Quickstart Community Curation with Canto and GMOD in the Cloud

Scott Cain (Generic Model Organism Database project), Amelia Ireland (Generic Model Organism Database project), Kim Rutherford (PomBase) and Val Wood (PomBase)

[○] Canto

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.

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

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:

Web Apollo

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
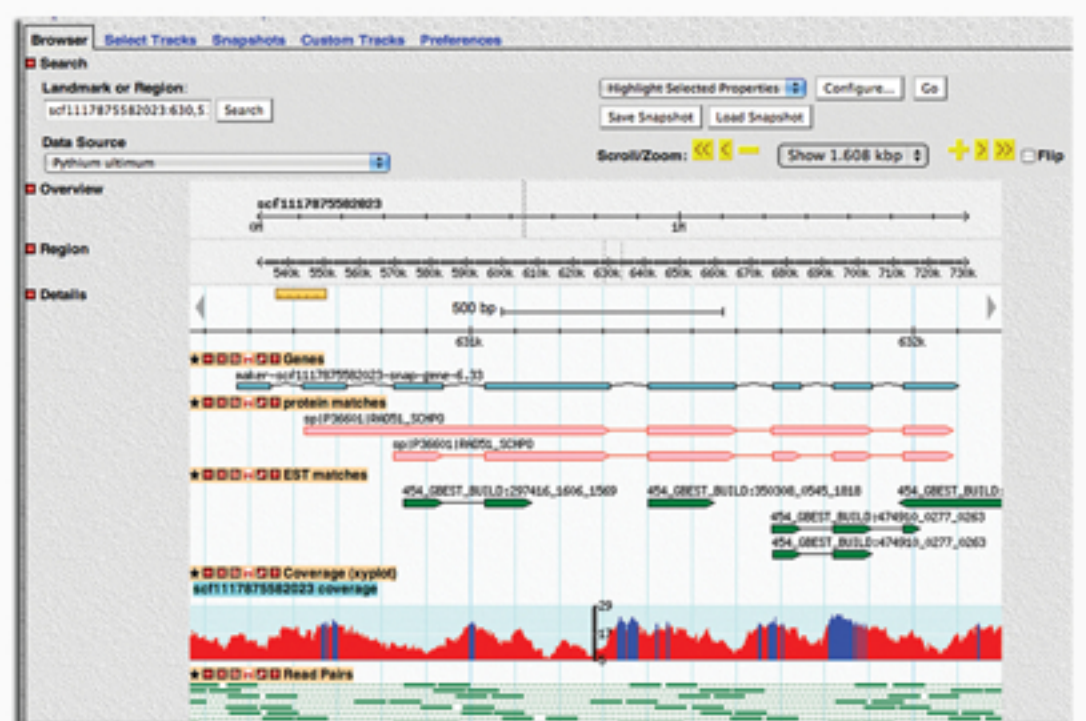
GBrowse

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
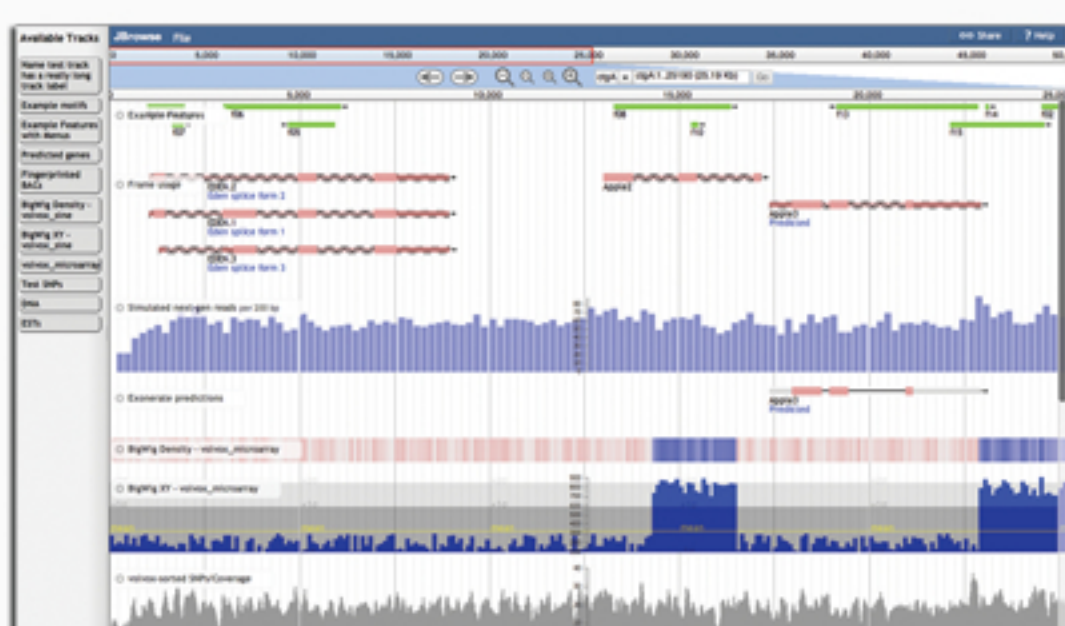
JBrowse

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

Tripal

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