



14th Annual Bioinformatics Open Source Conference

BOSC 2013 Schedule

Day 1 (Friday, July 19, 2013)

Time	Title	Speaker or Session Chair
7:30-9:00	Registration	
9:00-9:15	Introduction and Welcome	Nomi Harris (Chair, BOSC 2013)
9:15-10:15	Keynote: Network ready research--the role of open source and open thinking	Cameron Neylon
10:15-10:45	Coffee Break	
10:45-12:30	Session: Open Science	Chair: Hilmar Lapp
10:45-11:00	Open Science Data Framework: A Cloud enabled system to store, access, and analyze scientific data	Anup Mahurkar
11:00-11:15	myExperiment Research Objects: Beyond Workflows and Packs	Stian Soiland-Reyes
11:15-11:30	Empowering Cancer Research Through Open Development	Juli Klemm
11:30-11:45	DNAdigest - a not-for-profit organisation to promote and enable open-access sharing of genomics data	Fiona Nielsen
11:45-11:50	Jug: Reproducible Research in Python	Luis Pedro Coelho
11:50-11:55	OpenLabFramework: A Next-Generation Open-Source Laboratory Information Management System for Efficient Sample Tracking	Markus List
12:00-12:30	Ten Simple Rules for the Open Development of Scientific Software [discussion]	Andreas Prlic
12:30-1:30	Lunch	
1:00-2:00	Poster Session I	
2:00-3:30	Session: Visualization	Chair: Jan Aerts
2:00-2:25	Refinery Platform - Integrating Visualization and Analysis of Large-Scale Biological Data	Nils Gehlenborg
2:25-2:40	MetaSee: An interactive visualization toolbox for metagenomic sample analysis and comparison	Kang Ning
2:40-2:55	DGE-Vis: Visualisation of RNA-seq data for Differential Gene Expression analysis	David Powell
2:55-3:10	Genomic Visualization Everywhere with Dalliance	Thomas Down
3:10-3:25	Robust quality control of Next Generation Sequencing alignment data	Konstantin Okonechnikov
3:25-3:30	Visualizing bacterial sequencing data with GenomeView	Thomas Abeel

Time	Title	Speaker or Session Chair
3:30-4:00	Coffee Break	
4:00-5:30	Session: Bioinformatics Open Source Project Updates	Chair: Hans-Rudolf Hotz
4:00-4:15	BioRuby project updates - power of modularity in the community-based open source development model	Toshiaki Katayama
4:15-4:30	Biopython project update	Peter Cock
4:30-4:45	InterMine - Collaborative Data Mining	Alex Kalderimis
4:45-5:00	GenoCAD 2.2 Grammar Editor	Jean Peccoud
5:00-5:15	Improvements and new features in the 7th major release of the Bio-Linux distro	Timothy Booth
5:15-5:20	Announcements	Nomi Harris
5:20-6:30	Poster Session II	
5:20-6:30	BOFs	
7:00	Pay-your-own-way BOSC dinner, Hendrik's (www.hendriks-berlin.de), Straße des 17. Juni 13, 10623 Berlin. RSVP at bit.ly/BOSC2013-dinner	

Day 2 (Saturday, July 20, 2013)

Time	Title	Speaker or Session Chair
8:45-8:50	Announcements	Nomi Harris
8:50-9:00	Codefest 2013 Report	Brad Chapman (Codefest 2013 Organizer)
9:00-9:15	Open Bioinformatics Foundation: A Community For, By, and Of You	Hilmar Lapp (President, O B F)
9:15-10:15	Keynote: Biological sequence analysis in the post-data era	Sean Eddy
10:15-10:45	Coffee Break	
10:45-12:30	Session: Software Interoperability	Chair: Jeremy Goecks
10:45-11:10	BioBlend - Enabling Pipeline Dreams	Enis Afgan
11:10-11:35	Taverna Components: Semantically annotated and shareable units of functionality	Alan Williams
11:35-11:50	UGENE Workflow Designer – flexible control and extension of pipelines with scripts	Yuriy Vaskin
11:50-12:05	Oqtans: A Multifunctional Workbench for RNA-seq Data Analysis	Gunnar Räscher
12:05-12:10	PhyloCommons: community storage, annotation and reuse of phylogenies	Hilmar Lapp

Time	Title	Speaker or Session Chair
12:10-12:15	GEMBASSY: an EMBOSS associated package for genome analysis using G-language SOAP/REST web services	Kazuharu Arakawa
12:15-12:30	Rubra - flexible distributed pipelines for bioinformatics	Clare Sloggett
12:30-1:30	Lunch	
12:30-1:30	Poster Session III	
1:30-3:30	Session: Cloud and Genome-Scale Computing	Chair: Peter Cock
1:30-1:45	Towards Enabling Big Data and Federated Computing in the Cloud	Enis Afgan
1:45-2:00	MyGene.info: Making Elastic and Extensible Gene-centric Web Services	Chunlei Wu
2:00-2:15	An update on the Seal Hadoop-based sequence processing toolbox	Luca Pireddu
2:15-2:30	Open Source Configuration of Bioinformatics Infrastructure	John Chilton
2:30-2:55	An Open Source Framework for Gene Prioritization	Hoan Nguyen
2:55-3:10	RAMPART (aRobustAutomaticMultipleAssembleRToolkit)	Daniel Mapleson
3:10-3:30	OmicsConnect: flexible multi-omics data capture and integration tools for high-throughput biology	Joeri van der Velde
3:30-4:00	Coffee Break	
4:00-4:40	Session: Translational Genomics	Chair: Nomi Harris
4:00-4:25	Community development of human variant calling and validation pipelines	Brad Chapman
4:25-4:40	Understanding Cancer Genomes Using Galaxy	Jeremy Goecks
4:40-5:30	Panel: Strategies for Funding and Maintaining Open Source Software	<i>Moderator:</i> Brad Chapman <i>Panelists:</i> Peter Cock, Sean Eddy, Carole Goble, Richard Holland, Scott Markel, Jean Peccoud
5:30-5:40	Presentation of Student Travel Awards	Nomi Harris
5:40-6:40	BOFs	

Any last-minute schedule updates will be posted at
http://www.open-bio.org/wiki/BOSC_2013_Schedule