12th Annual Bioinformatics Open Source Conference
BOSC 2011

Day 1 (Friday, July 15, 2011)

Time	Title	Speaker or Session Chair
9:00-9:15	**Introduction**	Nomi Harris (Co-Chair, BOSC 2011)
9:15-10:15	**Keynote: The role of openness in knowledge-based systems for biomedicine**	Larry Hunter
10:15-10:45	*Coffee Break*	
10:45-12:30	**Session: Genome Content Management**	Chair: Peter Rice
10:45-11:05	Unipro UGENE: an open source toolkit for complex genome analysis	Konstantin Okonechnikov
11:05-11:25	Exploring the genome with Dalliance	Thomas Down
11:25-11:45	InterMine - Using RESTful Webservices for Interoperability	Alex Kalderimis
11:45-11:55	easyDAS: Automatic creation of DAS servers	Bernat Gel
11:55-12:05	Enacting Taverna Workflows through Galaxy	Kostas Karasavvas
12:05-12:15	Mobyle 1.0: new features, new types of services	Hervé Ménager
12:15-12:25	BioMart 0.8 offers new tools, more interfaces, and increased flexibility through plug-ins	Junjun Zhang
12:25-12:32	Running Workflows Through Taverna Server	Donal Fellows
12:30-2:00	*Lunch*	
1:30-2:30	**Poster Session**	
2:30-3:30	**Session: Visualization**	Chair: Jan Aerts
2:30-2:50	Cytoscape 3.0: Architecture for Extension	Michael Smoot
2:50-3:10	Applying Visual Analytics to Extend the Genome Browser from Visualization Tool to Analysis Tool	Jeremy Goecks
3:10-3:20	WebApollo: A web-based sequence annotation editor for community annotation	Nomi Harris
3:20-3:30	The isobar R package: Analysis of quantitative proteomics data	Florian P. Breitwieser
3:30-4:00	*Coffee Break*	
4:00-5:30	**Session: Next-Generation Sequencing**	Chair: Thomas Down
4:00-4:20	Stacks: building and genotyping loci de novo from short-read sequences	Julian Catchen
4:20-4:40	Large scale NGS pipelines using the MOLGENIS platform: processing the Genome of the Netherlands	Morris Swertz
4:40-4:50	Bio-NGS: BioRuby plugin to conduct programmable workflows for Next Generation Sequencing data	Raoul Bonnal
4:50-5:00	Goby framework: native support in GSNAP, BWA and IGV 2.0	Kevin C. Dorff

Time	Title	Speaker or Session Chair
5:00-5:10	A Scalable Multicore Implementation of the TEIRESIAS Algorithm	Frank Drews
5:10-5:20	Biomanycores, open-source parallel code for many-core bioinformatics	Jean-Frédéric Berthelot
5:20-5:30	GemSIM: General, Error-Model Based Simulator of next-generation sequencing	Kerensa McElroy
5:30-6:30	**Poster Session and BOFs**	
7:00	Optional dinner for BOSC attendees	Location TBA

Day 2 (Saturday, July 16, 2011)

Time	Title	Speaker or Session Chair
8:45-8:50	**Announcements**	Nomi Harris and Peter Rice
8:50-9:50	**Keynote: Into the Wonderful**	Matt Wood
9:50-10:15	Securing and sharing bioinformatics in the cloud	Richard Holland
10:15-10:45	*Coffee Break*	
10:45-12:30	**Session: Cloud Computing**	Chair: Brad Chapman
10:45-11:05	Mygene.info: Gene Annotation as a Service - GAaaS	Chunlei Wu
11:05-11:25	Cloud BioLinux: open source, fully-customizable bioinformatics computing on the cloud for the genomics community and beyond	Konstantinos Krampis
11:25-11:35	OBIWEE : an open source bioinformatics cloud environment	Jonathan Piat
11:35-11:45	SeqWare: Analyzing Whole Human Genome Sequence Data on Amazon's Cloud	Brian O'Connor
11:45-12:05	Sequencescape - a cloud enabled Laboratory Information Management Systems (LIMS) for second and third generation sequencing	Lars Jorgensen
12:05-12:15	Enabling NGS Analysis with(out) the Infrastructure	Enis Afgan
12:15-12:25	Hadoop-BAM: A Library for Genomic Data Processing	Aleksi Kallio
12:30-2:00	*Lunch*	
1:00-2:00	**Poster Session**	
2:00-3:30	**Session: Semantic Web and Misc. Open Source Projects**	Chair: Peter Cock
2:00-2:10	SADI for GMOD: Bringing Model Organism Data onto the Semantic Web	Ben Vandervalk
2:10-2:20	Scufl2: Because a workflow is more than its definition	Stian Soiland-Reyes
2:20-2:30	OntoCAT - an integrated programming toolkit for common ontology application tasks	Tomasz Adamusiak
2:30-2:50	Debian Med: individuals' expertise and their sharing of package build instructions	Steffen Möller

Time	Title	Speaker or Session Chair
2:50-3:10	The BALL project: The Biochemical Algorithms Library (BALL) for Rapid Application Development in Structural Bioinformatics and its graphical user interface BALLView	Andreas Hildebrandt
3:10-3:20	Biopython Project Update	Peter Cock
3:20-3:27	What's new with GMOD	Scott Cain
3:27-3:34	Exploring human variation data with Clojure	Brad Chapman
3:30-4:00	*Coffee Break*	
4:00-4:30	**Session: Misc. Open Source Projects**	Chair: Jim Procter
4:00-4:10	EMBOSS: New developments and extended data access	Peter Rice
4:10-4:20	G-language Project: the last 10 years and beyond	Kazuharu Arakawa
4:20-4:30	A Framework for Bioinformatics on the Microsoft Platform	Simon Mercer
4:30-5:20	**Panel: Multi-Institution Collaboration**	Moderator: Brad Chapman Panelists: Richard Holland, Hilmar Lapp, Jean Peccoud, Peter Rice
5:20-5:30	Presentation of awards	Nomi Harris
5:30-6:30	**BOFs**	

Last-minute schedule updates will be posted at http://www.open-bio.org/wiki/BOSC_2011_Schedule

Posters

No.	Poster Title and Author(s)
1	Unipro UGENE: an open source toolkit for complex genome analysis (Okonechnikov et al.)
2	Exploring the genome with Dalliance (Down, Hubbard)
3	InterMine - Using RESTful Webservices for Interoperability (Kalderimis et al.)
4	easyDAS: Automatic creation of DAS servers (Gel et al.)
5	Enacting Taverna Workflows through Galaxy (Karasavvas et al.)
6	Mobyle 1.0: new features, new types of services (Menager et al.)
7	BioMart 0.8 offers new tools, more interfaces, and increased flexibility through plug-ins (Zhang et al.)
8	Running Workflows Through Taverna Server (Fellows et al.)
9	Cytoscape 3.0: Architecture for Extension (Smoot)
10	Applying Visual Analytics to Extend the Genome Browser from Visualization Tool to Analysis Tool (Goecks et al.)
11	The isobar R package: Analysis of quantitative proteomics data (Breitwieser, Colinge)
12	Large scale NGS pipelines using the MOLGENIS platform: processing the Genome of the Netherlands (Byelas et al.)
13	Bio-NGS: BioRuby plugin to conduct programmable workflows for Next Generation Sequencing data (Bonnal et al.)
14	Goby framework: native support in GSNAP, BWA and IGV 2.0 (Dorff et al.)
15	Biomanycores, open-source parallel code for many-core bioinformatics (Berthelot et

	al.)
16	GemSIM: General, Error-Model Based Simulator of next-generation sequencing (McElroy et al.)
17	Mygene.info: Gene Annotation as a Service - GAaaS (Wu, Su)
18	Enabling NGS Analysis with(out) the Infrastructure (Afgan et al.)
19	Hadoop-BAM: A Library for Genomic Data Processing (Niemenmaa et al.)
20	SADI for GMOD: Bringing Model Organism Data onto the Semantic Web (Vandervalk et al.)
21	Scufl2: because a workflow is more than its definition (Sioland-Reves et al.)
22	OntoCAT - an integrated programming toolkit for common ontology application tasks (Adamusiak et al.)
23	Debian Med: individuals' expertize and their sharing of package build instructions (Moeller et al.)
24	The BALL project: The Biochemical Algorithms Library (BALL) for Rapid Application Development in Structural Bioinformatics and its graphical user interface BALLView (Hildebrandt et al.)
25	What's new with GMOD (Cain et al.)
26	EMBOSS: New developments and extended data access (Rice et al.)
27	A tool kit for pre-processing genome annotations in Generic Feature Format (GFF) (Sreedharan)
28	ADDAPTS: A Data-Driven Automated Pipeline and Tracking System (Naravan et al.)
29	BALLView: A versatile molecular visualization and modeling tool (Nickels et al.)
30	Beyond Web Services: Calling external programs from within Taverna (Williams et al.)
31	BioMart combines the power of the semantic web with the speed of relational database querying (Baran et al.)
32	BioSharing: standards, policies and communication in bioscience (Sansone et al.)
33	BioXSD: the XML Schema for everyday bioinformatics (Kalas et al.)
34	Cloudgene – A graphical MapReduce interface for cloud computing (Forer et al.)
35	Combining RapidMiner operators with bioinformatics services - a powerful combination (Jupp et al.)
36	Distributed Web Services for Bioinformatics: Multiple Sequence Alignment (Troshin et al.)
37	Endrov - an open source framework for image processing and analysis (Henriksson, Burglin)
38	fastapl -- a utility for processing fasta format data (Horton)
39	FLAME: An Open-Source Agent-Based Modelling Platform for High Performance Computing of Biological Systems (Bicak et al.)
40	GeneNomenclatureUtils: Tools for annotating genes and comparing gene lists with community resources (Croning, Grant)
41	GenomeTools - a versatile and efficient bioinformatics toolkit (Gremme et al.)
42	InterMine - An Open Source Data Warehouse and Query interface (Hu et al.)
43	Jalview 2: Transitions (Procter et al.)
44	jsDAS and DASTY3, enabling DAS protein visualization (Garcia et al.)
45	KNIME-CADDSuite – integration of the computer aided drug design suite (CADDSuite) into the Konstanz Information Miner (KNIME) (Roettig et al.)
46	OncoPortal: the power of BioMart for oncology research (Wong-Erasmus et al.)
47	SEQCRAWLER – A cloud ready indexing platform (Sallou)
48	SeqGI: Sequence Read Enrichment at Genomic Intervals (de Santiago et al.)
49	Web based pipeline frameworks for data processing (Ellrott et al.)
50	UniPAX – an integrative environment for biological networks (Gerasch et al.)

Ballot for Audience Favorite Talk

Please vote for one talk and give this form to Nomi Harris or Peter Rice (BOSC Co-Chairs) before 4:30pm on the second day. (Note that this ballot is two pages!)

The winner will be announced in the closing session at 5:20 on the second day.

Best Talk?	Title	Speaker
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