

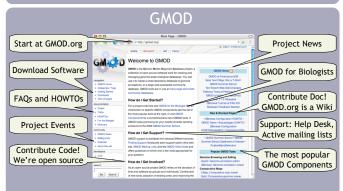
GMOD: Informatics Resources for Evolutionary Research

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Abstract

GMOD is a collection of interoperable open source software components for managing, annotating and visualizing genomic data. GMOD is used in many smaller research and emerging model organism communities, where informatics budgets are often tight. NESCent has recently joined GMOD to enhance and promote GMOD for evolutionary research. With the advent of more affordable sequencing technologies evolutionary biologists now have an unprecedented volume of data. At the same time, many established model organisms are venturing into comparative genomics and population genetics. GMOD can help both communities make this transition. Several GMOD components are particularly well-suited for evolutionary data.



GMOD is an active community of users and developers. GMOD support is available from mailing lists, the web site (http://gmod.org, a wiki), GMOD meetings, and the GMOD Help Desk. The Help Desk answers user questions, writes online tutorials and documentation, offers training



workshops at conferences and user sites, and coordinates the GMOD Summer School. If you have questions please

help@gmod.org



GBrowse Genome Browser

GBrowse is a web-based viewer for displaying genomes and their annotation. It is infinitely configurable by end-users and site administrators. If you have sequence and annotation GBrowse can show it.



Apollo Genome Editor

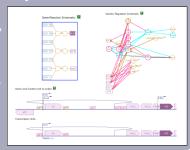
The Apollo genome editor is used to annotate genomic sequences. Apollo supports adding new annotations and refining computational annotations. It used in several community annotation efforts, and by full-time curators as well.



Pathway Tools

Pathway Tools is a system for predicting, annotating, visualizing and analyzing metabolic and regulatory pathways. It fully integrates with genomic annotation as well.

(Note: Pathway Tools has a restrictive commercial license, but is free to use for academic





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Chado Database Schema

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

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 rationalized.



Plus ...

... tools for comparative genomics (see other poster), generating web interfaces, automatic curation of papers, data warehousing, workflow management, data loading and export, middleware, gene expression visualization, ...

NESCent

The National Evolutionary Synthesis Center sponsors synthetic, interdisciplinary and transformative research in evolutionary biology.

NESCent hosts working groups, catalysis meetings, sabbaticals, post-doctoral fellowships, and a short-term visitor program. NESCent's informatics branch undertakes initiatives in support of software interoperability, data sharing, and informatics training. The center also solicits white-papers for projects that fall outside the scope of existing programs. More information is at the NESCent web

http://www.nescent.org

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.







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