JBrowse — 1.6.0 and beyond

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GMOD Summer School

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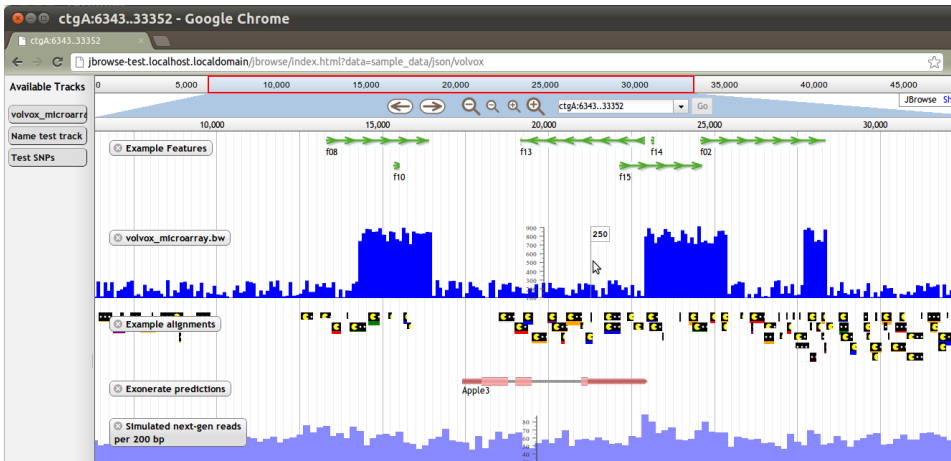
University of California, Berkeley

(JBrowse just released 1.6.0 yesterday)

ctgA:6343..33352 - Google Chrome
ctgA:6343..33352
jbrowse-test.localhost.localdomain/jbrowse/index.html?data=sample_data/json/volvox
Available Tracks
volvox_microarra
Name test track
Test SNPs
0
5,000
10,000
15,000
20,000
25,000
30,000
35,000
40,000
ctgA:6343..33352
Go
Example Features
f08
f10
f13
f14
f15
f02
volvox_microarray.bw
250
Example alignments
Exonerate predictions
Apple3
Simulated next-gen reads per 200 bp
Example motifs
m11
m08
m07
m12
m02
m05
m14
m13
m10
m03
Protein-coding genes
Frame usage
Apple2
Apple3

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)

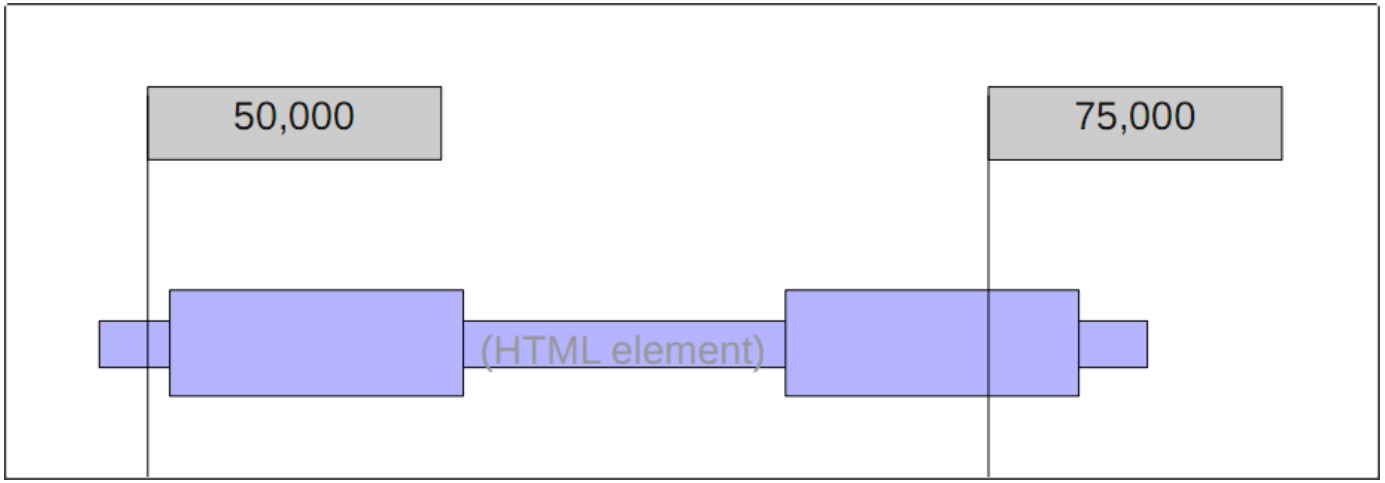
GBrowse-format configuration

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

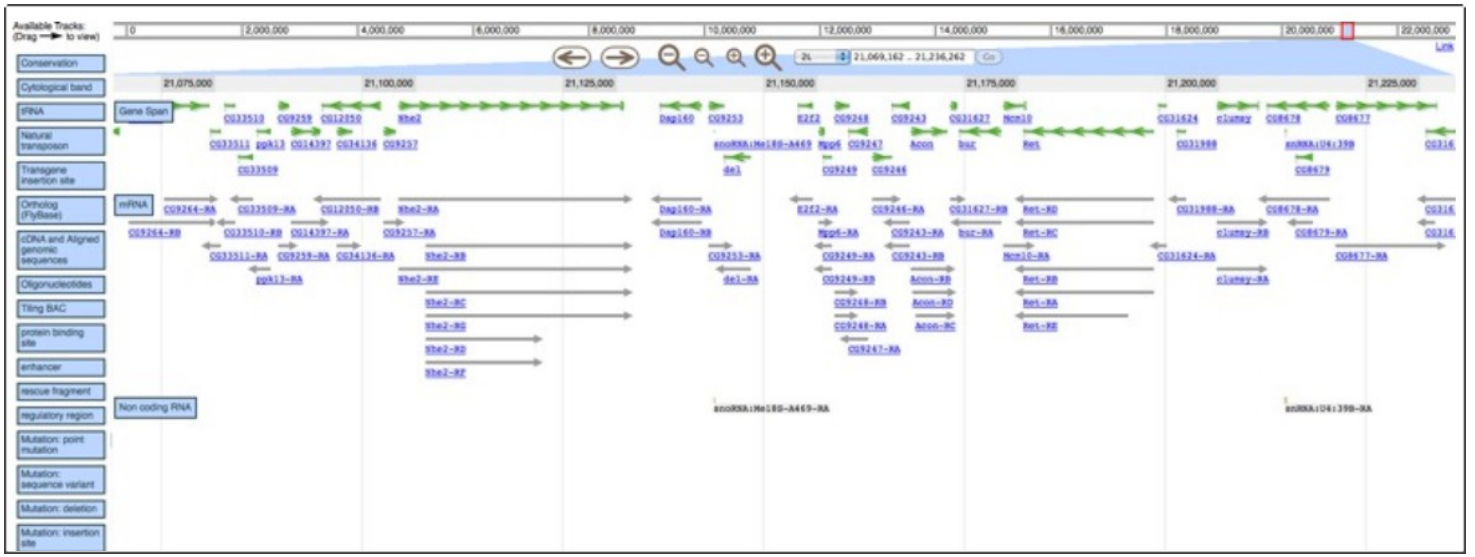
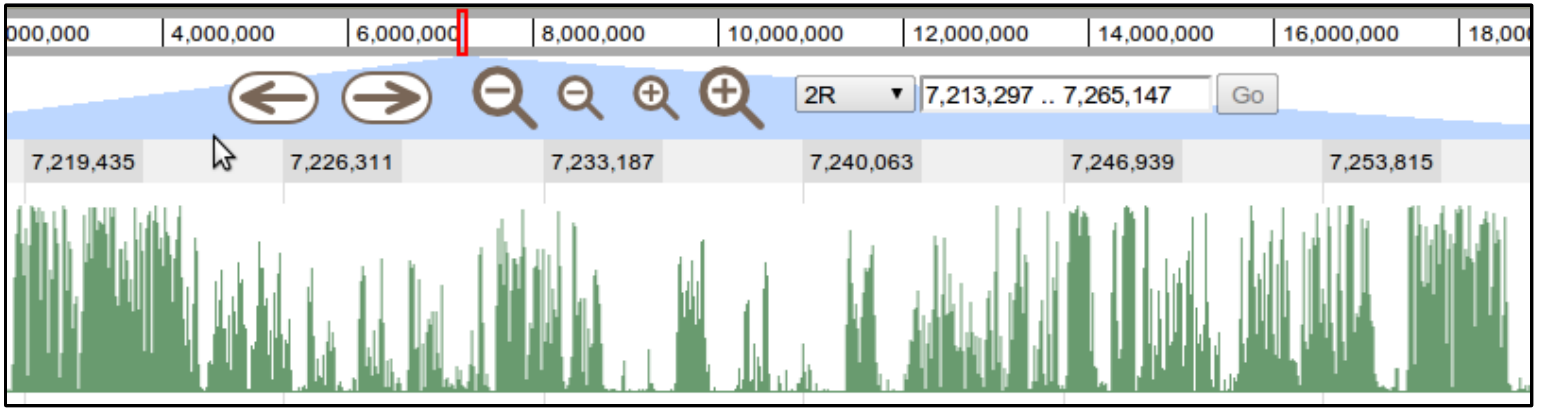


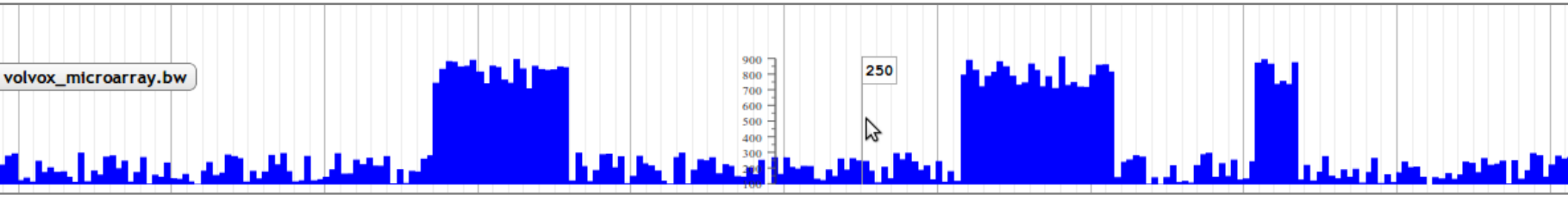
Image Tracks

- 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/

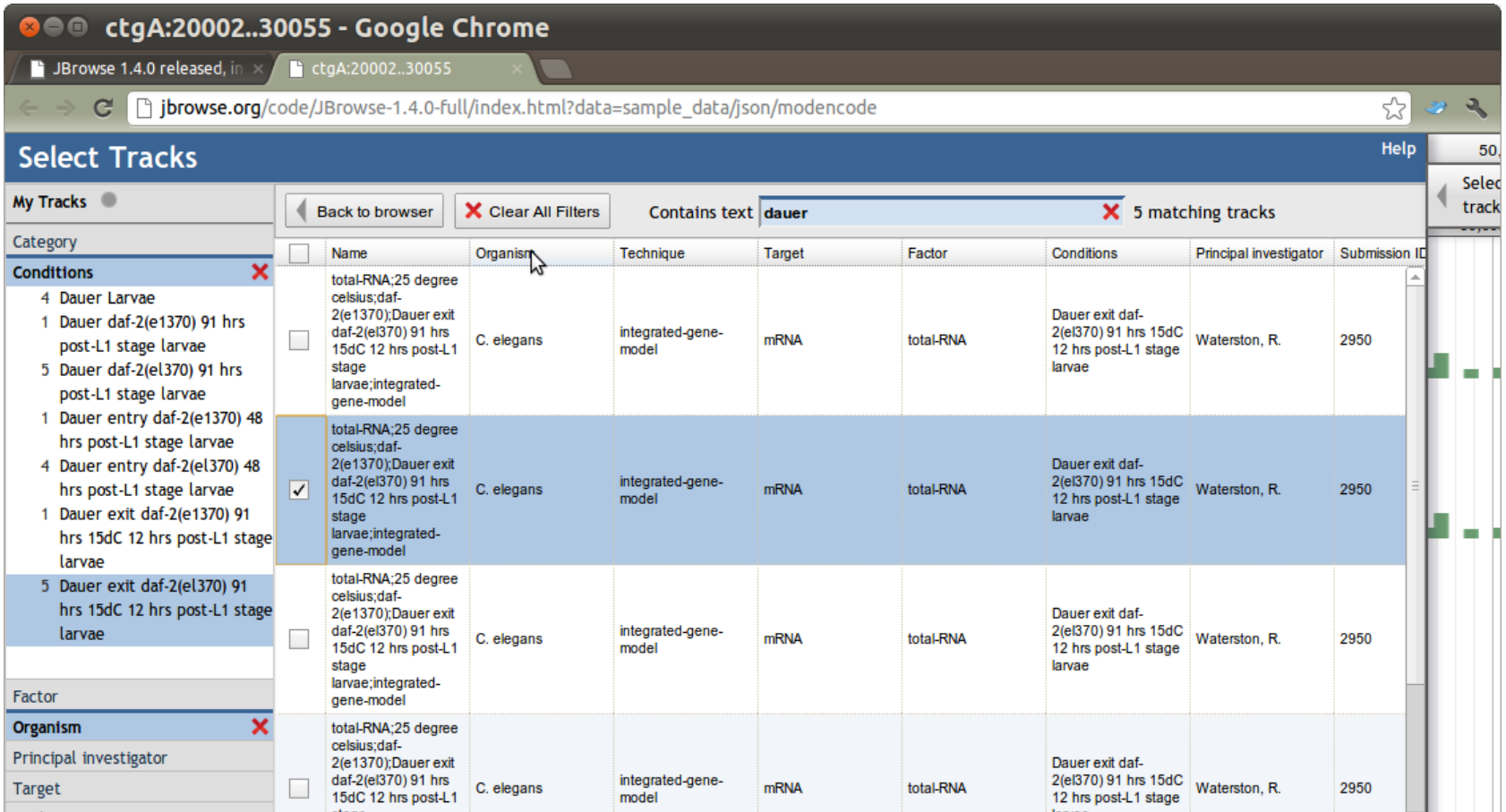


- Reads chunks of data directly from BigWig file on the web.
- Quite fast, and will get faster.
- Supported by all recent-ish (2-year-old) browsers, except Internet Explorer.
- IE is 4 years behind the tech curve, version 10 is required (released this month).

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



Hands-on time!

Course Set for 2.0

- [ ] Mostly-GBrowse2-compatible configuration.
- [x] 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

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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
- 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

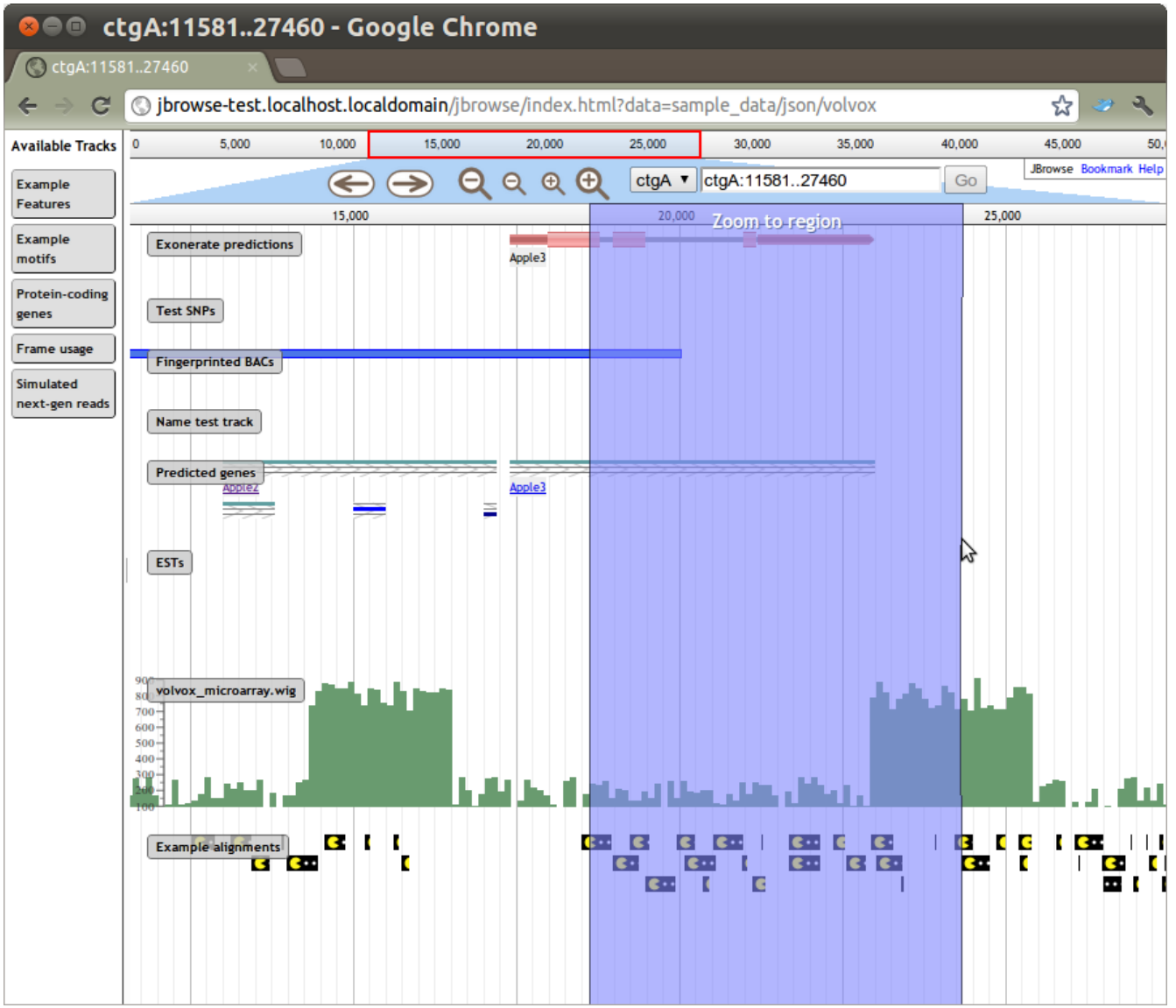
Julie Moon, OICR co-op student

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

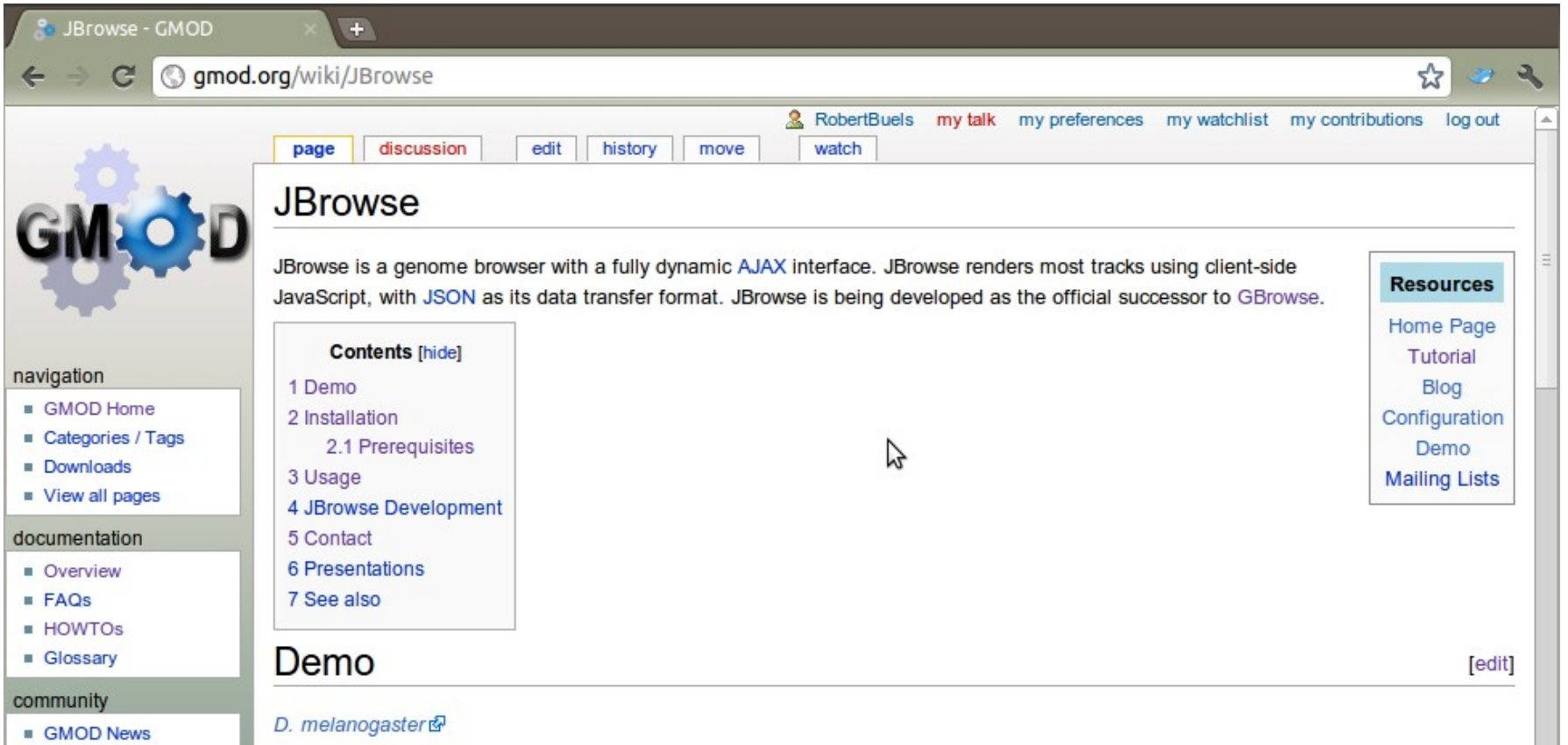
- gzips static data files on disk
- shrinks data directories by **about 60%**
  - takes ~~hg19~~GRCh37 from 19GB to 7.6GB.
- needs some webserver configuration for headers
  - Apache: AllowOverride FileInfo (.htaccess files)
  - `nginx`: add a smallish config snippet

Rubber-band Zooming



JBrowse Documentation

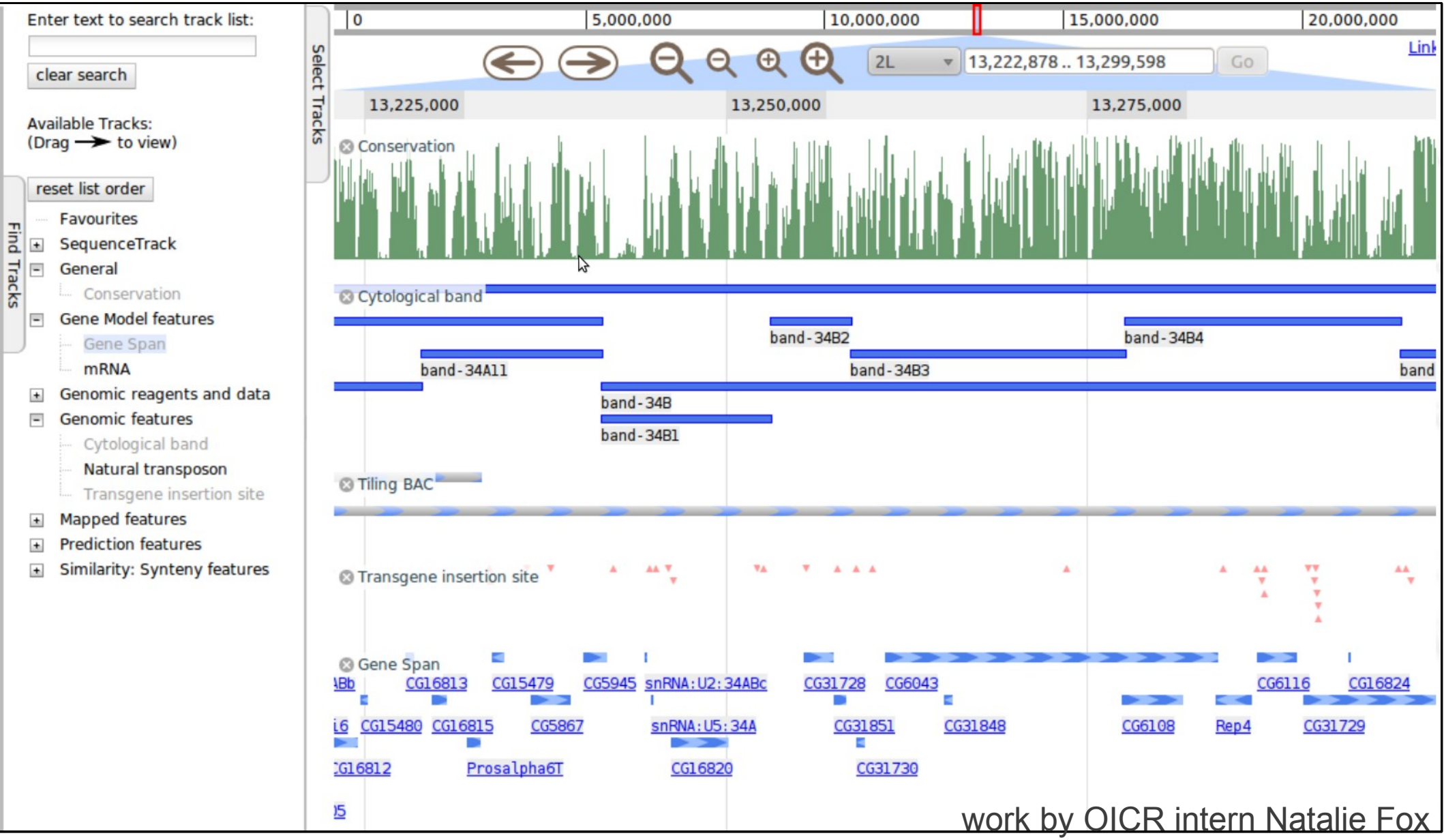
The GMOD wiki is the documentation hub
http://gmod.org/wiki/JBrowse



Coming Soon

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

Coming: Hierarchical Track Sel.

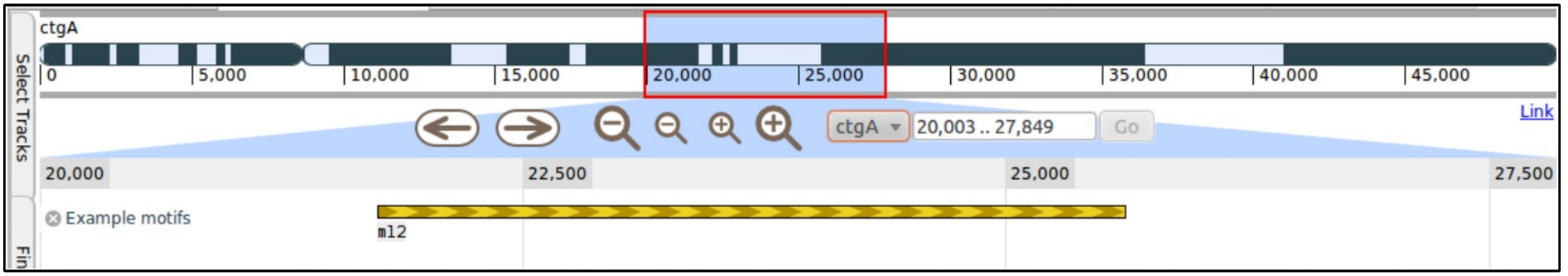


work by OICR intern Natalie Fox

Coming: Faceted Track Selection

work by OICR intern Natalie Fox

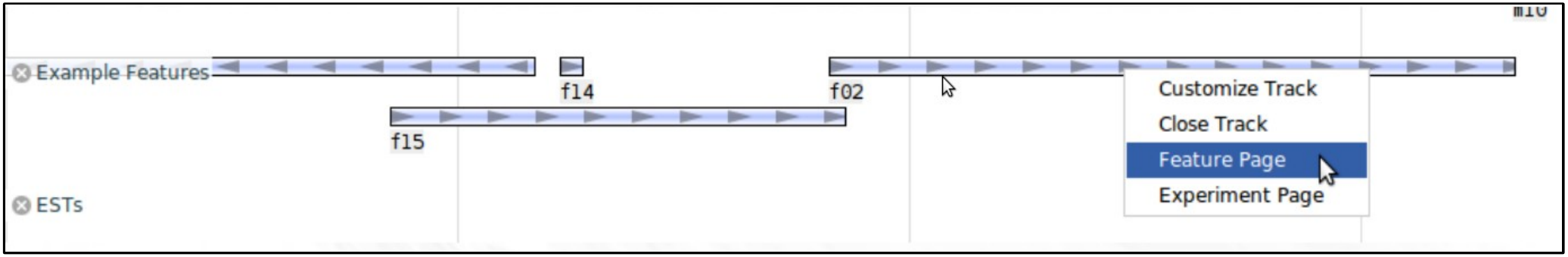
Coming: Overview Images



Can have a karyotype, or any other image.

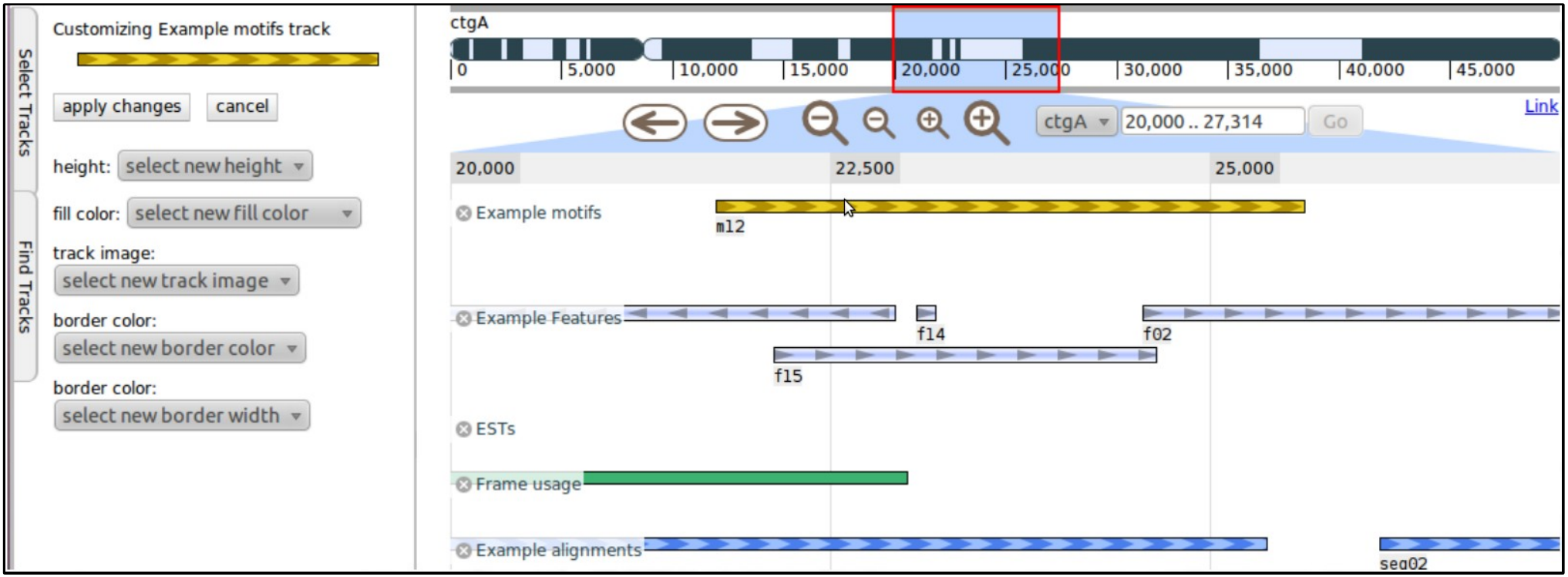
work by OICR intern Natalie Fox

Coming: Context Menus



work by OICR intern Natalie Fox

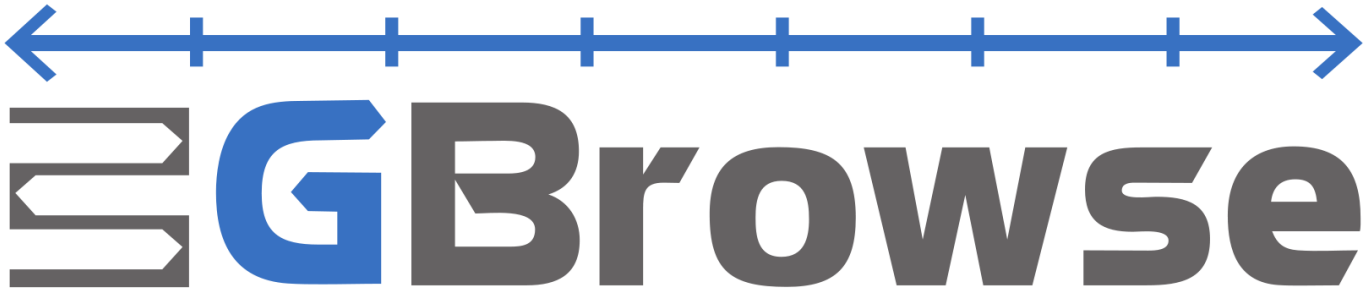
Coming: Track Customization



work by OICR intern Natalie Fox

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)

Apollo