Comparative Genomics Tools in GMOD

Dave Clements¹, Sheldon McKay², Ken Youns-Clark², Ben Faga², Scott Cain⁴, and the GMOD Consortium

¹National Evolutionary Synthesis Center, Durham, NC ²Cold Spring Harbor Laboratory, Cold Spring Harbor, NY ³University of Iowa, Iowa City, IA ⁴Ontario Institute for Cancer Research, Toronto, ON

Abstract

GMOD is a collection of interoperable open source software components for managing, annotating and visualizing genomic data. GMOD includes several components for managing and visualizing comparative genomics data. GMOD is used in many smaller research and emerging model organism communities, where informatics budgets are often tight. GMOD is also a community of developers and users that support and enhance it.

CMap: Comparative Map Viewer

The web-based CMap viewer enables users to view comparisons of many types of genomic data. CMap is data type agnostic and shows disparate data types together such as sequence, genetic, physical, QTL and deletion maps.

CMap displays correspondences between features such as markers, HGPS or any other annotation. CMap comes with tools for creating these correspondences based on feature names, or correspondences can be imported directly.

GBrowse_syn

GBrowse_syn, or the Generic Syntenic Browser, is a GBrowse-based syntenic browser designed to display multiple genomes, with a central reference species compared to two or more additional species. It can be used to view multiple sequence alignment data, synteny or co-linearity data from other sources against genome annotations provided by GBrowse.

Sybil

Sybil is a web based tool for visualizing and mining comparative genomic data. It uses a Chado database containing clusters of orthologous genes. Sybil visualizes information in several ways. Cluster reports show the genomic context of orthologous genes. Gradient displays are a tool for comparing whole genomes. Region comparisons display regions that match a reference. Gene reports display genomic context of genes, cluster assignments, and top BLAST hits.

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