

# JBrowse

## A next-generation genome browser

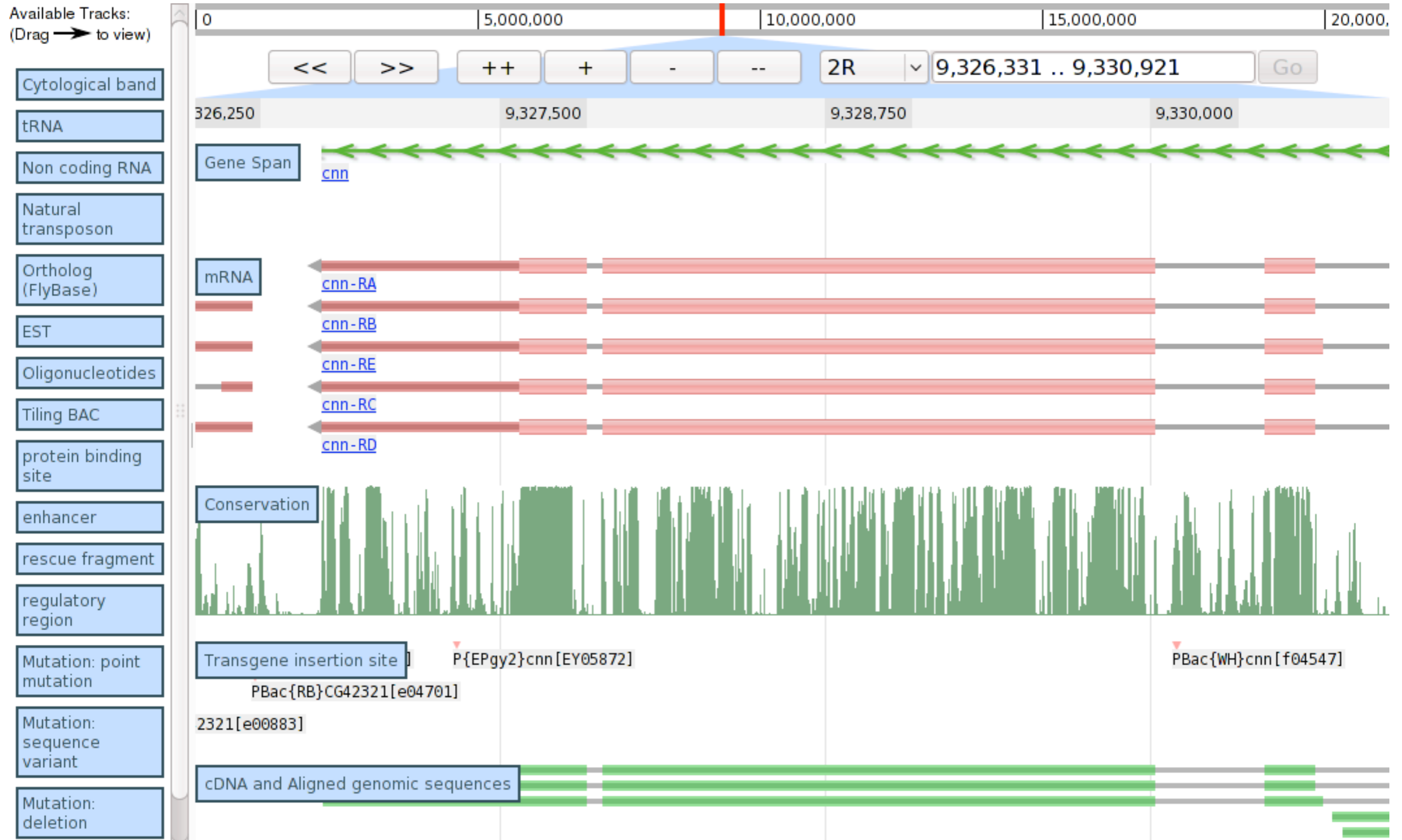
*Skinner, Uzilov, Stein, Mungall, Holmes*

**Genome Research**, September 2009

(advance online access)

<http://jbrowse.org/>

# A Javascript genome browser: <http://jbrowse.org/>



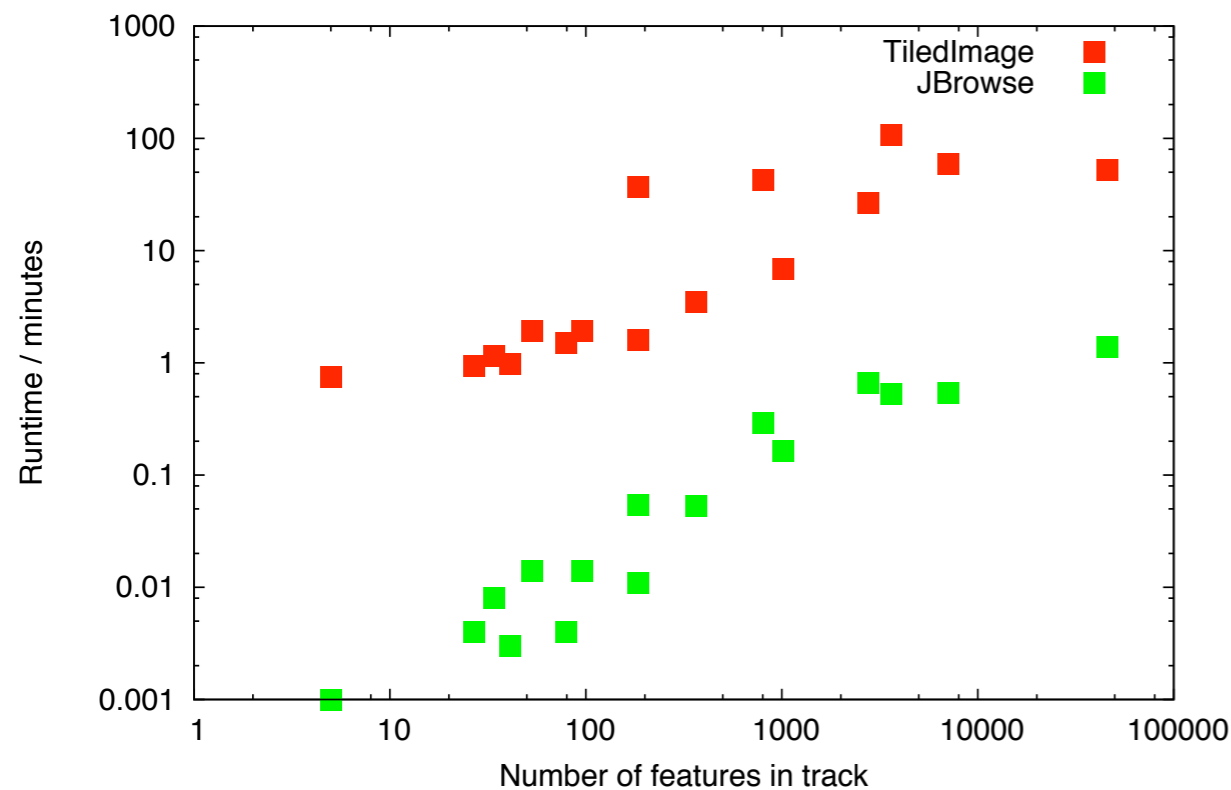
# History

- Prototype (TiledImage)
  - Server-side rendering (c.f. Google Maps, Genome Projector, X:Map)
- Current version (JBrowse)
  - Client-side rendering

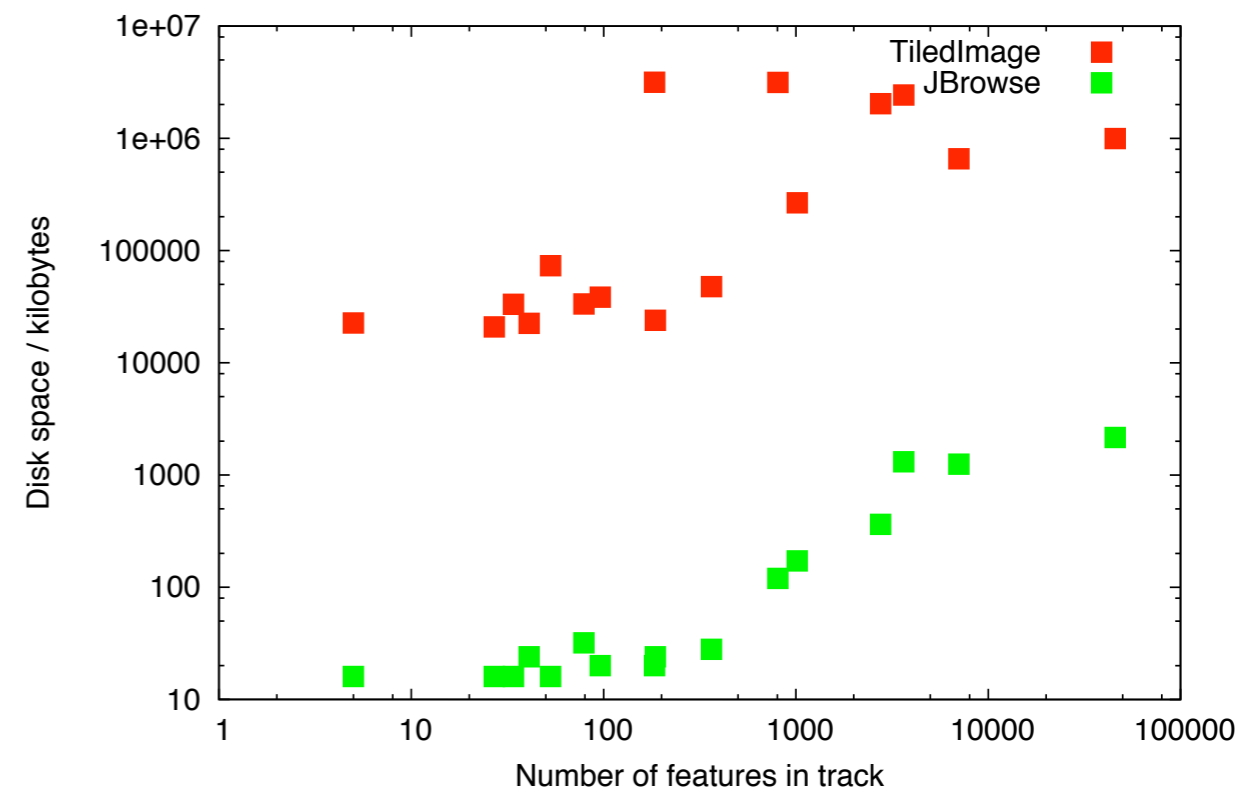
# Pre-rendering does not scale

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

Time to generate tracks: TiledImage vs JBrowse

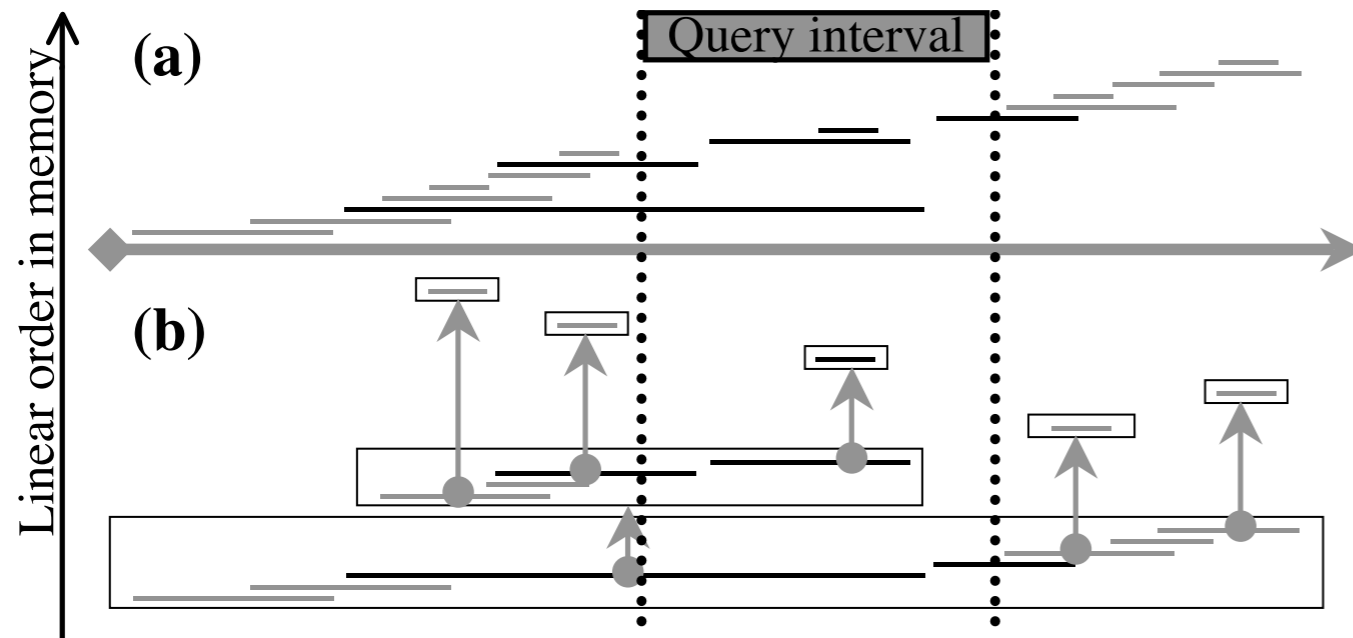


Disk space required to store track: TiledImage vs JBrowse



Figures compare server-side rendering (TiledImage) to client-side rendering (JBrowse)

# Nested Containment Lists



Query:  **$O(n + \log N)$**

$N$ =database

$n$ =number of results

5-500x faster than

R-trees, MySQL B-trees

(indexing/binning),

Ensembl, UCSC...

**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.

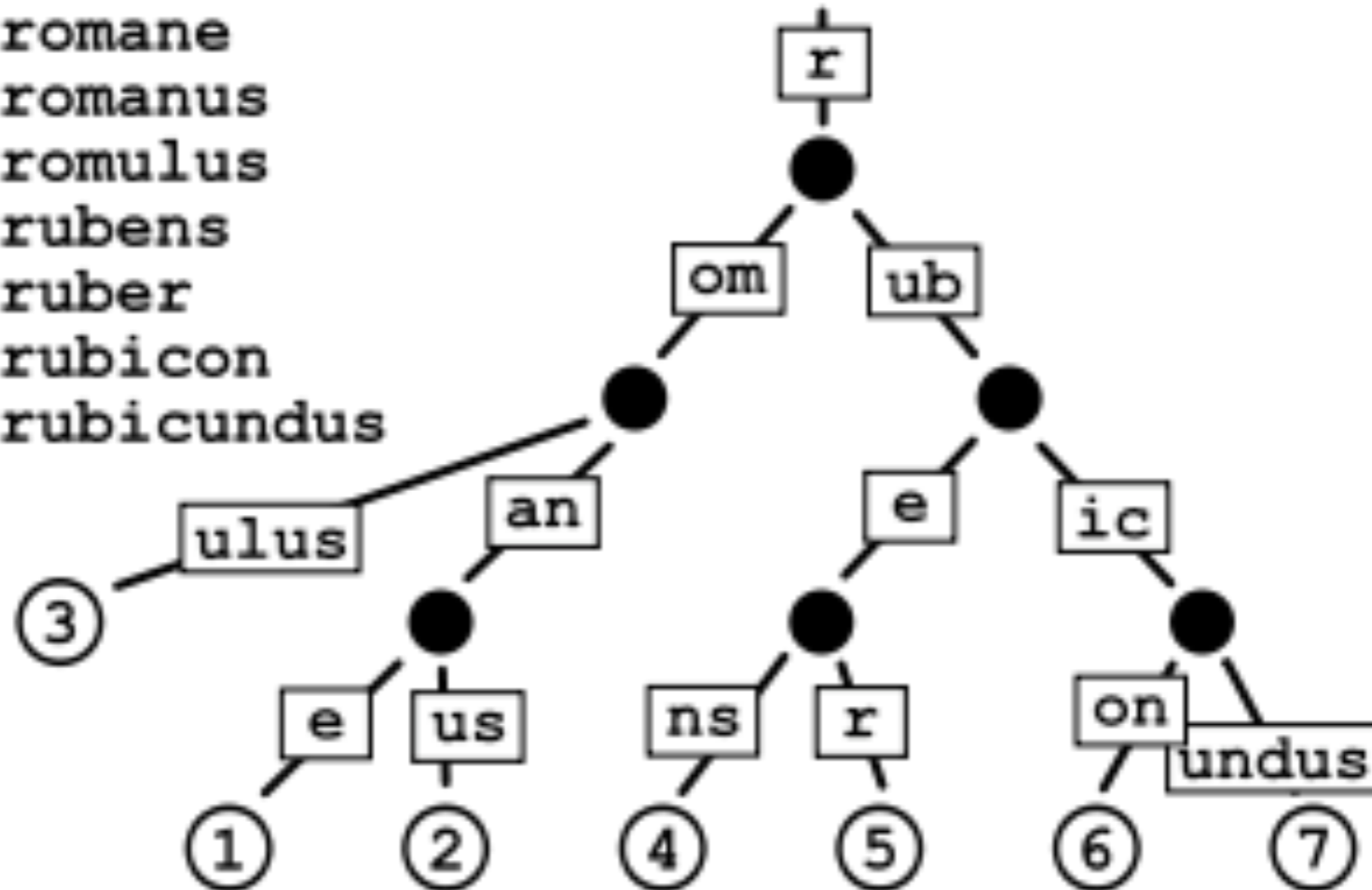
Construction:  **$O(N \log N)$**

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

Alekseyenko & Lee  
Bioinformatics, 2007

# Lazily-loaded Patricia Tries

- 1 romane
- 2 romanus
- 3 romulus
- 4 rubens
- 5 ruber
- 6 rubicon
- 7 rubicundus



# TWiki plugin

The screenshot shows a Safari browser window displaying a TWiki page. The address bar shows the URL `http://genome.biowiki.org/twiki/bin/view/Main/TestTestPage`. The page content includes a breadcrumb trail, a "Raw View" and "Attach" link, and several paragraphs of text explaining the JBrowsePlugin and file attachments. At the bottom, there is a genomic track visualization for the region `ctgA:18,860 .. 29,450`. The track shows a scale from 0 to 45,000 with major ticks every 5,000. A blue shaded region highlights the current view from 18,861 to 28,293. Below the scale, there are several tracks, with the first one labeled "DNA" and showing coordinates 18,861, 21,219, 23,577, 25,935, and 28,293. On the left side, there is a list of "Available Tracks" with a scroll bar, including "DNA", "volvox", "volvox Example Features", "volvox Name test track", "volvox Example motifs", and "volvox Example alignments".

TWiki > Main Web > TestPage > TestTestPage (11 Jun 2009, IanHolmes) [Raw View](#) [Attach](#)

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 `%JBROWSE%` somewhere in the page. (Admins can edit the [WebTopicEditTemplate](#) to set this up as the default, so it happens automatically.) See also [DeepLinkTest](#) 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 suffices should be lower case, otherwise the files may not be recognized as JBrowse-friendly attachments.

(last JBrowse build Sat May 9 17:48:05 2009; [transcript](#); [diagnostic information](#))

Available Tracks:  
(Drag → to view)

- DNA
- volvox
- volvox Example Features
- volvox Name test track
- volvox Example motifs
- volvox Example alignments

0 5,000 10,000 15,000 20,000 25,000 30,000 35,000 40,000 45,000

← → 🔍 🔍 🔍 🔍 ctgA 18,860 .. 29,450 Go

18,861 21,219 23,577 25,935 28,293

# 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](http://jbrowse.lighthouseapp.com)





Mitch Skinner