JBrowse
A next-generation genome browser

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(advance online access)

http://jbrowse.org/
A Javascript genome browser:

http://jbrowse.org/
History

- Prototype (TiledImage)
- Server-side rendering (c.f. Google Maps, Genome Projector, X:Map)
- Current version (JBrowse)
- Client-side rendering
Pre-rendering does not scale

*D. melanogaster* at pixel resolution is an order of magnitude wider than the continental US

Figures compare server-side rendering (TiledImage) to client-side rendering (JBrowse)
Fig. 1. Storage and querying for interval overlap. In (a), we demonstrate that using conventional sorting of interval database by start, end coordinates the interval overlap query cannot halt at first non-qualifying interval (see text), but has to continue until the end/start of the database, scanning on average half of the stored intervals. In NCList (b), however, the result set intervals (in black) are located back to back in each of the sublists (each sublist is shown in a separate box) and sublists potentially containing more results are linked to each other by containment links. Therefore, the scanning problem is eliminated in this case, resulting in lower query complexity.

Within each sublist, there are no containments
Sorting by startpoint leaves endpoints sorted too

Query: $O(n + \log N)$
$N = \text{database}$
$n = \text{number of results}$

5-500x faster than R-trees, MySQL B-trees
(indexing/binning), Ensembl, UCSC...

Construction: $O(N \log N)$
Lazily-loaded Patricia Tries

1. romane
2. romanus
3. romulus
4. rubens
5. ruber
6. rubicon
7. rubicundus
TWiki plugin

This test-test page uses the TWiki JBrowsePlugin. See TestPage for a bare-bones version, without a config file.

Edit the wiki source text for a page to include the string "$JBROWSER$" somewhere in the page. (Admins can edit the WebTopicEditTemplate to set this up as the default, so it happens automatically.) See also DeepLinkText for an example of how to deep-link to a particular region.

Attach a FASTA file, one or more GFF files and (optionally) a config file to the page. As you attach annotations, they are processed by a Makefile and anyone who visits the page after that, or reloads the page, can see them. (To attach files, you will need to register.)

GFF filenames must end in ".*gff" or ".*gff3". FASTA files must end in ".*fa" or ".*fasta". BED files (if you have them) in ".*bed". All of these suffixes should be lower case, otherwise the files may not be recognized as JBrowse-friendly attachments.

(test JBrowse build Set May 9 17:46:05 2009: transcript: diagnostic information)
Imminent developments

- Lazily-loaded NCLists
- Text autocompletion; “proper” search
- **Nextgen sequence data**
  - Start with basic summarization, then custom tracks
- **Community annotation**
  - Persistent upload & sharing of tracks
  - Editing/curation over the web (ackles...)
- Documented image-track API
- Synteny browser (c.f. GBrowse-syn)
- Much more at jbrowse.lighthouseapp.com