





## Help Desk Update

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September 2010 GMOD Meeting 13-45 September 2010

Help Desk

**Events** 

Grant Proposal / GBrowse → JBrowse

**New Stuff** 

Interesting Documents

GMOD on the Web



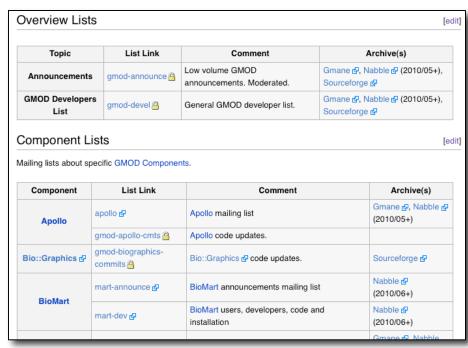


#### Mailing List Archive(s): GMOD @ Nabble

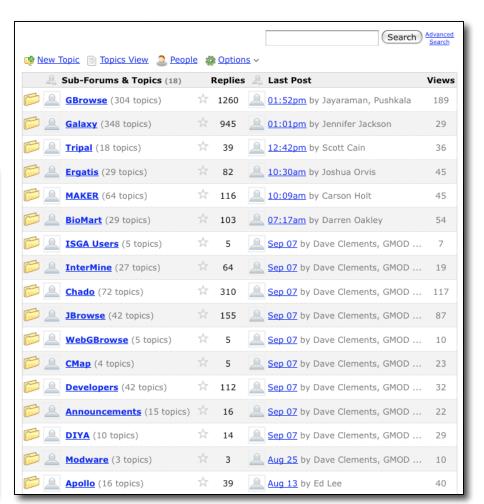
#### Unified search - no matter where list is hosted

All active lists

SF.net search < good



http://gmod.org/wiki/GMOD\_Mailing\_Lists



http://gmod.827538.n3.nabble.com/

#### Software Membership Requirements

- Codified in Feb 2010, following Jan 2010 meeting
- Version 1 Requirements:
  - Meets a common need
  - Useful over time
  - Configurable and Extensible
  - Open source license for all users
  - Interoperable with existing GMOD components
  - Commitment of support
- Want to add:
  - Support mailing list that is publicly archived
  - Publicly accessible code repository
- Thoughts, changes?





#### **Promotion**

- Why?
  - Increased visibility
    - → Increased adoption
      - → More projects contributing back
  - Increased adoption & development → funding
- How?
  - Cite GMOD, GMOD Components
  - Powered by GMOD icons
  - Speakers at your event
  - Graphics & slides for your presentations, posters
  - Presentation and event promotion
  - Brochures (GMOD project, events)
  - Bling!











### **GMOD Logo Program**





















Logos by John Aikman's Spring 2010 Advanced Design class @ Linn-Benton Community College, Albany, Oregon, United States





## 2010 GMOD Community Survey is Coming

- 2008
  - Covered components and project wide topics
- 2009
  - Focused on genome and comparative genomics browsing
- 2010
  - Will cover components and project wide topics
  - Use it to produce a GMOD Project publication.
  - Suggestions for general topics to cover?
  - Free bling to random survey takers!





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#### Satellites

- Birds of a Feather
- Wednesday, 9:30am, Part II Room
- Can still sign up!
- Topics:
  - Post Reference Genome Tools
  - You've got two days to come up with other topics
  - Rare opportunity to meet with others facing similar issues







#### Summer Schools

- 2010: 4th school, 3rd year
  - In May @ NESCent, North Carolina, US
  - 62 applicants for 25 slots
- 2011
  - During Summer @ NESCent
  - Will charge tuition; seeking sponsors
- Summer school sessions become online tutorials:
  - Starting and ending VMware images
  - Step by step instructions
  - Example datasets
  - Apollo, Artemis-Chado Integration,
     BioMart, Chado, CMap, Galaxy,
    - GBrowse, GBrowse\_syn, JBrowse, MAKER, Tripal



NESCent ~ Durham, NC

**GMOD Summer School** 

Americas, May 6-9





## **Upcoming Events of Note**

- Biocuration 2010
  - October, Tokyo, Japan
- Pathway Tools Workshop
  - October, Menlo Park, California, US
- GMOD Evo Hackathon
  - November, Durham, North Carolina, US
- Computational and Comparative Genomics
  - November, Cold Spring Harbor, New York, US
- Plant and Animal Genome
  - January, San Diego, California, US
- Workshop on Molecular Evolution
  - January, Cesky Krumlov, Czech Republic
- Galaxy Developers Conference
  - 2011, Europe















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### **Grant Proposal**

- Enhancing the GMOD Suite of Genome Annotation and Visualization Tools
  - JBrowse, GBrowse → JBrowse, Help Desk
  - Submitted Summer 2010
  - If approved, will start early 2011
- Help Desk
  - JBrowse, GBrowse → JBrowse, NGS data, transcriptomics, developmental atlases, population genomic and natural diversity data, workflow and pipeline tools for processing large data sets, and software interoperability
  - Continue with documentation, user support, gmod.org, training, (longer) summer schools, outreach, annual survey





#### JBrowse Development

#### 1.1 just released

- Scalability: very large data sets, including NGS reads, human EST/SNP tracks
- Extensibility: custom tracks
- Backward incompatible JSON format

# JBrowse 1.1 custom tracks e.g., base-pairing interactions of RNA secondary structure

3.000 3.500

mahoney 0 822

#### 1.2 Release (December 2010)

 improved NGS display (paired-end reads, possibly readto-genome alignments)

Available Tracks:

Genes

Xdecoder

Xdecoderm

Posterior pp,

(Drag -> to view)

slightly wrong

coordinates (RNAdecoder) 1.000

Shape Reactivity

SHAPEstructure

Xdecoder structure

2,000

- reduced memory usage for NGS
- minor UI enhancements including y-axis labels for wiggle tracks





## JBrowse Grant Proposal

- GBrowse → JBrowse
  - JBrowse concepts have proven themselves
  - Scalable to coming data set sizes
  - GBrowse development will wind down during the grant.
- New Features:
  - JBrowse ecosystem on par with what GBrowse has
  - DAS and web services support
  - Scalability and NGS
  - Large numbers of tracks
  - Community annotation (upload/publish, tagging, comment, ...)
  - Mobile device support?
- GBrowse → JBrowse Migration Support
  - Migration Scripts: Config files, data (data is easy)
  - Simultaneous GBrowse and JBrowse support
  - JBrowse running on top of GBrowse config and data





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#### **New Components**

- ISGA: Chris Hemmerich et al. at Indiana U.
  - Bioinformatics pipeline service software built on Ergatis
  - Newest GMOD component
- WebGBrowse: Ram Podicheti et al. at Indiana U
  - Hosted GBrowse and GUI for GBrowse configuration
  - Nominated and approved, almost in.
- SOBA: Ginger Fan et al. U of Utah
  - GFF3 file analysis and reporting
  - Tabular and graphical reports
  - Nominated and approved, code being refactored
- GMOD-DBSF, genes4all, ...: Alexie Papanicolaou at CSIRO
  - Drupal based toolkit for building organism web sites
  - Submitted for publication; not yet nominated





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#### Some Interesting Documents

- How to load a Chado Database into BioMart
  - AO Keliet, J Amselem, S Derozie, and D Steinbach, all @ INRA URGI

**EURGI**bio: mart

- http://gmod.org/wiki/BioMart
- Choosing a genome browser for a Model Organism Database: surveying the Maize community







- How and why MaizeGDB picked GBrowse
- Appeared in *Database*,
   http://database.oxfordjournals.org/







# Nature Methods Supplement on visualizing biological data, March 2010

- Visualizing biological data now and in the future
  - SI O'Donoghue, et al.
- Visualizing genomes: techniques and challenges
  - CB Nielsen, et al.
- Visualization of multiple alignments, phylogenies and gene family evolution
  - JB Proctor, et al.
- Visualization of image data from cells to organisms
  - T Walker, et al.
- Visualization of macromolecular structures
  - SI O'Donoghue, et al.
- Visualization of omics data for systems biology
  - N Gehlenborg, et al.





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### **GMOD.org**

- Moving from CSHL to OICR
  - In Jan/Feb 2010 Real soon now
  - MediaWiki upgrade
  - Probably lots of new extensions
  - Maybe a modified skin
- Look into adding
  - User log section
  - Scrapbook for contributed code
  - Membership directory (TableEdit based)
  - Semi-automated publication listing/linking





#### Should GMOD have a social presence?

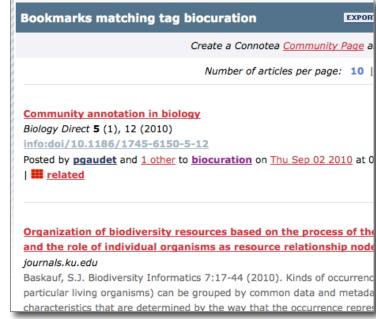
# GMOD already has mailing lists, wiki, GMOD News (RSS), IRC

#### What should the goals be?

- Community building / forums?
- Social bookmarking?
  - ISB uses Connotea to bookmark biocuration, text mining, and semantic annotation papers
- Outreach?

#### Which tools?

Twitter, Facebook, Connotea,
 StumbleUpon, Technorati, ...



http://www.connotea.org/tag/biocuration



#### Textpresso Update

- Textpresso
  - Stand-alone tool for text analysis.
  - Hard to tightly interface with external website
  - Dated user interface
  - Nathan Liles of Jim Hu's group at Texas A&M is working with CalTech on these issues
- Textpresso developers also have plans for a community website and mailing list.





#### Odds and Ends

- Get a name tag at next break!
- Hang on to it.

- Upload your talk, or just send it to me:
  - clements@nescent.org





#### Acknowledgements

## Summer School Oregon NESCent TAMU GMOD Europe PAG LBCC Hackathon

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Hilmar Lapp
Candace Brown
Jon Auman
Dan Blankenberg
Dave Matthews
Steve Heller
John Aikman
Robert Buels
Richard Smith
Nicole Washington
Suzi Lewis

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#### Thank You!



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