

JBrowse

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Scott Cain

Ontario Institute for Cancer Research

GMOD Coordinator

WormBase Developer

scott@scottcain.net

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?



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?

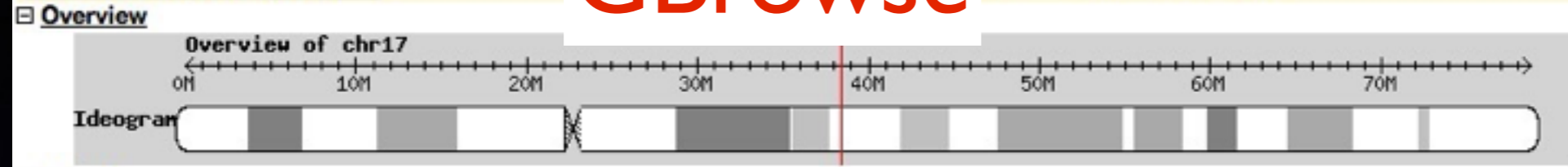
- Visualizing dense data from a multitude of sources (genes from a GFF file, RNASeq data from a BAM file, variation data from a VCF file)
- Homology and gene expression support for gene models

GBrowse

Landmark or Region: chr17:38350227..384002; Search

Reports & Analysis: Download GFF File... Configure... Go

Data Source: Welcome to eqtl.uchicago.edu! kbp + >>> Flip



Details

Entrez genes: NM_025267 AARS1: alanyl-tRNA synthetase domain containing 1; NM_173079 RUNDC1: RUN domain containing 1

Degner, Pai, Pique-Regi et al. (2012): $-\log_{10}(P)$, LCLs, 70 Nigerian HAPMAP ids, DNase sensitivity QTLs (dsQTLs) by

Schadt et al. (2007): $-\log_{10}(P)$, liver, 427 ids, European descent

Myers et al. (2007): $-\log_{10}(P)$, cortex from control brain, 279 ids, European descent

Stranger et al. (2007): $-\log_{10}(P)$, LCLs, 210 HAPMAP ids, 4 single populations.

Veyrieras et al. (2008): $-\log_{10}(P)$, LCLs, 210 HAPMAP ids, multi-population.

Veyrieras et al. (2008): posterior probability, LCLs, 210 HAPMAP ids, multi-population.

Pickrell et al. (2010): $-\log_{10}(P)$, LCLs, 69 Nigerian HAPMAP ids, RNA-Seq for eQTLs.

Innocenti et al. (2011): $\log_{10}(\text{Bayes Factor})$, Liver, 266 ids, RNA-Chip for eQTLs.

Pickrell et al. (2010): $-\log_{10}(P)$, LCLs, 69 Nigerian HAPMAP ids, RNA-Seq for splicing QTLs.

Montgomery et al. (2010): $-\log_{10}(P)$, LCLs, 60 European HAPMAP ids, RNA-Seq for transcript QTLs.

Zeller et al. (2010): $-\log_{10}(P)$, Monocytes, 1,490 ids recruited in Germany.

Montgomery et al. (2010): $-\log_{10}(P)$, LCLs, 60 European HAPMAP ids, RNA-Seq for exon QTLs.

Dinas et al. (2009): $-\log_{10}(P)$, Fibroblasts, 75 Europeans

Dinas et al. (2009): $-\log_{10}(P)$, LCLs, 75 Europeans

Dinas et al. (2009): $-\log_{10}(P)$, T-cells, 75 Europeans

Track height: Drag/Select:

32.40 Mb .80 Mb

32.40 Mb 32.60 Mb 32.80 Mb

processed transcript RNA gene

IFIT1P1-001 > processed pseudogene

BRCA2-002 > nonsense mediated decay

BRCA2-004 > processed transcript

BRCA2-005 > nonsense mediated decay

BRCA2-006 > retained intron

< N4BP2L1-001 protein coding

- 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

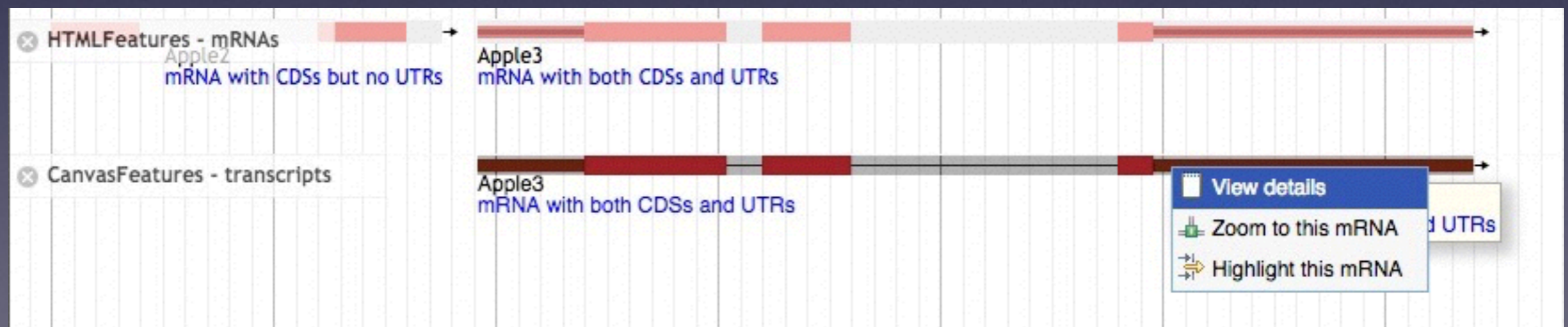
- Do everything possible on the client side, in JavaScript.
- Fast, smooth navigation.
- Supports GFF3, BED, Bio::DB::*, Chado, WIG, BAM, BigWig, VCF, and UCSC import (intron/exon structure, name lookups, quantitative plots).
- Is stably funded by NHGRI.
- Is open source, of course.
- Did I mention it's 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>
- Pls most involved: Ian Holmes, Lincoln Stein, Suzi Lewis

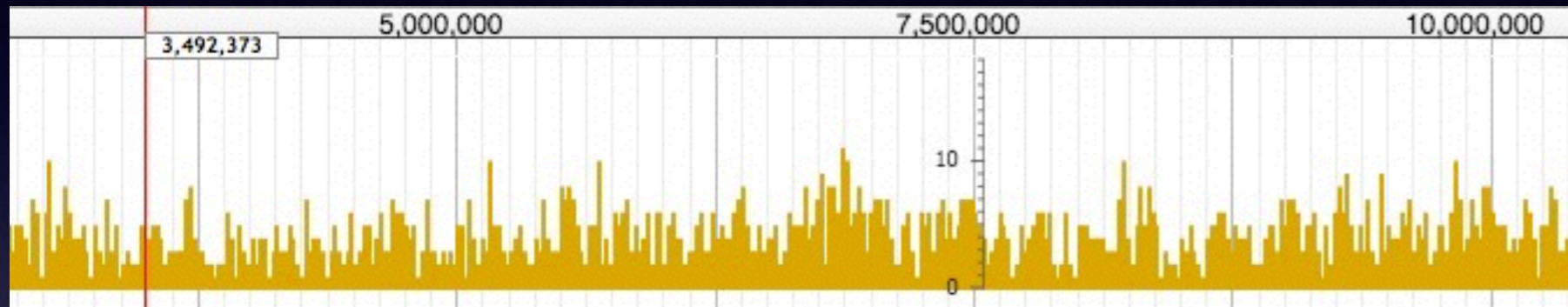
Feature Tracks

- 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

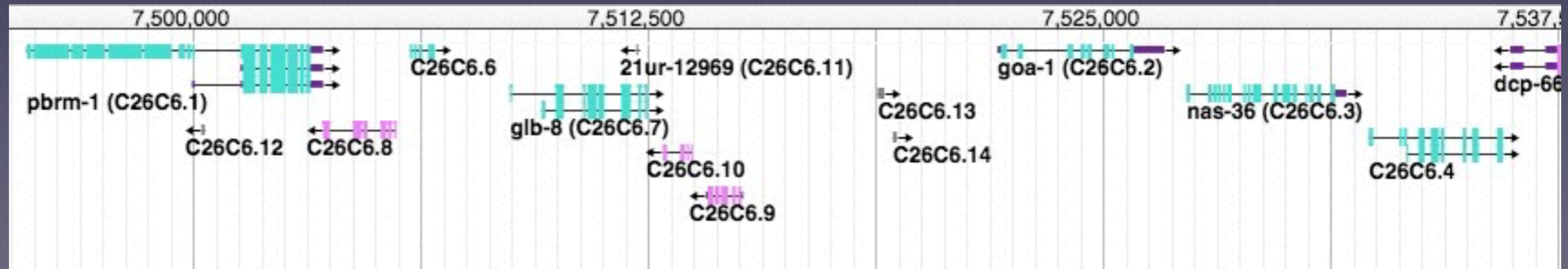


Feature Density Plots

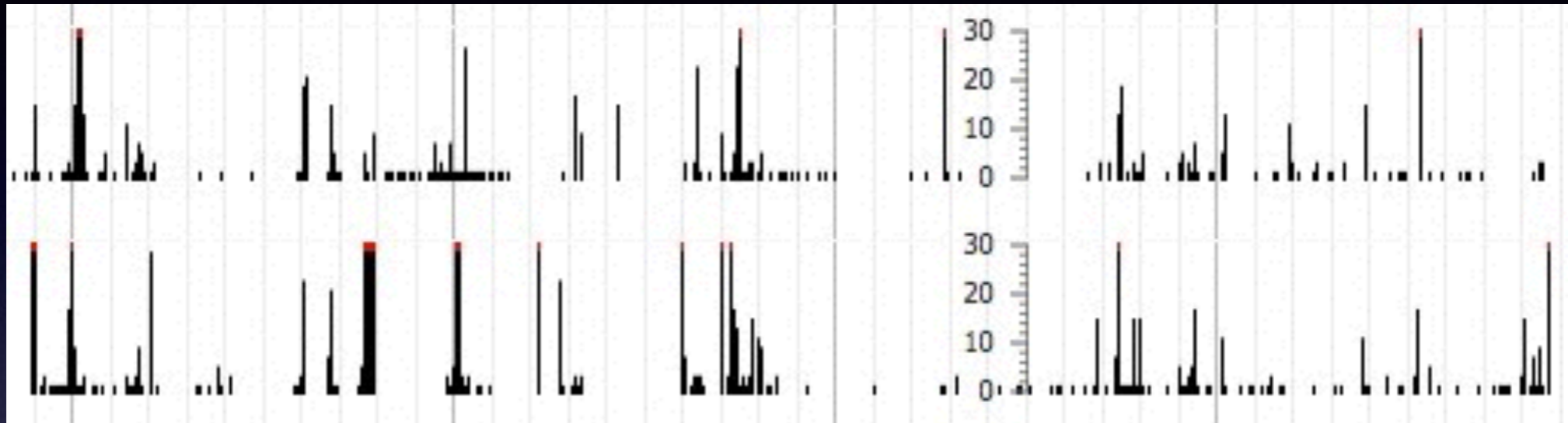
Zoomed out



Zoomed in

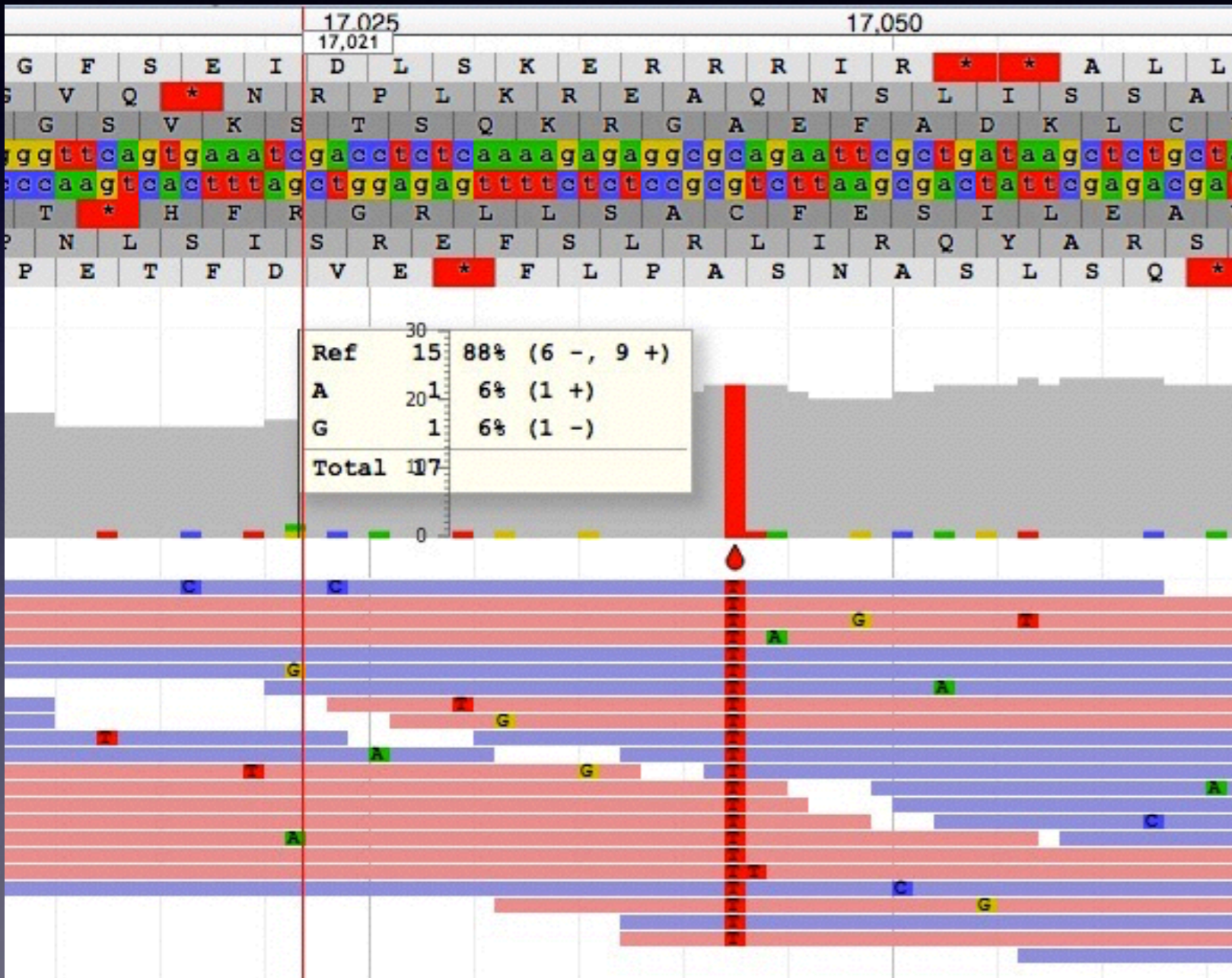


Wiggle/BigWig Tracks



- 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

SNV

Primary Data

| | |
|-------------|-------------------------------|
| Type | SNV |
| Score | 104 |
| Description | SNV A -> T |
| Position | scf1117875582023:88017..88017 |
| Length | 1 bp |

Attributes

| | |
|---------------------|------------------|
| AC1 | 2 |
| AF1 | 1 |
| DP | 17 |
| DP4 | 0 0 11 6 |
| FQ | -78 |
| MQ | 57 |
| VDB | 0.0507 |
| alternative_alleles | T |
| description | SNV A -> T |
| reference_allele | A |
| seq_id | scf1117875582023 |

Genotypes (1)

| | | |
|--------------|----------|-------------|
| variant | 1 | 100% |
| homozygous | 1 | 100% |
| T variant | 1 | 100% |
| Total | 1 | 100% |

| Name | GT | PL | GQ |
|----------------------|-------|----------|----|
| simulated-sorted.bam | T / T | 137 51 0 | 99 |

- 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

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

- Based on JBrowse, using plugin system
- Next generation of the popular Apollo annotation editor
- Online annotation editing and curation!

Web  pollo

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)

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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>