

Managing Genomic Data

Scott Cain
GMOD Project Coordinator
Senior WormBase Developer
Alliance of Genome Resources Developer
Ontario Institute for Cancer Research (OICR)
scott@scottcain.net

Programming for Biology
CSHL
October 2018

One problem people in bioinformatics may face:

Some nice people (possibly you) sequenced one or more organisms or strains, and then built them into assemblies (or if you're really lucky, full chromosomes). What now?

In addition, again if you're really lucky, you may have all sorts of data associated with these sequences, like expression, strains, genotypes, phenotypes, breeding info, physical maps. Seriously, now what?



GMOD is ...

- A set of interoperable open-source **software** components for visualizing, annotating, and managing biological data.
- An active **community** of developers and users asking diverse questions, and facing common challenges, with their biological data.



Who uses GMOD?



GMOD Project

- Open Source
- Used to have two full time project staff:
 - Project Coordinator: Scott Cain
 - Help Desk: Amelia Ireland
- Components
 - Some have dedicated funding
 - Others are contributed
 - New components must have:
 - An open source license
 - Interoperability with other GMOD components
 - A good faith commitment of at least 2 years of support
 - ...



GMOD is Software

Algorithms?

```
INEXACTSEARCH( $W, z$ )
    CALCULATED( $W$ )
    return INEXCUR( $W, |W| - 1, z, 1, |X| - 1$ )

CALCULATED( $W$ )
     $k \leftarrow 1$ 
     $l \leftarrow |X| - 1$ 
     $z \leftarrow 0$ 
    for  $i = 0$  to  $|W| - 1$  do
         $k \leftarrow C(W[i]) + O'(W[i], k - 1) + 1$ 
         $l \leftarrow C(W[i]) + O'(W[i], l)$ 
        if  $k > l$  then
             $k \leftarrow l$ 
             $l \leftarrow |X| - 1$ 
             $z \leftarrow z + 1$ 
         $D(i) \leftarrow z$ 

INEXCUR( $W, i, z, k, l$ )
    if  $z < D(i)$  then
        return  $\emptyset$ 
    if  $i < 0$  then
        return  $\{[k, l]\}$ 
     $I \leftarrow \emptyset$ 
     $I \leftarrow I \cup \text{INEXCUR}(W, i - 1, z - 1, k, l)$ 
    for each  $b \in \{A, C, G, T\}$  do
         $k \leftarrow C(b) + O(b, k - 1) + 1$ 
         $l \leftarrow C(b) + O(b, l)$ 
        if  $k \leq l$  then
             $I \leftarrow I \cup \text{INEXCUR}(W, i, z - 1, k, l)$ 
        if  $b = W[i]$  then
             $I \leftarrow I \cup \text{INEXCUR}(W, i - 1, z, k, l)$ 
        else
             $I \leftarrow I \cup \text{INEXCUR}(W, i - 1, z - 1, k, l)$ 
    return  $I$ 
```

Not really.

Plumbing!



GMOD Software

- Configurability and extensibility are central goals of GMOD.
 - GMOD tools are built to be reused
- Emphasize local installs
- Not a hosted solution (with a few exceptions)
- Not monolithic.
 - Most components can stand alone
 - Allows organizations to start slowly



GMOD Software

- Interoperability and data integration are also central goals of GMOD.
- You'll see several mechanisms in this talk
 - GFF3
 - Chado
 - Ontologies



Software

GMOD components can be categorized as

- V** Visualization
- D** Data Management
- A** Annotation and Analysis



Software

You have

Sequence
Gene models
Mapping data
Alternative transcripts
Expression
SNP / variation
Methylation
GO terms
Stocks / lines
Publications / Attribution
Orthology

GMOD Has

 MAKER
 Galaxy
 Ergatis
 (ISGA)
 SOBA
 Textpresso
 Apollo
  Table Edit

 GBrowse
 (WebGBrowse)
 JBrowse
 CMap (CMap-js)
 GBrowse_syn
 Sybil

 Chado
 Bio::Chado::Schema
 ModWare
  Tripal

 BioMart
 InterMine



 Annotation & Analysis

 Data Management

 Visualization

GMOD Requirements

- Server
 - Most use Linux
- GMOD Systems Administrator
 - Understands Linux package management, a scripting language, command line interfaces, relational databases, ...
 - Grad/Undergrad, half time when starting up.



MAKER

- Genome annotation pipeline for creating gene predictions
- Incorporates
 - SNAP, RepeatMasker, exonerate, BLAST
 - Augustus, FGENESH, GeneMark, MPI
- Other capabilities
 - Map existing annotation onto new assemblies
 - Merge multiple legacy annotation sets into a consensus set
 - Update existing annotations with new evidence
 - Integrate raw InterProScan results
- Maker Web Annotation Service

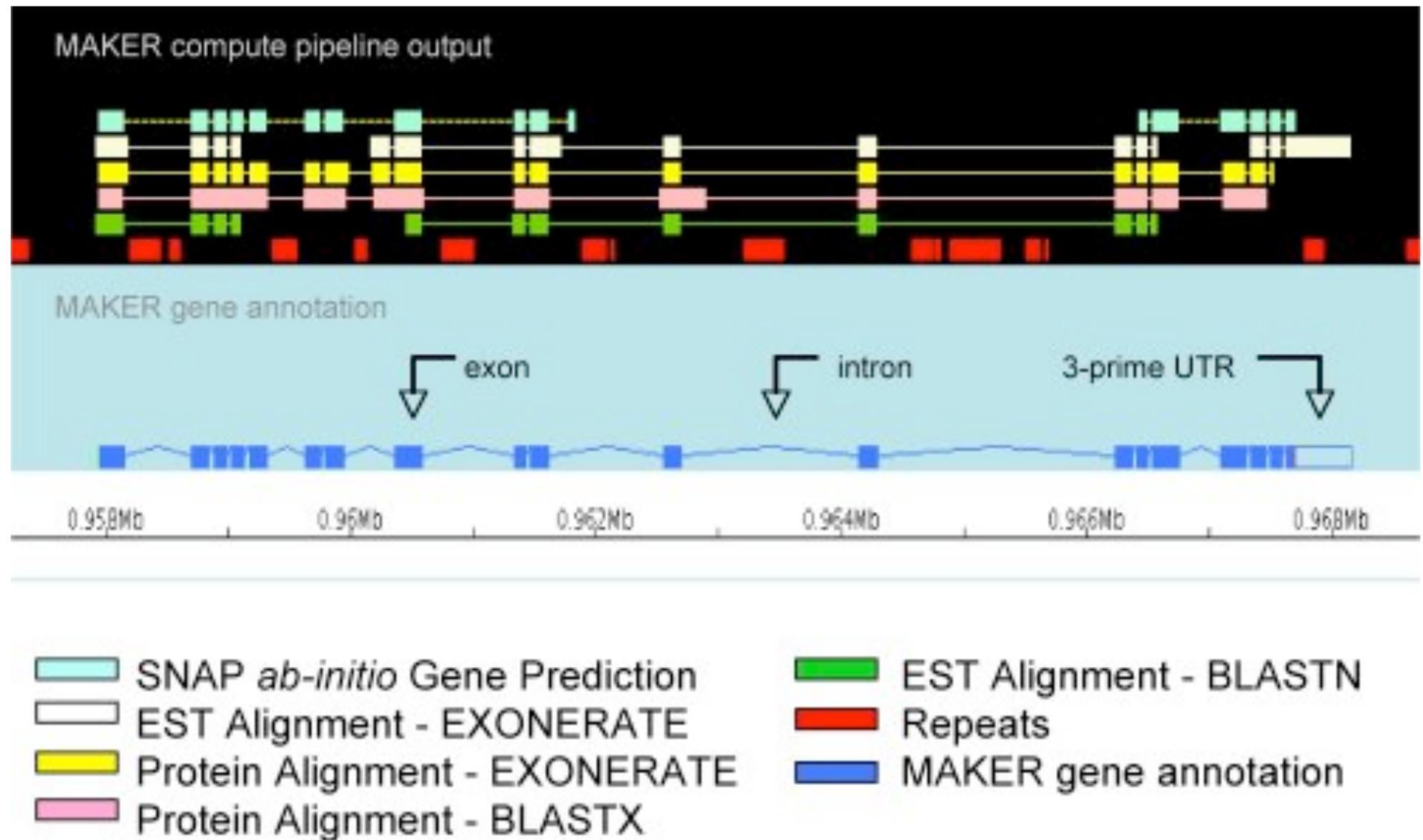


MAKER
Annotate this!



MAKER: An easy-to-use annotation pipeline designed for emerging model organism genomes, Brandi L. Cantarel, *et al.*, *Genome Res.* 2008. 18: 188-196

Minimizing “Edit distance”



MAKER Development

■ MAKER

2008. Based on early annotation pipelines developed by Mark Yandell at Celera.

■ MAKER 2

2011. Introduction of MPI parallelization, support for multiple gene predictors, GFF3 pass-through, and quality metrics like AED (Annotation Edit Distance) from the Sequence Ontology consortium.

■ MAKER-P

2015. Support for tRNA and snoRNA annotation. Improved parallelization on large plant genomes.

■ MAKER 3

2016. EVM (Evidence Modeler) support for improved annotation and user defined evidence probability weighting.

■ WQ-MAKER

2018. Wrapper for MAKER to run on XSEDE (free compute resource)

MAKER Resources

Home Page

<http://www.yandell-lab.org/software/maker.html>

Tutorial

http://gmod.org/wiki/MAKER_Tutorial

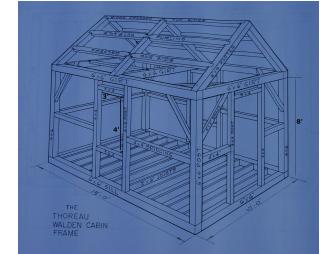
Mailing List

http://yandell-lab.org/mailman/listinfo/maker-devel_yandell-lab.org



Chado: A database schema for biological data

- A *schema* is a database design
 - Blueprint for a database, a way of organizing data
- Independent of specific data
 - Chado provides structure
 - You provide the hard work and data



+



=

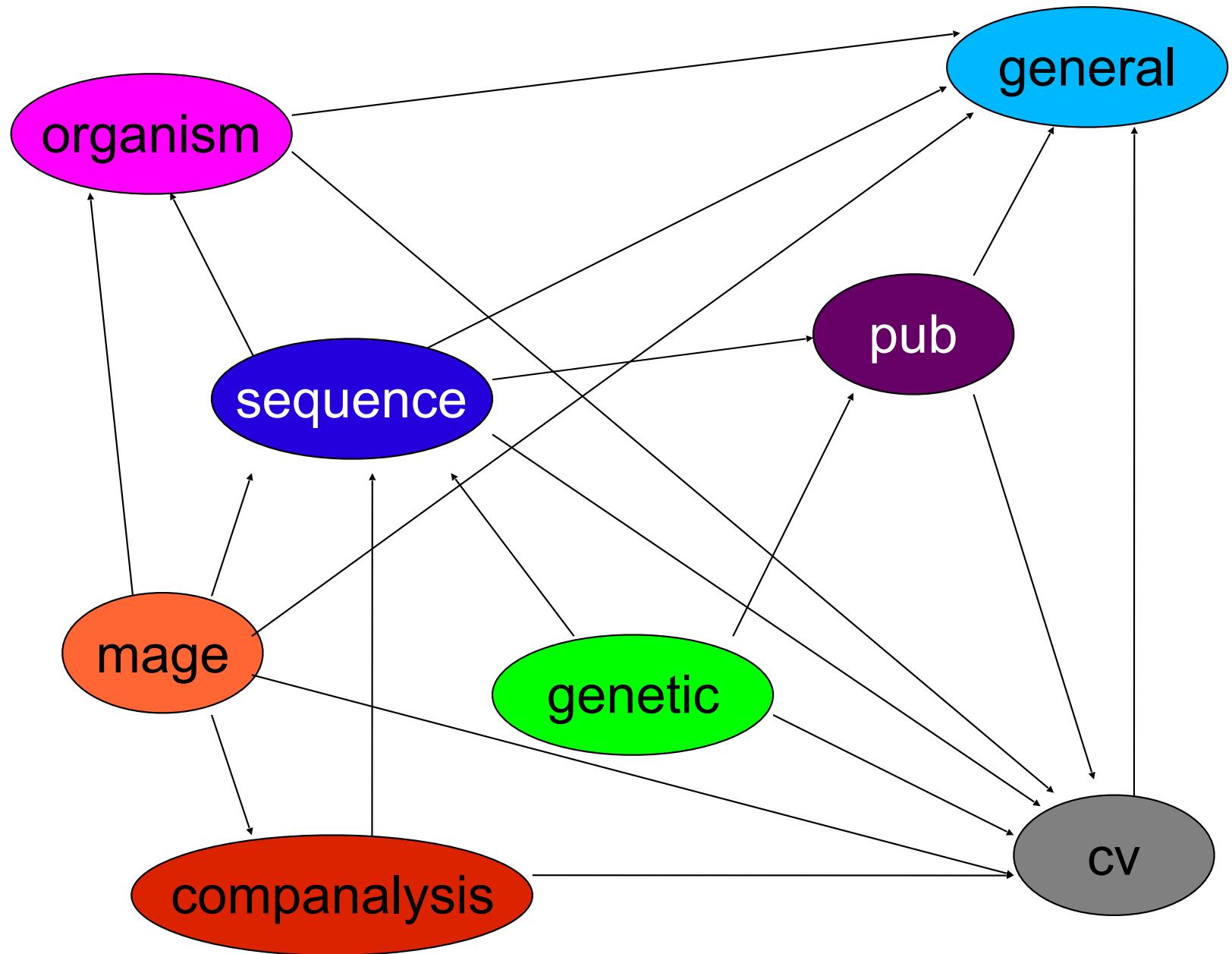


Why use Chado?

- Very good at genomic data
- Widely used
 - AphidBase, BeetleBase, dictyBase, FlyBase, SGN, SpBase, VectorBase, wFleaBase, Banana Genome Hub, Hardwood Genomics...
- Integrates with other GMOD tools
- Community of support
- Modular, flexible and extensible
- Normalized (boring but important for data integrity)



Chado Modules

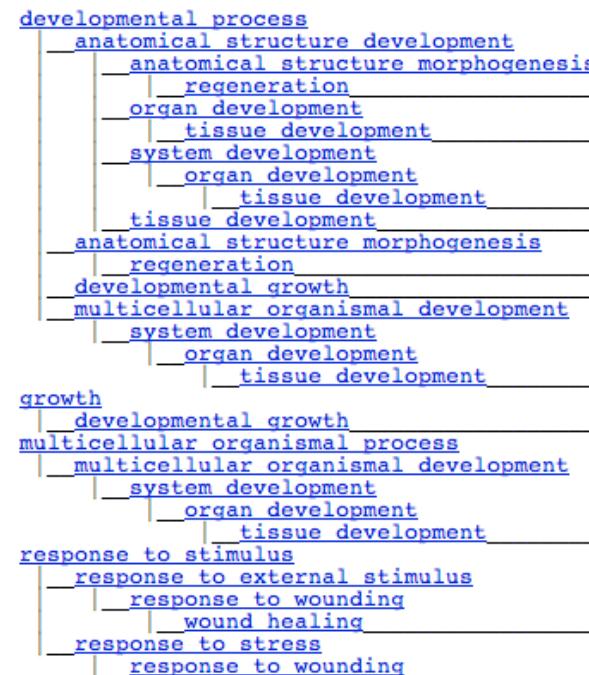


Controlled Vocabularies and Ontologies

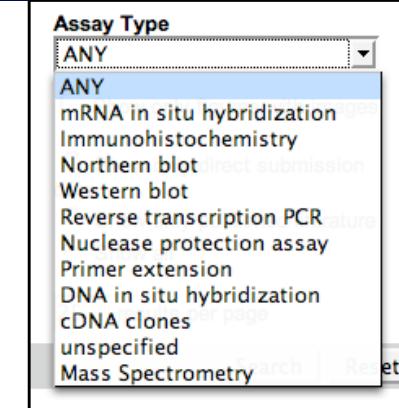
Controlled Vocabulary (CV)

List of terms from which a value *must* come

Pull down menus are examples of CVs



FlyBase CV Term Viewer:
GO term “tissue regeneration”



ZFIN assay type CV

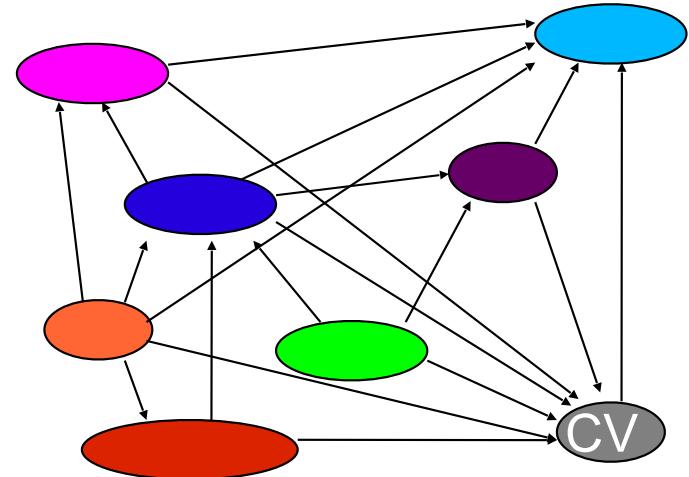
Ontology

Ontology = CV + rules + relationships
between terms

Gene Ontology, Sequence Ontology
Many standard ontologies available
from OBO

CVs and Ontologies in Chado

- Controlled vocabularies and ontologies are key in Chado
- Maximally used for
 - Integrity
 - Interoperability
- Can create your own, *but* ...
 - Please use standard ontologies when they exist
 - See OBO: <http://www.obofoundry.org/>



Chado Resources

Home Page	http://gmod.org/wiki/Chado
Tutorial	http://gmod.org/wiki/Chado_Tutorial
Introduction	http://gmod.org/wiki/Introduction_to_Chado
Manual	http://gmod.org/wiki/Chado_Manual
Modules	http://gmod.org/wiki/GBrowse_Modules
Mailing List	https://lists.sourceforge.net/lists/listinfo/gmod-schema



Chado Web Front Ends

- Chado is a schema, a server side technology
- It is not a web front end or a desktop client
- Options for Chado web front ends:
 - Do it yourself
 - Tripal



Do it yourself

- GMOD provides some support in form of libraries
- Perl
 - Chado::AutoDBI (phasing out)
 - Modware → Bio::Chado::Schema
- Java
 - At least two projects under development
 - GOBL (the Berkeley/Apollo people)
 - INRA (France) Hibernate-based
- Drupal / PHP
 - Three projects underway



Tripal

- Set of Drupal modules
 - Feature, Organism, Library, Analysis
 - Modules roughly correspond to Chado modules
 - Easy to create new modules
- Includes user authentication, job management, and data entry support

The screenshot shows the homepage of the Marine Genomics Project. At the top, there's a navigation bar with links for Species/Projects, Tools, Search, Contribute, About MG.org, Mailing Lists, and Login. The main title "The Marine Genomics Project" is displayed above a banner image of a coral reef. Below the banner, a section titled "Welcome to the Marine Genomics Project" features a photograph of a coral reef and text about MG.org being a web-based interface for public transcriptomic and genomic data and analysis tools. To the right, there's a graphic of an envelope containing a document and a link to "Join our MG.org mailing list". A sidebar on the left lists site features: Species ESTs, Unigenes, Blast, Mailing List, and Flag Features.

Species/Projects Tools Search Contribute About MG.org Mailing Lists Login

Welcome to the Marine Genomics Project

MG.org: a web-based interface for public transcriptomic and genomic data and analysis tools.

The Marine Genomics project is an inclusive organization that welcomes all investigators who are interested in applying genomic approaches to furthering our knowledge of marine organisms.

Site Features:

- **Species ESTs:** Search annotated ESTs.
- **Unigenes:** Search annotated assemblies of ESTs (unigenes).
- **Blast:** Blast your sequences against MG.org ESTs and unigenes.
- **Mailing List:** Sign up for the MG.org mailing list in your user account preferences.
- **Flag Features:** Registered users can flag ESTs/contigs for quick future access.

MarineGenomics.org



Stephen Ficklin, Meg Staton, Chun-Huai Cheng, ...
Washington State University, Clemson University Genomics Institute

Tripal Resources

Home Page

<http://gmod.org/wiki/Tripal>

Tutorial

http://gmod.org/wiki/Tripal_Tutorial

User Guide

<http://tripal.info/tutorials/v3.x>

Example

<https://www.rosaceae.org>

Mailing List

<https://lists.sourceforge.net/lists/listinfo/gmod-tripal>



Chado Web: DIY or Tripal?

Do It Yourself

More work

Get exactly what you want

Tripal

User authentication

Data entry

Actively developed

Well documented

Easy to extend

Drupal

What really made us decide to switch over to Drupal was that we needed authentication mechanisms, customized data entry mechanisms, and the ability to add social networking features and other non-biological components to our sites. Drupal supported all of this and was widely used, well documented, and well supported.

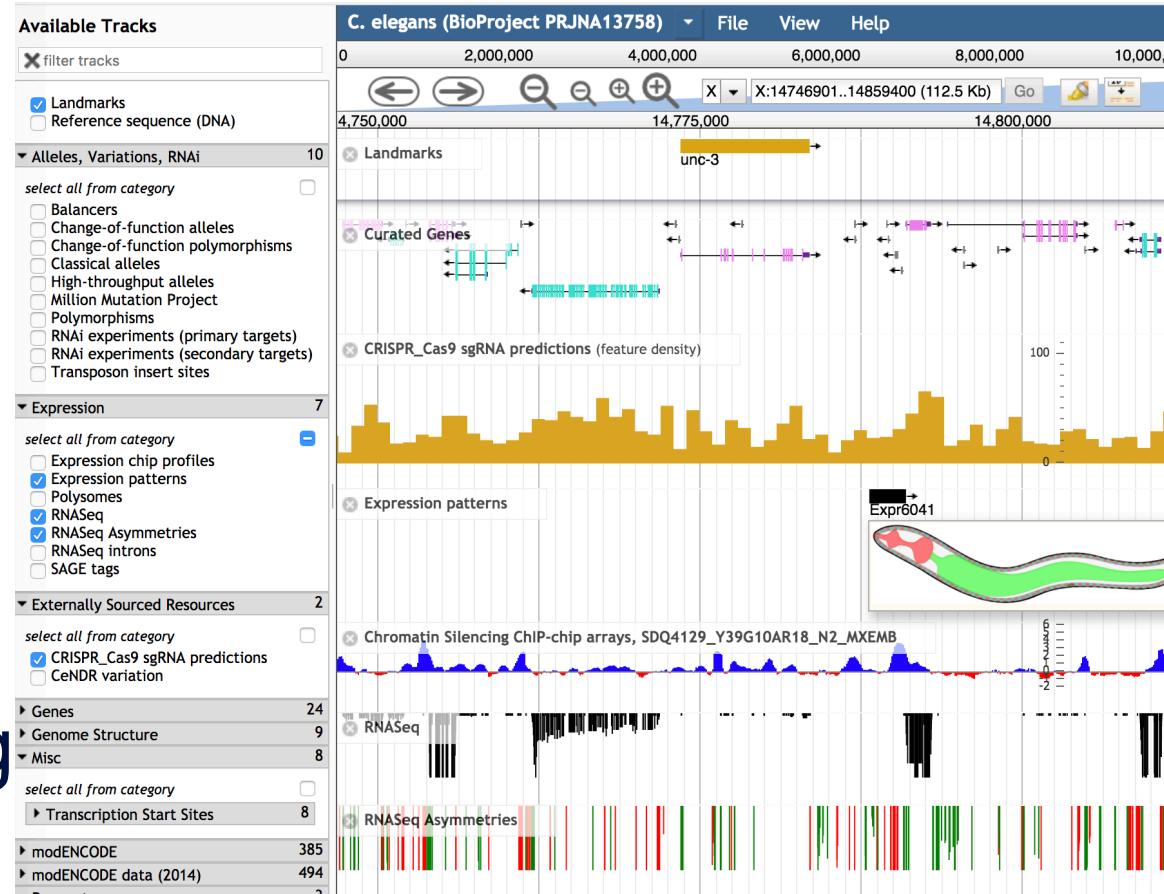
Stephen Ficklin, Lead Tripal Developer



This is not necessarily an either/or choice

JBrowse

- GMOD's 2nd generation genome browser
- It's fast
- Completely new
 - Client side rendering
 - Heavily AJAX
 - JSON, Nested Containment Lists



JBrowse: A next-generation genome browser, Mitchell E. Skinner,
Andrew V. Uzilov, Lincoln D. Stein, Christopher J. Mungall and Ian
H. Holmes, Genome Res. 2009. 19: 1630-1638



JBrowse Future Plans

- An ecosystem comparable to GBrowse
 - Glyph library, user defined glyphs, callbacks, track sharing, ...
- Comparative genomics (more on that later)
- Community Annotation
 - User authentication
 - User uploadable and sharable tracks and annotation
- Server side tools for integrated analysis



JBrowse Resources

Home Page	http://jbrowse.org
Admin Tutorial	http://gmod.org/wiki/JBrowse_Tutorial_PAG_2017
Configuration	http://jbrowse.org/code/jbrowse-master/docs/config.html
Example site	http://staging.wormbase.org/tools/genome/jbrowse/
Mailing List	https://lists.sourceforge.net/lists/listinfo/gmod-ajax



GBrowse or JBrowse

GBrowse

Robust ecosystem
Feature rich
Large user base
Track sharing

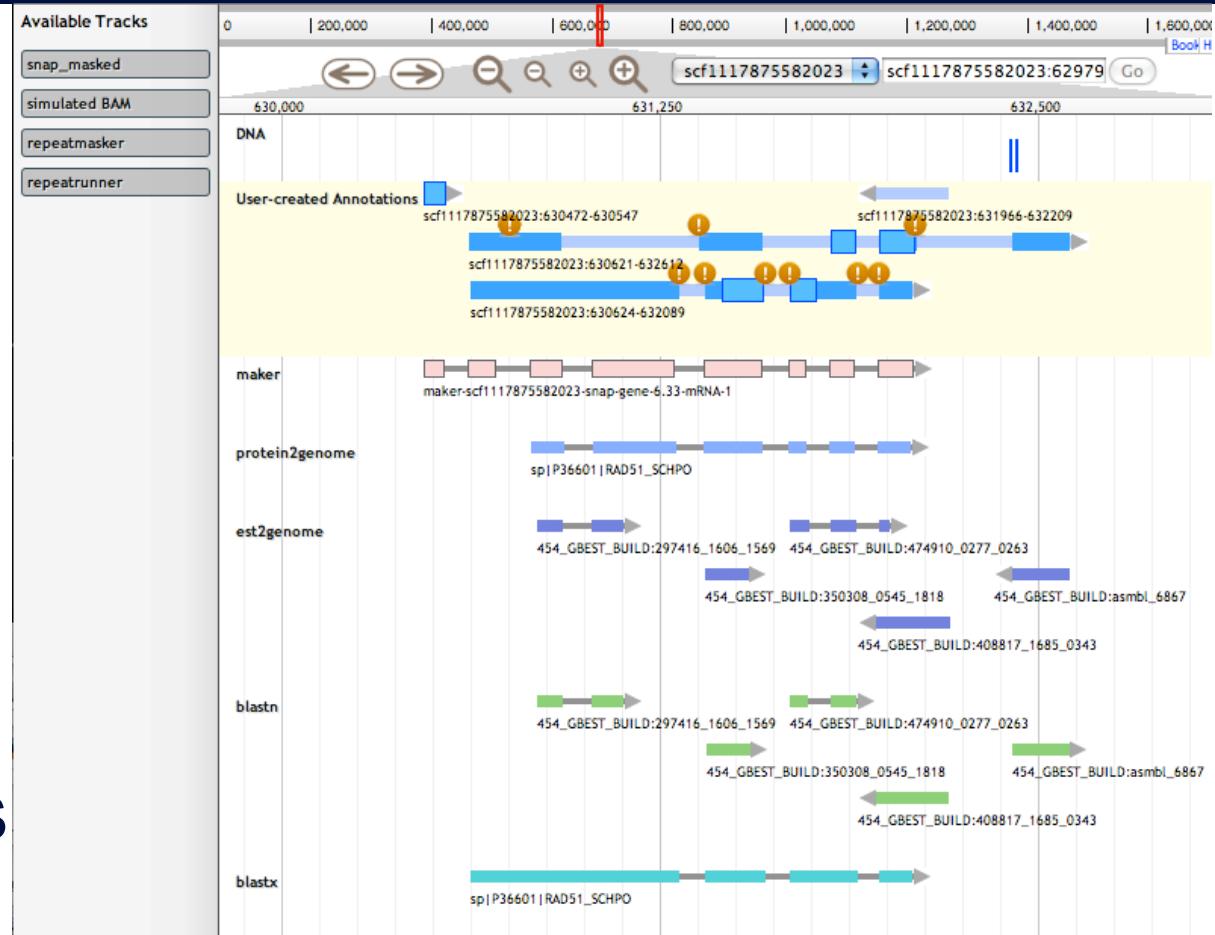
JBrowse

Very fast
Rapidly growing user base
Lots of future development
Easy to configure

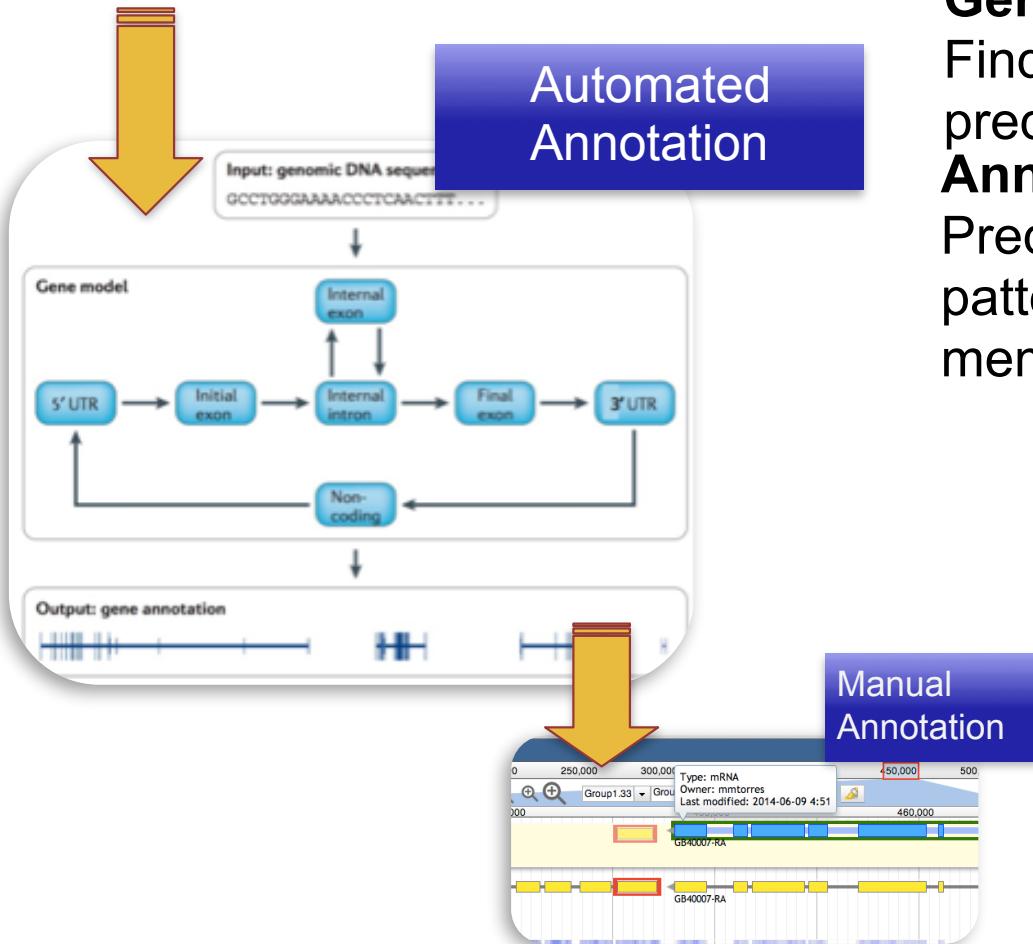


Apollo (used to be called WebApollo)

- GMOD's genome annotation editor
- Add and refine annotations.
- Based on JBrowse
- Multiple simultaneous users
- Keep track of evidence, curator
- Used in several community annotation efforts



Automated Identification is not Perfect



Generation of Gene Models

Find ORFs, multiple rounds of gene prediction

Annotation of Gene Models

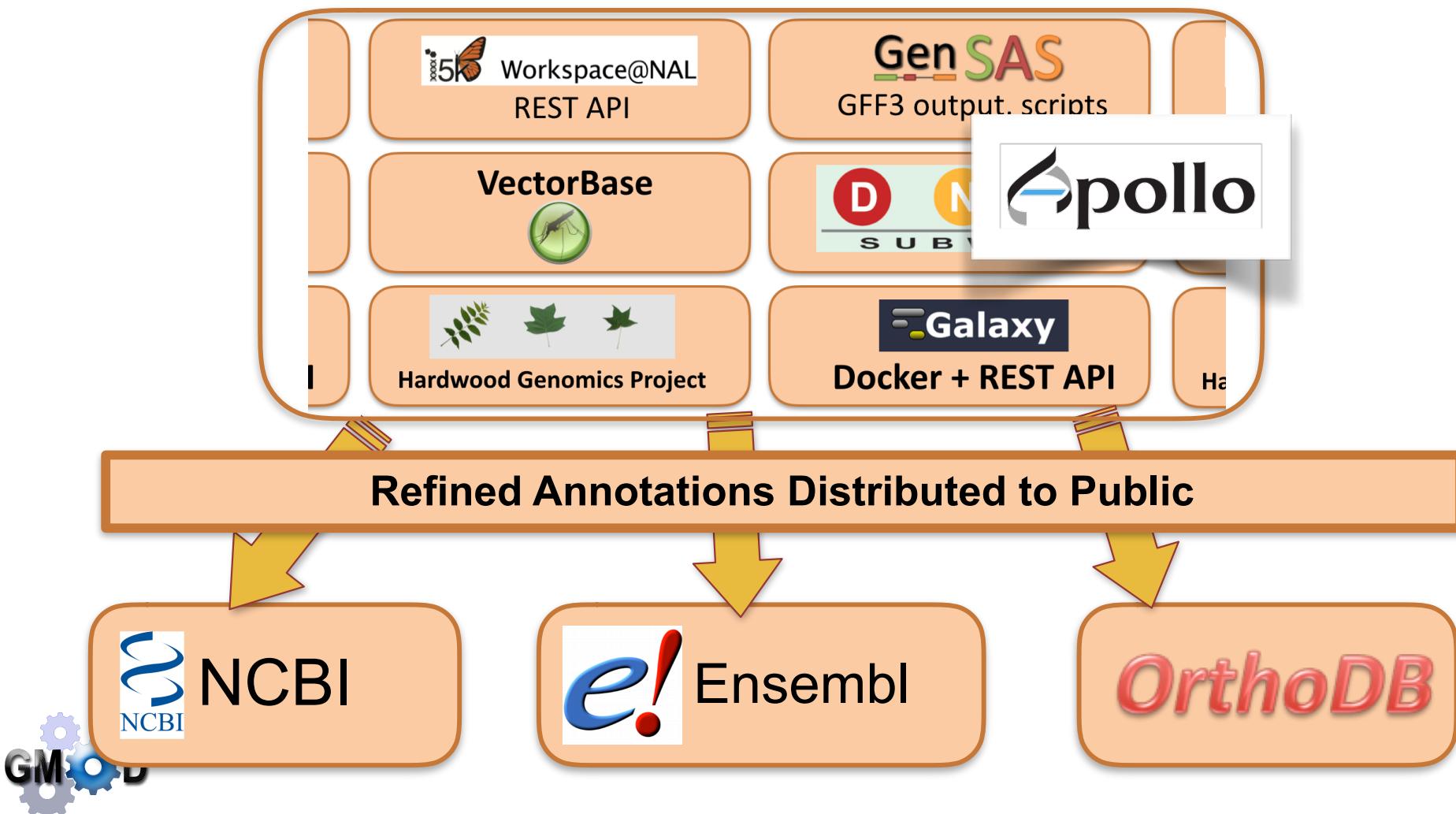
Predicting function, expression patterns, metabolic network memberships



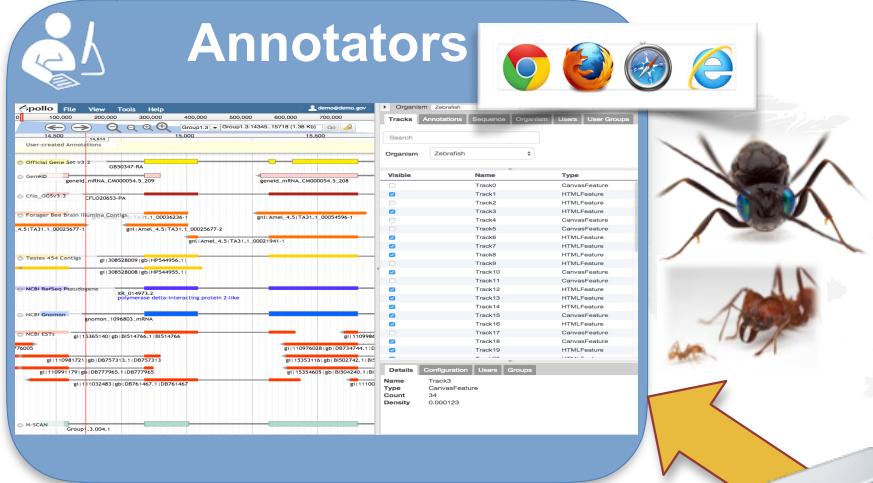
- Assembly errors can cause fragmented annotations
- Limited coverage makes precise identification difficult

Apollo: Used to Produce High Quality Annotations

- Over 100 organizations use Apollo
- Multiple genomes and labs per server



Apollo is a Tool for Collaborative Annotation



- Web-based Editor
- Visual feedback
- Real-time collaborative
- **JBrowse** browser

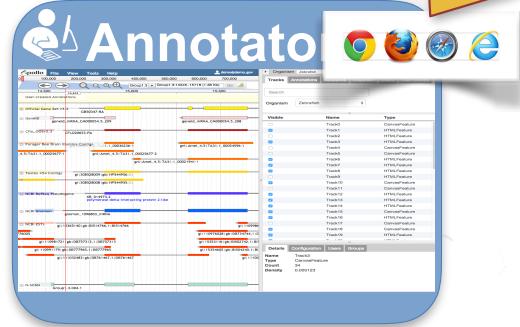
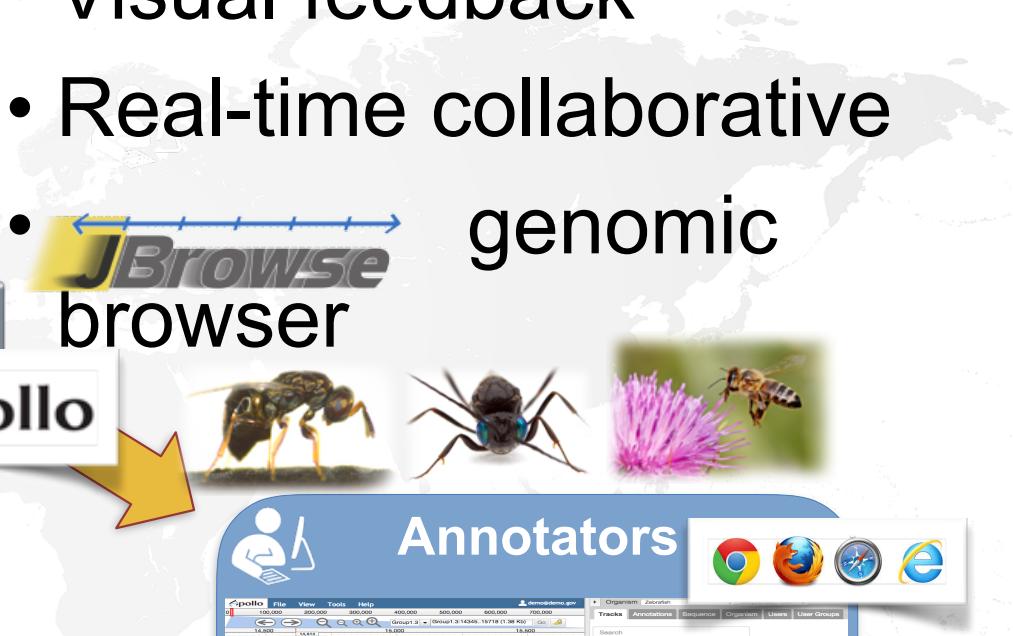


Photo Credits: i5K; Alex Wild at <http://www.alexanderwild.com/>; leaf cutter ant, ensign wasp; Leo Bukeboom: *Nasonia vitripennis* jewel wasp; Wikimedia Commons: *Apis mellifera* honey bee; Mike MacNeil USDA/ARS Fort Keogh LARRL: *Bos taurus* cow.

Apollo Resources

Home Page

<http://apollo.berkeleybop.org/>

Documentation

<http://genomearchitect.github.io/documentation/>

Demo

<http://genomearchitect.github.io/demo/>

Mailing List

apollo@lists.lbl.gov



GBrowse_syn

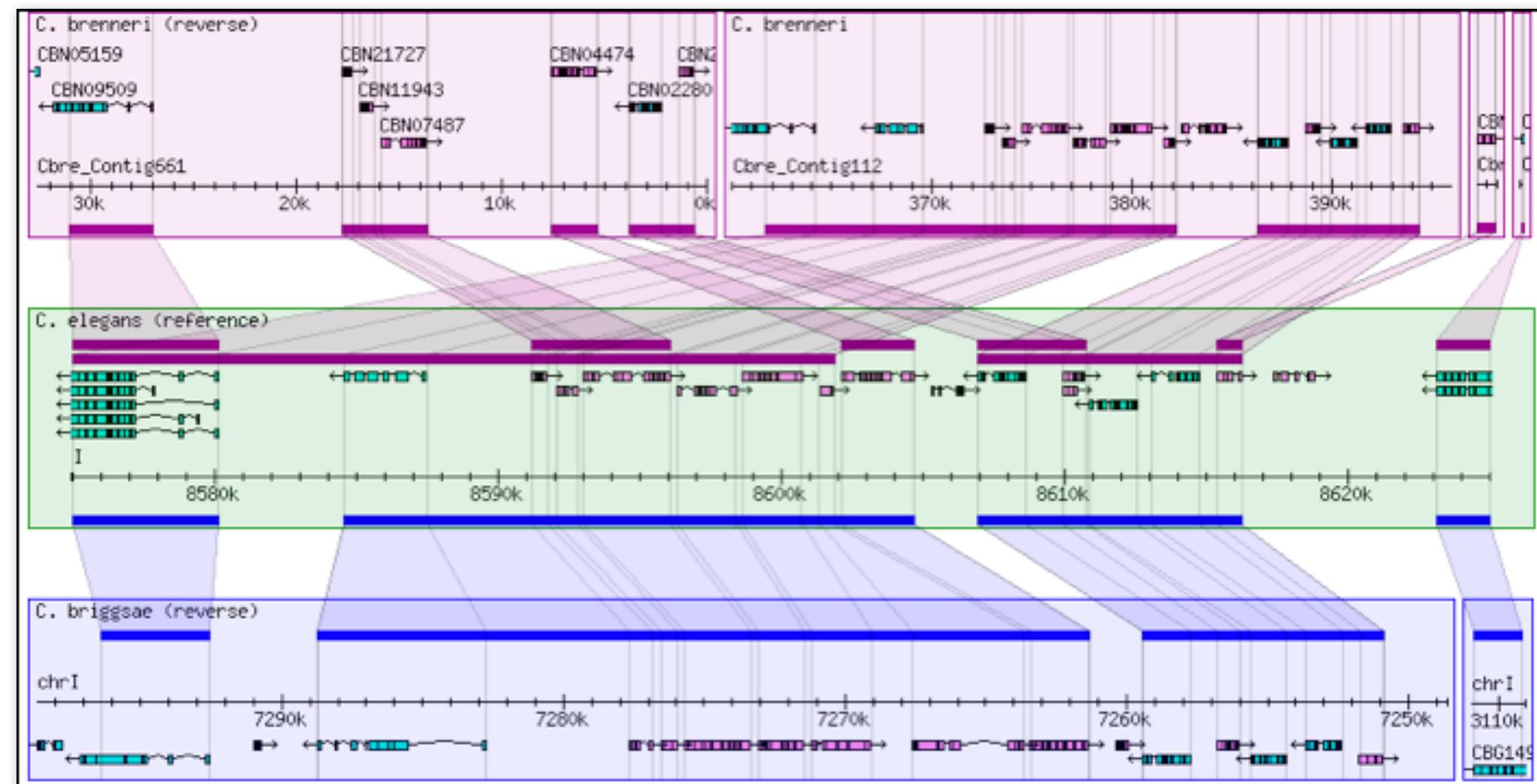
- GBrowse based comparative genomics viewer
- Shows a reference sequence compared to 2 or more others
- Can also show any GBrowse-based annotations



Example comparing *C. elegans* to 4 other species at WormBase

Sheldon McKay, University of Arizona

GBrowse_syn



Syntenic blocks do not have to be colinear
Can also show duplications

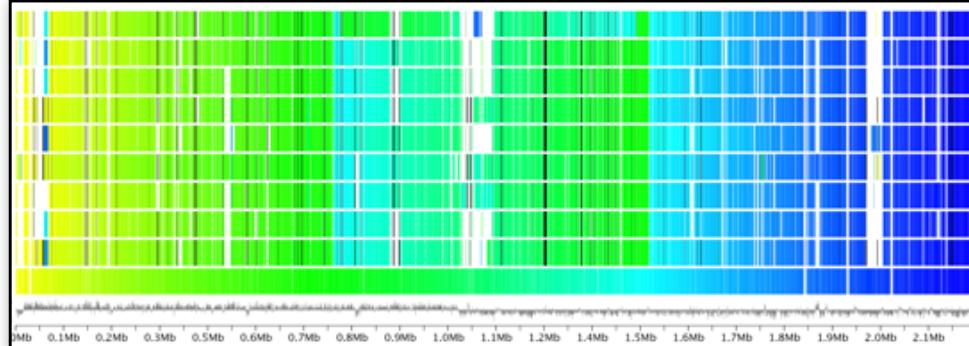
GBrowse_syn Resources

Home Page	http://gmod.org/wiki/GBrowse_syn
Tutorial	http://gmod.org/wiki/GBrowse_syn_Tutorial
User Help	http://gmod.org/wiki/GBrowse_syn_Help
Configuration	http://gmod.org/wiki/GBrowse_syn_Configuration
Example	http://www.wormbase.org/cgi-bin/gbrowse_syn/
Mailing List	https://lists.sourceforge.net/lists/listinfo/gmod-gbrowse

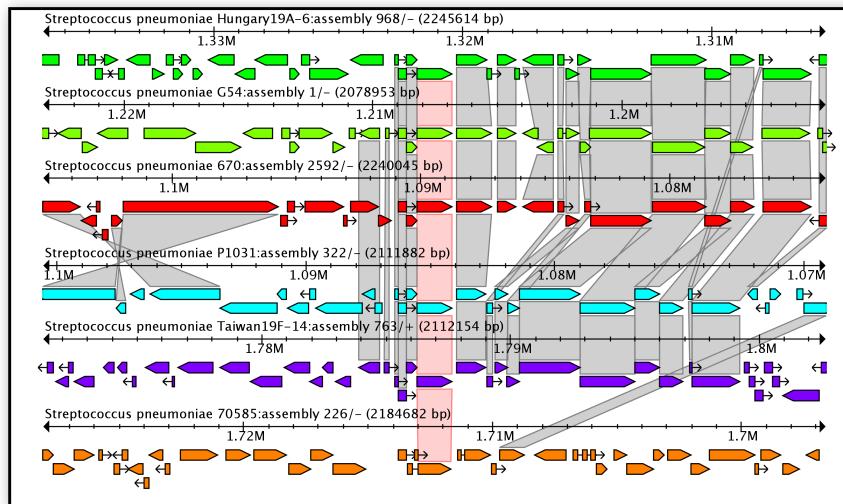


SynView and Sybil

Sybil



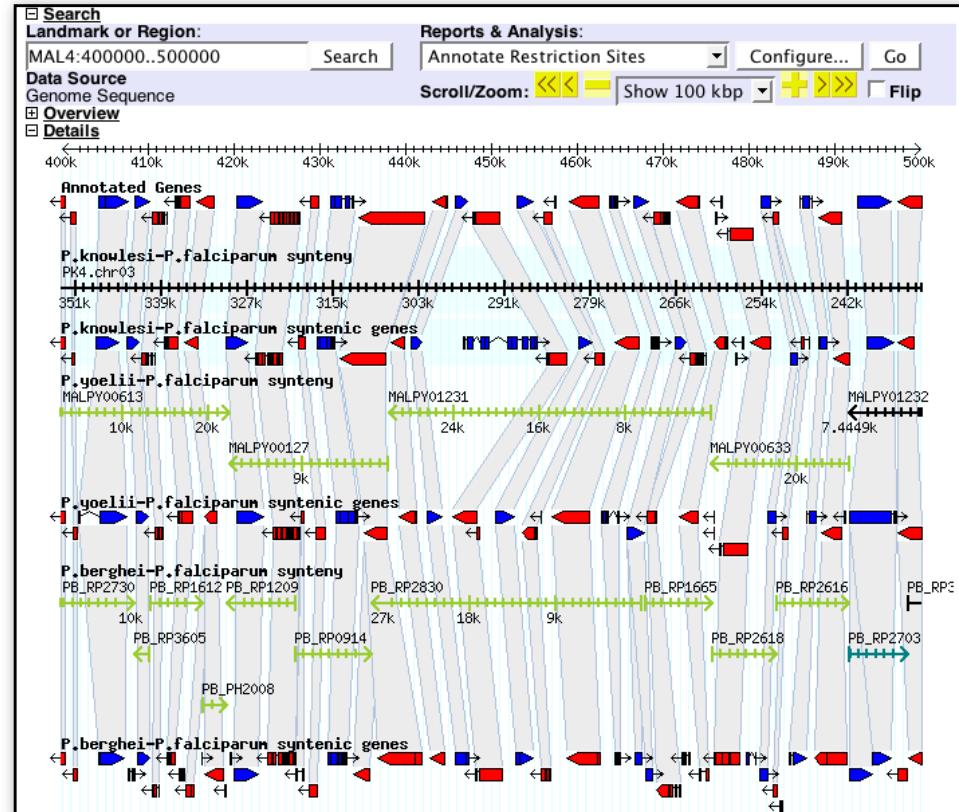
Whole Genome Gradient Display



Cluster Report

Sybil: Methods and Software for Multiple Genome Comparison and Visualization.
Crabtree, *et al.*; in Gene Function Analysis,
ed. by Michael F. Ochs (2007)

SynView



SynView: a GBrowse-compatible approach to visualizing comparative genome data. Haiming Wang, *et al.*; in Bioinformatics 22 (18)

GBrowse_syn or Sybil or SynView?

GBrowse_syn

Scalable (sort of)
Familiar interface
Extensive documentation
Growing user community

SynView

Scalable
Runs inside GBrowse 1
Good luck getting it to work

Sybil

Scalable
Whole genome and
other unique visualizations
Built on Chado



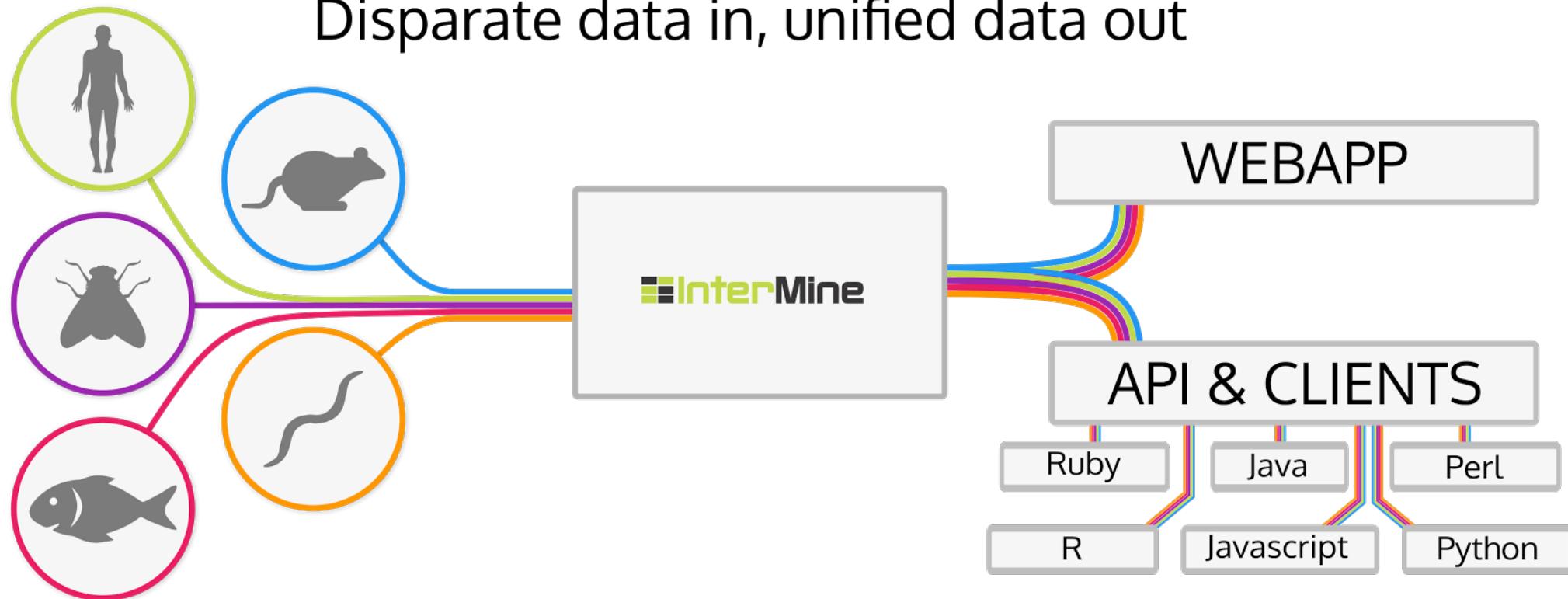
BioMart and InterMine

- Chado well-suited for setting up organism databases that have
 - Easy to use query interface to support common types of questions
 - Unified, coherent presentation of information
- BioMart and InterMine
 - Allow users to ask complex queries on all data
 - At the expense of having to do more work



InterMine: What is it?

Disparate data in, unified data out



Model organism images Designed by Freepik and distributed by Flaticon

Who uses InterMine

Over 30 installations, mostly at MODs, like FlyMine, YeastMine, WormMine, Wheat3BMine.

Others as well though, like TargetMine (drug discovery) and Shaare (gene candidate prioritization).

What do they use it for:

1. Genomic
2. Pathways
3. Interactions (complex and binary)
4. Protein structures
5. GO and other ontologies
(Mammalian phenotype, etc)
6. Protein domains
7. Variation
8. Expression and regulation
9. Lots more ...



What can you do with InterMine

1. Keyword search
2. Query results
 1. Column summaries
3. List Analysis
 1. Visualizations - heat maps, expression.
 2. Enrichment
4. Template queries - quick forms to make for searches that your users do often
5. My account
6. All data is integrated, fast performance



GFF3

- The common file format of GMOD for genomic annotation
- Tab delimited, 9 column format
- Supported by Chado, GBrowse, JBrowse, CMap, Apollo, InterMine, BioMart, Galaxy,



<http://gmod.org/wiki/GFF3>

A wiki, of course.
GMOD.org is the hub
 for all things related
 to the project:

- Documentation
- News
- Links
- Calendar
- Tutorials
- HOWTOs
- Glossary
- Overview
- Talks/Posters
- Mailing Lists
- ...



[navigation](#)

- [GMOD Home](#)
- [Categories / Tags](#)
- [Downloads](#)
- [View all pages](#)

[documentation](#)

- [Overview](#)
- [FAQs](#)
- [HOWTOs](#)
- [Glossary](#)

[community](#)

- [GMOD News](#)
- [Support / Training](#)
- [Calendar](#)
- [Outreach / Promotion](#)

[developers](#)

- [SVN](#)
- [SourceForge Site](#)

[search](#)

[Go](#) [Search](#)

[toolbox](#)

- [What links here](#)
- [Related changes](#)
- [Upload file](#)
- [Special pages](#)
- [Printable version](#)
- [Permanent link](#)
- [Print as PDF](#)

The March 2011 GMOD Meeting starts this weekend. [Register now.](#)

Welcome to GMOD

GMOD is the Generic Model Organism Database 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](#). The next meeting will be held March 5-6, 2011 at NESCent in Durham, North Carolina, as a part of [GMOD Americas 2011](#).

Contributing Organizations



March
2011
GMOD
Meeting &
Satellites

Start this weekend!
Register Now
(Satellites are free)



Abstracts due Feb 28

[GMOD News](#)

Planned downtime for gmod.org

InterMine 0.96 Release

GMOD Helpdesk Position Open

Galaxy Conf. Abstracts Due Feb 28

GMOD Wiki Migration Complete

March 2011 GMOD Meeting

Openings @ Xerbase

GMOD @ PAG 2011

GMOD Roadshow in San Diego

New GMOD.org Beta site

[New & Revised Pages](#)

- March 2011 GMOD Meeting • GSoC • GBrowse 2.0 Prerequisites • GMOD Schools • GMOD in the Sequencing Center • News/Planned downtime for gmod.org • News/InterMine 0.96 Release
- GBrowse syn • Galaxy • News/GMOD Helpdesk Position Open

Popular GMOD Tools

Genome Browsing and Editing

GBrowse: Genome annotation viewer
 Apollo: Genome annotation editor

Comparative Genomics

CMap: Comparative map viewer
 GBrowse_syn: Synteny viewer

Database Tools

Chado: Biological database schema
 BioMart: Data mining system
 GMODTools: Chado to Fasta, GFF, ...
 InterMine: Data warehousing

Analysis and Annotation

Galaxy: Data analysis & integration
 MAKER: Genome annotation pipeline

Biological Pathways

Pathway Tools: Metabolic, regulatory

Publication Curation

Textpresso: text mining

Mailing Lists

- Several project and topic based lists
- Many component-specific lists
- Mailing lists are very active
- Nabble archive of all lists

Overview Lists

Topic	List Link	Comment	Archive(s)
Announcements	gmod-announce	Low volume GMOD announcements. Moderated.	Gmane (2010/05+) , Nabble (2010/05+) , Sourceforge (2010/05+)
GMOD Developers List	gmod-devel	General GMOD developer list.	Gmane (2010/05+) , Nabble (2010/05+) , Sourceforge (2010/05+)

Component Lists

Mailing lists about specific GMOD Components.

Component	List Link	Comment	Archive(s)
Apollo	apollo	Apollo mailing list	Gmane (2008/04-2010/10) , Nabble (2010/05+)
	gmod-apollo-commits	Apollo code updates.	
Bio::Graphics	gmod-biographics-commits	Bio::Graphics code updates.	Sourceforge (2010/06+)
	announce	BioMart announcements mailing list	Nabble (2010/06+)
BioMart	users	BioMart users, developers, code and installation	Nabble (2010/06+)
	gmod-schema	All Chado issues	Gmane (2010/05+) , Nabble (2010/05+) , Nabble (new, 2010/05+) , Sourceforge (2010/05+)
Chado	gmod-schema-commits	Chado code updates.	Sourceforge (2010/05+)
	gmod-cmap	Discussion of CMap development, installation problems, etc.	Nabble (old) , Nabble (new, 2010/05+) , Sourceforge (2010/05+)
CMap	gmod-cmap-commits	Notification of SVN activity for CMap.	Sourceforge (2010/05+)
	diyg-pub-l	DIYA general discussion and support.	Nabble (2010/05+)
DIYA	diyg-dev-l	DIYA developer discussion.	
	ergatis-users	Ergatis users mailing list.	Nabble (2010/05+) , Sourceforge (2010/05+)
Ergatis	announcement	Ergatis announcements.	Nabble (2010/05+) , Sourceforge (2010/05+)
	ergatis-devel	Ergatis developers.	Nabble (2010/05+) , Sourceforge (2010/05+)
Galaxy	galaxy-dev	Discussion and questions regarding local installations and development of Galaxy.	Nabble (2010/05+) , Mail-Archive.com (2010/05+) , GMane (2010/05+) , Penn State (2010/05+)
	galaxy-user	General questions and discussion regarding Galaxy usage, especially pertaining to the public sites hosted by the Galaxy Team. Also used for announcements relevant to the Galaxy user community.	Nabble (2010/05+) , Mail-Archive.com (2010/05+) , GMane (2010/05+) , Penn State (2010/05+)
	galaxy-commits	Galaxy source control commit messages.	Penn State (2010/05+)
GBrowse & GBrowse_syn	gmod-gbrowse	GBrowse and GBrowse_syn users and developers.	Gmane (2010/05+) , Nabble (2010/05+) , Nabble (new 2010/05+) , Sourceforge (2010/05+)
	gmod-gbrowse-commits	Code updates.	Sourceforge (2010/05+)
InterMine	dev	InterMine support and development list.	InterMine (2010/05+) , Nabble (2010/05+)
ISGA	isga-users	ISGA support, development, and announcements mailing list	Nabble (2010/05+)
JBrowse	gmod-ajax	AJAX based genome browser.	Nabble (2010/05+) , Sourceforge (2010/05+)
MAKER	maker-devel	MAKER developers and users list.	Bluehost (2010/05+) , Google (2010/05+)
Modware	gmod-ware-users	Modware support and developer mailing list.	Nabble (2010/05+) , Sourceforge (2010/05+)
Pathway Tools	ptools-users@ai.sri.com	Pathway Tools users list. To subscribe to this list, send a request to ptools-support@ai.sri.com.	None
Sybil	sybil-info	Sybil mailing list.	Sourceforge (2010/05+)
Textpresso		A support mailing list and a community web site are under development for Textpresso. In the mean time, if you have support questions, please send them to textpresso@caltech.edu. See the User Guide for help.	
	gmod-tripal	Tripal-related announcements, questions, and requests for help from developers and the community.	Nabble (2010/05+) , Sourceforge (2010/05+)
Tripal	gmod-tripal-devel	Tripal development list	Nabble (2010/05+) , Sourceforge (2010/05+)
	gmod-webgbrowse	Questions, announcements, and development postings about the WebGBrowse front end to GBrowse configuration.	Nabble (2010/05+) , Sourceforge (2010/05+)

Topic Based Lists

These mailing lists are about general topics of interest, rather than about specific software components.

Name	List Link	Topics	Archive(s)
CoGePhy	gmod-cogephy	Discussion of comparative genomics, phylogeny, and related topics.	Nabble (2010/05+) , SourceForge (2010/05+)
PhenDiver	gmod-phendiver	Discussion of phenotype, natural diversity, population genetics and related topics.	Nabble (2010/05+) , SourceForge (2010/05+)



http://gmod.org/wiki/GMOD_Mailing_Lists

Acknowledgements

Literally, too many to count (OK, that was figurative, but it's really a lot!)

Each of these projects has a group of people that contribute code or testing or feedback. Actually counting them up would be too hard.

Thanks, and now lets look at some of the websites I referred to earlier...

