October 2011 GMOD Meeting

12-13 October 2011
Ontario Institute for Cancer Research
Toronto, Canada

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The next GMOD meeting is being held in October 12-13, 2011 at the Ontario Institute for Cancer Research (OICR) in Toronto, Canada. OICR is the home of GBrowse and BioMart.

If you're curious to see what happens at a GMOD meeting, see the writeup of the September 2010 GMOD Meeting, or the March 2011 GMOD Meeting page.

Registration

Registration is now closed.

Agenda

Keynote speakers

Gary D. Bader

Gary works on biological network analysis and pathway information resources as an Associate Professor at The Donnelly Centre at the University of Toronto. He completed post-doctoral work in the group of Chris Sander in the Computational Biology Center (cBio) at Memorial Sloan-Kettering Cancer Center in New York. Gary developed the Biomolecular Interaction Network Database (BIND) during his Ph.D. in the lab of Christopher Hogue in the Department of Biochemistry at the University of Toronto and the Samuel Lunenfeld Research Institute at Mount Sinai Hospital in Toronto. He completed a B.Sc. in Biochemistry at McGill University in Montreal. See http://baderlab.org for more information on Gary.

Michael Brudno

Mike's main research interest is the development of computational methods for the analysis of High throughput, a.k.a. Next-Generation sequencing data. His group is working on algorithms for assembly, mapping, visualization, and variation discovery with short reads. In addition, they also work on cloud computing, whole-genome alignment, as well as on detection and analysis of genome variation in the sea squirt *C. savignyi*.

After receiving a BA in Computer Science and History from UC Berkeley, Mike worked on his PhD at the Computer Science Department of Stanford University, developing several approaches for comparison of genomic sequences, including the LAGAN Alignment Toolkit. He then completed a postdoc at the Computer Science Division, UC Berkeley and was a Visiting Scientist at CSAIL (MIT) before starting as an Assistant Professor at the University of Toronto in January 2006. He is the recipient of the Alfred P. Sloan Research Fellowship, Ontario Early Researcher Award, and a Canada Research Chair in Computational Biology. See http://www.cs.toronto.edu/~brudno/ for more information on Mike.

Agenda

The Main meeting (Days 1 and 2) will take place at HL31 in the MaRS Centre. Here are the directions once you are outside the building:

Directions to the HL31 are as follows:

- Enter the MaRS Centre (101 College Street, Toronto ON M5G 1L7) through the main doors (with the stairs & ramp)
- In the main lobby area, turn right and walk towards the west end of the building
- Pass the RBC bank machine and proceed through a glass door on your right
- Go down the stairs marked ?Stair 16, Ground Floor? (or take the elevator)
- At the bottom of the stairs, enter the hallway through the door marked ?Stair 16, Upper Concourse?
- The corridor to HL31 boardroom is immediately on your left

Day 1: Wednesday

Time	Topic	Presenter(s)	Links
9:15	Introductions	Scott Cain	
9:35	Welcome to OICR and the State of GMOD	Scott Cain	slides
10:10	Keynote: Network and pathway information for systems biology	Gary Bader	PPT
11:00	Coffee break		
11:30	GBrowse2: What's New	Lincoln Stein	PPT

12:00	Lunch		
1:30	JBrowse and WebApollo	Mitch Skinner	PDF
2:00	The Mycoplasma Genome Database: marrying microscopy and genomics	Andrew Oberlin	PDF
2:30	Coffee break		
3:00	MAKER	Carson Holt	PDF
3:30	InterMine	Alex Kalderimis and/or Richard Smith	PDF
4:00	Improving MOD interoperation (A Discussion)	Josh Goodman	PDF,PPT
4:45	Wrap up and dinner Mata Hari Grill 39 Baldwin St. Toronto		PDF

Day 2: Thursday

Time	Topic	Presenter(s)	Links
9:15	Keynote: The Savant Browser and MedSavant	Michael Brudno	PDF,PPT
10:00	Galaxy	Dan Blankenberg	PDF
10:30	Coffee		
11:00	SADI for GMOD: An RDF/OWL Interface to GMOD Data	Ben Vandervalk	Prezi, PDF
11:30	The Comprehensive Antibiotic Resistance Database	Andrew McArthur	PDF,PPT
12:00	Lunch		
1:30	Lightning talks (Please feel free to give a 5-10 minute talk on whatever; if you are interested enough to put together a talk, others will likely be interested in the content! :-)		

Day 3: Friday

Time	Workshop	Location
9:00	BioMart	OICR, 8th floor Boardroom
9:00	Galaxy	OICR room HL-31
2:30	MAKER	OICR, 8th floor Boardroom

Suggested agenda items

Please feel free to add suggested talks or topics for the meeting.

- The Mycoplasma Genome Database: marrying microscopy and genomics (Andrew Oberlin & Iddo Friedberg)
- Improving MOD interoperability (Scott Cain, Josh Goodman will lead the discussion)
- BioMart, Chado, Galaxy, GBrowse, and InterMine updates - since representatives of all those groups will be there (suggested by Dave C)
- SADI for GMOD: An RDF/OWL Interface to GMOD Data (Ben Vandervalk)
- Running GBrowse2 without root and without Apache (Todd Harris)
- The Comprehensive Antibiotic Resistance Database (Andrew McArthur)
- JBrowse update (Mitch Skinner)
- web application integration, the Ambikon integration server (Rob Buels)

Scheduled Satellite Meetings

- BioMart workshop (half day, morning), Friday, 14 October
- Galaxy workshop (half day, morning), Friday, October 14 - details to be forthcoming
- InterMine development meeting, Thursday and Friday
- MAKER workshop (half day, afternoon), Friday, October 14

You can register for the BioMart, Galaxy, and MAKER Workshops on the meeting registration site. If you are interested in the InterMine development meeting, please let Richard Smith know.

Galaxy Workshop

This workshop will cover an introduction to Galaxy, including analyzing data with tools and visualizations, using Galaxy in the cloud, and running your own instance and adding new tools. Dan Blankenberg of the Galaxy Project will lead the workshop.

Galaxy is an open-source analysis and data integration framework that is available as a free public service and as open source software that can be deployed both locally or on cloud resources. The Galaxy platform empowers transparent and reproducible research by providing interactive access to popular tools, including those that allow manipulation of raw sequencing reads, mapping, peak calling, genomic interval operations, visualization at genome browsers and more, as well as a point-and-click workflow system.

The Galaxy workshop will be held on Friday, 14 October, from 9am-2pm in the Ontario Institute for Cancer Research, room OICR HL-31. Table seating is limited to 18 participants, with space for an additional 10 participants, so please register and arrive early.

Workshop Slides

An Introduction to Galaxy

Using Galaxy for High-throughput Sequencing (HTS) Analysis and Visualization

Running and Enhancing your own Galaxy

Second Half: Running Your Own Instance

InterMine Development Meeting

This meeting is intended for organisations that have an InterMine, or are thinking of setting one up, to discuss development priorities, as well as production and implementation issues. This meeting is part of the InterMod project, which involves supporting InterMine data-warehouses for *D. melanogaster*, *R. norvegus*, *M. musculus*, *S. cerevisiae*, *D. rerio* and *C. elegans*. Groups representing other efforts to use InterMine for biological data-warehousing are welcome to attend (as indeed some aleady are) - please contact Richard Smith for more details.

BioMart Workshop

This workshop will include an introduction to the BioMart system, followed by a brief demonstration of BioMart applications in the BioMart Central Portal (http://central.biomart.org) and the International Cancer Genome Consortium (ICGC) Data Portal (http://dcc.icgc.org), and a hands-on tutorial to show how to create and configure a local data mart, how to import external mart and link it with the local mart, how to deploy the BioMart server to provide data access, and how to query BioMart server via web GUI and REST API. Junjun Zhang of the BioMart Project will lead the workshop.

Requirements: Parts of the tutorial will be taught using a VirtualBox Open Virtualization Appliance (OVA) image file. You will need a laptop with the latest version of VirtualBox, VMware Player, or VMware Workstation installed and running. VirtualBox is freely available from http://www.virtualbox.org/wiki/Downloads. VMware player for Linux and Windows operating systems is freely available from VMware (http://vmware.com/products/player/). Mac users may use VMware Fusion (http://www.vmware.com/products/fusion/ on a 30 day free trail).

The BioMart workshop will be held on Friday, October 14, from 9-12 in the Ontario Institute for Cancer Research, 8th floor NorthEast Boardroom.

MAKER Workshop

The MAKER workshop will include a brief introduction to MAKER as well as demonstrations in using the pipeline to generate gene annotations, perform downstream analysis of the gene models, and ingrate the output into other GMOD tools. To make demonstrations as hands on as possible, the web version of MAKER will be used to give everyone access to the pipeline (http://www.yandell-lab.org/software/mwas.html). Examples will include demonstrations of the command line version of MAKER as well (but the online examples will be hands on). You can follow along online, or you can just watch and take notes.

Requirements for online examples: WiFi capable laptop, a javascript enabled web browser, and Java 6 or greater.

The MAKER workshop will be held on Friday, October 14, from 2:30-5:00 in the Ontario Institute for Cancer Research, 8th floor NorthEast Boardroom.

Logistics

Hotel

We don't have a block of rooms reserved due to unfavorable contracts offered. We're suggesting staying at Delta Chelsea hotel, as it is convenient to OICR.

Next Meeting

April 2012 GMOD Meeting