JBrowse

PAG 2017

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What is GMOD?

- A set of interoperable open-source **software** components for visualizing, annotating, and managing biological data.

- An active **community** of developers and users asking diverse questions, and facing common challenges, with their biological data.

Who uses GMOD?

Plus hundreds more organizations.

Other GMOD Projects

- GBrowse - "old school" Genome Browser, based on BioPerl

- MAKER - Tool for doing whole genome *de novo* annotation

- Chado - Organism-agnostic database schema for genomics and related data

- Apollo - Web-based feature annotation editor based on JBrowse

- Tripal - Web framework based on Drupal/PHP; provides user interface to data in Chado (Right behind me at 4:00!)

- InterMine - Very powerful query engine/web UI for biological data (loaders for GFF, Chado)

- Galaxy - Very powerful workflow editor—lets you create and easily rerun complex workflows.

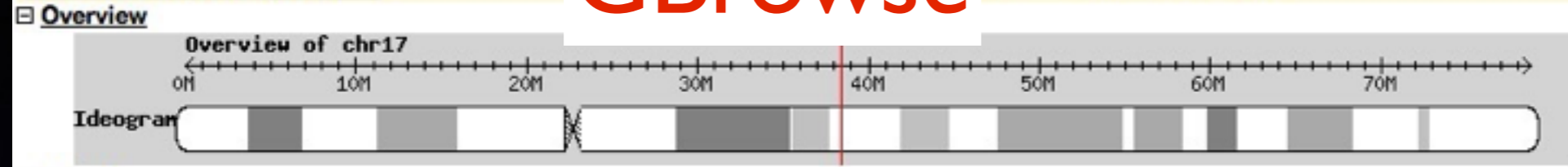# What are Genome Browsers good for?

- Visualizing dense data from a multitude of sources (genes from a GFF file, RNASeq data from a BAM file, variation data from a VCF file)

- Homology and gene expression support for gene models

GBrowse

Ensembl

- Many "specialty" browsers (eg, Biodalliance, Savant)

Why Install Your Own?

- You have data no one else has

- You want to be able to share it with your group, community, the world (potentially with "less savvy" users)

- You want to have control over how it looks

Why JBrowse?

- (Fairly) Easy install

- Good user experience (getting close to a browser-desktop hybrid)

- Good community support (mailing lists, tutorials, software updates)

Installation

- Only requires:
  - Web server (apache, lighttpd, nginx, etc)
  - Perl/make/standard unix-y tools
  - Really easy to get via AWS (Docker too, but we won't be using that)

JBrowse Attributes

- 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

- free and open source (license: LGPL / Artistic)

- a GMOD project

  - http://gmod.org

- developed using git, hosted on GitHub

  - http://github.com/GMOD/jbrowse

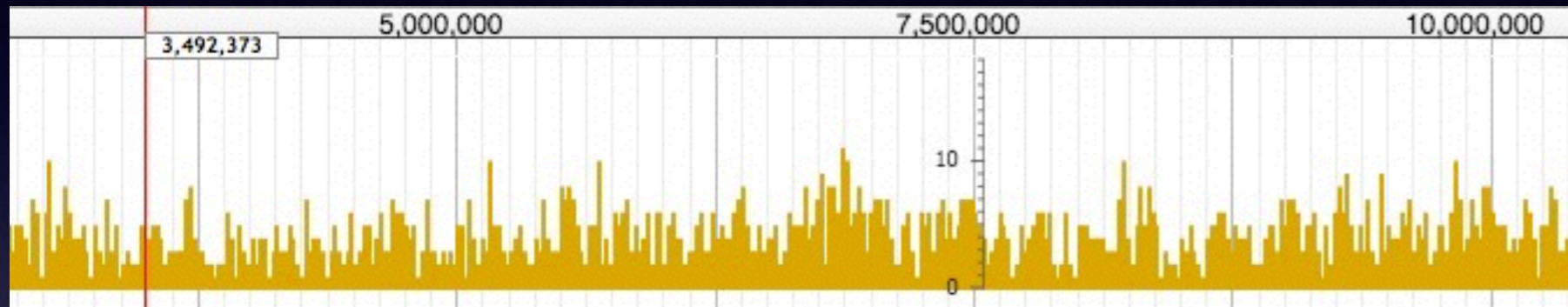- PIs most involved: Ian Holmes, Lincoln Stein, Suzi Lewis

Feature Tracks

- HTMLFeatures: Rectangles (<div>s) with various fills and heights to represent the feature spans (more compatible)

- CanvasFeatures: Much prettier, more configurable glyphs

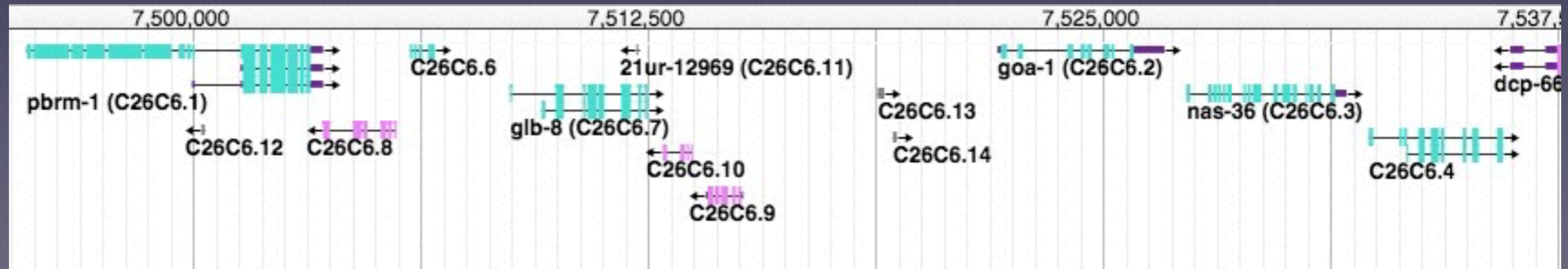- Super-configurable left clicking and right-click
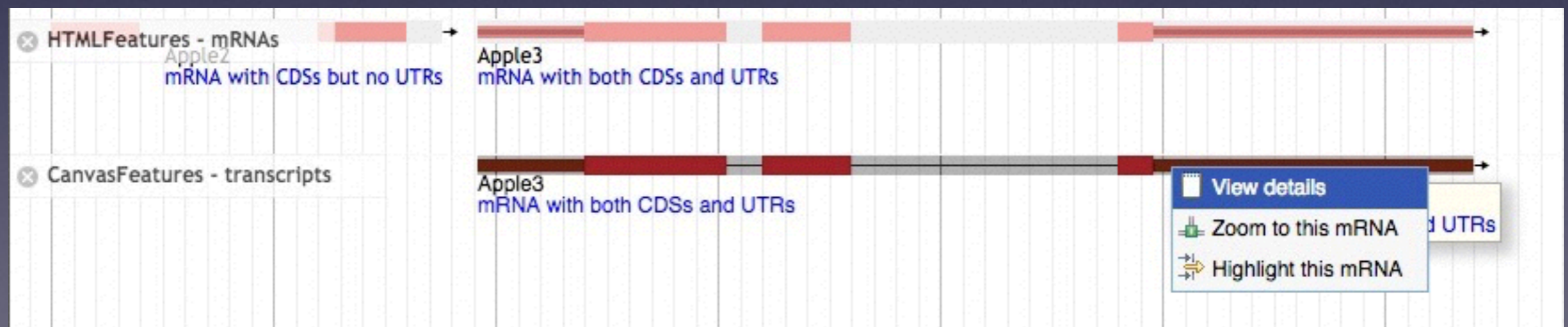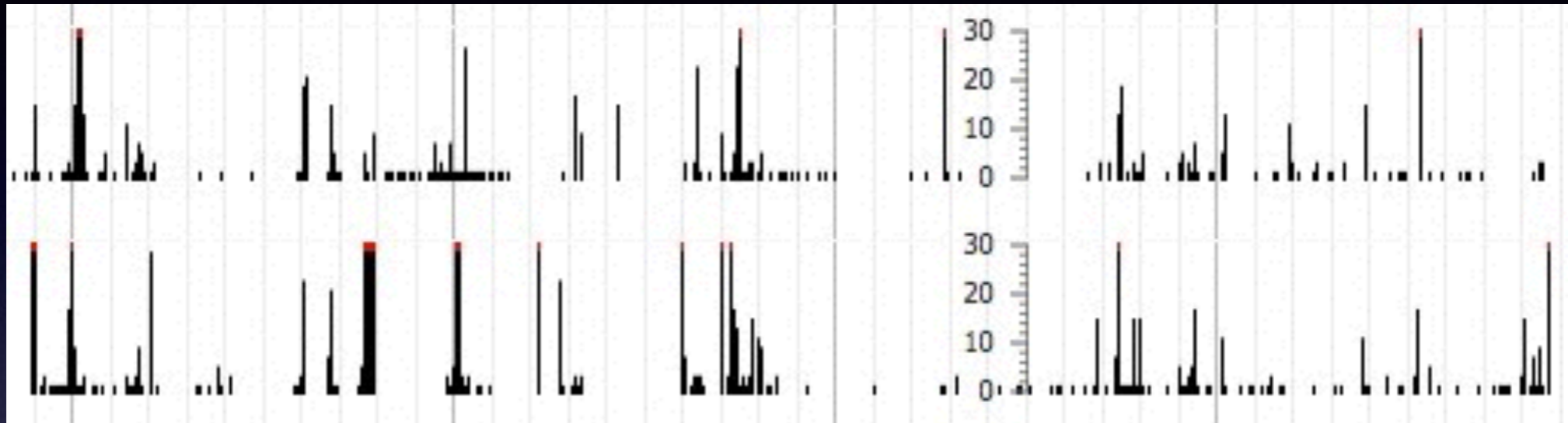
Feature Density Plots
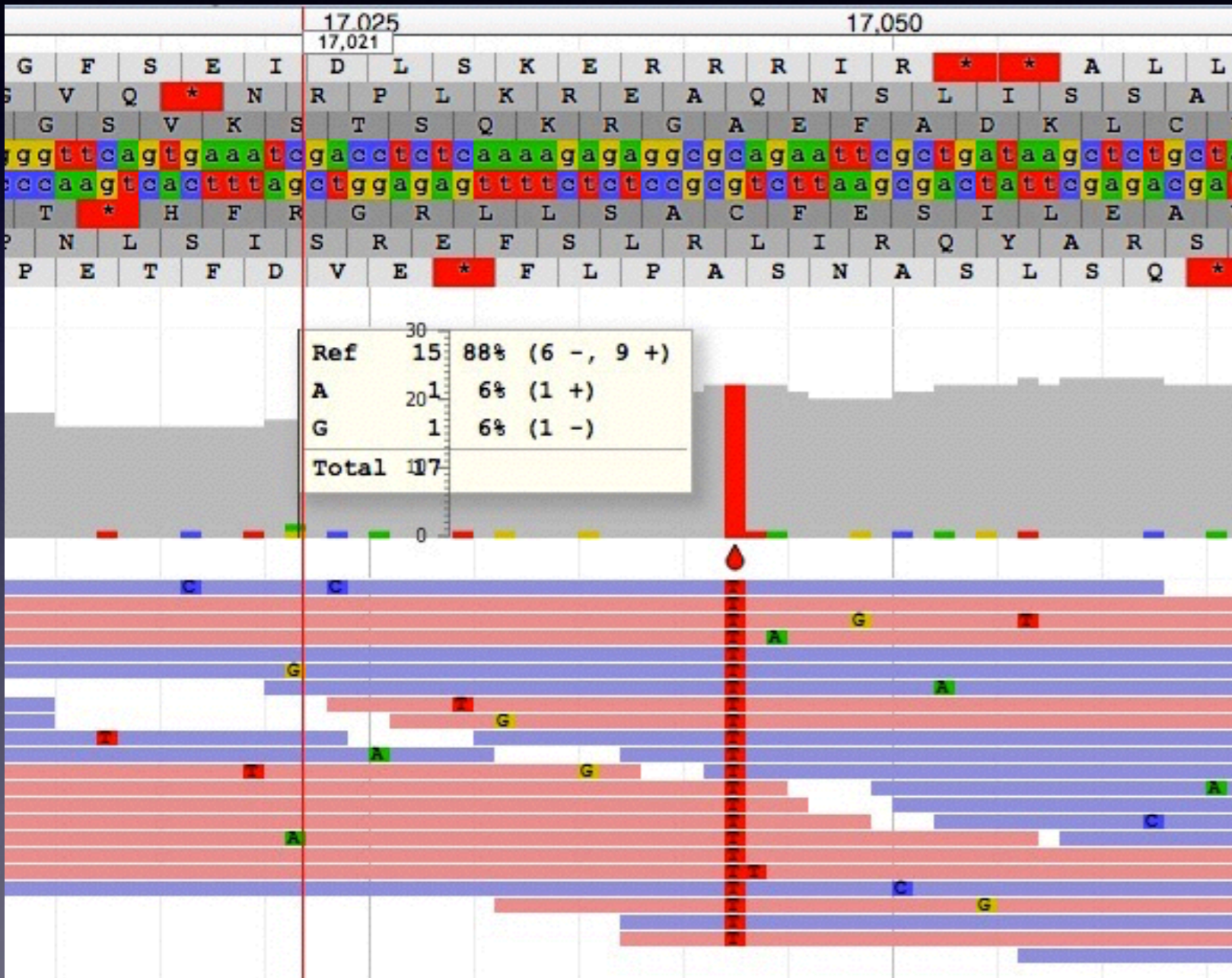
Zoomed out

Zoomed in

Wiggle/BigWig Tracks

- Reads small chunks directly from BigWig file.
- Needs only a not-super-old (< 5 yrs) browser, except for Internet Explorer.
- IE requires version 10.

BAM Alignment Tracks

- 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

- Open local files directly on client, no data transfer required

- Highly customizable, embeddable, integratable, programmable

Apollo

- Based on JBrowse, using plugin system

- Next generation of the popular Apollo annotation editor

- Online annotation editing and curation!

Apollo

- 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 a live demo (later)

- http://genomearchitect.org/WebApolloDemo/

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!

- Apollo client is a JBrowse plugin

Coming in 2.X
(see the talk during the GMOD workshop on Wednesday!)

- MORE: data types, sorting options, speed

- Graphical configuration

- Multiple views, linked or independent

- Logins, uploading, track sharing

- Circular genomes

Big Thanks

Ian Holms (UC Berkeley)
Rob Buels
Mitch Skinner
Amelia Ireland
Eric Yao

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

Suzi Lewis (LBNL)
Gregg Helt
Ed Lee
Justin Reese (UofMo)
Colin Diesh (UofMo)

NHGRI
Cold, hard cash

The End
(on to the workshop)

http://jbrowse.org/

GMOD: http://gmod.org/wiki/JBrowse

Github: http://github.com/GMOD/jbrowse