2013 GMOD Summer School

Comprehensive training on current GMOD components at the GMOD Summer School. More information and applications.

GMOD is Social

Follow **The Tweet of GMOD**
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GMOD News

Add

- GCC2013 Early Reg closes 24 May
- New WebApollo Release
- 2013 Meeting Notes Online
- Apply For GSoC 2013 Now!
- Accepting Applications For GMOD Summer School 2013
- JBrowse 1.9.0 released
- Pathway Tools 17.0 Released
- SGD and ENCODE DCC Jobs
- New NGDx Group at Novartis
- 2013 Meeting: Keynote Announcement

More GMOD

Early registration closes May 24

GMOD is the **G**eneric **M**odel **O**rganism **D**atabase project, a collection of open source software tools for creating and managing genome-scale biological databases. You can use it to create a small laboratory database of genome annotations, or a large web-accessible community database. GMOD tools are in use at many large and small community databases.

How do I Get Started?

See Overview for the big picture. For an introduction to specific GMOD components see the list of the most popular tools at the right, or visit GMOD Components for a comprehensive list of GMOD tools. If GMOD looks promising for your needs, consider attending the next GMOD community meeting.

How do I Get Support?

GMOD support is available from several different sources. Support introduces each support option (this web site, GMOD Mailing Lists, Training and Outreach activities (including GMOD Schools), and the GMOD Help Desk) and offers guidance on which one is the most appropriate for your question.

How do I Get Involved?

As an open source project GMOD relies on the donation of time and software by groups and individuals. Contribution of new tools, adoption of existing ones, and improving the documentation are all welcome. Existing and potential users are encouraged to provide feedback via mailing lists or the help desk. The GMOD Project Page lists projects in need of ideas and developers. You can also attend project meetings.

Popular GMOD Tools

See the full list of GMOD components

GMOD in the Cloud toolset

GBrowse: Genome annotation viewer

Galaxy: Data analysis & integration

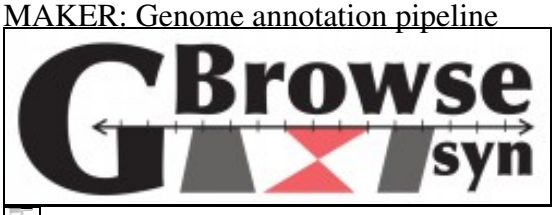
Chado: Biological database schema

JBrowse: Super-fast genome annotation viewer

BioMart: Data mining system

WebApollo: browser-based annotation editor

MAKER: Genome annotation pipeline

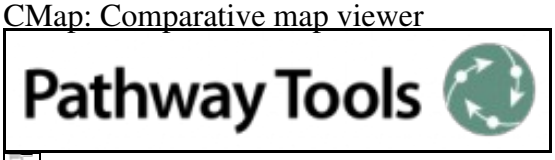


GBrowse_syn: Synteny viewer

Tripal: Chado web interface

InterMine: Data warehousing

CMap: Comparative map viewer



Pathway Tools: Metabolic, regulatory pathways

Contributing Organizations

EcoliWiki
BERKELEY LAB
ParameciumDB
sol genomics network
Ontario Institute for Cancer Research
CUGI
Clemson University Genomics Institute
PENNSTATE
iPlant Collaborative
EMORY UNIVERSITY
Berkeley
UNIVERSITY OF CALIFORNIA
tair
WASHINGTON STATE UNIVERSITY
UNIVERSITY OF SASKATCHEWAN