

JBrowse – 1.6.0 and beyond

Robert Buels
GMOD Summer School
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University of California, Berkeley



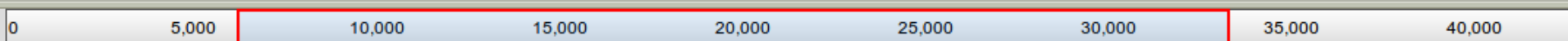
(JBrowse just released 1.6.0 yesterday)

Available Tracks

volvox_microarray

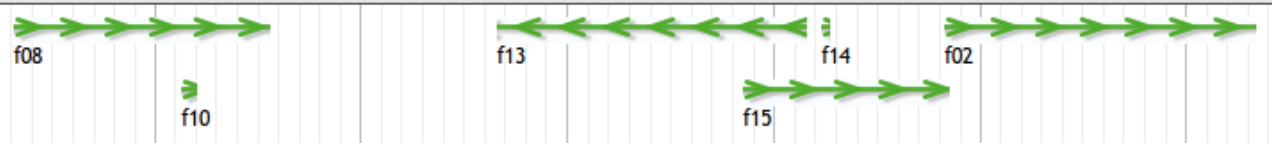
Name test track

Test SNPs

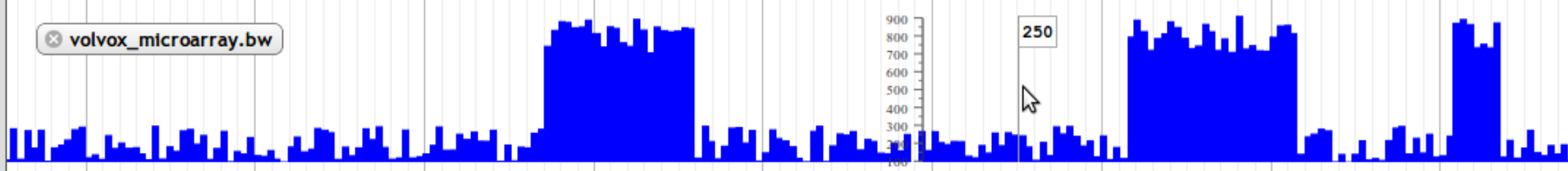


Navigation controls: left arrow, right arrow, zoom in, zoom out, search input (ctgA:6343..33352), and Go button.

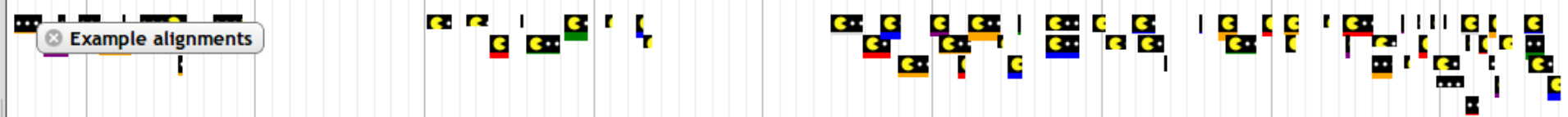
Example Features



volvox_microarray.bw



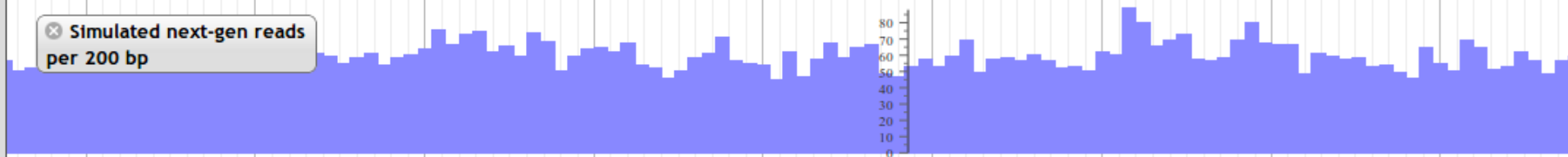
Example alignments



Exonerate predictions



Simulated next-gen reads per 200 bp



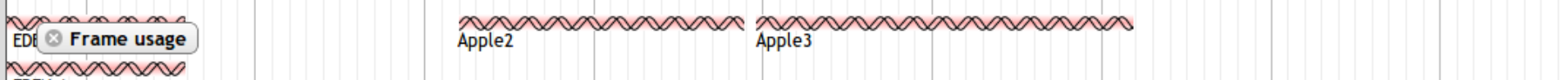
Example motifs



Protein-coding genes

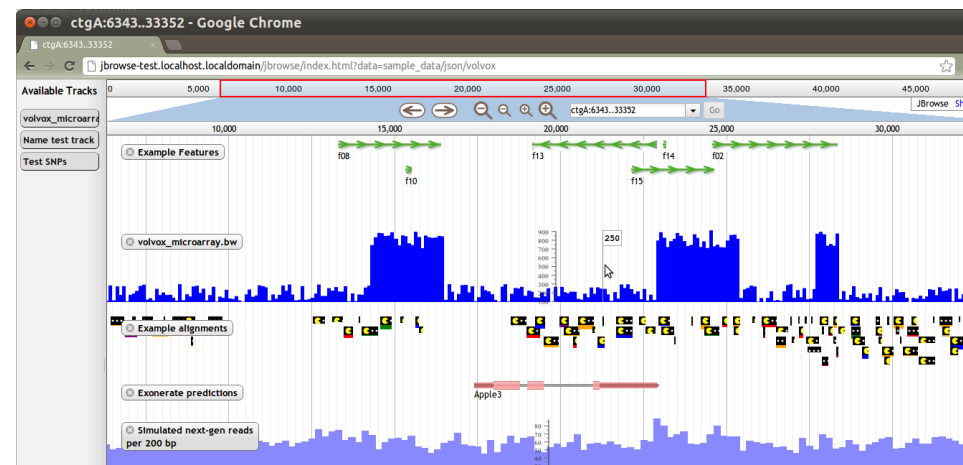


Frame usage



JBrowse...

- Do everything possible on the client side.
- **Fast**, smooth navigation (*think Google Maps*) for genomes).
- Supports BED, GFF, Bio::DB::*, Chado, WIG, BAM, BigWig, UCSC (*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).
NHGRI funds 3yr development of project.
Mitch Skinner joins the team.
- 2007 CSHL Biology of Genomes: scaling.
- 2008 JavaScript-only rendering.
- 2009 Genome Research paper.
- 2010 WebApollo funded to develop JBrowse.
NHGRI renews for 6mo.
JBrowse dubbed “official” GBrowse successor.
- 2011 Mitch Skinner joins genomics startup.
US politicians play chicken with economy.
NHGRI renews for 3yr.
- 2012 (January) **Robert Buels joins the team.**

The JBrowse Project

- free and open source (license: GPL / 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
- just got 3 more years of funding from NHGRI!



± Particular Strengths

- **very, very** fast, smooth, scalable
- easy to get running
- Faceted Track Selector - thousands of tracks!
- Direct-to-browser BigWig support.
 - coming soon for BAM and BigBED also

± Particular Weaknesses

- no user-uploaded data or end-user customization
- no data export
- few pre-made glyph options

**We're working on these,
of course.**

Release Roadmap

1.3.0 – April 13

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

1.4.0 – June 14

faceted track selector, auto-completion

1.5.0 – August 13

direct BigWig, nice Wiggle tracks
popups and context menus

1.6.0 – August 25

Feature descriptions, bugfixes for class.

today

(more intermediate releases)

UI plugin system (pub/sub events)

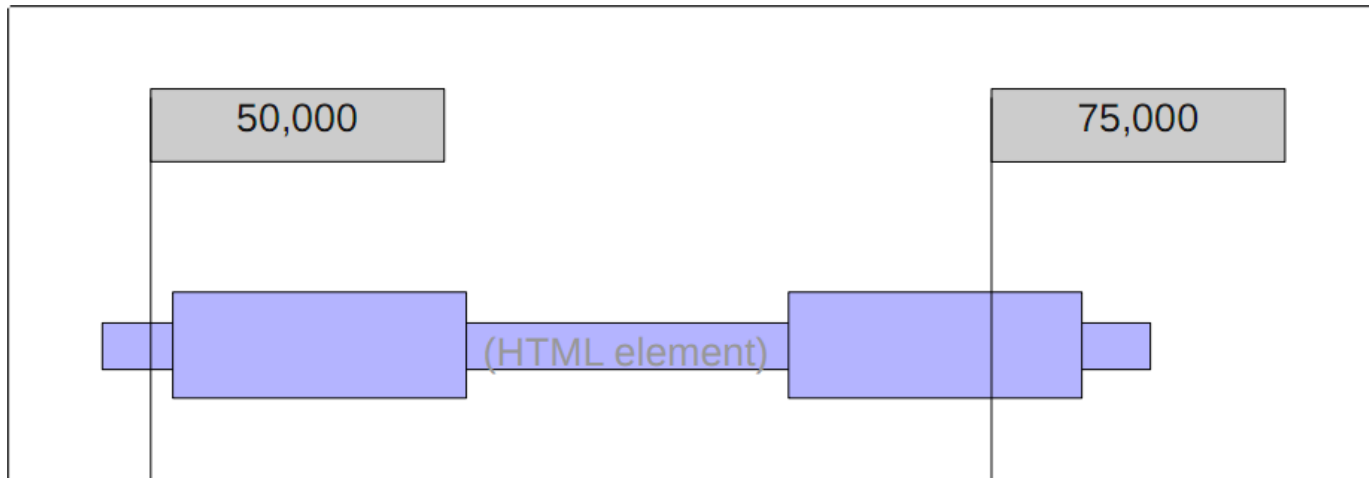
GBrowse-format configuration

2.0.0 – February?

Formatting scripts decoupled from config,
more GBrowse compatibility

Feature Tracks

- rectangles (`<div>s`) with various fills and dimensions to represent the features
- can do a surprising amount



Feature Tracks: Density Plots

Zoomed out



Zoomed in

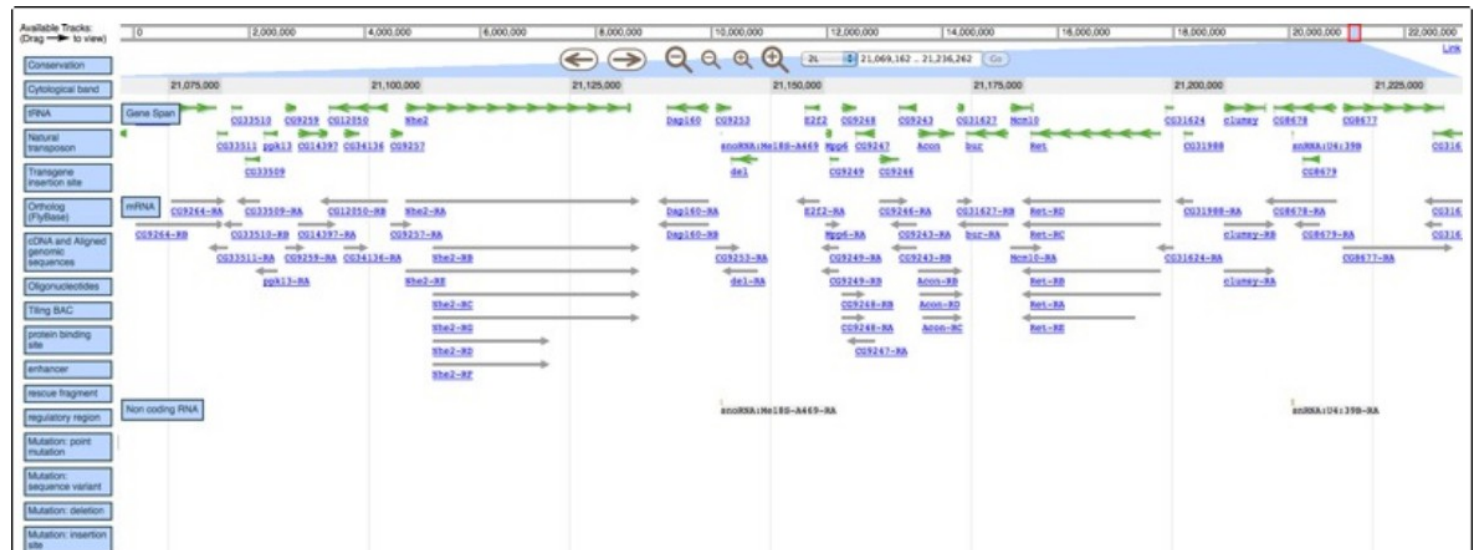
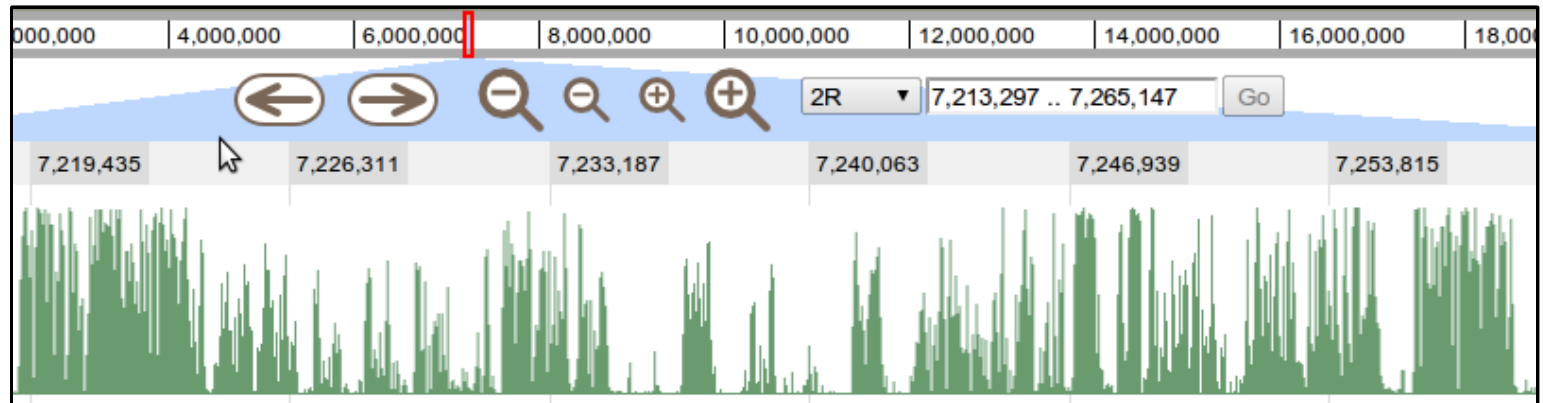


Image Tracks

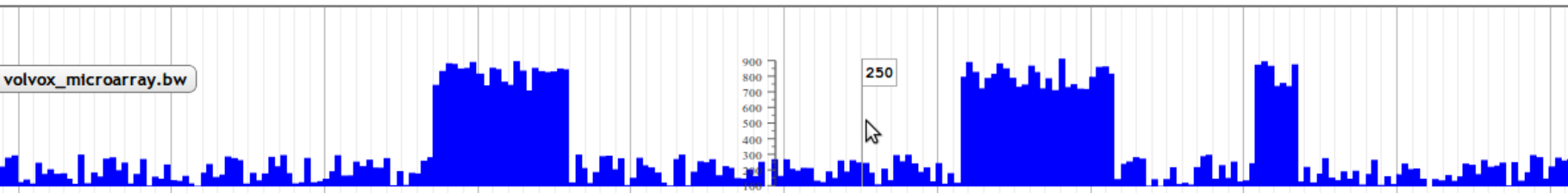
- any pre-generated images that cover the genome
- quantitative data (wiggle/BigWig)
 - wig-to-json.pl
- RNA base-pairing



Wiggle/BigWig Tracks

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

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



- Reads chunks of data directly from BigWig file on the web.
- Quite fast, and will get faster.
- Supported by all recent-ish (2-year-old) browsers, except Internet Explorer.
- IE is 4 years behind the tech curve, version 10 is required (released this month).

Faceted Track Selection

- just make a CSV file of track metadata
 - join to JBrowse track configuration with **name** column

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

The screenshot shows the JBrowse 'Select Tracks' interface. The browser address bar displays the URL: http://jbrowse.org/code/JBrowse-1.4.0-full/index.html?data=sample_data/json/modencode. The interface includes a search bar with the text 'dauer' and a filter for '5 matching tracks'. A table of track metadata is displayed, with columns for Name, Organism, Technique, Target, Factor, Conditions, Principal investigator, and Submission ID. The table contains five rows, with the second row selected. The 'Conditions' and 'Organism' facets are expanded on the left side of the interface.

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
4 Dauer Larvae	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
1 Dauer daf-2(e1370) 91 hrs post-L1 stage larvae	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
5 Dauer daf-2(e1370) 91 hrs post-L1 stage larvae	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
1 Dauer entry daf-2(e1370) 48 hrs post-L1 stage larvae	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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Hands-on time!

Course Set for 2.0

- Mostly-GBrowse2-compatible configuration.
- Load and search rich track metadata for thousands of tracks.
- GBrowse compatibility backend (2.1?)
 - rendering service with Bio::Graphics glyphs
 - fetch and render GBrowse remote tracks
 - hopefully not much configuration, probably a standalone server

Course Set for 2.0

- ❑ Solid data-source plugin system, including direct BAM, ~~BigWig~~, BigBed.
- ❑ New, documented pub/sub event API ties together JBrowse itself, and is available to **any other JavaScript code**.
- ❑ Decouple data and configuration: formatting data and configuring tracks need to be separate steps.

Plans: Configuration

- GBrowse format
 - as much backward compatibility as possible
- dynamic changes to configuration information (probably more like at 2.1 or 2.2)

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!

Big Thanks To:

Suzi Lewis (LBNL)

Gregg Helt

Ed Lee



Nomi Harris

Ian Holmes



Mitch Skinner

Stephen Cummings

Lincoln Stein (OICR)

Julie Moon

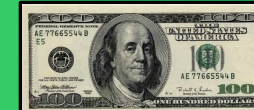
Natalie Fox

Adam Wright



Lukas Mueller (BTI, SGN)

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)



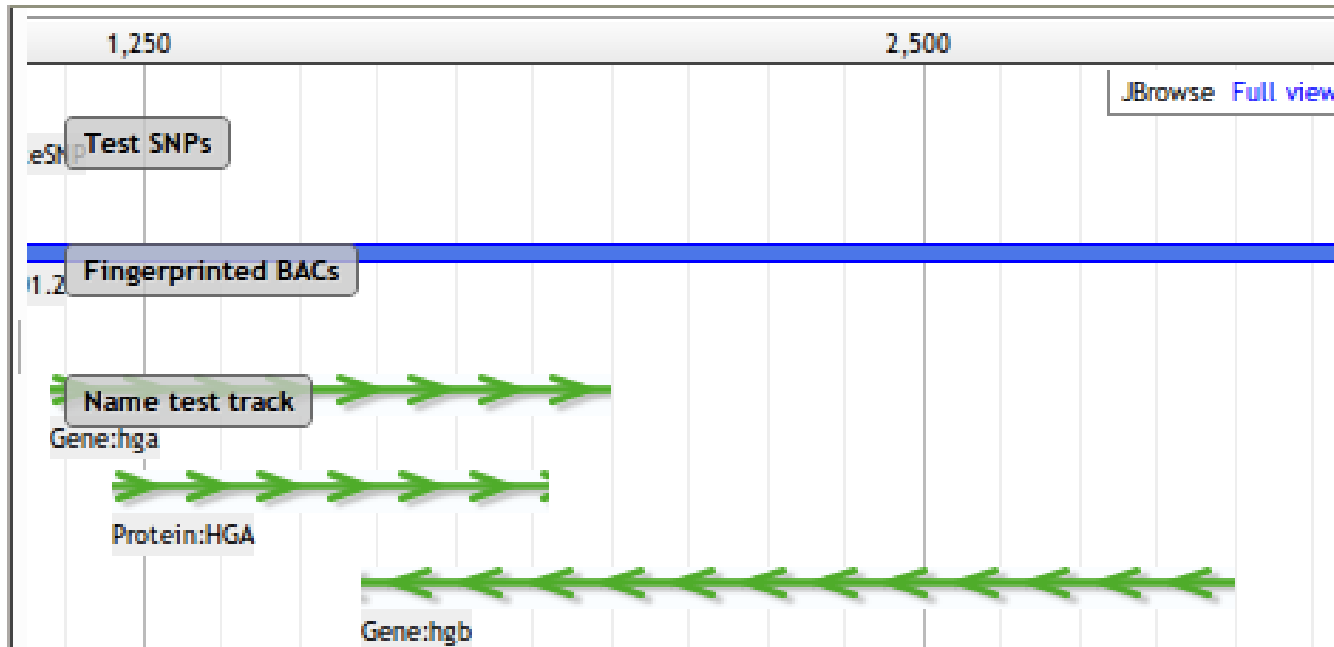
- Was Engineering Lead at Sol Genomics Network <http://solgenomics.net>, at BTI with Lukas Mueller
- Became new JBrowse Lead Developer as of January 2012 at UC Berkeley with Ian Holmes

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 hack the data/trackList.json to use these >:-{

Embedded Mode



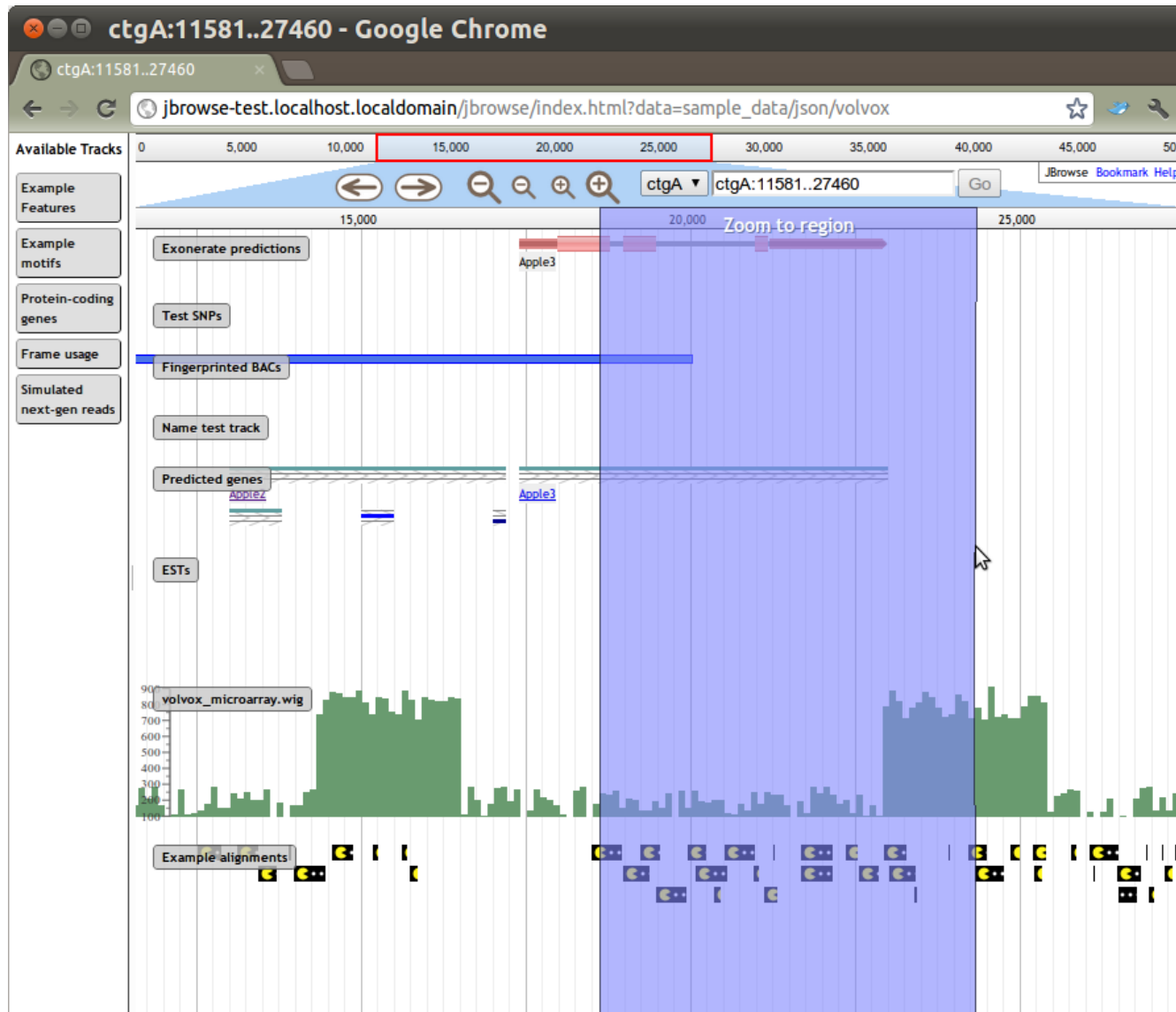
Julie Moon, OICR co-op student

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


Pre-Compression

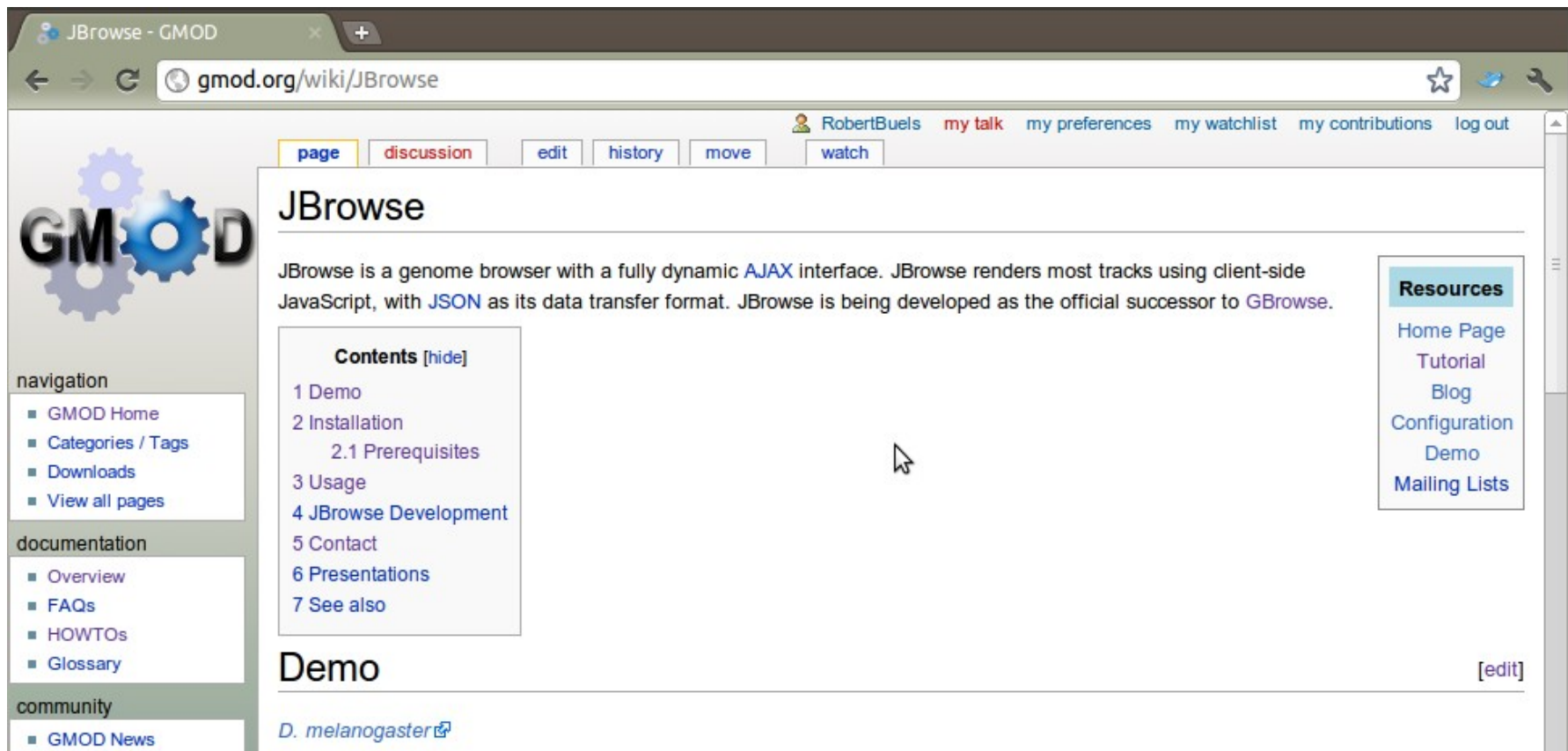
- gzips static data files on disk
- shrinks data directories by **about 60%**
 - takes ~~hg19~~GRCh37 from 19GB to 7.6GB.
- needs some webserver configuration for headers
 - Apache: AllowOverride FileInfo (.htaccess files)
 - nginx: add a smallish config snippet

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

[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

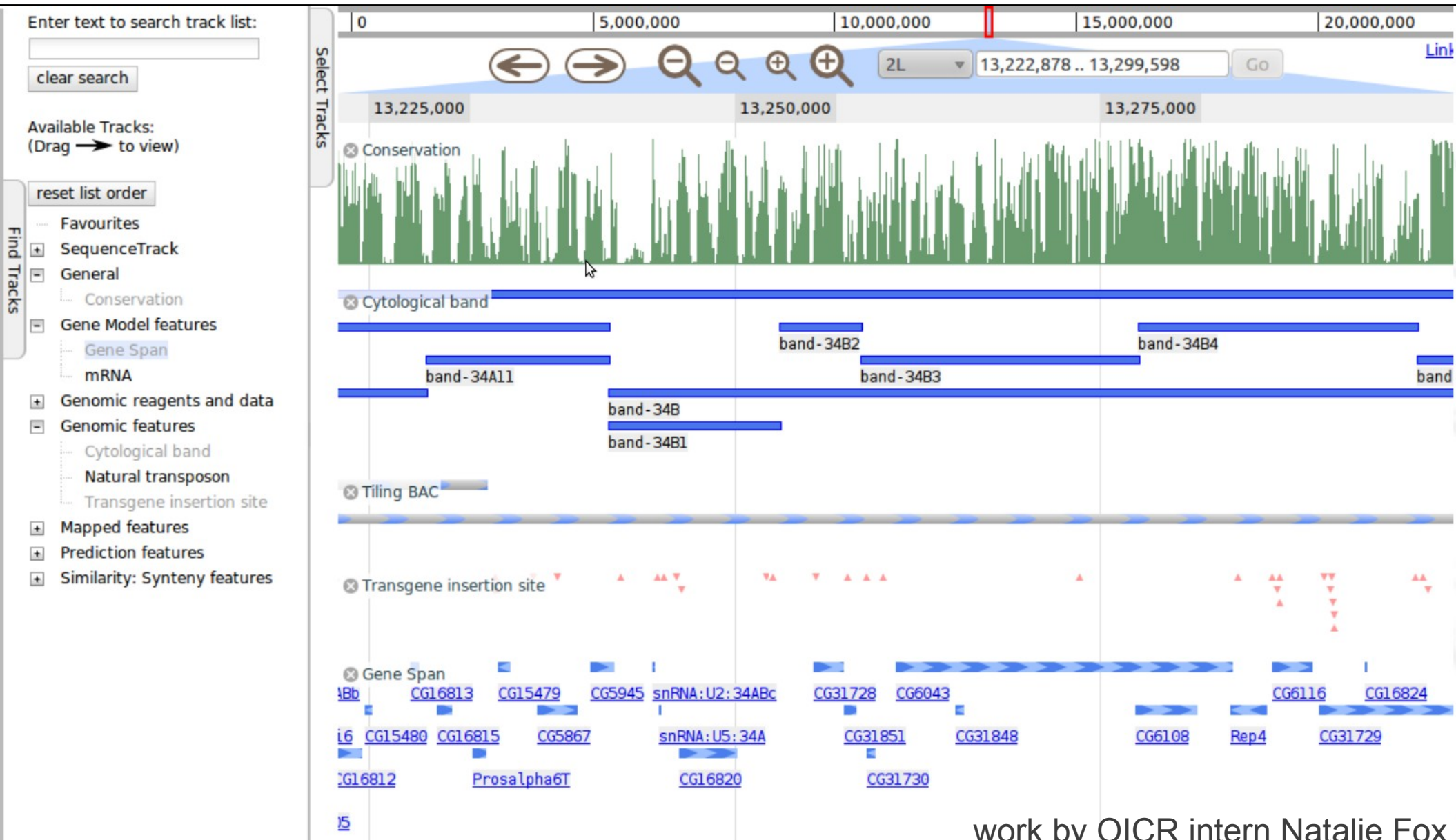
community

- GMOD News

Coming Soon

- new track selection
- overview images
- context menus
- track customization
- drag to zoom!

Coming: Hierarchical Track Sel.



Coming: Faceted Track Selection

clear selected tracks

Click on the track name below to display/hide the track.

22 Items

sorted by: labels; then by... • grouped as sorted

- cDNA and Aligned genomic sequences
- Conservation
- Cytological band
- DNA
- enhancer
- Gene Span
- mRNA
- Mutation: deletion
- Mutation: insertion site
- Mutation: point mutation
- Mutation: sequence variant
- Natural transposon
- Non coding RNA
- Oligonucleotides
- Ortholog (FlyBase)
- protein binding site
- regulatory region
- rescue fragment
- Tiling BAC
- Transgene insertion site
- tRNA
- XRate predictions

Show only the first 10 results

0 5,000,000 10,000,000 15,000,000 20,000,000

← → 🔍 🔍 🔍 🔍 2L

13,222,878 .. 13,274,458 Go

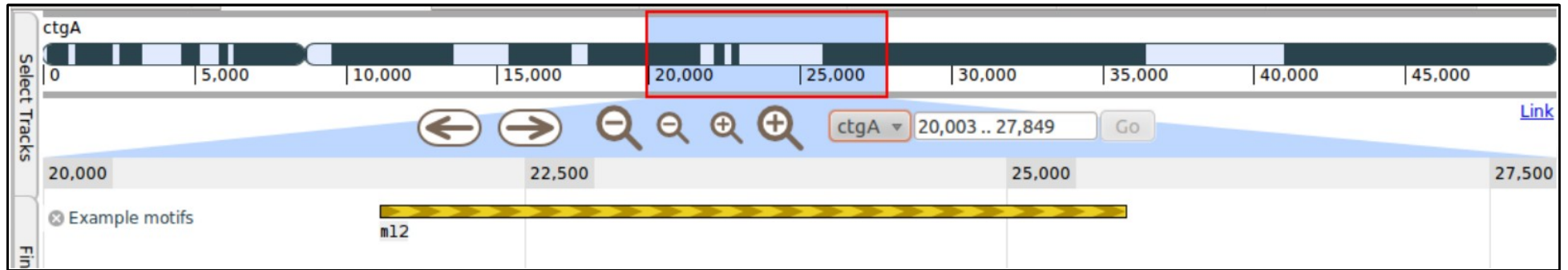
13,225,000 13,250,000

Find Tracks

- Conservation
- Cytological band
 - band - 34A11
 - band - 34B1
 - band - 34B2
 - band - 34B3
- Tiling BAC
- Transgene insertion site
- Gene Span
 - lBb
 - CG16813
 - CG15479
 - CG5945
 - snRNA:U2:34ABc
 - CG31728
 - CG6043
 - l6
 - CG15480
 - CG16815
 - CG5867
 - snRNA:U5:34A
 - CG31831
 - CG31848

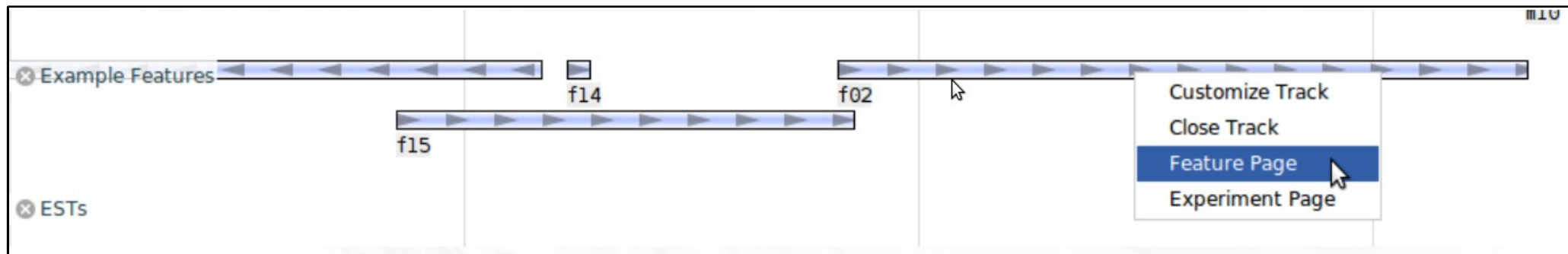
work by OICR intern Natalie Fox

Coming: Overview Images



Can have a karyotype, or any other image.

Coming: Context Menus



Coming: Track Customization

The image displays a genomic track viewer interface. On the left, a sidebar titled "Select Tracks" and "Find Tracks" provides customization options for the "Example motifs track". The options include:

- Customizing Example motifs track: A yellow dashed bar is shown.
- Buttons: "apply changes" and "cancel".
- height: "select new height" dropdown.
- fill color: "select new fill color" dropdown.
- track image: "select new track image" dropdown.
- border color: "select new border color" dropdown.
- border color: "select new border width" dropdown.

The main track area shows a genomic track for "ctgA" with a scale from 0 to 45,000. A red box highlights the region from 20,000 to 25,000. Below this, a zoomed-in view shows the region from 20,000 to 25,000 with a search bar containing "ctgA" and "20,000..27,314". The zoomed view includes several tracks:

- Example motifs: A yellow dashed bar labeled "m12".
- Example Features: A blue bar with arrows pointing right, labeled "f15", "f14", and "f02".
- ESTs: A track with no visible features.
- Frame usage: A green bar.
- Example alignments: A blue bar with arrows pointing right, labeled "seq02".

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 ;-)



WebApollo

- next generation of the popular Apollo annotation editor
- genome editing in your browser
- based on JBrowse



WebApollo

- clients receive annotation updates **in real time** (like Google Docs)
- saves edits to a central database
- has produced several extensions that will be coming to core JBrowse
 - highlighting and selecting features
 - HTML5 Canvas tracks for wiggle data (opening the door for many more canvas-based techniques)

