

GMOD: Managing Genomic Data from Emerging Model Organisms

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Abstract

GMOD is a collection of interoperable open-source software components for managing, visualizing and annotating genomic data. GMOD components are used at hundreds of organizations, ranging from major model organism databases to individual labs. GMOD is well positioned to serve the converging interests of genomic model organism communities and evolutionary biology. In the past year there have been new releases of several core GMOD components, and a new wiki-based project website (http://gmod.org) has been launched.

What can GMOD Do?

If you have	& you need to	then GMOD can help with
Genomic Sequence	View/search	GBrowse
	Annotate	Apollo, MAKER
	Organize	Chado Sequence Module
Comparative Genomics	View/search	CMap, SynView, Sybil, GBrowse_syn, SynBrowse
	Annotate	Sybil
Phylogenies	Organize	Chado Phylogeny Module
Phenotype,	Organize	Chado Genetics Module
Genotype	Annotate	Phenote
Microarray &	View/search	Java TreeView
Expression	Organize	Chado Mage, Expression
Ontologies	Curate	Chado CV module
	View	GO Term Viewer
Pathways	View, predict, organize	Pathway Tools
Publications	Curate/search	TextPresso, PubSearch
	Organize	Chado Publication Module
Data!	Organize	Chado, BioMart, InterMine
	View/Query	GMODWeb,BioMart,InterMine

Who Uses GMOD?

AphidBase, ApiDB, ChromDB, CGD, DictyBase, FlyBase, Gramene, ParameciumDB, PlasmoDB, PossumBase, SGN, SmedGD, SpBase, VectorBase, wFleaBase, Xenbase, and hundreds of other large and small communities.

GMOD Community Resources



http://gmod.org

Comparative Genomics

GMOD supports visualizing comparative genomics data. Sybil shows syntenic regions and whole genome comparisons. CMap shows comparative maps of any type (genetic, physical, sequence, ...). SynView (shown), GBrowse_syn a



(shown), **GBrowse_syn** and **SynBrowse** are GBrowsebased synteny browsers.

What's New in GMOD?

New Components

MAKER is an annotation pipeline for eukaryotic genomes that produces GMOD compatible databases. MAKER identifies repeats, aligns ESTs and proteins to a genome and produces *ab initio* gene predictions.

The **Community Annotation System** (CAS) is a set of popular GMOD components prepackaged into a single system. It comes with GBrowse, Chado, Apollo, Modware, and MediaWiki with the TableEdit extension installed. CAS is under development.

Phenote is used to annotate biological phenotypes using ontologies, and pairs phenotypes with genotypes.

Phenote-Chado integration is coming soon.

GBrowse_syn is a GBrowse-based synteny browser for displaying multiple genomes.

New Features

GBrowse: automatic installation, rubberbanding, popup balloons, draggable and collapsible tracks, and track sharing

Apollo: undo function, preferences editor, Chado adapter enhancements, and improved graph and GFF3 support.

CMap: ribbon and dot-plot displays, new feature glyphs, embeddable image generation, and directory guessing for easier installation.

Chado: ontology updates, materialized views, stock module, easier GFF loading and delete by GFF.

Chado Database Schema

Chado is the unifying data model for GMOD. It is a modular and extensible database design for biological data. Chado supports sequence, genetic, phenotypic, ontology, gene expression and many other datatypes.

Natural Diversity in GMOD

Chado has recently been extended with the Natural Diversity module, which supports stocks, individuals, pedigrees, crosses, geolocations, and phenotype and genotype experiments. Taxonomy and phylogenetic trees in Chado's core modules have also been





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http://nescent.org