

August 2009 GMOD Community Meeting



GMOD Help Desk

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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



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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 Synthesis 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.

ANISEED Ascidian Network for *InSitu* Expression and Embryological Data

Tutorials Genes/Clones /Cis-Reg Explore Genome Explore Anatomy Expression data Explore Literature Down

CniSearch

ANISEED version 3: A model organism database for *Ciona intestinalis*, *Ciona savignyi*, *Halocynthia roretzi* and *Phallusia mammillata*

Picture of the month:
Vegetal view of a reconstructed 128-cell *Ciona* gastrula. Muscle and mesenchyme are in red, endoderm in blue, notochord in orange, TLC in green, and A-line neural cells in yellow.
Image communicated by F. Robin and P. Lemaire.

<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

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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.
- (5) Is modular; allowing for extension and custom pipeline.
- (6) Outputs common file formats.

2 METHODS AND RESULTS

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

Thank You!



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http://gmod.org/GMOD_Help_Desk
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GMOD: Who uses it?



Plus several *hundreds* others.

