

JBrowse: a Modern Genome Browser

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PAG XX

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2R:9,865,964 .. 9,915,264 - Google Chrome

2R:9,865,964 .. 9,915,264

jbrowse.org/genomes/dmel/

Available Tracks: (Drag → to view)

0 | 2,000,000 | 4,000,000 | 6,000,000 | 8,000,000 | 10,000,000 | 12,000,000 | 14,000,000 | 16,000,000 | 18,000,000 | 20,000,000

Navigation: ← → 🔍 - 🔍 + 🔍 2R 9,865,964 .. 9,915,264 Go [Link](#)

9,875,000 | 9,887,500 | 9,900,000 | 9,912,500

Tracks:

- tRNA
- Non coding RNA
- Natural transposon
- Ortholog (FlyBase)
- cDNA and Aligned genomic sequences
- protein binding site
- enhancer
- rescue fragment
- regulatory region
- Mutation: point mutation
- Mutation: sequence variant
- Mutation: deletion
- Mutation: insertion site
- XRate predictions

Conservation

Transgene insertion site

Oligonucleotides

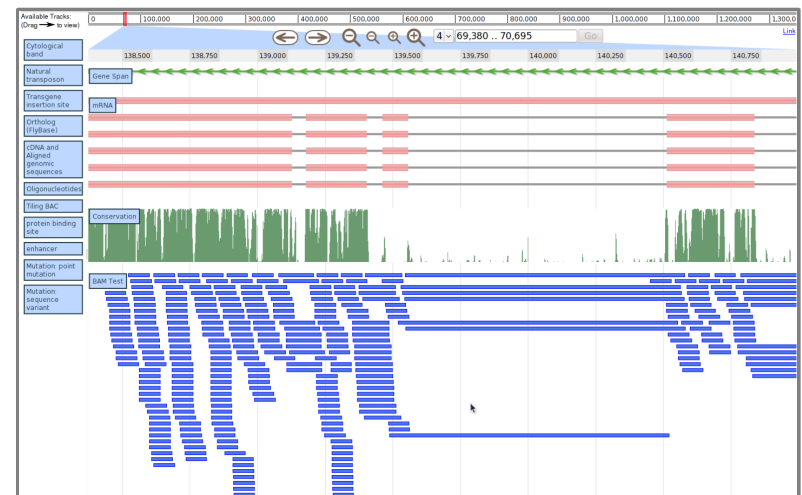
mRNA: [513350-RA](#), [RN-tre-RC](#), [CG30482-RA](#), [mam-RE](#)

Ortholog (FlyBase): [CG8067-RA](#), [mam-RA](#)

cDNA and Aligned genomic sequences: [RN-tre-RA](#), [RN-tre-RE](#)

JBrowse...

- Smooth, fast navigation (*think Google Maps for genomes*)
- Supports BED, GFF, Bio::DB::*, Chado, WIG, BAM, UCSC (*intron/exon structure, name lookups, quantitative plots*)
- Relies on pre-indexing to minimize security exposure and runtime bandwidth/CPU load on the server (*future versions more likely to do some server work at runtime*)
- Has an API for customized track/glyph extensions
- Is stably funded by NHGRI, with many interesting innovations implemented & pending integration
- Is open source software



The JBrowse Project

- free and open source (license: GPL / Artistic)
- a **GMOD** project
<http://gmod.org>
- development uses `git`, hosted on GitHub
<http://github.com/GMOD/jbrowse>
- PIs most involved: Ian Holmes, Suzi Lewis, Lincoln Stein
- just got 3 more years of funding from NHGRI!

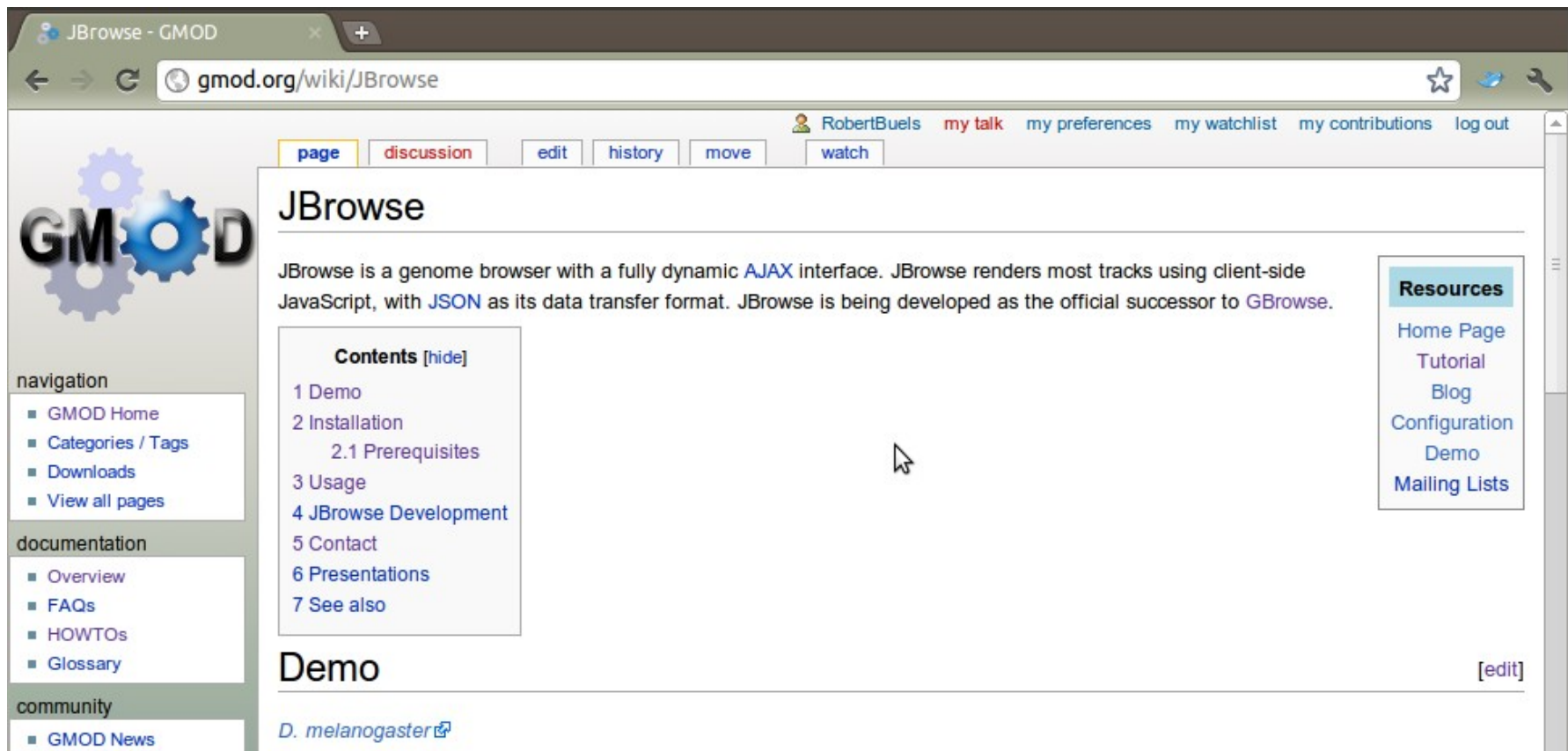


A Brief History of JBrowse

- 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 = “official” successor to GBrowse
- 2011 Mitch Skinner joins genomics startup
US politicians play chicken with economy
NHGRI renews for 3yr
- 2012 Robert Buels joins the team

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-section "Demo" with a link to [D. melanogaster](#).

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

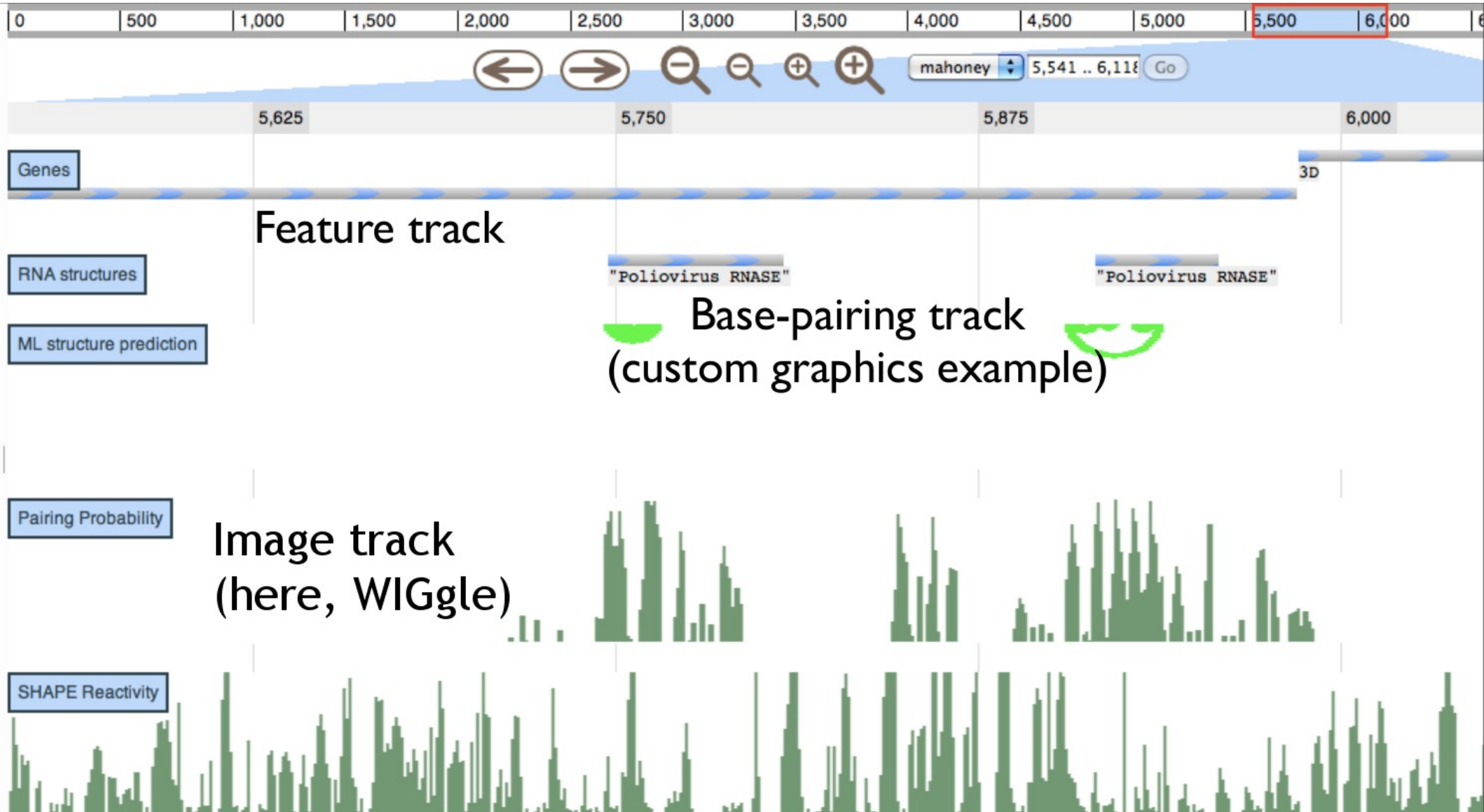
community

- GMOD News

First look: Live Demo

- a couple of JBrowsers around the web
 - <http://intron.ccam.uchc.edu/JBrowse/Dmel/>
 - <http://jbrowse.org/ucsc/hg19/>
- maybe install a demo JBrowse locally with the tutorial

Types of Tracks



Feature Tracks

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

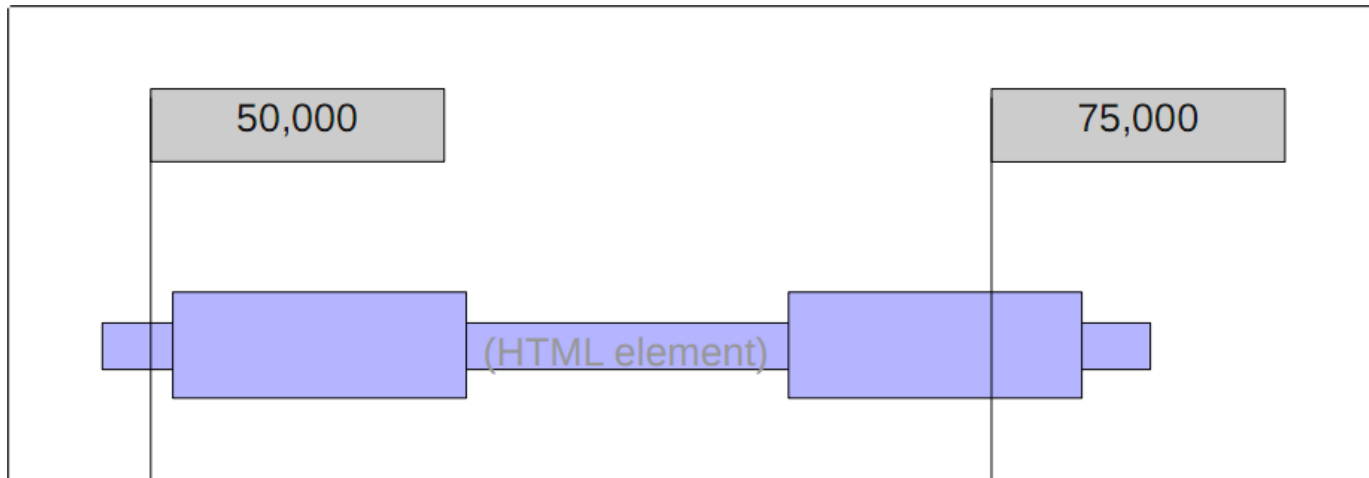
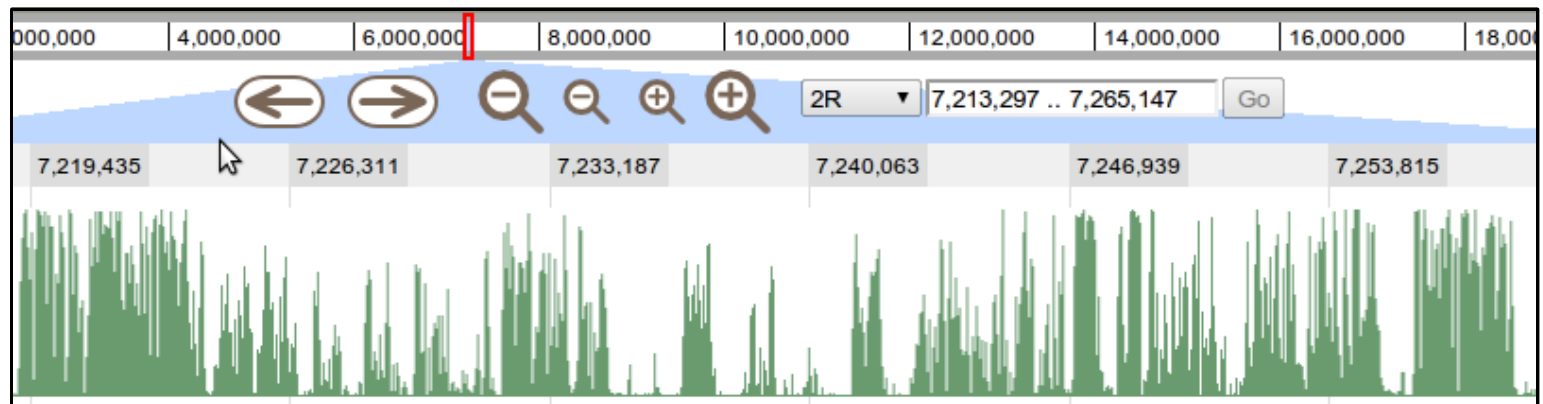


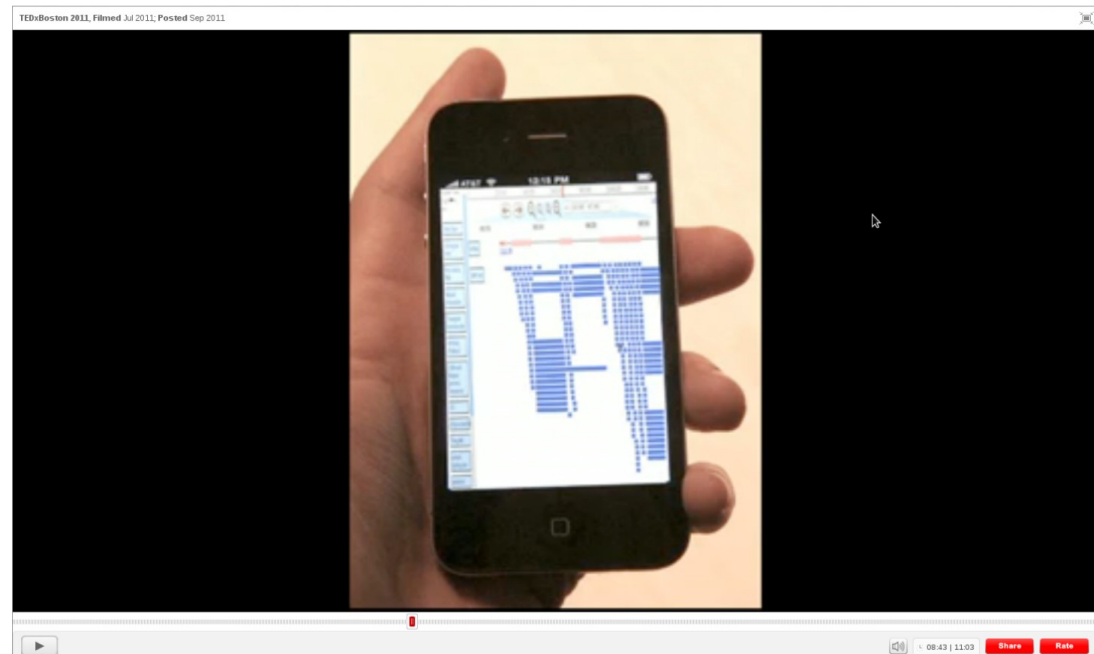
Image Tracks

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



± Particular Strengths

- fast and smooth!
- easy things are easy!
- works nicely on an iPad/iPhone



JBrowse on an iPhone
video frame from TEDx Boston talk by Richard Resnick

± Particular Weaknesses

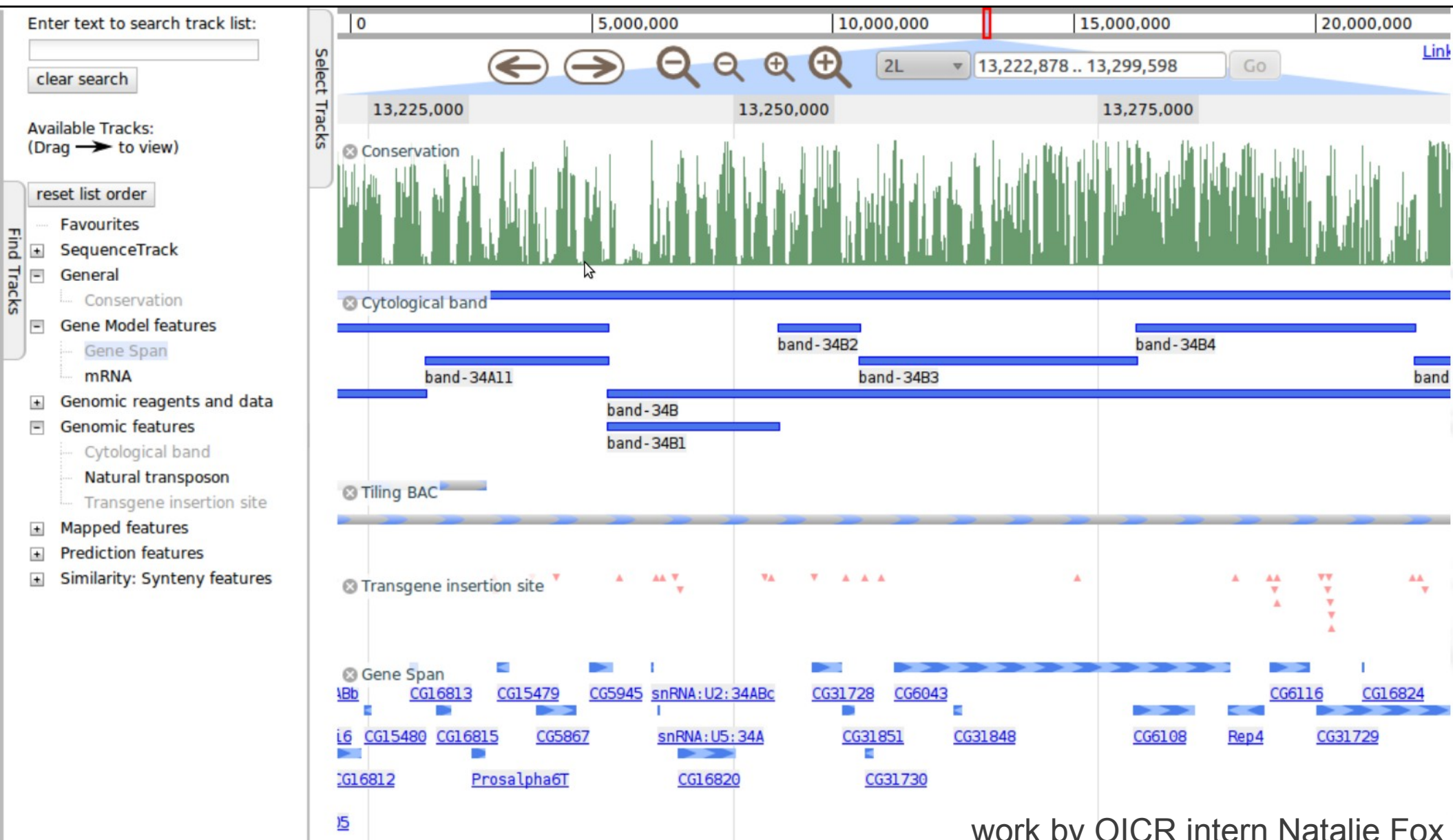
- no user-uploaded data support
- slow for big numbers of reference seqs (e.g. 5,000 annotated contigs)
- few glyph options, feature tracks are limited by the facts of `<div>`

These will all be improved.

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

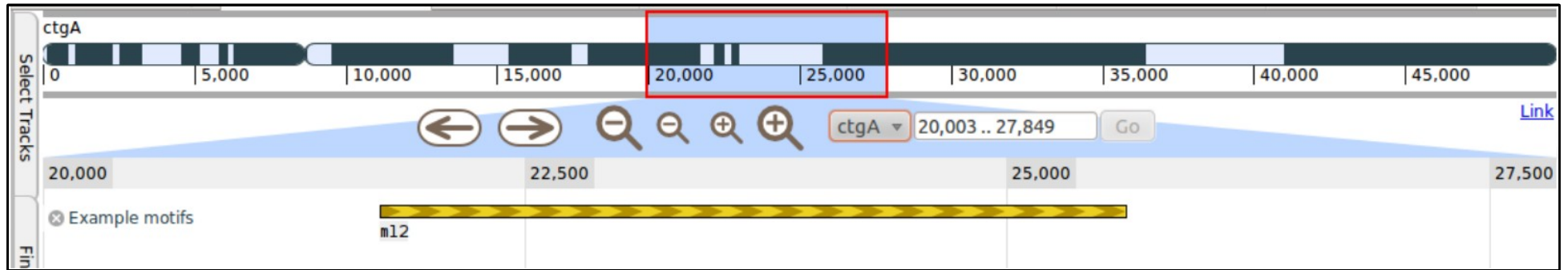
13,225,000 13,250,000

Find Tracks

- Conservation
- Cytological band
 - band - 34A11
 - band - 34B
 - 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

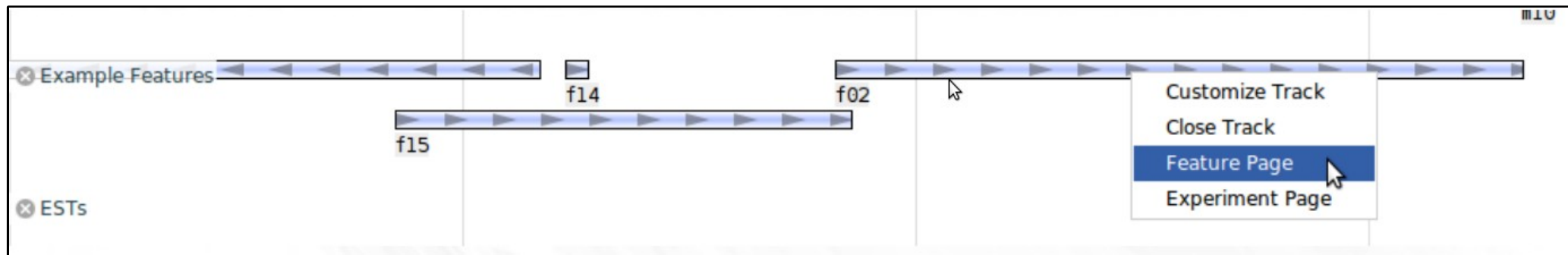
work by OICR intern Natalie Fox

Coming: Overview Images



Can have a karyotype, or any other image.

Coming: Context Menus



Coming: Track Customization

The image displays a genomic browser interface with a customization panel on the left and a main track view on the right.

Customization Panel (Left):

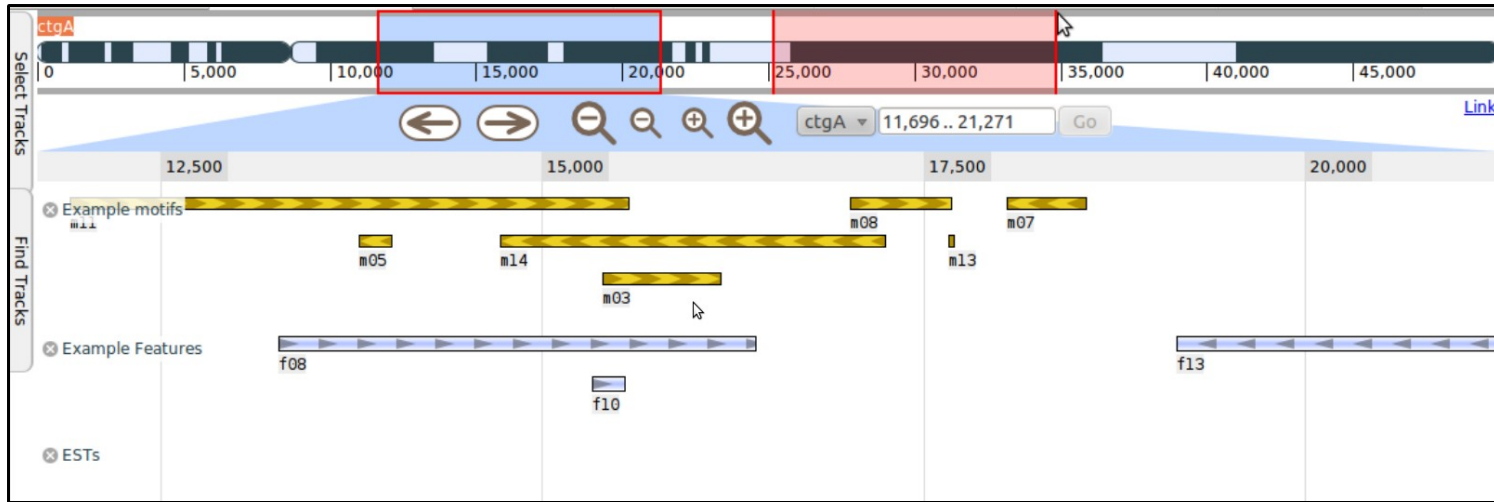
- Select Tracks:** A section for managing track visibility.
- Find Tracks:** A section for finding tracks.
- Customizing Example motifs track:** A section for customizing the 'Example motifs' track, including:
 - Buttons: `apply changes`, `cancel`
 - height: `select new height` (dropdown)
 - fill color: `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)

Main Track View (Right):

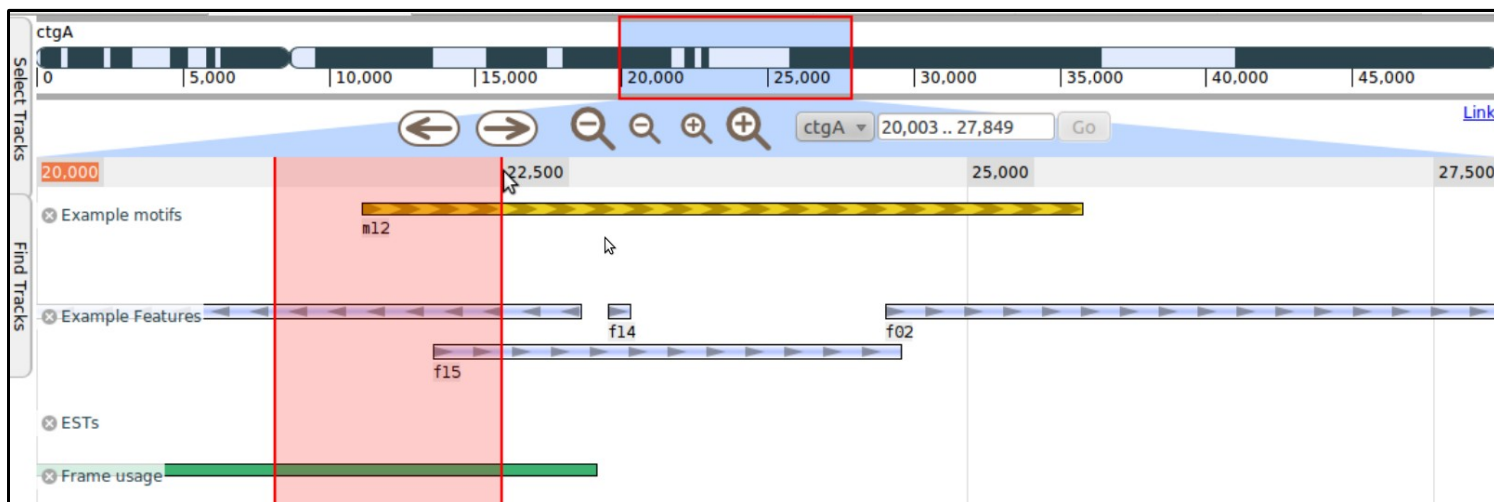
- ctgA:** A genomic track with a scale from 0 to 45,000. A red box highlights the region from 20,000 to 25,000.
- Navigation:** Navigation icons (left, right, zoom in, zoom out) and a search bar with `ctgA` and `20,000..27,314`, and a `Go` button.
- Zoomed View:** A detailed view of the 20,000 to 25,000 region with markers at 20,000, 22,500, and 25,000.
- Tracks:**
 - Example motifs:** A yellow track with a dashed border and a mouse cursor over a feature labeled `m12`.
 - Example Features:** A blue track with arrowheads and features labeled `f15`, `f14`, and `f02`.
 - ESTs:** A track for ESTs.
 - Frame usage:** A green track.
 - Example alignments:** A blue track with arrowheads and a feature labeled `seq02`.

Coming: Drag to Zoom

In the overview

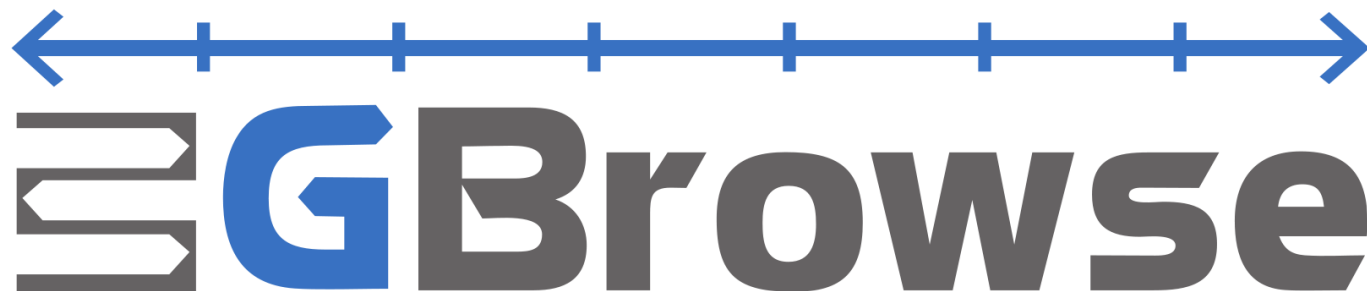


In the main view



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)



WebApollo Live Demo!

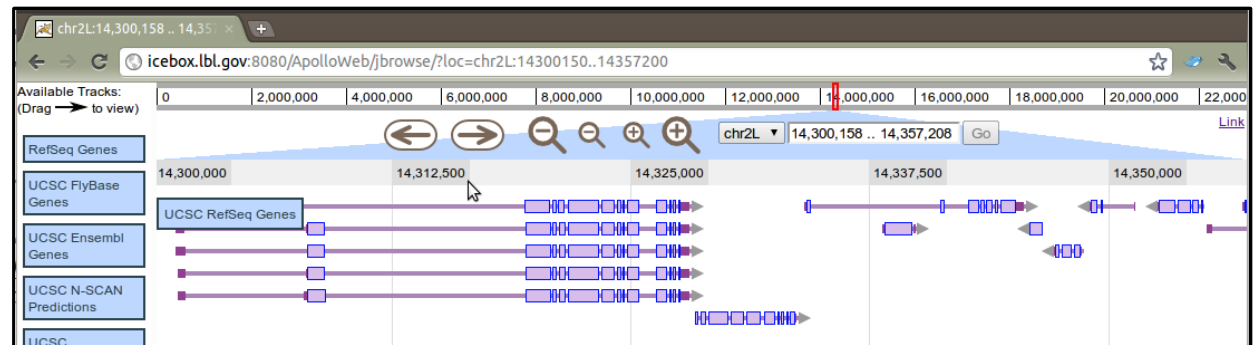
Step
1

<http://goo.gl/SHByG>

User name: **write_1**
Password: **write_1**

Step
2

<http://goo.gl/mSh3w>



Big Thanks To:

Suzi Lewis (LBNL)

Gregg Helt

Ed Lee



Nomi Harris

Ian Holmes (Berkeley)

Mitch Skinner

Stephen Cummings

Lincoln Stein (OICR)

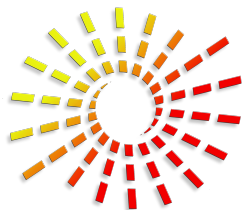
Natalie Fox

Adam Wright



Lukas Mueller (BTI, SGN)

NHGRI



<http://jbrowse.org>



<http://gmod.org/wiki/JBrowse>

github

<http://github.com/GMOD/jbrowse>

(yes, jbrowse needs a logo)

The End

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(#bioperl, #gmod)



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