2014 GMOD Community Meeting
January 16, 2014

JBrowse: Robert Buels, Mitchell Skinner, Lincoln Stein, Ian Holmes

WebApollo: Ed Lee, Gregg Helt, Justin Reese, Monica Munoz-Torres, Chris Childers, Robert Buels, Lincoln Stein, Ian Holmes, Christine Elsik, Suzanna Lewis

University of California, Berkeley
Talk outline

1. JBrowse quick tour
2. Comparison to GBrowse
3. Integrating it
4. Extending it
5. JBrowse 2! The next-next browser
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.

2014  JBrowse 2 release! Really! Need to write a paper!
Stores and Tracks

**Stores**
- BAM
- SNPCoverage
- BigWig
- NCList
- GFF3
- SequenceChunks
- SPARQL
- VCF

**Tracks**
- Reference Sequence
- Features
- Alignments
- XYPlot
- Color density
- SNPCoverage
Feature Tracks

- Clicks on features and menu items can open URLs in popup dialogs or new windows, or can run any JavaScript code.

From any quantitative source (BigWig, JSON, etc)
Image Tracks

- any pre-generated images that cover the genome
  - RNA base-pairing
  - Images from other genome browsers
  - Legacy JBrowse .wig formatter uses this

Base-pairing track
(custom graphics example)

Image track
(here, WIGgle)
Track Visualizations
++ Particular Strengths ++

- online, but fast and smooth
- easy to administer
- compressed NGS data: direct-to-browser BAM, BigWig, and VCF
- optional faceted track selector - efficiently search thousands of tracks
++ Particular Strengths ++

• combination tracks

• open local files directly on client, no data transfer required

• highly customizable, embeddable, integratable, programmable
Faceted Track Selection

- make CSV file(s) of track metadata, and/or put track metadata in JSON config files
Combination Tracks

- Combine spans: set ops
- Combine quantitative: arithmetic ops
- “Mask” one track with spans from another
Open Local Files

- Select lots of files
- Paste lots of URLs
- Files are never transferred anywhere.
- More like a desktop app than an old-style web app.
¡Live Demos!

http://jbrowse.org/demos
<table>
<thead>
<tr>
<th>All query and display runs on the server computer. Send images.</th>
<th>All browsing code runs in the user's web browser. Servers send only data.</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Bottleneck: server CPU and mem</strong></td>
<td><strong>Bottleneck: client network, client CPU and mem</strong></td>
</tr>
<tr>
<td>Local files must be <strong>sent to the server.</strong></td>
<td>Local files are <strong>opened in-place.</strong></td>
</tr>
<tr>
<td><strong>15-year development</strong> history.</td>
<td>6-year development history (but only 2 years of Rob, heh).</td>
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<tr>
<td>Few demands on web browsers, compatible with <strong>very old browsers.</strong></td>
<td>Browsers <strong>newer than 4 years old</strong> are all fine. For IE, version 9 is minimum (Windows 7).</td>
</tr>
</tbody>
</table>
• Lincoln would like everyone to please hurry up and move to JBrowse, thanks.

• JBrowse is ready for most users to move.

• Some users need more things. Please help me!
WebApollo
http://www.gmod.org/wiki/WebApollo

- next generation of the popular Apollo annotation editor
- UI built on top of JBrowse as a plugin
- realtime annotation editing and curation on the web!
Integrating JBrowse

- Your systems can directly drive JBrowse by emitting JSON
  - JSON Configuration
  - Data (JBrowse/Store/SeqFeature/REST)
  - Name searches and completions (Jbrowse/Store/Names/REST)

- JBrowse is static and self-contained, can go to the data
  - e.g. put it on the end of your cloud-based SNP-calling pipeline to visually validate SNPs

- Plugin system: can build on top of JBrowse!
Web Apollo

- Users see updates in real time (like Google Docs)
- saves edits to a central Chado database
- front-end is a JBrowse plugin (Gregg Helt)
- back-end is extensive server-side Java (Ed Lee)
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.

• WebApollo front-end is a JBrowse plugin
JBrowse 2

• Not vaporware! But very delayed!

• Because I prioritized caring for existing users.

• They needed a lot of things very badly that I could still do in 1.x (JBrowse 1.10 and 1.11)
JBrowse 2 Plans

• Even more of a desktop-web hybrid
  • go to http://jbrow.se and just open your local or network files

• Tiled, related views of one or many genomes

• Show only regions of interest (e.g. collapse introns)

• Advanced authentication - OAuth2, Google, Dropbox, iPlant?

• Graphical conf - both admins and users
JBrowse 2 UI Mockup
Beyond JBrowse 2

• JBrowse 2 architecture lays solid groundwork for advanced features.

• Multiple views lays foundation for:
  • Synteny views
  • Circular views
  • Whole-genome vertical views
  • Network views

• Juxtaposing regions lays foundations for:
  • List of interesting regions
  • Showing gene fusions (e.g. in cancer)
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

Ian Holmes (UC)
Amelia Ireland
Mitch Skinner

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

NHGRI

Apollo

GMOD
The End

http://jbrowse.org

http://gmod.org/wiki/JBrowse

http://github.com/GMOD/jbrowse

(yes, jbrowse needs a logo)
Robert Buels

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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, also at OICR with Lincoln Stein