JBrowse

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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)

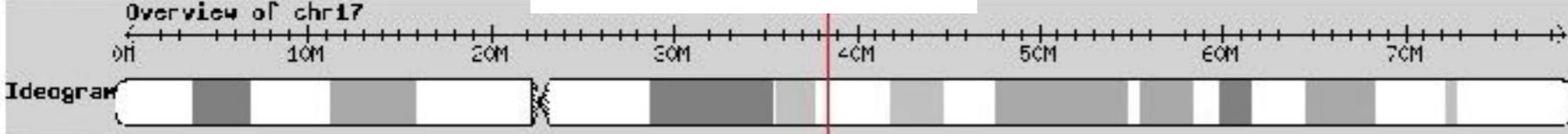- Homology and gene expression support for gene models

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

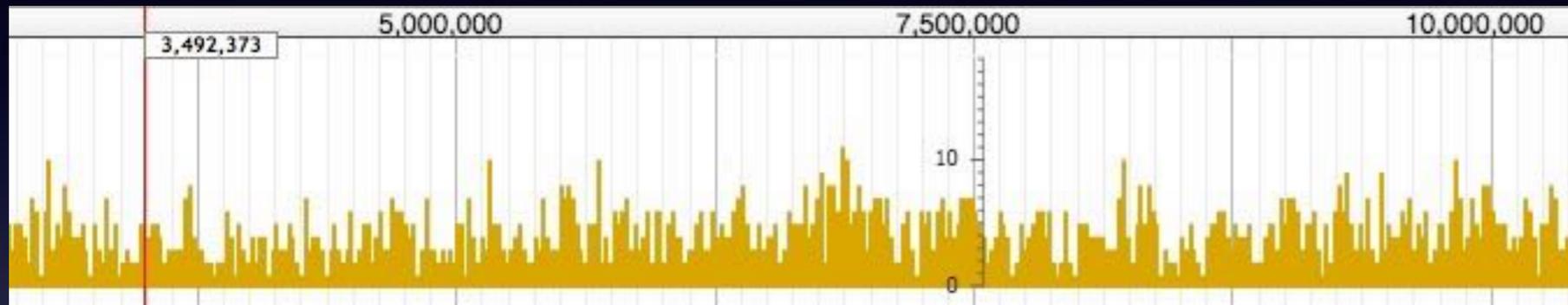- PIs most involved: Ian Holmes, Lincoln Stein, Suzi Lewis

Feature Tracks

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

- CanvasFeatures: Much prettier, more configurable glyphs

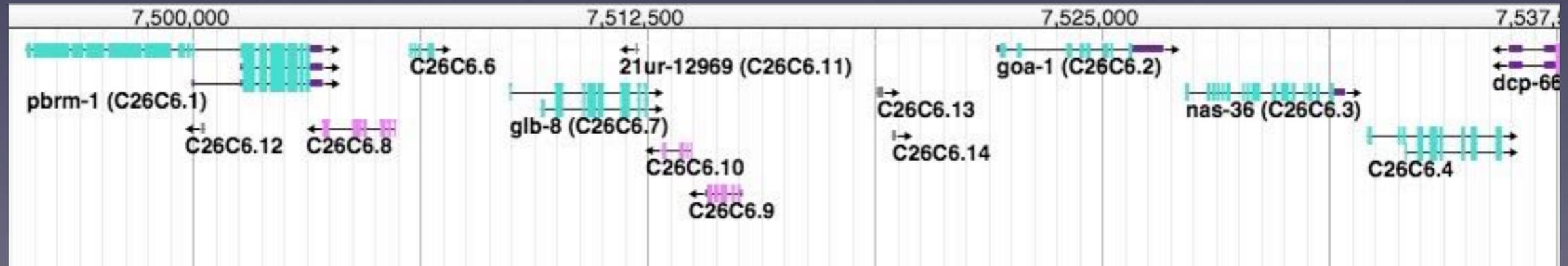- Super-configurable left clicking and right-click
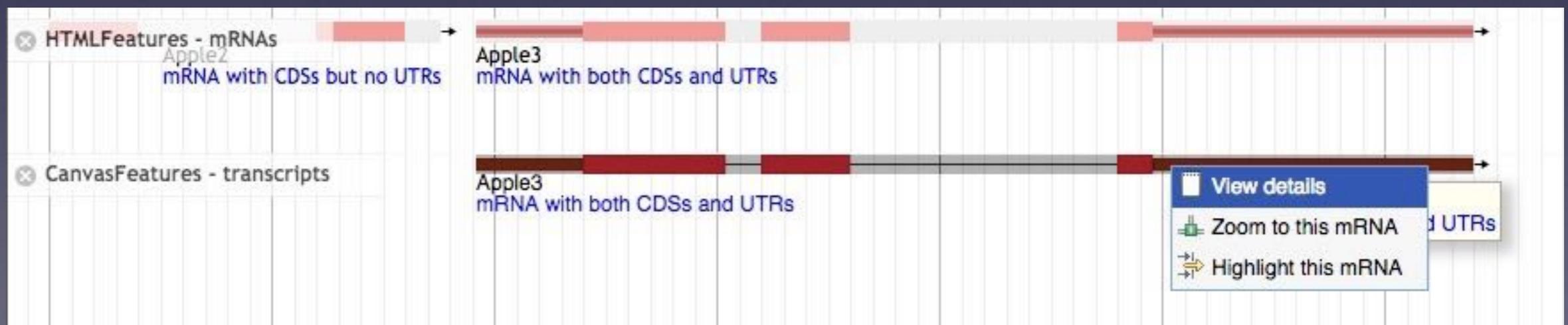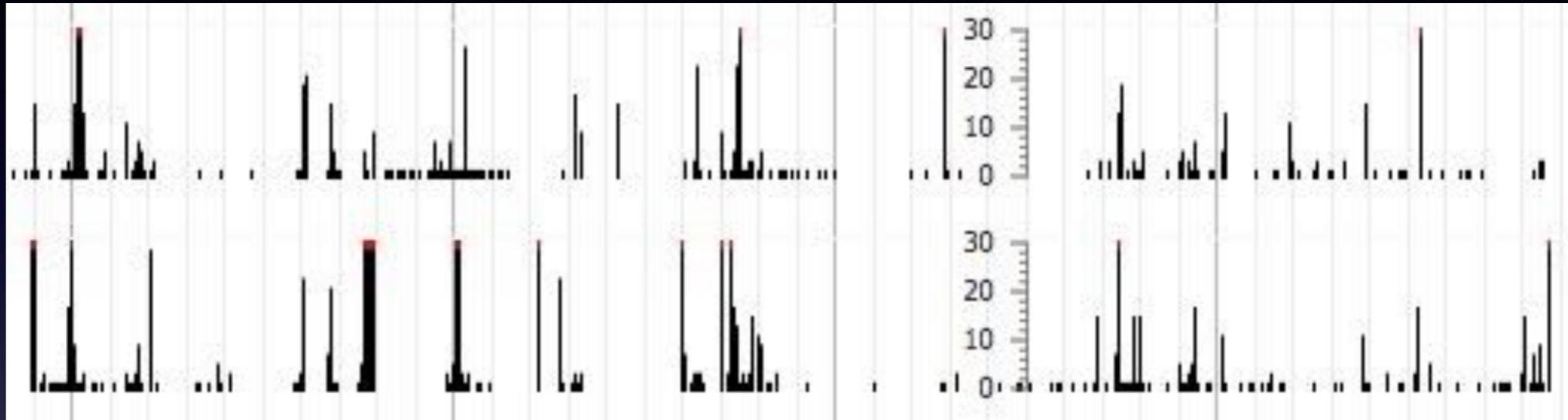
Feature Density Plots

Zoomed out

Zoomed in

Wiggle/BigWig Tracks

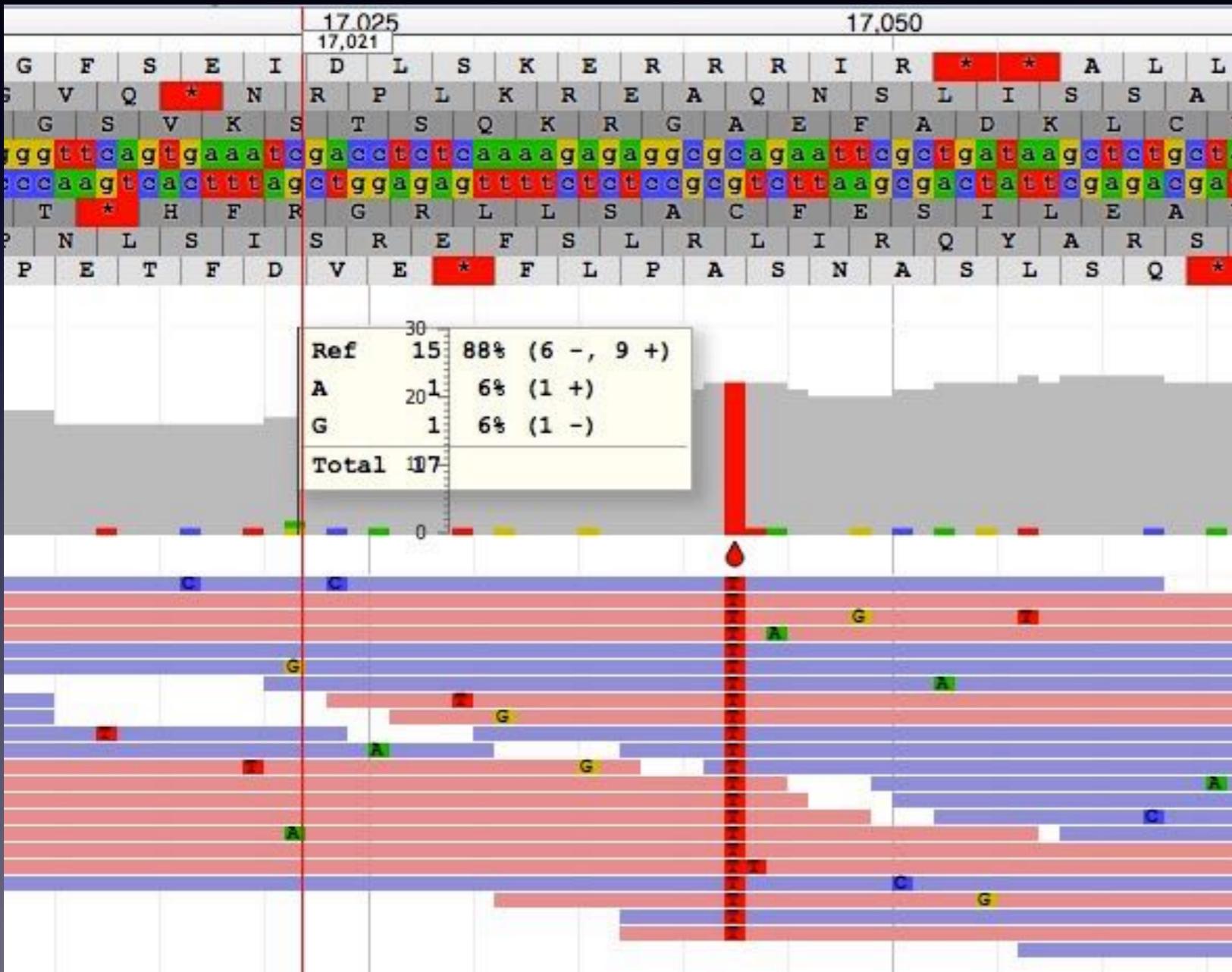- Reads small chunks directly from BigWig file.
- Needs only a not-super-old (< 5 yrs) browser, except for Internet Explorer.
- IE requires version 10.

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 future releases

(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

- Server side component, BLAST integration

Big Thanks

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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