

JBrowse – 1.9.0 and beyond

Gregg Helt
(channeling Robert Buels)
GMOD April 2013 Meeting
April 5, 2013



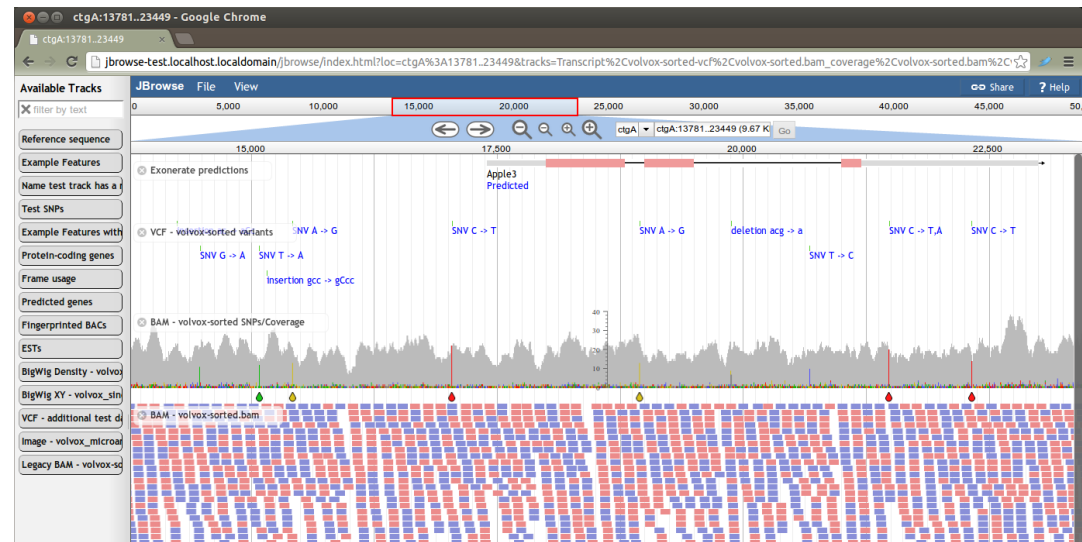
Lawrence Berkeley National Laboratory
Joint Genome Institute
(University of California, Berkeley)



(JBrowse 1.9.0 is coming Any Day Now)

JBrowse

- Do everything possible on the client side, in JavaScript.
- **Fast**, smooth navigation (*think Google Maps for genomes*).
- Supports BED, GFF, Bio::DB::*, Chado, WIG, BAM, BigWig, VCF, and UCSC import (*intron/exon structure, name lookups, quantitative plots*).
- Is stably funded by NHGRI, many interesting innovations implemented and/or pending integration.
- 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.

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

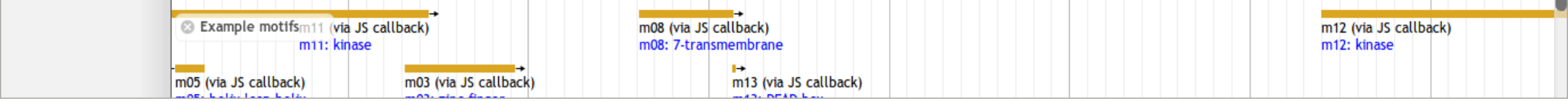
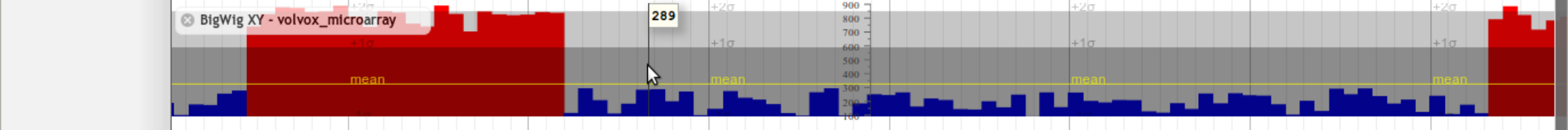
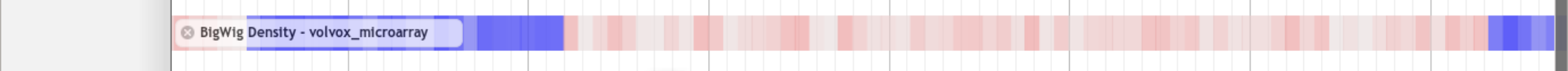
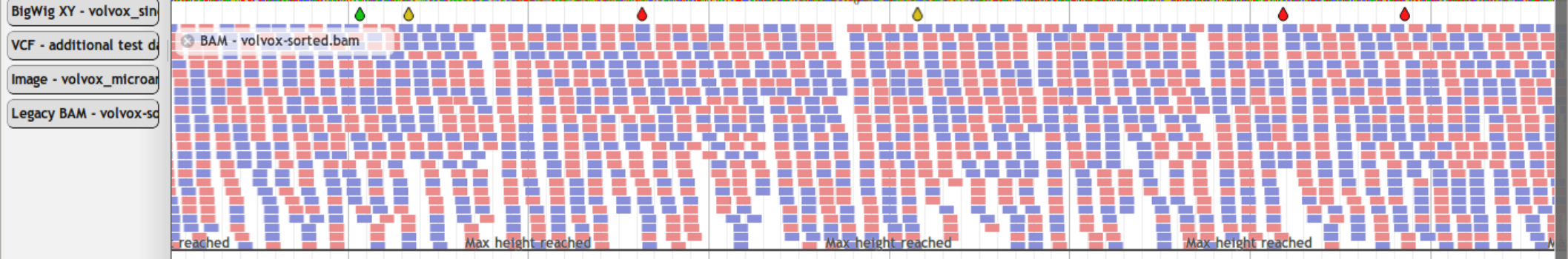
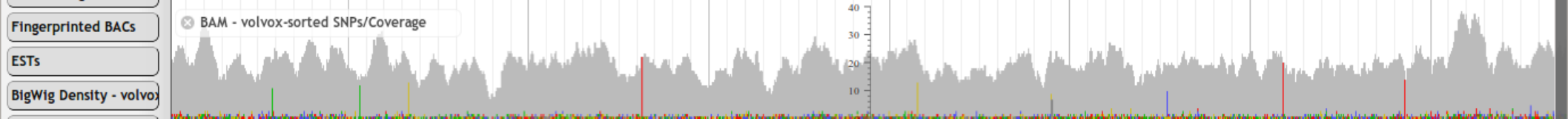
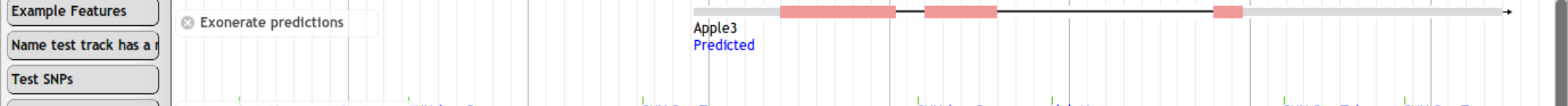
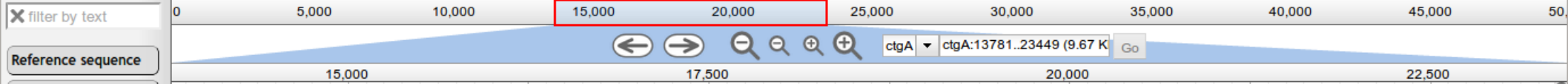
The JBrowse Project

- 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

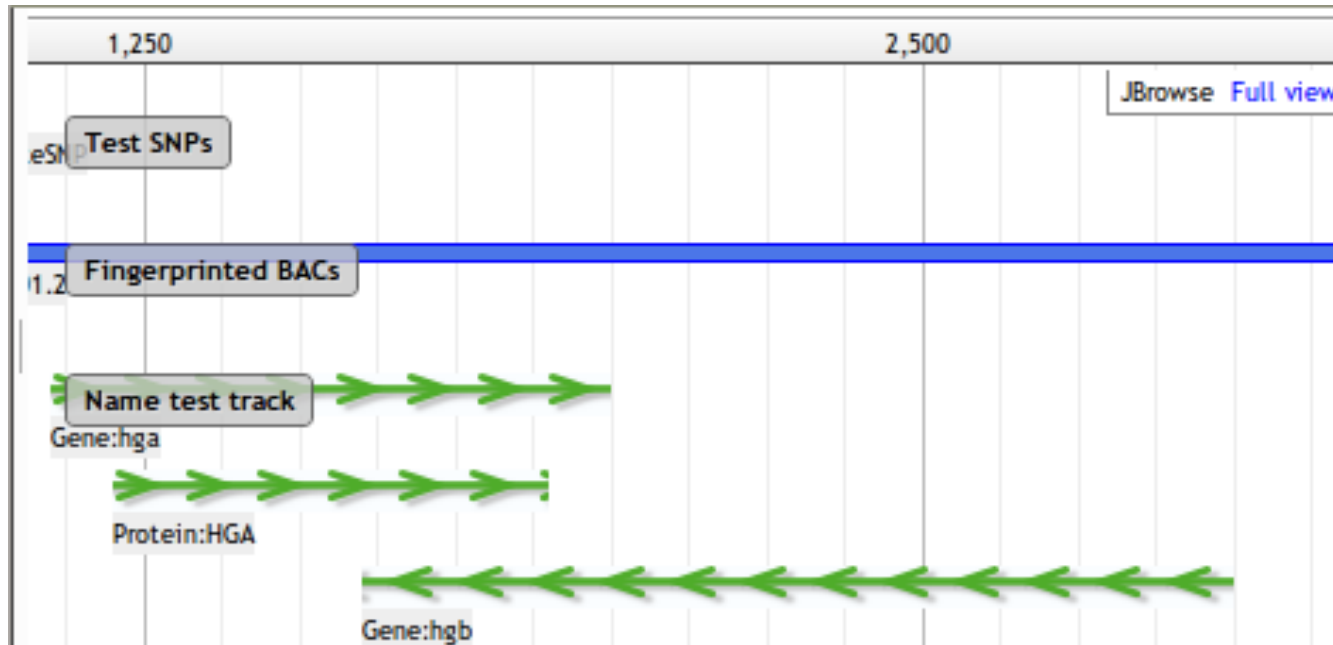


++ Particular Strengths ++

- Web-based, but still fast, smooth, scalable
- easy to set up
- compressed NGS data: direct-to-browser BAM, BigWig, and VCF
- optional faceted track selector - efficiently search thousands of tracks
- open local files directly on client, no data transfer required
- highly customizable



Embedded Mode

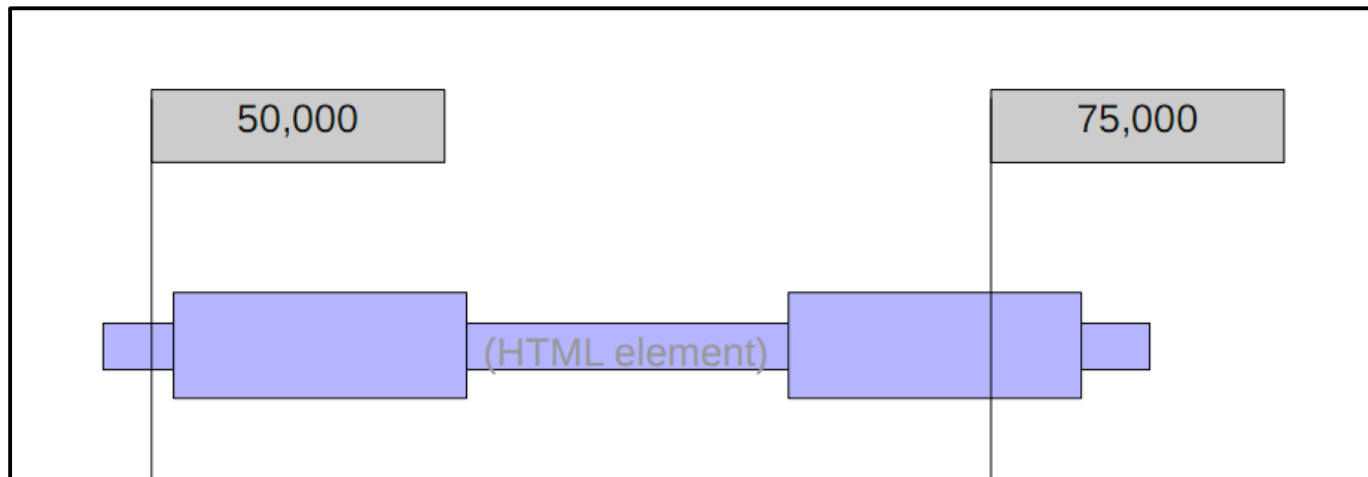


Julie Moon, OICR co-op student

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

HTML Feature Tracks

- rectangles (<div>s) with various fills and dimensions to represent the features
- surprisingly versatile



Feature Density Plots

Zoomed out



Zoomed in

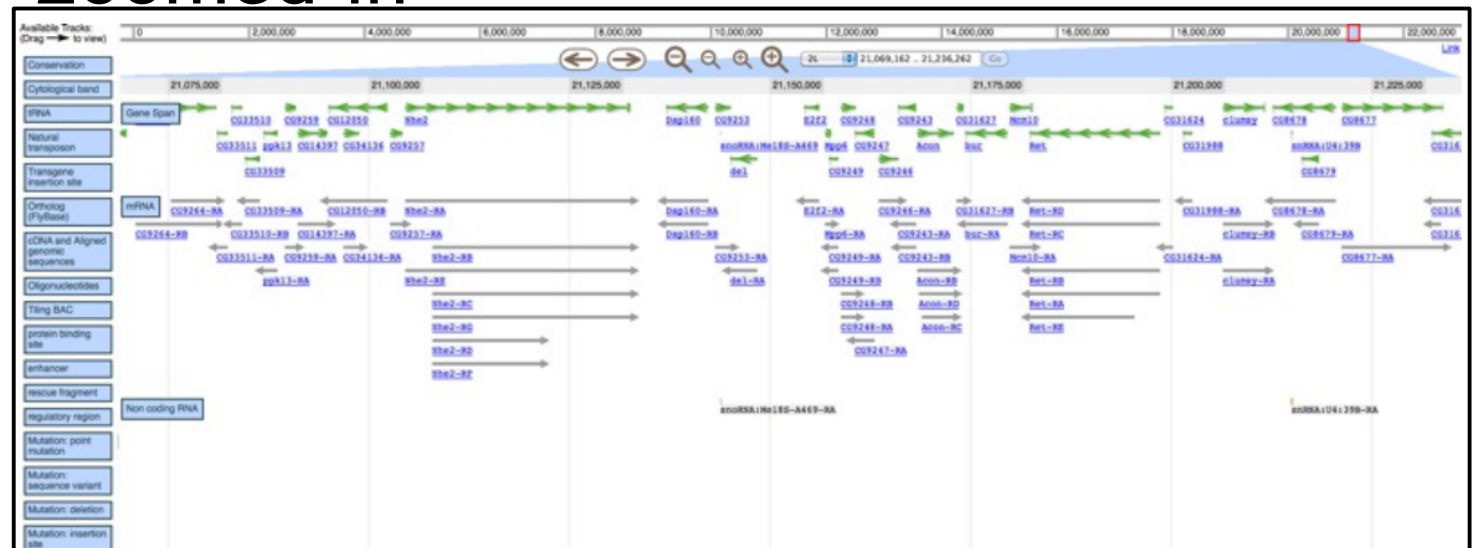
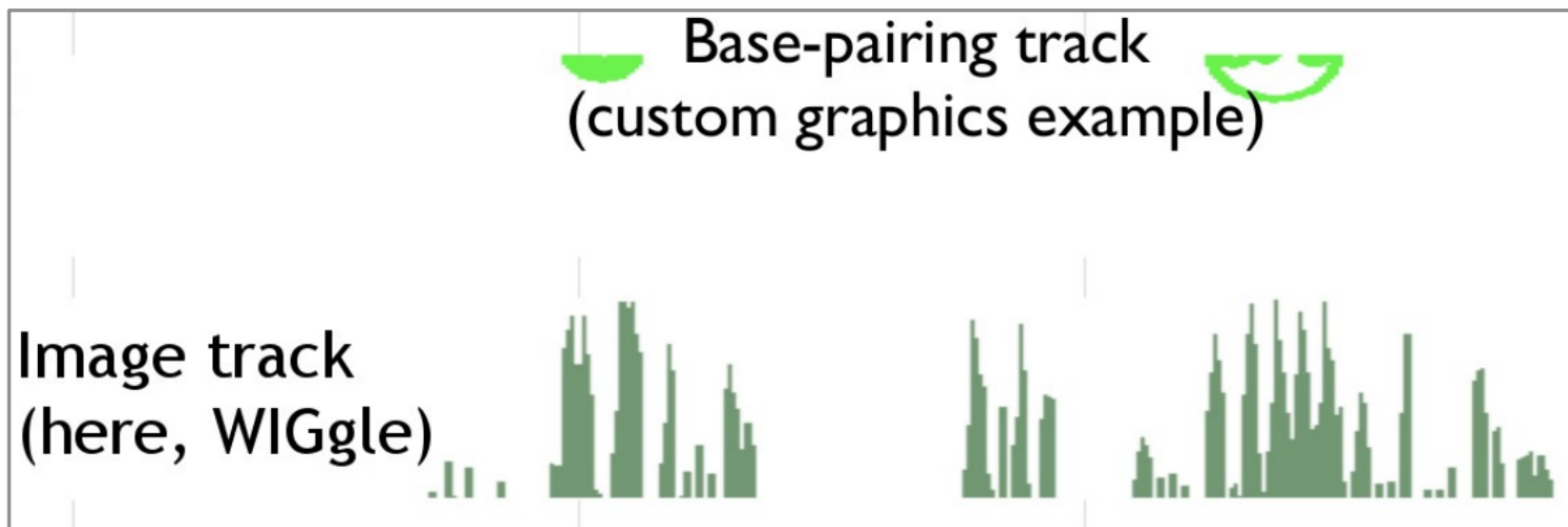


Image Tracks

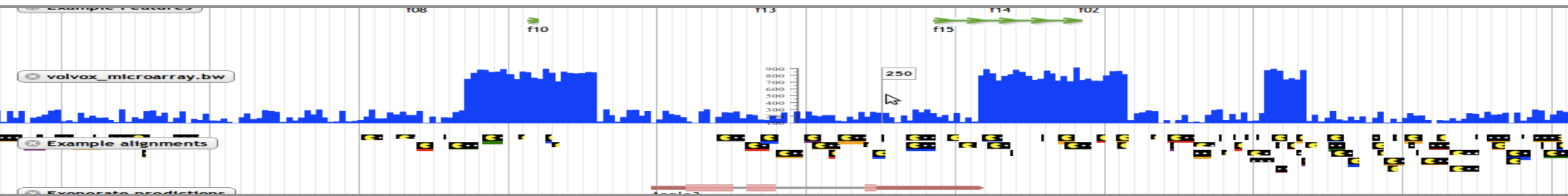
- any pre-generated images that cover the genome
 - RNA base-pairing
 - Images from other genome browsers
 - Legacy JBrowse .wig formatter used this also



Wiggle/BigWig Tracks

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

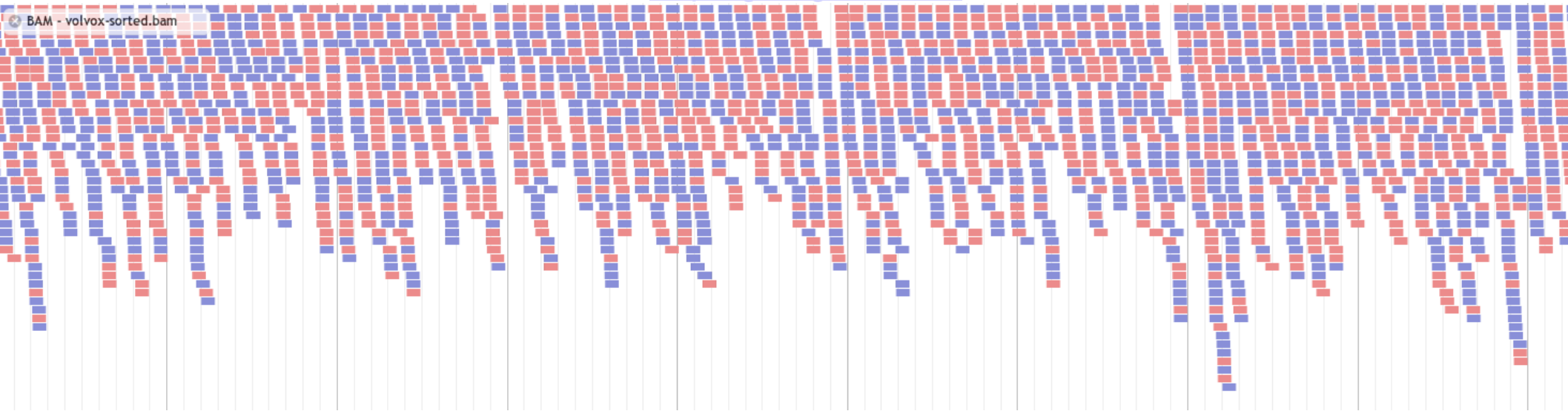
<http://jbrowse.org/genomes/tomato/>



- Very efficient; reads small chunks directly from BigWig file on the web.
- Needs only a recent-ish (4-year-old) browser, except for Internet Explorer.
- IE is years behind the curve, so requires latest version 10.

BAM Alignment Tracks

<http://goo.gl/XSVN2>



- Very efficient, reads small chunks directly from BAM file on the web.
- Again, browser support very good except for IE, which requires version 10.

VCF Tracks

- Reads directly from VCF files compressed and indexed with bgzip and tabix.
- Displays all VCF data, with descriptions.

The image shows a genomic browser interface with two tracks on the left: 'VCF - volvox-sorted variants' and 'BAM - volvox-sorted.bam'. The BAM track displays sequencing reads with colored bases (red, blue, green, yellow). A central window titled 'SNV' provides detailed information for a variant. The variant is a single nucleotide polymorphism (SNV) at position ctgA:15078..15078, with a score of 96 and a description of 'SNV T -> A'. The window also lists various attributes such as AC1, AF1, DP, DP4, FQ, MQ, and VDB. A tooltip for DP4 explains it as the number of high-quality ref-forward bases, ref-reverse, alt-forward, and alt-reverse bases. At the bottom, the region sequence is shown as '>ctgA ctgA:15078..15078 class=SNV length=1' followed by the sequence 't'. On the right, another track shows a zoomed-in view of the variant with the label 'SNV T -> A'.

SNV

Primary Data

Type	SNV
Score	96
Description	SNV T -> A
Position	ctgA:15078..15078
Length	1 bp

Attributes

AC1	2
AF1	1
DP	12
DP4	0 0 4 8
FQ	# high-quality ref-forward bases, ref-reverse, alt-forward and alt-reverse bases
MQ	
VDB	0.0404

alternative_alleles A

description SNV T -> A

genotypes

sample_data/raw/volvox/volvox-sorted.bam	GQ	69
	GT	1/1
	PL	129 36 0

reference_allele T

seq_id ctgA

Region sequence

```
>ctgA ctgA:15078..15078 class=SNV length=1
t
```


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.
- Example: WebApollo (see next talk)

Coming Soon

- Graphical configuration
- Multiple independent views
- Track sharing
- Circular genome support

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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github

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(yes, jbrowse needs a logo)

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~~

1.8.0 – January 31

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

1.9.0 – April 1

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

2.0.0 – June 2013?

Graphical configuration, multiple independent views, more GBrowse compatibility.

2012
2013

today

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 >:-{

Publish / Subscribe Example

- JBrowse publishes

`/jbrowse/v1/v/region/highlighted chr1:12345..67890`

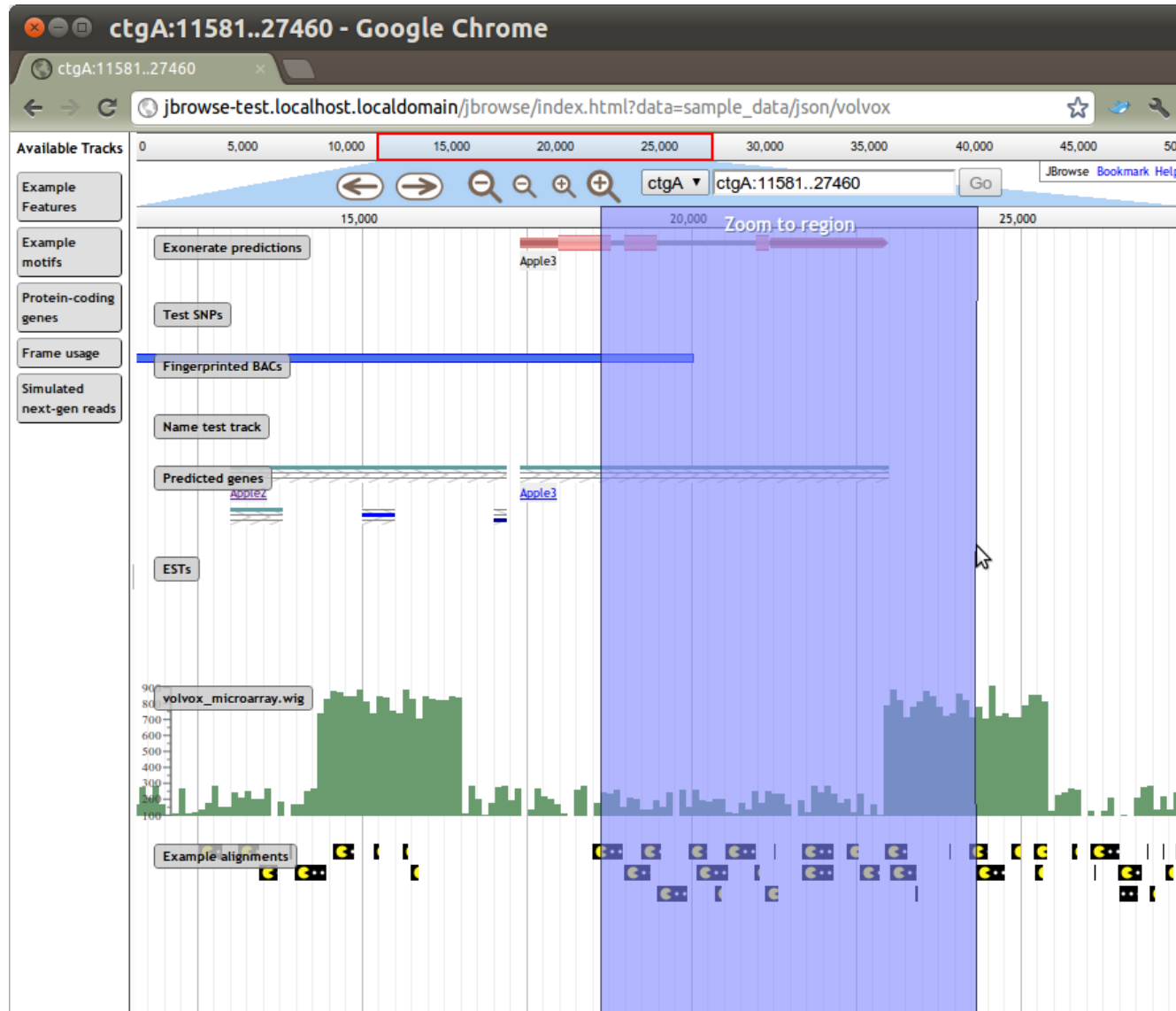
- Some **other code** has subscribed to this, and
 - calls a web service to launch an analysis on that region
 - pops up a notification saying it has done so
- When the analysis is done, it publishes

`/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

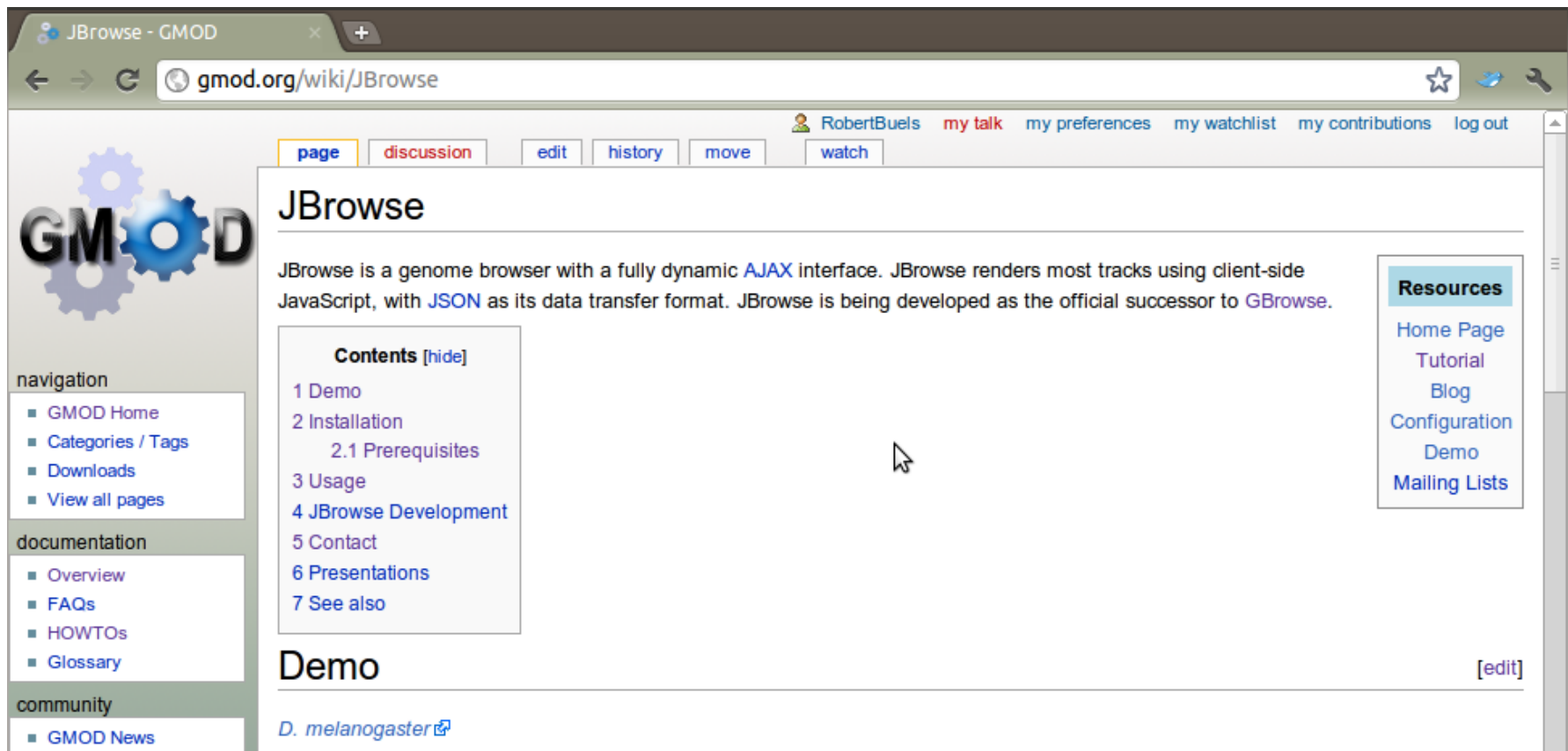
Rubber-band Zooming



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 navigation menu on the left, a main text area with a "Contents" table of contents, and a "Resources" sidebar on the right.

Navigation:

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

Documentation:

- Overview
- FAQs
- HOWTOs
- Glossary

Community:

- GMOD News

Page Actions: page, discussion, edit, history, move, watch

User Profile: RobertBuels, my talk, my preferences, my watchlist, my contributions, log out

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

Resources

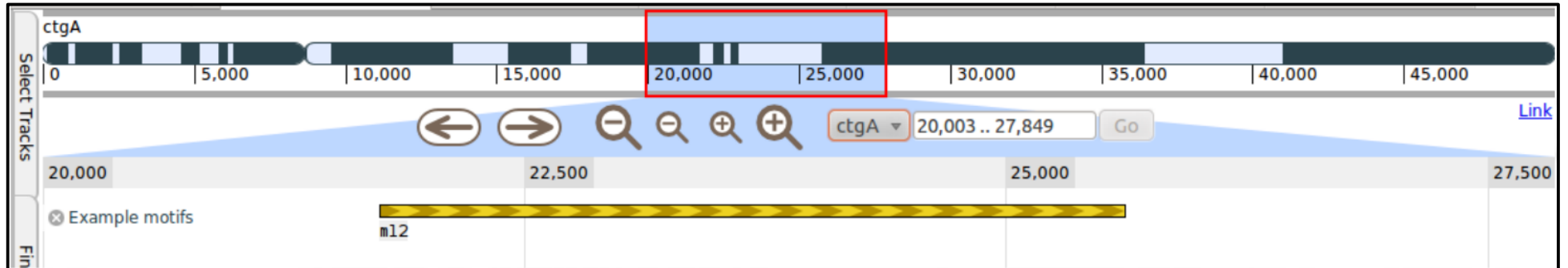
- Home Page
- Tutorial
- Blog
- Configuration
- Demo
- Mailing Lists

Demo

[D. melanogaster](#)

[edit]

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 ;-)



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

