JBrowse — 1.10.0 and beyond

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GMOD Summer School 2013

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University of California, Berkeley

(JBrowse 1.10.0 will be released Any Day Now)

ctgA:13781..23449 - Google Chrome
ctgA:13781..23449
jbrowse-test.localhost.localdomain/jbrowse/index.html?loc=ctgA%3A13781..23449&tracks=Transcript%2Cvolvox-sorted-vcf%2Cvolvox-sorted.bam_coverage%2Cvolvox-sorted.bam%2C
Available Tracks
filter by text
Reference sequence
Example Features
Name test track has a
Test SNPs
Example Features with
Protein-coding genes
Frame usage
Predicted genes
Fingerprinted BACs
ESTs
BigWig Density - volvox
BigWig XY - volvox_sin
VCF - additional test d
Image - volvox_microar
Legacy BAM - volvox-sc
JBrowse
File
View
Share
Help
0
5,000
10,000
15,000
20,000
25,000
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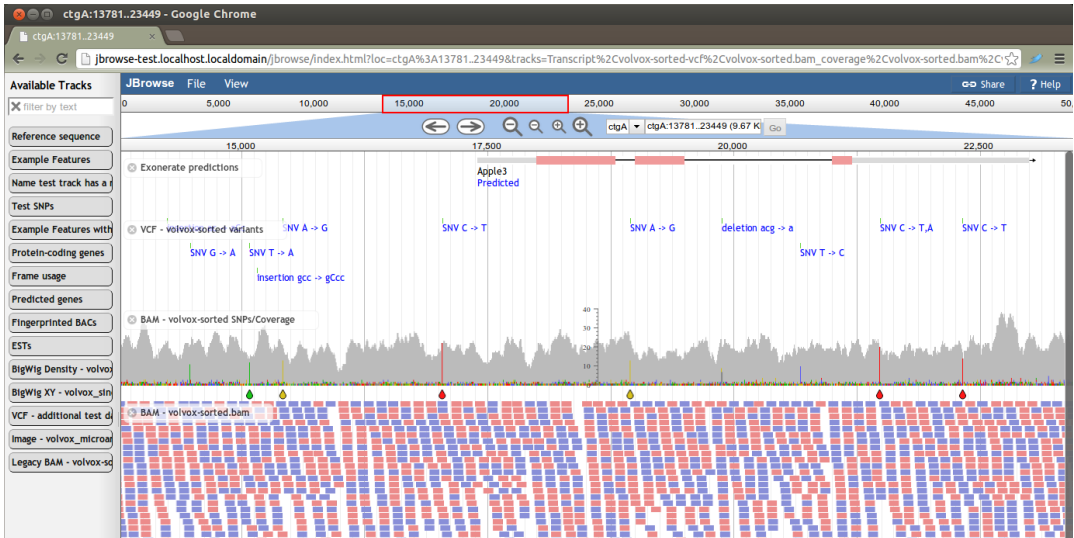
50,
ctgA
ctgA:13781..23449 (9.67 K
Go
15,000
17,500
20,000
22,500
Exonerate predictions
Apple3
Predicted
VCF - volvox-sorted variants
SNV A -> G
SNV C -> T
SNV A -> G
deletion acg -> a
SNV C -> T,A
SNV C -> T
SNV G -> A
SNV T -> A
SNV T -> C
insertion gcc -> gCcc
BAM - volvox-sorted SNPs/Coverage
40
30
20
10
0
BAM - volvox-sorted.bam
reached
Max height reached
Max height reached
Max height reached
BigWig Density - volvox_microarray
BigWig XY - volvox_microarray
289
+2σ
+1σ
mean
900
800
700
600
500
400
300
200
100
Example motifs
m11 (via JS callback)
m11: kinase
m08 (via JS callback)
m08: 7-transmembrane
m12 (via JS callback)
m12: kinase
m05 (via JS callback)
m03 (via JS callback)
m13 (via JS callback)

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.

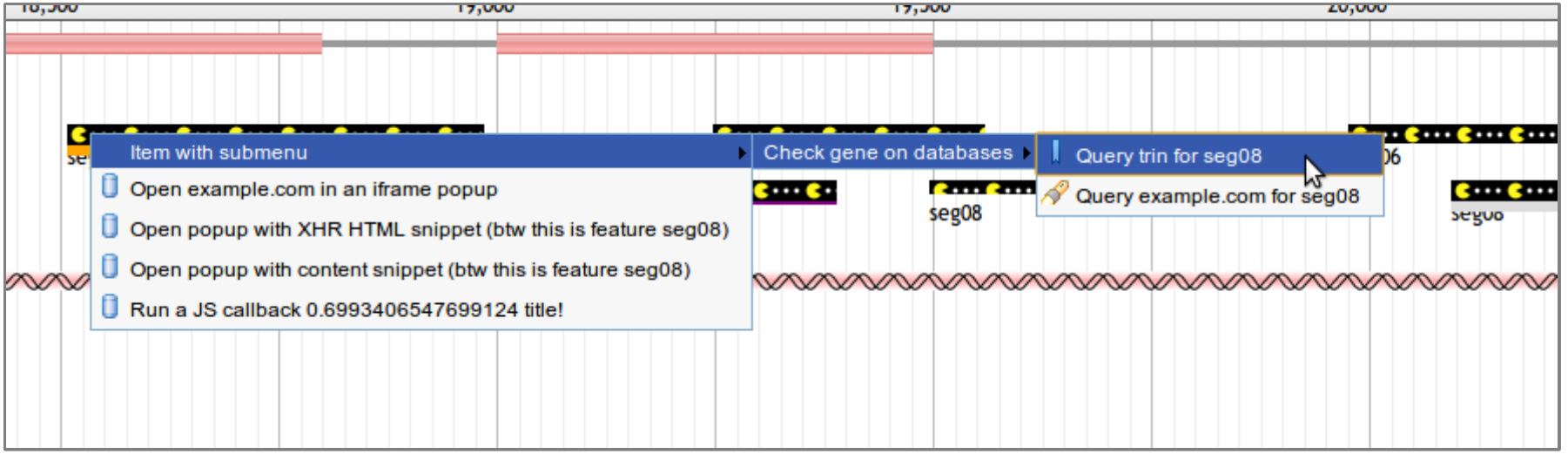
The JBrowse Project

- 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

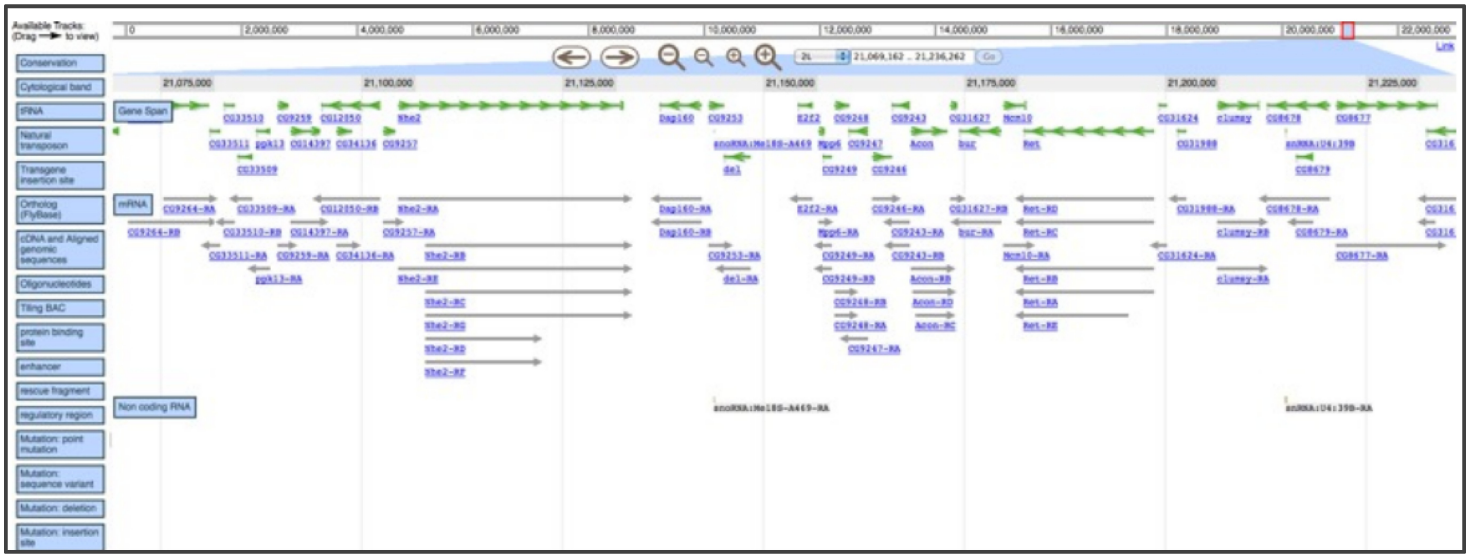
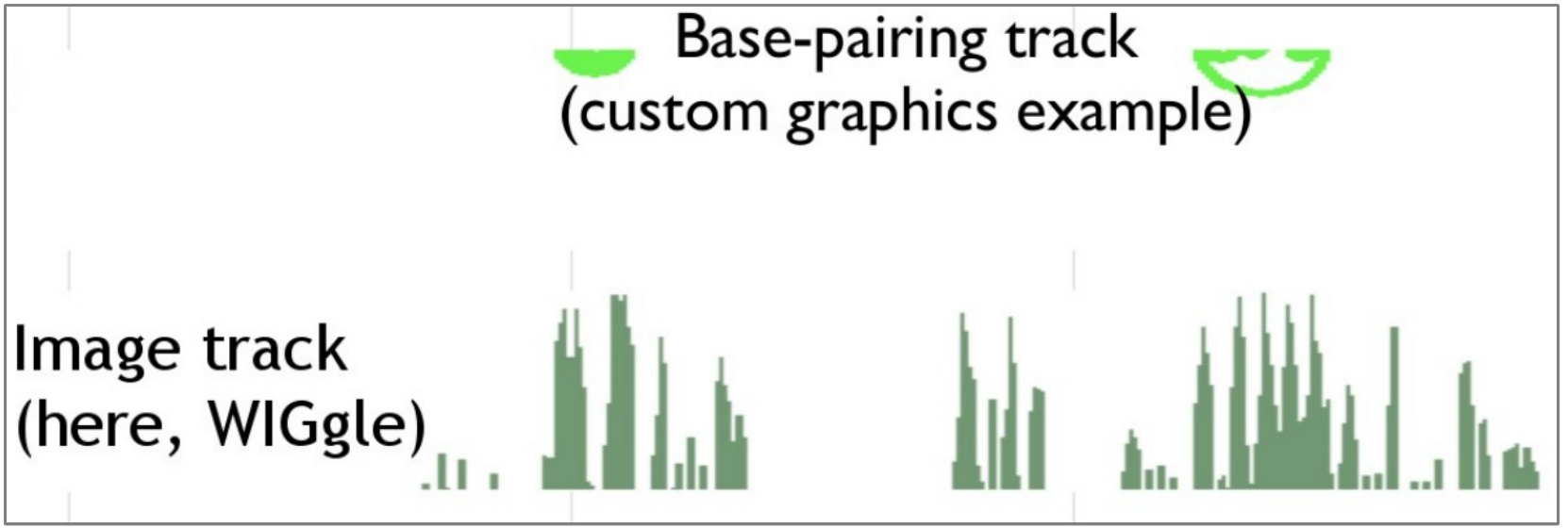


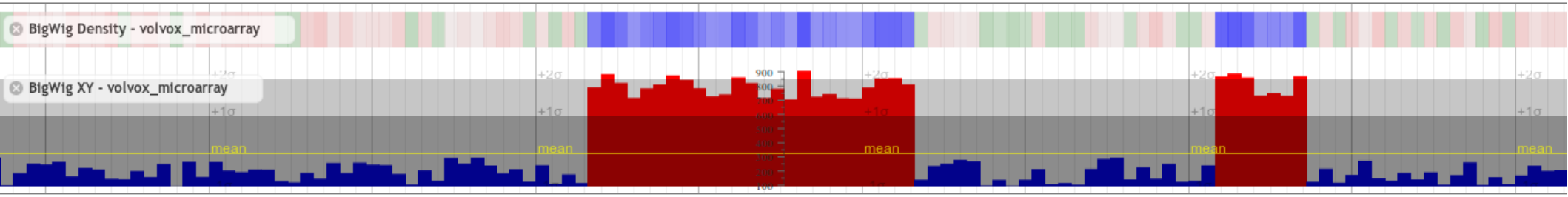
Image Tracks

- 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

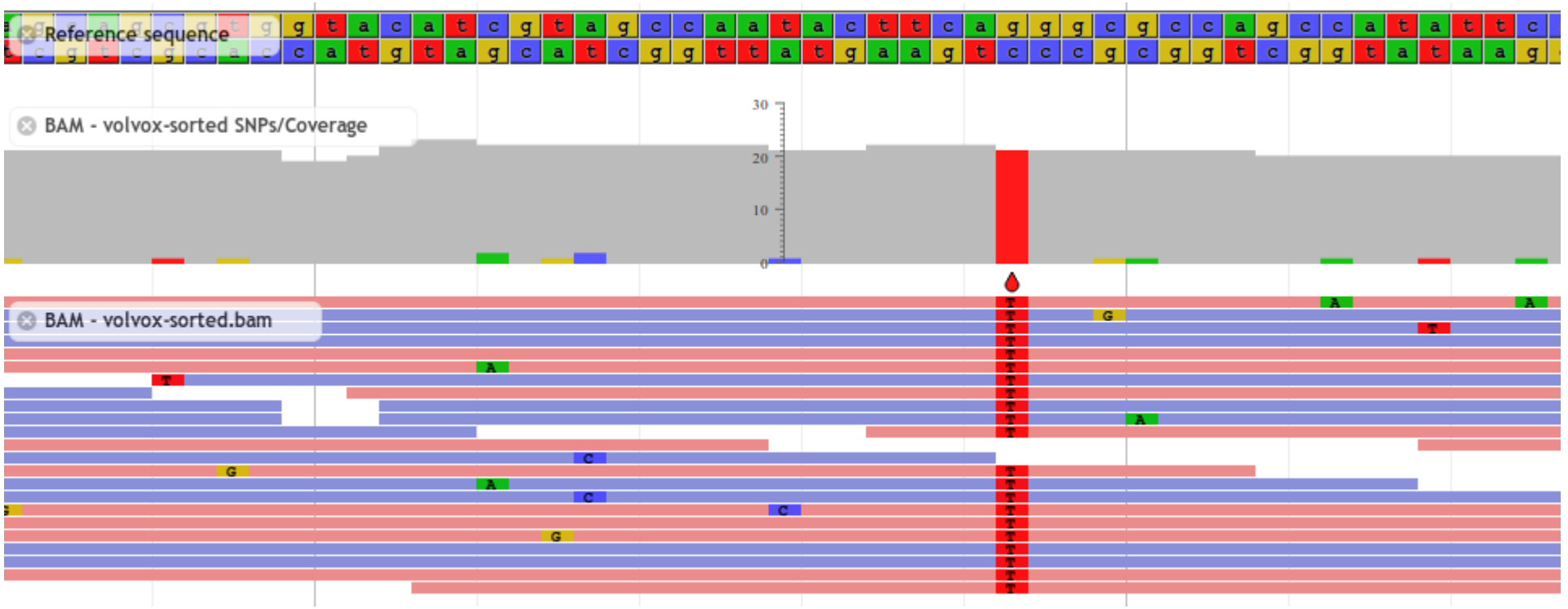
http://goo.gl/4kWFP http://jbrowse.org/genomes/tomato/



- 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

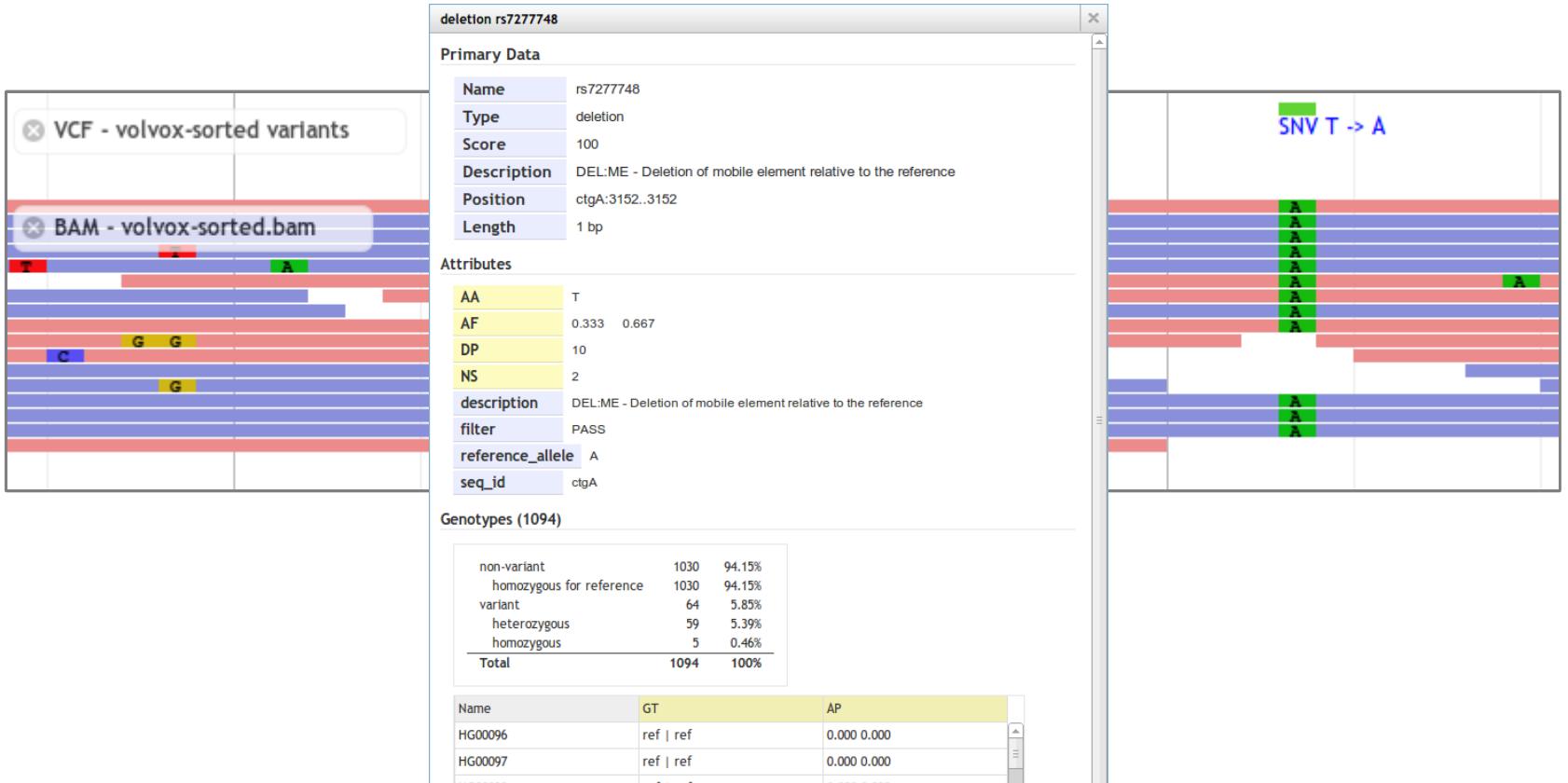
http://goo.gl/XSVN2



- 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

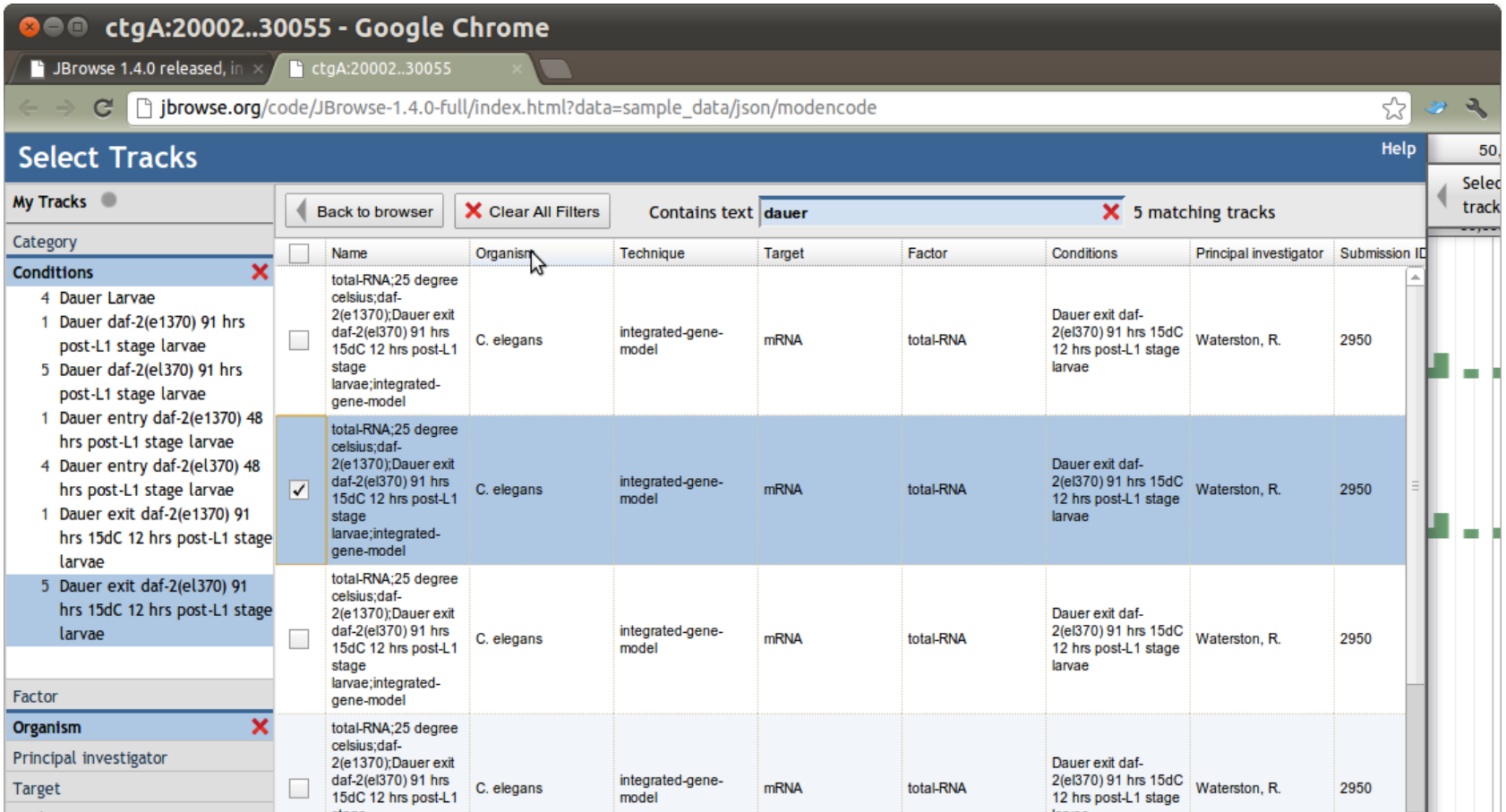
++ Particular Strengths ++

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

Faceted Track Selection

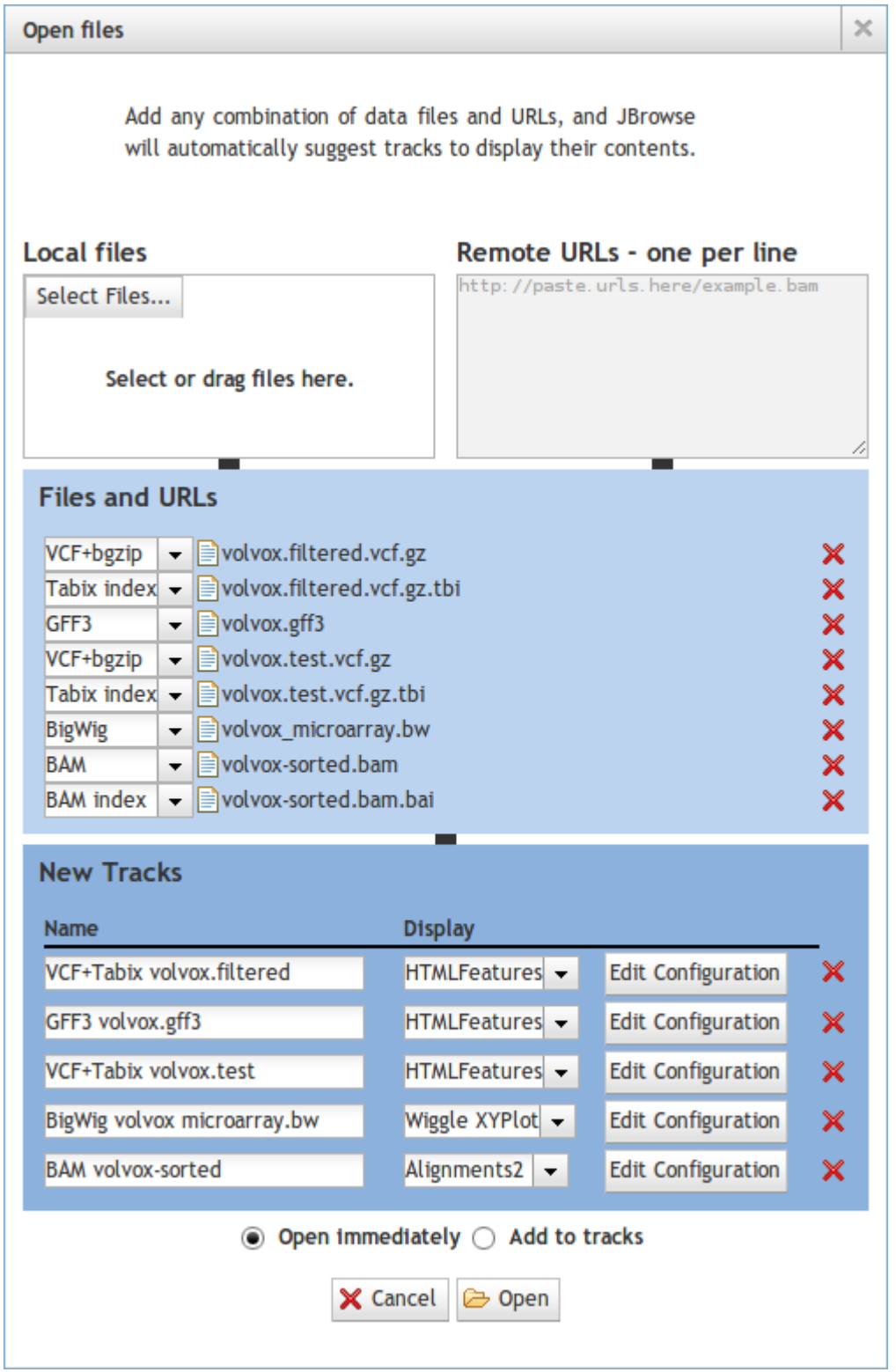
- make a CSV file of as much track metadata, and/or put track metadata in JSON config files

http://jbrowse.org/code/JBrowse-1.4.0-full/index.html?data=sample_data/json/modencode



Open Local Files

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



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/

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 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

Apollo

Ian Holmes (UC)
Amelia Ireland
Mitch Skinner

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

GMOD

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

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

2012 Direct BAM, alignment tracks, data export, coverage tracks, wiggle density

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?

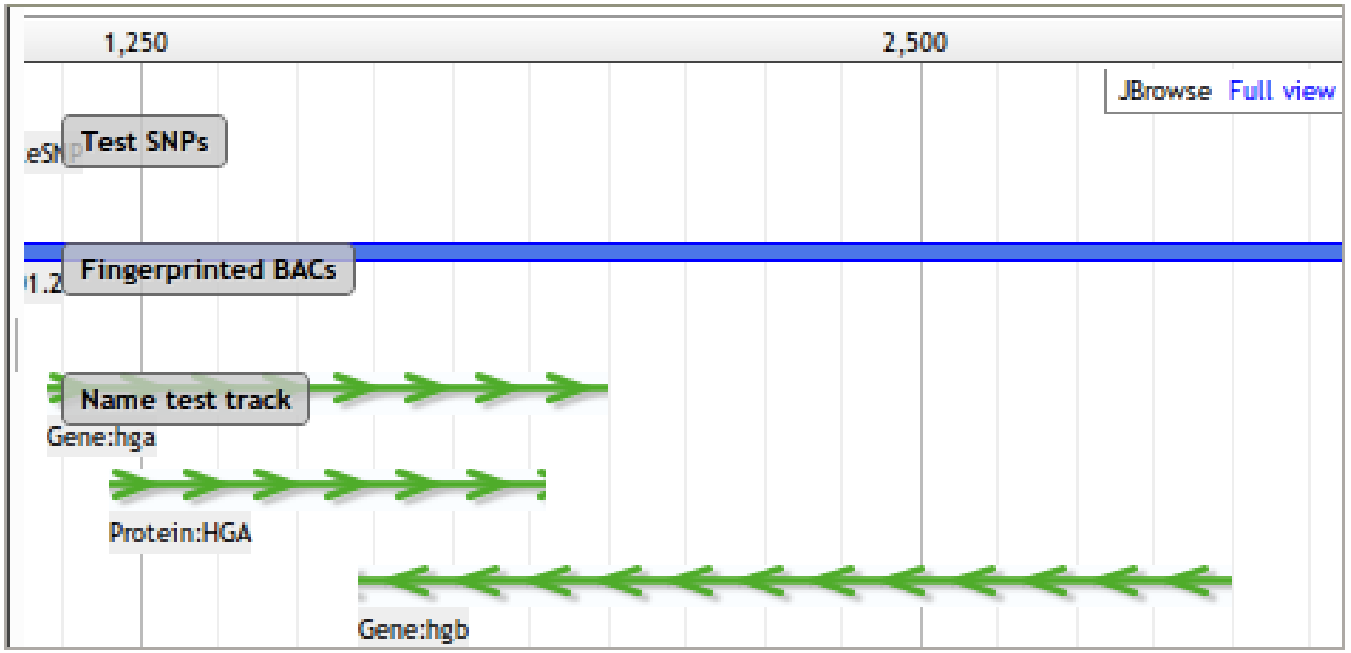
Graphical configuration, multiple independent views, more GBrowse compatibility.

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

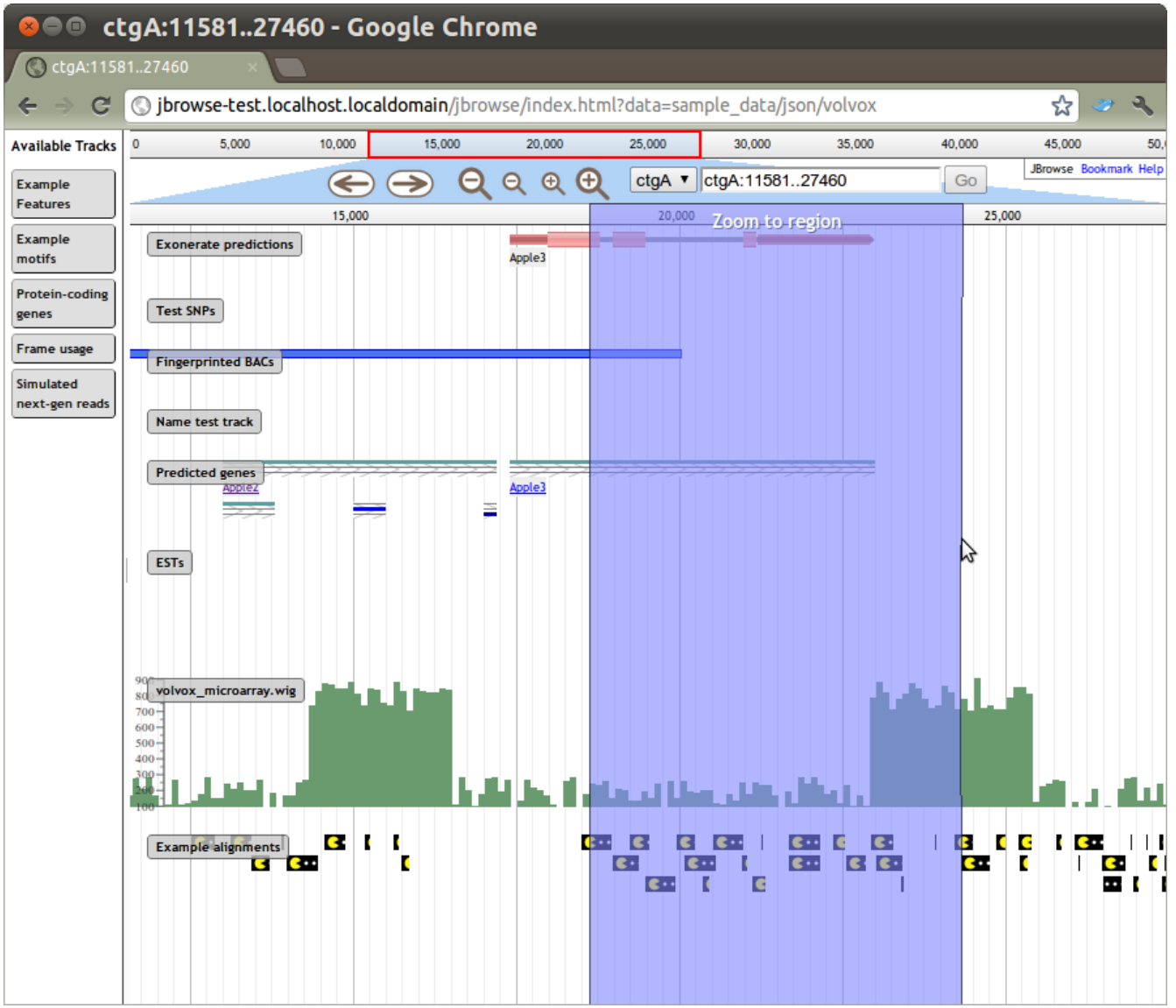
  `/jbrowse/v1/c/track/add  {track config JSON}`

- Track with the analysis results appears in the browser!

Pre-Compression

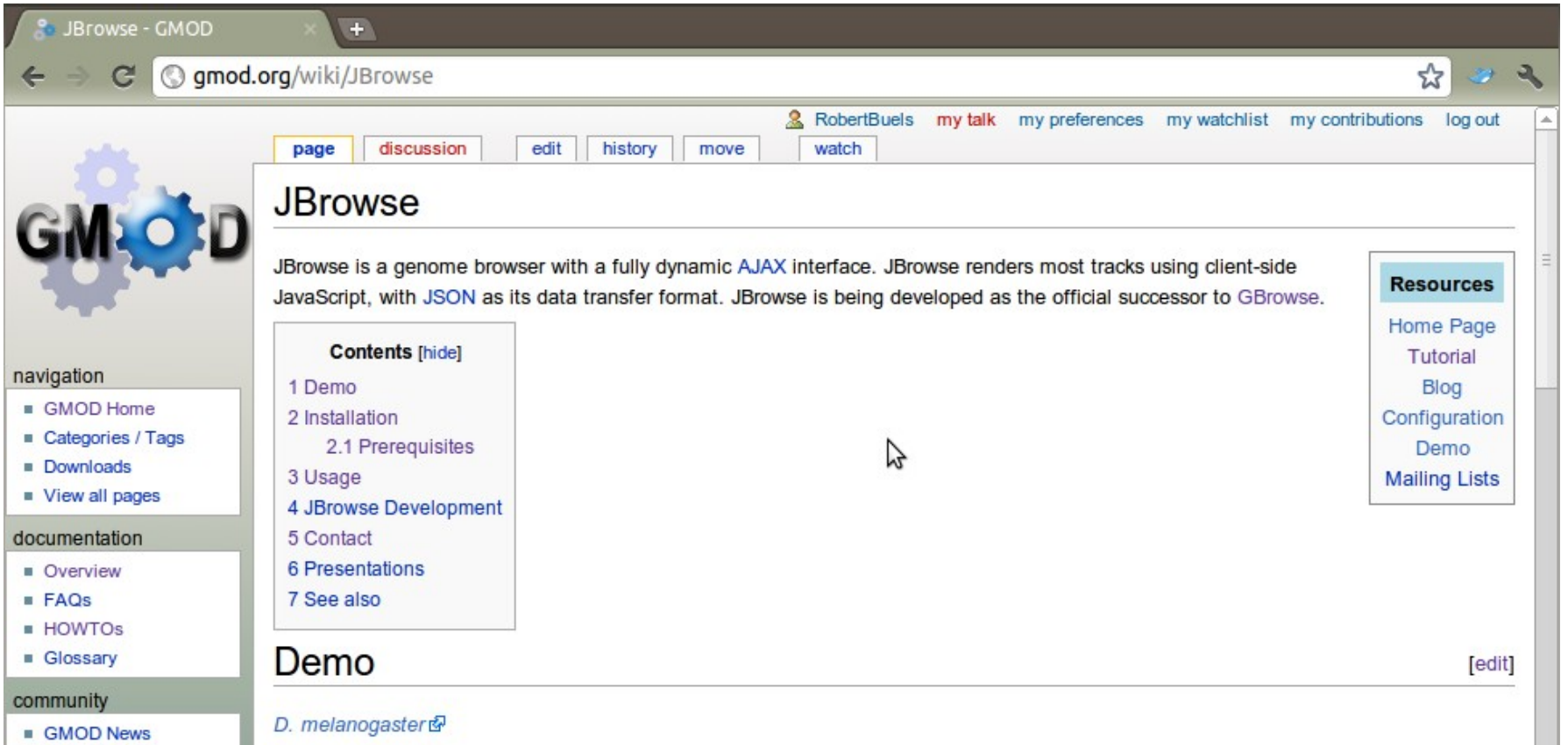
- gzips static data files on disk
- shrinks data directories by **about 60%**
  - takes GRCh37 from 19GB to 7.6GB.
- needs some webserver configuration for headers
  - Apache: AllowOverride FileInfo (.htaccess files)
  - `nginx`: add a smallish config snippet

Rubber-band Zooming



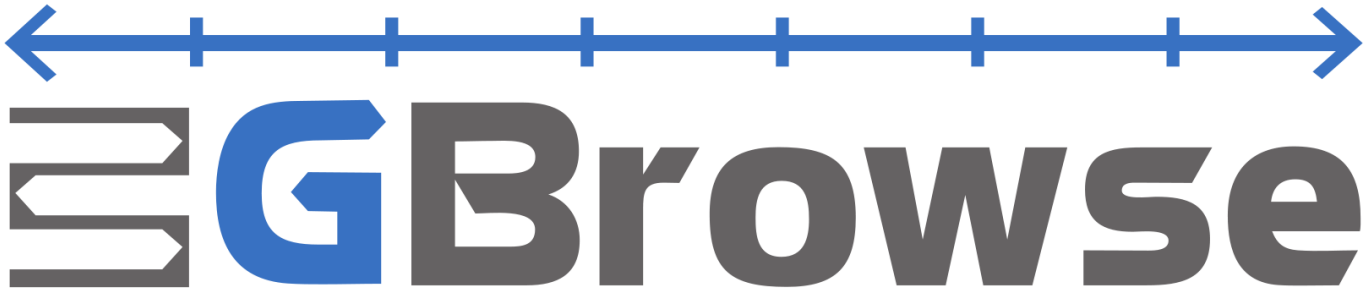
JBrowse Documentation

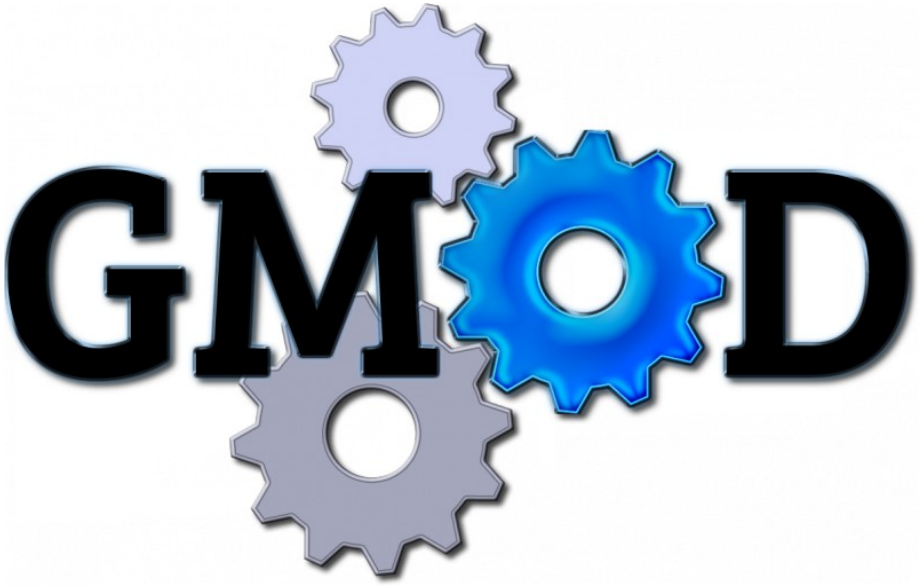
The GMOD wiki is the documentation hub
http://gmod.org/wiki/JBrowse



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.