

GMOD Meeting August 6-7, 2009

Oxford, UK



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What is GMOD?

- Set of interoperable tools for managing, annotating, and viewing genomic data:
 - GBrowse genome viewer
 - Apollo genome annotation editor
 - CMap comparative mapping viewer
 - Sybil and GBrowse_syn comparative genomics viewers
 - plus many other tools.
- Active community of users and developers
 - Mailing lists, semi-annual meetings



What's New

- Gbrowse2
- GBrowse_syn
- JBrowse (formerly GBrowse 3)
- NextGen sequencing support for GBrowse
- Tripal/Drupal

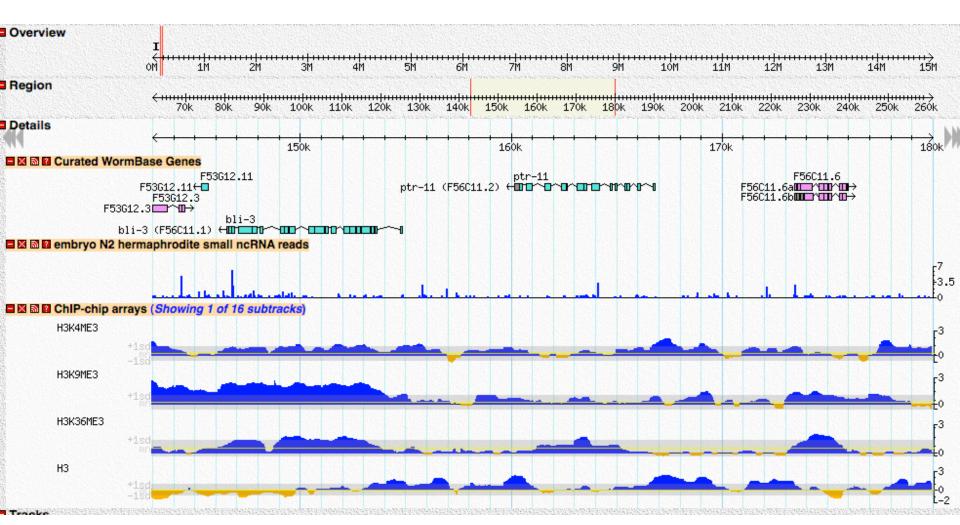


GBrowse2

- Backend rearchitecture, including:
 - Distributed databases and render servers
 - AJAX track loading
 - Improved configuration management



GBrowse2





JBrowse

- Another complete rearchitecture
- Uses AJAX for client side rendering, Google Maps style
- http://gmod.org/wiki/JBrowse

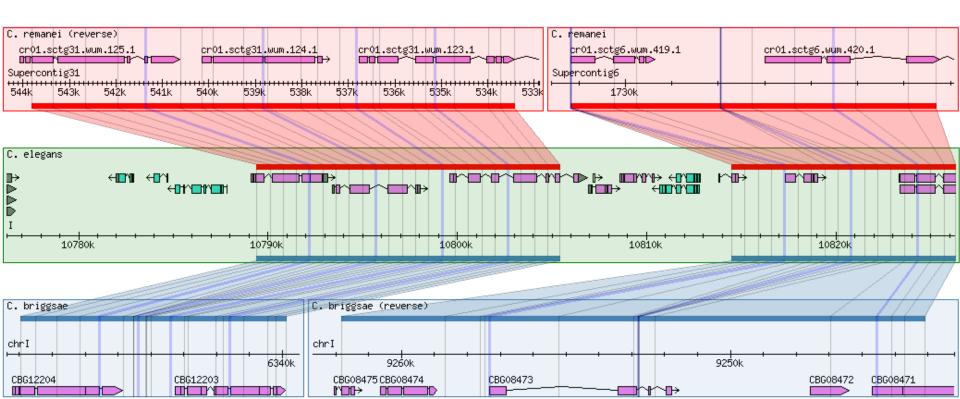


GBrowse_syn

- Distributed with GBrowse 1.70
- Makes use of data adaptors/databases that GBrowse uses

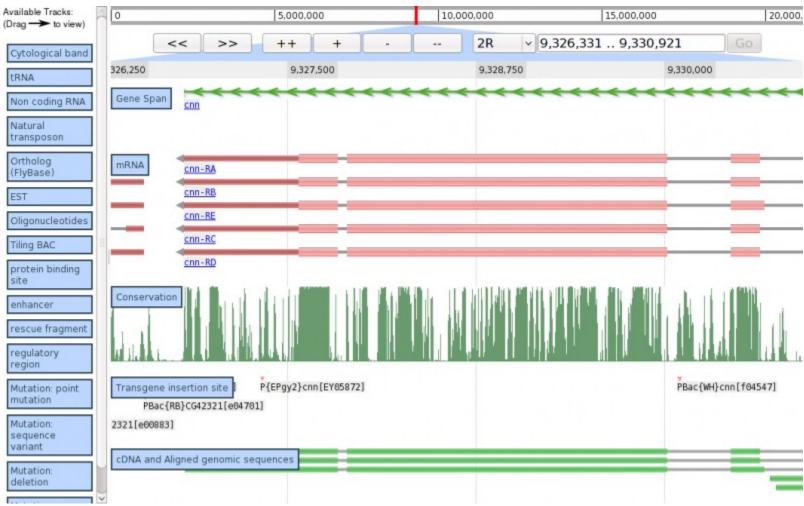


GBrowse_syn





JBrowse



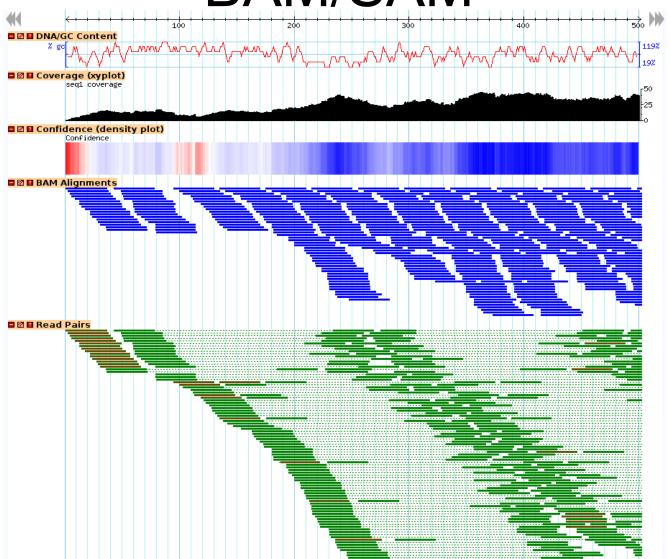


NextGen Sequencing

- Supported in GBrowse2; GBrowse1 may work with some finagling.
- Support for SAM/BAM databases
 - http://samtools.sourceforge.net/
- Coverage XY-plot
- Confidence density plot
- Individual alignments
- Paired reads



BAM/SAM



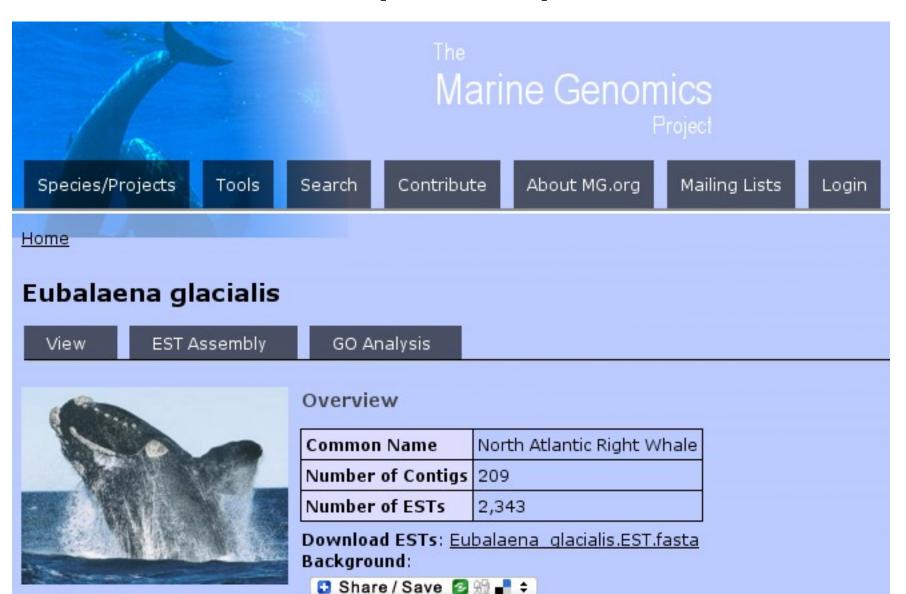


Drupal/Tripal

- Drupal: Widely used CMS, very extensible
- Tripal is a set of modules for Drupal to interact with a Chado database.
- Can integrate GBrowse/CMap
- Modules for:
 - organism
 - library
 - sequence



Drupal/Tripal



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