JBrowse — 1.6.0 and beyond

Robert Buels
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University of California, Berkeley
(JBrowse just released 1.6.0 yesterday)
JBrowse...

- Do everything possible on the client side.
- Fast, smooth navigation (think Google Maps) for genomes.
- Supports BED, GFF, Bio::DB::*\*, Chado, WIG, BAM, BigWig, UCSC (intron/exon structure, name lookups, quantitative plots).
- Is stably funded by NHGRI, many interesting innovations implemented and/or pending integration.
- Is open source, of course.
- Did I mention it's fast?
The JBrowse Project

2006  First prototype (pre-rendered GBrowse). NHGRI funds 3yr development of project.
      Mitch Skinner joins the team.


2008  JavaScript-only rendering.

2009  Genome Research paper.

2010  WebApollo funded to develop JBrowse.
      NHGRI renews for 6mo.
      JBrowse dubbed “official” GBrowse successor.

2011  Mitch Skinner joins genomics startup.
      US politicians play chicken with economy.
      NHGRI renews for 3yr.

2012  (January) Robert Buels joins the team.
The JBrowse Project

- free and open source (license: GPL / Artistic)
- a GMOD project
  [GMOD](http://gmod.org)
- developed using git, hosted on GitHub
  [http://github.com/GMOD/jbrowse](http://github.com/GMOD/jbrowse)
- PIs most involved: Ian Holmes, Lincoln Stein, Suzi Lewis
- just got 3 more years of funding from NHGRI!
Particular Strengths

- very, very fast, smooth, scalable
- easy to get running
- Faceted Track Selector - thousands of tracks!
- Direct-to-browser BigWig support.
  - coming soon for BAM and BigBED also
Particular Weaknesses

- no user-uploaded data or end-user customization
- no data export
- few pre-made glyph options

We're working on these, of course.
Release Roadmap

1.3.0 – April 13
rubberbanding, y-axis scales, embedded mode, many other small fixes

1.4.0 – June 14
faceted track selector, auto-completion

1.5.0 – August 13
direct BigWig, nice Wiggle tracks
popups and context menus

1.6.0 – August 25
Feature descriptions, bugfixes for class.

(today)

(more intermediate releases)
UI plugin system (pub/sub events)
GBrowse-format configuration

2.0.0 – February?
Formatting scripts decoupled from config, more GBrowse compatibility
Feature Tracks

- rectangles (\texttt{<div>})s with various fills and dimensions to represent the features
- can do a surprising amount
Feature Tracks: Density Plots

Zoomed out

Zoomed in
Image Tracks

- any pre-generated images that cover the genome
- quantitative data (wiggle/BigWig)
  - wig-to-json.pl
- RNA base-pairing
Wiggle/BigWig Tracks

- Reads chunks of data directly from BigWig file on the web.
- Quite fast, and will get faster.
- Supported by all recent-ish (2-year-old) browsers, except Internet Explorer.
- IE is 4 years behind the tech curve, version 10 is required (released this month).

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

- just make a CSV file of track metadata
  - join to JBrowse track configuration with `name` column

Hands-on time!
Course Set for 2.0

☐ Mostly-GBrowse2-compatible configuration.

☒ Load and search rich track metadata for thousands of tracks.

☐ GBrowse compatibility backend (2.1?)
  - rendering service with Bio::Graphics glyphs
  - fetch and render GBrowse remote tracks
  - hopefully not much configuration, probably a standalone server
Course Set for 2.0

Solid data-source plugin system, including direct BAM, BigWig, BigBed.

New, documented pub/sub event API ties together JBrowse itself, and is available to any other JavaScript code.

Decouple data and configuration: formatting data and configuring tracks need to be separate steps.
Plans: Configuration

- GBrowse format
  - as much backward compatibility as possible
- dynamic changes to configuration information
  (probably more like at 2.1 or 2.2)
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!
Big Thanks To:

Suzi Lewis (LBNL)
Gregg Helt
Ed Lee
Nomi Harris

Ian Holmes
Mitch Skinner
Stephen Cummings

Lincoln Stein (OICR)
Julie Moon
Natalie Fox
Adam Wright

Lukas Mueller (BTI, SGN)
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

• Became new JBrowse Lead Developer as of January 2012 at UC Berkeley with Ian Holmes
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 hack the data/trackList.json to use these >:-{
Embedded Mode

Julie Moon, OICR co-op student

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

• gzips static data files on disk
• shrinks data directories by **about 60%**
  - *takes hg19* 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
Coming Soon

- new track selection
- overview images
- context menus
- track customization
- drag to zoom!
Coming: Hierarchical Track Sel.

work by OICR intern Natalie Fox
Coming: Faceted Track Selection

work by OICR intern Natalie Fox
Coming: Overview Images

Can have a karyotype, or any other image.

work by OICR intern Natalie Fox
Coming: Context Menus

work by OICR intern Natalie Fox
Coming: Track Customization

work by OICR intern Natalie Fox
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, has worked on automated migration tools to help
- Another thing I need to merge into master ;-)
WebApollo

- next generation of the popular Apollo annotation editor
- genome editing in your browser
- based on JBrowse
WebApollo

- clients receive annotation updates in real time (like Google Docs)
- saves edits to a central database
- has produced several extensions that will be coming to core JBrowse
  - highlighting and selecting features
  - HTML5 Canvas tracks for wiggle data (opening the door for many more canvas-based techniques)