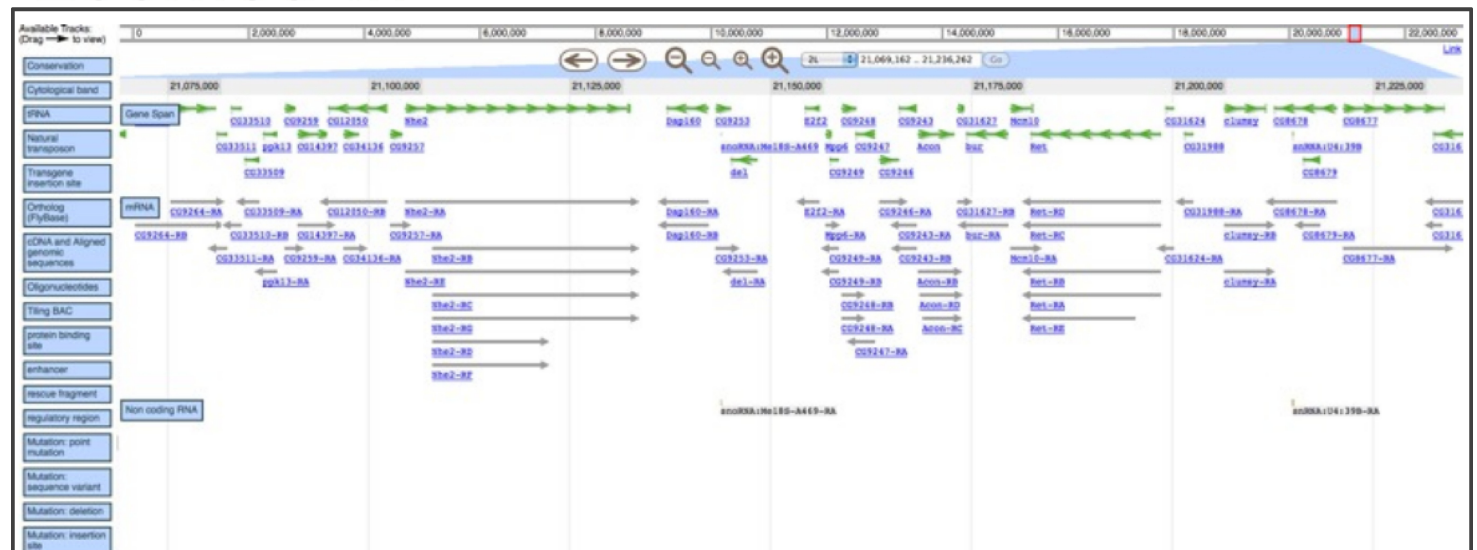
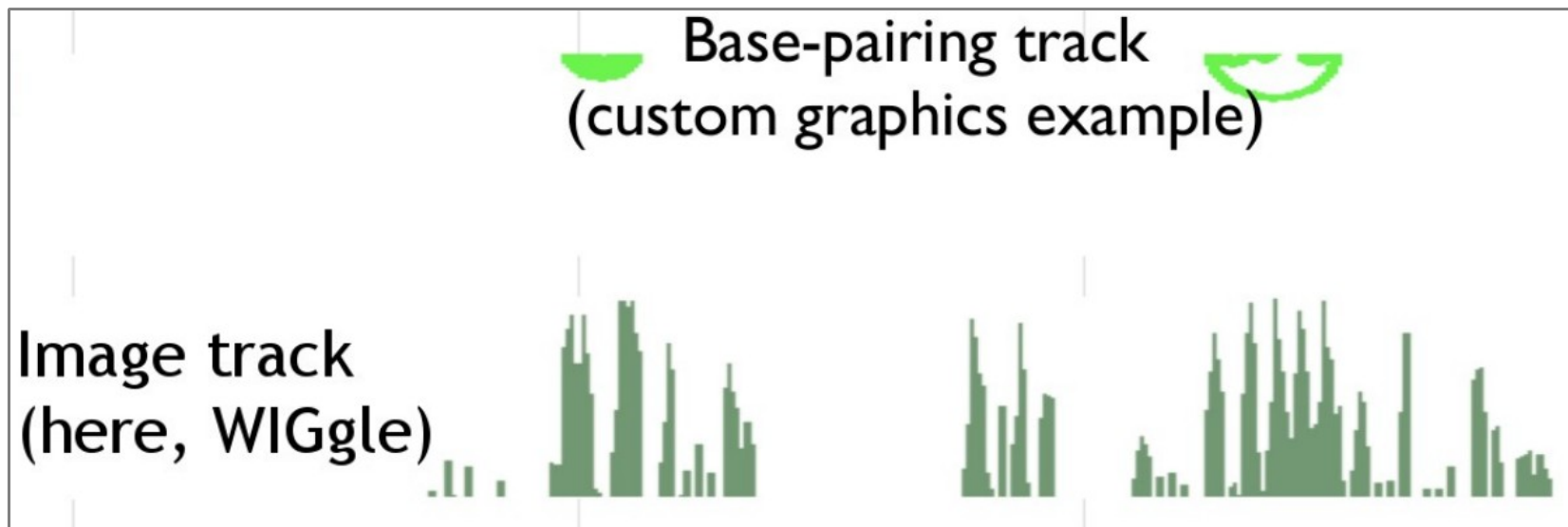


Image Tracks

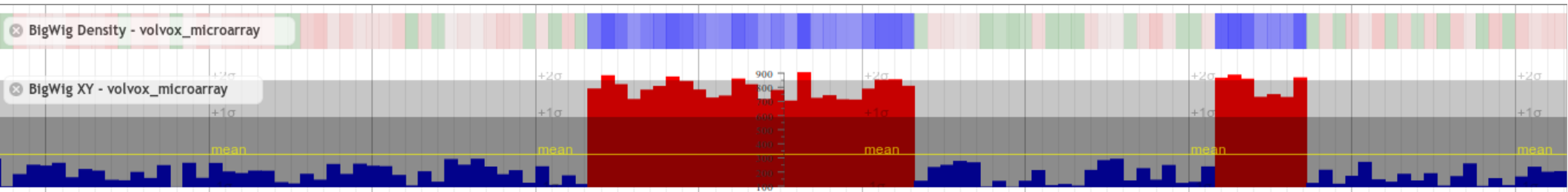
- any pre-generated images that cover the genome
 - RNA base-pairing
 - Images from other genome browsers
 - Legacy JBrowse .wig formatter used this also



Wiggle/BigWig Tracks

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

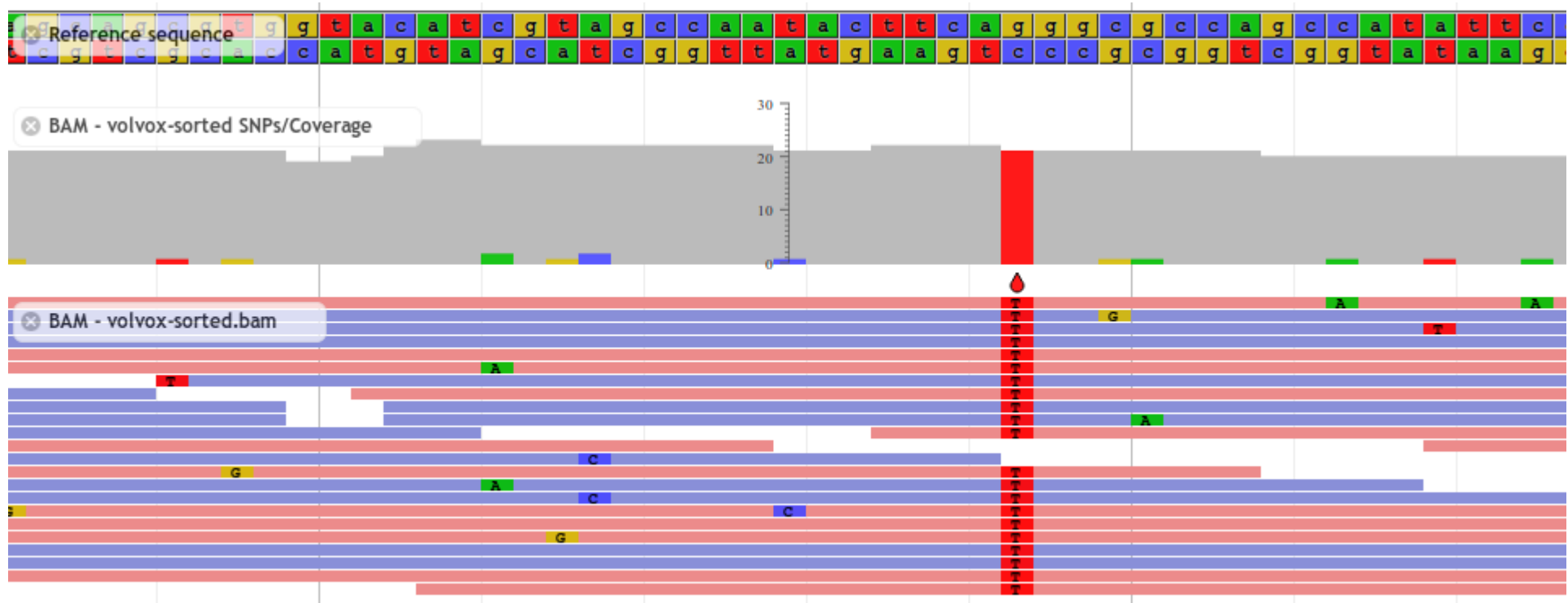
<http://jbrowse.org/genomes/tomato/>



- 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

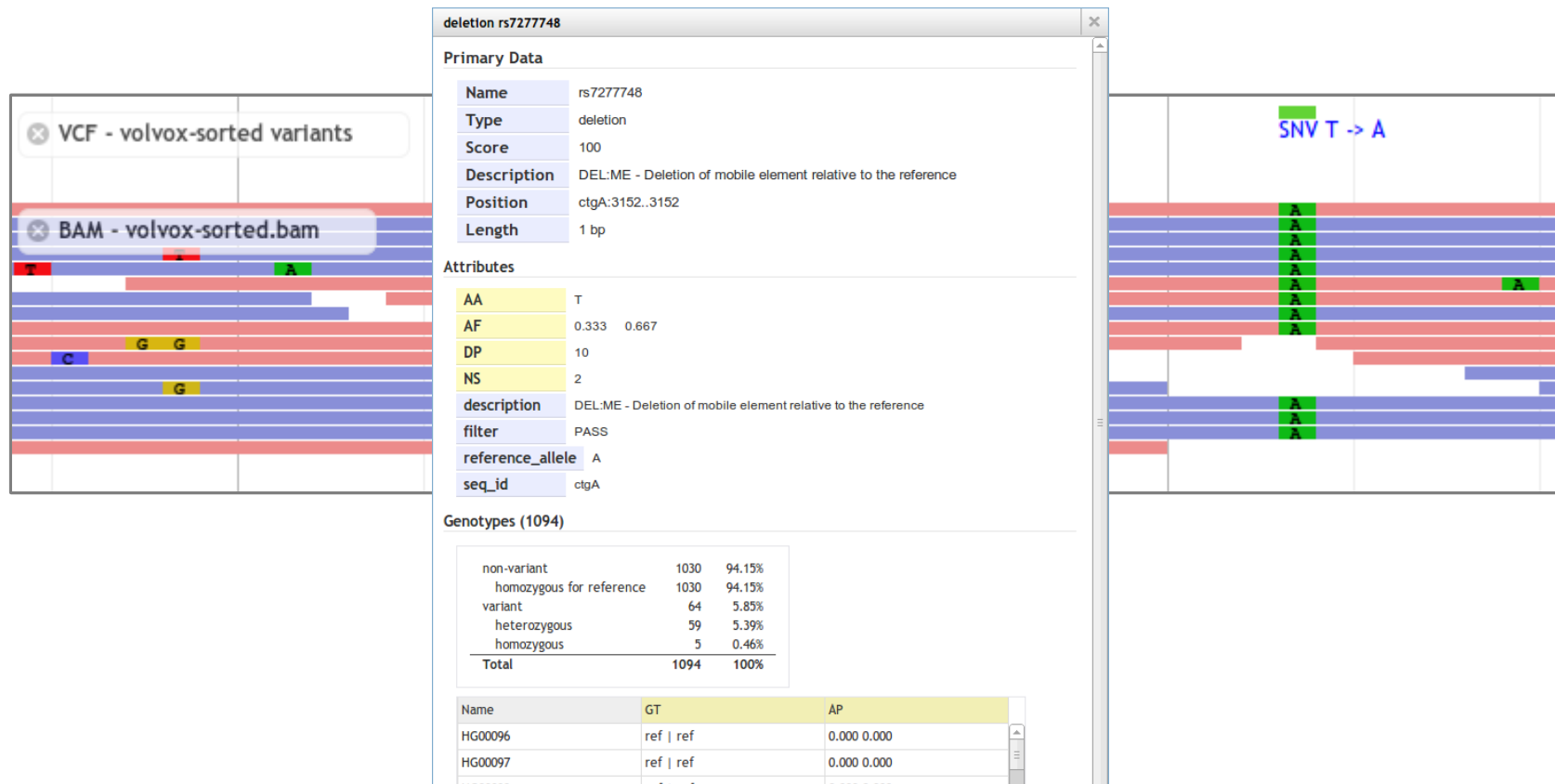
<http://goo.gl/XSVN2>



- 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

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. The interface has a blue header with 'Select Tracks' and 'Help' buttons. Below the header, there are navigation buttons: 'Back to browser', 'Clear All Filters', and a search box containing 'dauer' with a red 'X' icon and the text '5 matching tracks'. The main content 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' from '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'. On the left, there are faceted filters for 'Conditions', 'Organism', 'Principal investigator', and 'Target'. The 'Conditions' filter is expanded, showing a list of conditions with checkboxes. The 'Organism' filter is also expanded, showing 'C. elegans' as the selected option.

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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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	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

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 in 2.x Series

- **MORE:** data types, sorting options, speed
- Graphical configuration
- Multiple views, linked or independent
- Logins, uploading, track sharing
- Circular genomes

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

Justin Reese



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

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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

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

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

2.0.0 – September 2013?

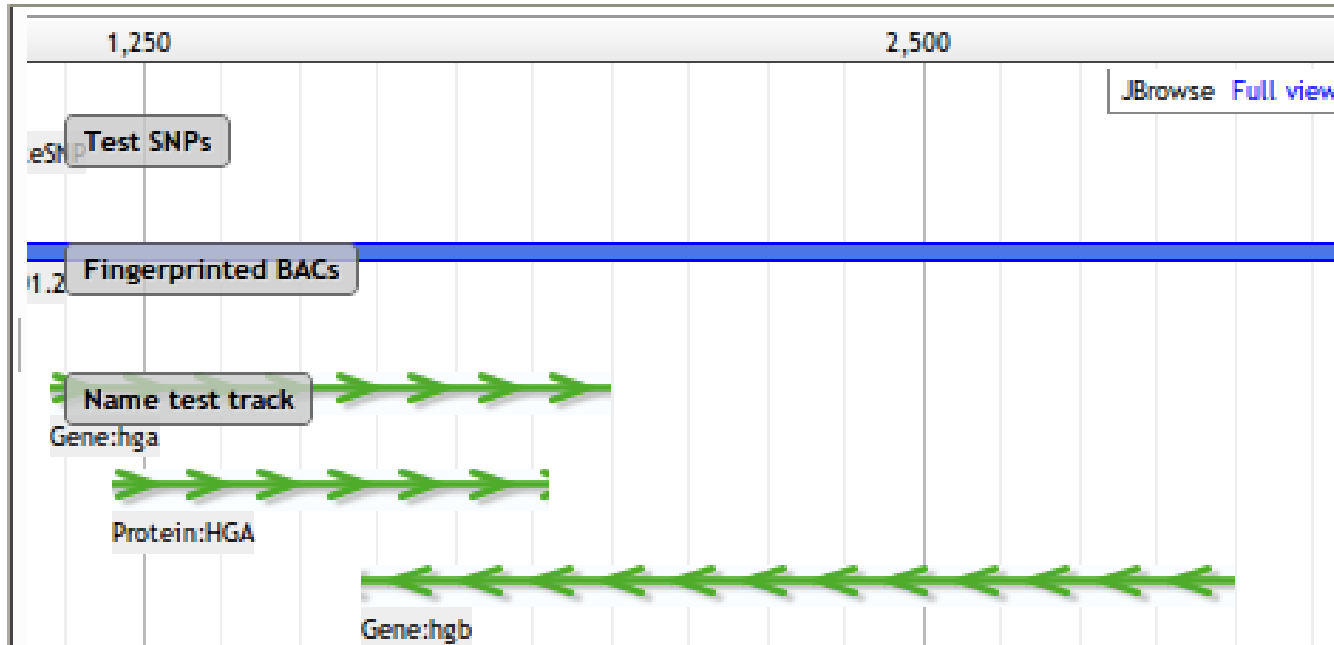
Graphical configuration, multiple independent views, more GBrowse compatibility.

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

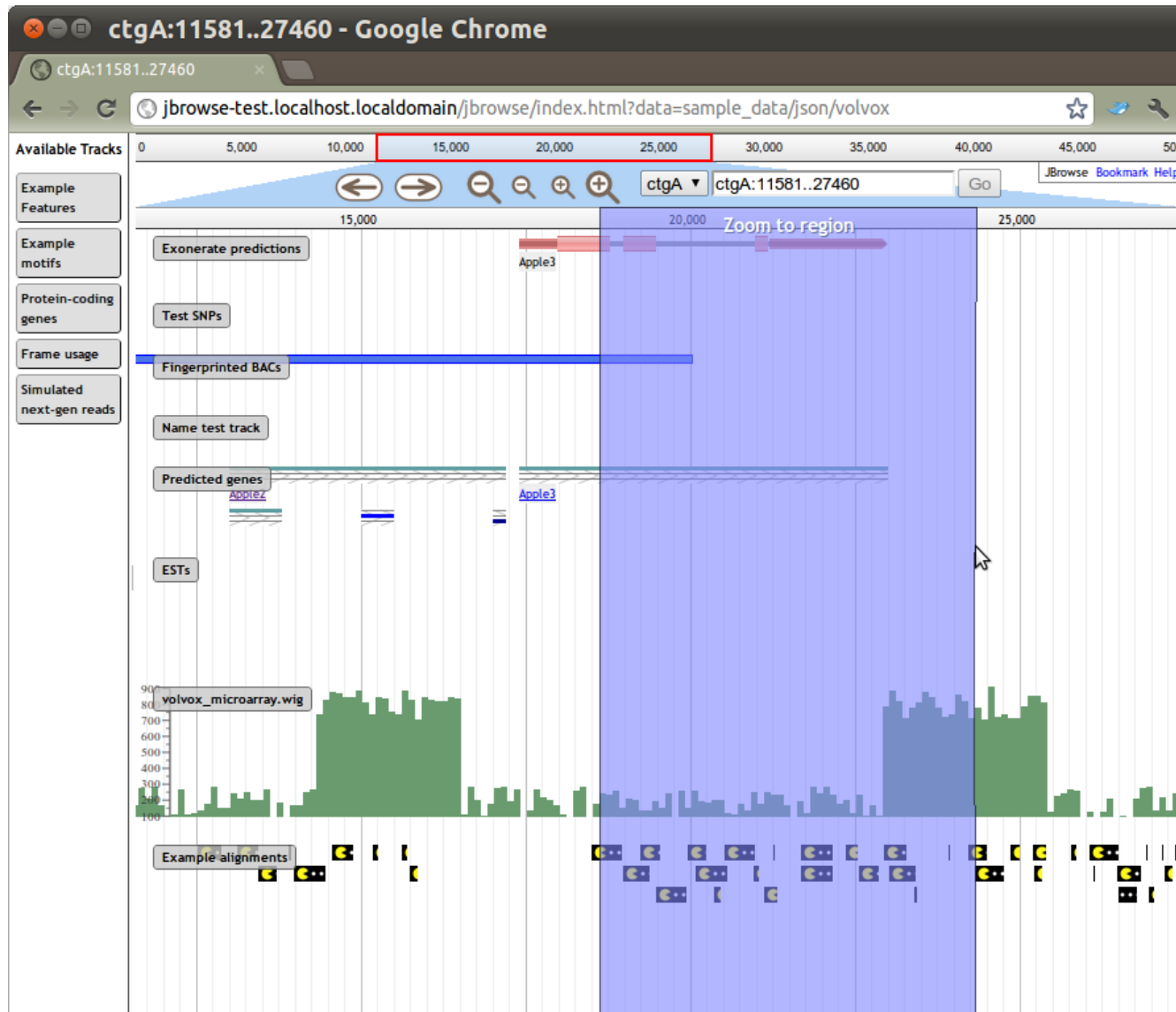
```
/jbrowse/v1/c/track/add {track config JSON}
```

- Track with the analysis results appears in the browser!

Pre-Compression

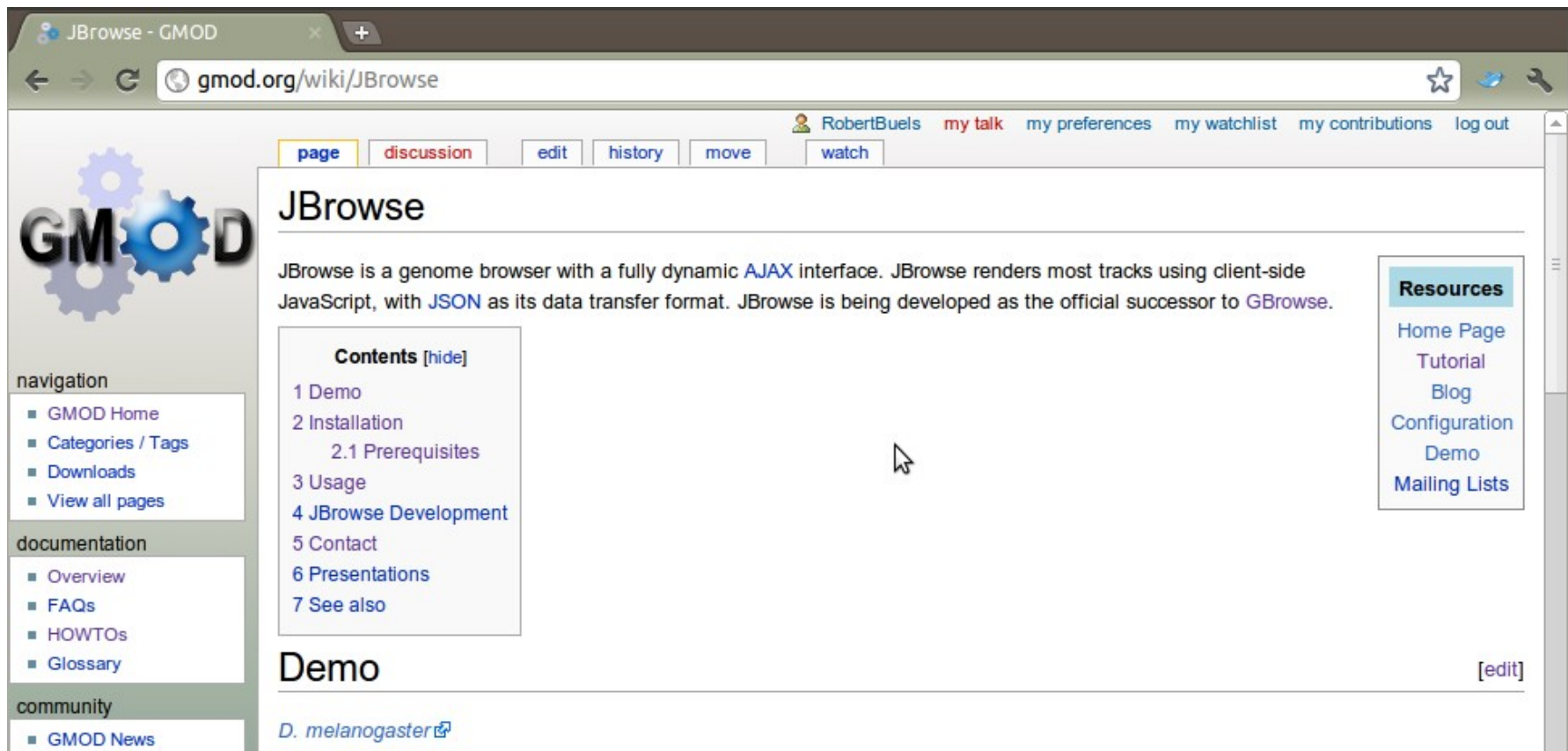
- gzips static data files on disk
- shrinks data directories by **about 60%**
 - takes GRCh37 from 19GB to 7.6GB.
- needs some webserver configuration for headers
 - Apache: AllowOverride FileInfo (.htaccess files)
 - nginx: add a smallish config snippet

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 with links to GMOD Home, Categories / Tags, Downloads, and View all pages, and a Resources sidebar on the right with links to Home Page, Tutorial, Blog, Configuration, Demo, and Mailing Lists. The page is titled "JBrowse" and has a sub-header "Demo" with an [edit] link.

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 [edit]

[D. melanogaster](#)

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

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, did some preliminary work on tools to assist.
- Much work still to be done.





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