# August 2009 GMOD Community Meeting



# **GMOD Help Desk**

#### **Dave Clements**

National Evolutionary Synthesis Center 6-7 August 2009 Oxford, UK

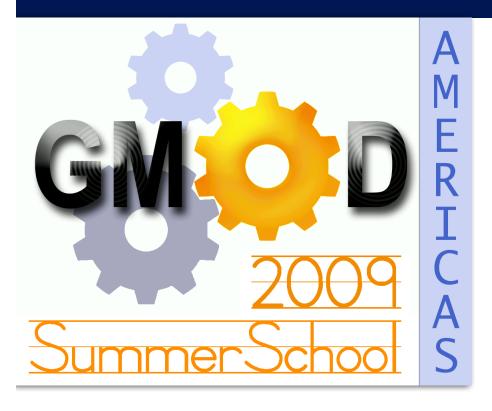
## **GMOD Help Desk**

- Summer Schools
- Outreach
- Community Surveys
- GMOD Hackathon
- Aniseed & Atlases
- Natural Diversity
- DIYA
- Tomorrow:
  - Visualizing Next Generation Sequence in GBrowse using SAMtools





#### **GMOD Summer Schools**





Multi-day, hands-on tutorials on installation and configuration of GMOD components

Both 2009 courses were full: 100+ applications for 50 openings Offered again in 2010, Considering one in Asia/Pacific. Class content will be made available on GMOD.org by Sep 2009.





#### Outreach

- GBrowse for Next Gen Data Talks
- Lutherstadt-Wittenberg, April
- U. Connecticut in June
- SMBE GMOD Workshop, Iowa City, June
  - Sheldon McKay, Mark Yandell, Ben Faga
- Bioinformatics Australia, Melbourne, October, maybe
- Insect Pests, Rennes, November

http://gmod.org/wiki/Training\_and\_Outreach





# **GMOD Community Surveys**

- Now doing annual community survey
- 2008
  - 89 responses
  - Very informative about how GMOD is used
    - http://gmod.org/wiki/2008\_GMOD\_Community\_Survey
- 2009 survey in October





#### **GMOD** Hackathon

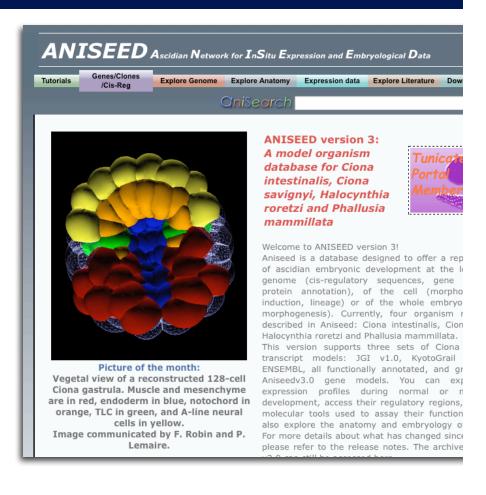
- Likely March-May Timeframe
- Likely at US National Evolutionary Sythesis Center (NESCent) in Durham, NC
- Focus:
  - Extending GMOD for evolutionary biology
- Contact me if you want to
  - Be on organizing committee
  - Participate in Hackathon





#### Atlases & Aniseed

- Ascidians / Tunicates
- Atlases for:
  - Expression
  - Anatomy
  - Cell Fate
- Converting to Chado
  - Extending Chado to better support atlases
  - Will make web front end part of GMOD.





http://aniseed-ibdm.univ-mrs.fr/



## Natural Diversity Chado Module

- Same status as at Nov 2007 Meeting ....
- Um, sorry about that. It's coming!

- Better support for phenotypes, crosses, individuals, geolocation, ...
- Based on GDPDM from Cornell U
  - Terry Casstevens et al.





#### DIYA

- Gene prediction pipeline for prokaryotes
- Actually a generic, lightweight pipeline framework
- Becoming part of GMOD as we speak

#### BIOINFORMATICS APPLICATIONS NOTE

Vol. 25 no. 7 2009, pa

#### Genome analysis

#### DIYA: a bacterial annotation pipeline for any genomics lab

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#### ABSTRACT

**Summary:** DIYA (Do-It-Yourself Annotator) is a modular and configurable open source pipeline software, written in Perl, used for the rapid annotation of bacterial genome sequences. The software is currently used to take DNA contigs as input, either in the form of complete genomes or the result of shotgun sequencing, and produce an annotated sequence in Genbank file format as output.

Availability: Distribution and source code are available at (https://sourceforge.net/projects/diyg/).

Contact: tread@emory.edu

Supplementary information: Supplementary data are available at Bioinformatics online.

- (3) Is relatively straightforward to configure.
- (4) Can be installed on a wide a range of hardware.
- Is modular; allowing for extension and customi pipeline.
- (6) Outputs common file formats.

#### 2 METHODS AND RESULTS

DIYA is written in object-oriented Perl and uses the Bioperl l et al., 2002) for sequence conversion and annotation. It configuration of DIYA requires basic knowledge of Perl an DIYA component is tested on installation. All DIYA pipelines





## Thank You!



### Dave Clements GMOD Help Desk

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http://gmod.org/GMOD\_Help\_Desk http://nescent.org





#### GMOD: Who uses it?









