Quickstart Community Curation with Canto and GMOD in the Cloud

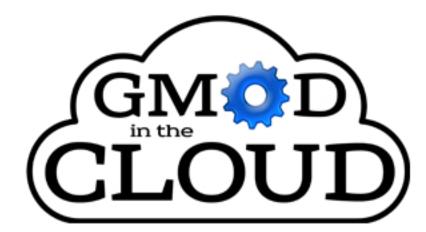
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[Canto Section 2017]

Canto is an easy-to-use web-based tool for literature curation by researchers and professional biocurators alike. Canto provides a simple, intuitive interface for capturing gene product properties using ontologies such as the Gene Ontology.

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Canto is one of the tools installed on GMOD in the Cloud.





GMOD in the Cloud is a virtual machine available in the Amazon Compute Cloud. It comes with software from the Generic Model Organism Database (GMOD) project already installed and configured.

Getting started with GMOD in the Cloud is quick and easy: choose a configuration for your virtual machine and launch!

When your virtual machine is running, upload a gene list and ontology files to Canto, and you are ready to start curating.

Other software installed on GMOD in the Cloud:



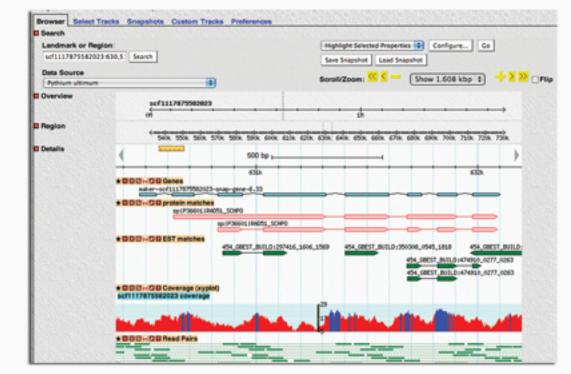


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Browser-based genome editor for distributed community annotation Drag-and-drop feature editing with exon-level zoom Real time updating enables concurrent usage by multiple editors

∃GBrowse

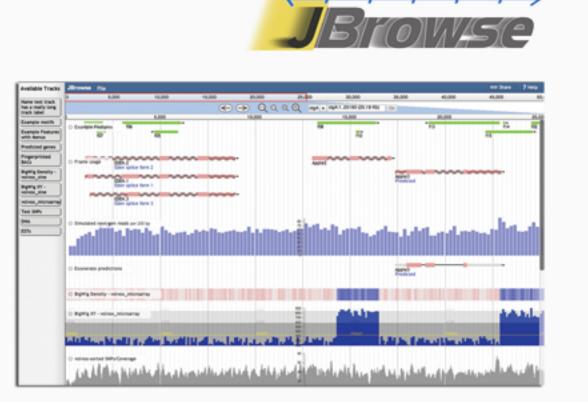


Popular, widely-used genome browser with Google Maps-style scrolling Supports many formats, including GFF3, SAM/BAM, Wiggle, BigWig, DAS Can read directly from a Chado database

CHADO

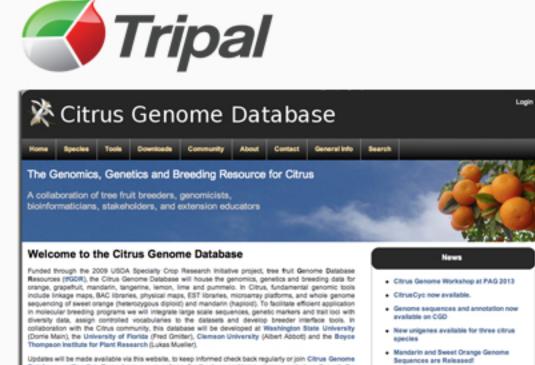
Organism-agnostic database schema

covers many biological data types



Super-speedy, next-gen genome browser

Javascript-based rendering for smooth, responsive scrolling and zooming Supports GFF3, BED, FASTA, Wiggle, BigWig, BAM, and Chado databases



Updates will be made available via this website, to keep informed check back regularly or join Citrus Genome Database mailing list. If you have any questions, feedback or problems, please contact us through the contact link on the navigation bar.

Drupal-based web front end for Chado databases Easy creation of a slick, powerful interface for viewing and editing data Integrate other GMOD tools, such as GBrowse and Galaxy