(JBrowse 1.10.0 will be released Any Day Now)
JBrowse

- 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

2006  First prototype (pre-rendered Gbrowse tiles).
      NHGRI funds 3yr development of project.
      Mitch Skinner joins as lead developer.


2008  All-JavaScript rendering on the client.

2009  Paper in Genome Research.

2010  WebApollo funded for development based on JBrowse.
      NHGRI renews for 6mo.
      JBrowse dubbed “official” successor of GBrowse.

2011  Mitch Skinner moves on.
      NHGRI renews for 3yrs.

2012  Robert Buels joins as lead developer.
      Aggressive development on NGS formats, scalability, configurability.

2013  WebApollo first public release.
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

- rectangles (<div>s) with various fills and heights to represent the feature spans
- Super-configurable left clicking and right-click menus.

![Screenshot of feature tracks with examples of clicks and menus](image-url)
Feature Density Plots

Zoomed out

Zoomed in
Image Tracks

- any pre-generated images that cover the genome
  - RNA base-pairing
  - Images from other genome browsers
  - Legacy JBrowse .wig formatter used this also
Wiggle/BigWig Tracks

http://goo.gl/4kWFP  http://jbrowse.org/genomes/tomato/

- Reads small chunks directly from BigWig file.
- Needs only a not-super-old (< 4 yrs) browser, except for Internet Explorer.
- IE requires version 10.
- 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
++ Particular Strengths ++

- open local files directly on client, no data transfer required
- highly customizable, embeddable, integratable, programmable
Faceted Track Selection

- make a CSV file of as much track metadata, and/or put track metadata in JSON config files

Open Local Files

- Select multiple files
- Paste multiple URLs
- Blurring the line between “desktop” and “web”
Integrating JBrowse

• Your systems can drive JBrowse by emitting JSON
  – Configuration
  – Data (Jbrowse/Store/SeqFeature/REST)

• JBrowse is self-contained, can **go to the data**
  – E.g. put it in the end of your cloud-based SNP-calling pipeline to visually validate SNPs

• Plugin system: build on top of JBrowse
WebApollo
http://www.gmod.org/wiki/WebApollo

• based on JBrowse, using plugin system
• next generation of the popular Apollo annotation editor
• online annotation editing and curation!
WebApollo

• 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 Live Demo!

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.
- WebApollo client is a JBrowse plugin
Coming in 2.x Series

- **MORE**: data types, sorting options, speed
- Graphical configuration
- Multiple views, linked or independent
- Logins, uploading, track sharing
- Circular genomes
It's an Open Source Project

• If you are interested in seeing all this happen sooner
  – Can you spare your time?
  – Some of your developers' time?

• My door is always open
Big Thanks

Suzi Lewis (LBNL)
Gregg Helt
Ed Lee
Justin Reese

Ian Holmes (UC)
Amelia Ireland
Mitch Skinner

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

NHGRI

GMOD
The End

http://jbrowse.org

http://gmod.org/wiki/JBrowse

http://github.com/GMOD/jbrowse

(yes, jbrowse needs a logo)
Robert Buels

rbuels@gmail.com

rbuels on freenode IRC
(#bioperl, #gmod)

• Was Engineering Lead at Sol Genomics Network
  http://solgenomics.net, at BTI with Lukas Mueller

• Jan. 2012, became new JBrowse Lead Developer
  at UC Berkeley with Ian Holmes
Releases

1.3.0 – April 13
  Rubberbanding, y-axis scales, embedded mode, many other small fixes
1.4.0 – June 14
  Faceted track selector, name autocompletion
1.5.0 – August 13
  Direct BigWig, wiggle XY plot tracks, detail popups, context menus
1.6.0 – August 25
  Feature descriptions, bugfixes for GMOD summer school
1.7.0 – November 5
  Direct BAM, alignment tracks, data export, coverage tracks, wiggle density
1.8.0 – January 31
  Open local BAM, BigWig, and GFF3 files, faster BAM.
1.9.0 – April 1
  Direct VCF, faster BAM, more configurability, wiggle track autoscaling

2.0.0 – September 2013?
  Graphical configuration, multiple independent views, more GBrowse compatibility.

2012
2013
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 edit data/trackList.json to use these >:-{
Embedded Mode

http://localhost/jbrowse/index.html
?loc=ctgA:1386..6057
&tracks=<list of tracks>
&data=sample_data/json/volvox
&nav=0
&overview=0
&tracklist=0
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!
Pre-Compression

- gzips static data files on disk
- shrinks data directories by **about 60%**
  - takes 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
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, did some preliminary work on tools to assist.
- Much work still to be done.
• Umbrella organization of open source bioinformatics (mostly genomics) projects.
• All try to be interoperable.
• Holds satellite meetings, summer schools, etc.