JBrowse — 1.9.0 and beyond

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(channeling Robert Buels)
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(JBrowse 1.9.0 is coming Any Day Now)
JBrowse

- Do everything possible on the client side, in JavaScript.
- Fast, smooth navigation *(think Google Maps for genomes)*.
- Supports BED, GFF, Bio::DB::**, Chado, WIG, BAM, BigWig, VCF, and UCSC import (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?
<table>
<thead>
<tr>
<th>Year</th>
<th>Event</th>
</tr>
</thead>
</table>
| 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. |
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
The JBrowse Project

- free and open source (license: LGPL / 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
++ Particular Strengths ++

- Web-based, but still fast, smooth, scalable
- 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
Faceted Track Selection

- make a CSV file of track metadata, or put track metadata key/value in config
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
HTML Feature Tracks

- rectangles (<div>s) with various fills and dimensions to represent the features
- surprisingly versatile
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

- Very efficient; reads small chunks directly from BigWig file on the web.
- Needs only a recent-ish (4-year-old) browser, except for Internet Explorer.
- IE is years behind the curve, so requires latest version 10.

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

- Very efficient, reads small chunks directly from BAM file on the web.
- Again, browser support very good except for IE, which requires version 10.

http://goo.gl/XSVN2
VCF Tracks

- Reads directly from VCF files compressed and indexed with bgzip and tabix.
- Displays all VCF data, with descriptions.
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.

- Example: WebApollo (see next talk)
Coming Soon

- Graphical configuration
- Multiple independent views
- Track sharing
- Circular genome support
The End

http://jbrowse.org

http://gmod.org/wiki/JBrowse

http://github.com/GMOD/jbrowse

(Yes, jbrowse needs a logo)
The End

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(yes, jbrowse needs a logo)
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 – June 2013
   Graphical configuration, multiple independent views, more GBrowse compatibility.
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  >:-{
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 webservers 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: Overview Images

Can have a karyotype, or any other image.

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 ;-)

![GBrowse](image)
Big Thanks

Suzi Lewis (LBNL)
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Julie Moon
Natalie Fox
Adam Wright

NHGRI

Apollo

GMOD