

GMOD: Database Resources for **Emerging Model Organisms**

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Abstract

More affordable sequencing technologies have given many emerging model organism communities an unprecedented volume of data. GMOD enables small research communities to establish web-accessible genomic databases with minimal informatics investment. GMOD is a collection of interoperable open source software components for managing, annotating and visualizing genomic data. GMOD components are used in many smaller research and emerging model organism communities, where informatics budgets are often tight. NESCent has recently joined GMOD and sponsors the GMOD

What Can GMOD Do?

GMOD has components for many common genomic data tasks Chado, GMOD includes Chado, a modular database schema, that supports many common needs.

If you have	& you need to	then GMOD can help with
Genomic Sequence	View	GBrowse
	Annotate	Apollo
	Organize	Chado Sequence Module
Comparative, Synteny	View	CMap,SynView,SynBrowse,Sybil
	Annotate	Sybil
	Organize	Chado Map Module
Phylogenetic Trees	Organize	Chado Organism, Phylogeny modules
	View	GMODWeb
Phenotype,	Organize	Chado Genetics Module
Genotype	View	GMODWeb
Microarray and Expression	View	Java TreeView, Caryoscope, GeneXplorer
	Organize	Chado Mage, Expression Modules
Ontologies	Curate	Chado CV module
	View	GO Term Viewer
Pathways	View, predict, organize	Pathway Tools
Publications	Curate/search	TextPresso, PubSearch
	Organize	Chado Publication Module

Who Uses GMOD?

AphidBase, BeeBase, BeetleBase, ButterflyBase, FlyBase, GnpAnnot-Lep, HeliconiusBase, VectorBase, wFleaBase, and hundreds of other large and small communities.

Getting Started with GMOD



GMOD Support

Support is available from active mailing lists, the web site, GMOD meetings, and a new GMOD Help Desk. The Help Desk answers user questions, writes documentation and online



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tutorials, and offers training workshops, Summer School. If you have guestions please contact the help desk.

help@gmod.org



GBrowse Genome Browser

GBrowse is a web-based viewer for displaying genomes and their configurable by end-users and site administrators. If vou have sequence and/or GBrowse can show it.



Apollo Genome Editor

The Apollo genome edito is used to annotate genosupports adding new annotations and refining computational annotations. It is used in severa community annotation efforts, and by full-time curators as well.





The GMOD Help Desk is hosted by NESCent and is funded

Chado Database Schema

Chado is the unifying data and extensible database design for biological data. Chado supports sequence, phylogenetic, phenotypic, gene expression and many other datatypes. Chado has recently been extended with the Natural Diversity module, which supports stocks, individuals, pedigrees, crosses, geogenotype experiments. Taxonomy and phylogenetic trees in Chado's core module

have also been rationalized.



National Evolutionary Synthesis Center (NESCent)

NESCent sponsors synthetic, interdisciplinary and transformative research in evolutionary biology. NESCent is located in

Durham NC and is a collaborative effort of Duke University, North Carolina State University, and the University of North Carolina at Chapel Hill.

http://www.nescent.org





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