

13th Annual Bioinformatics Open Source Conference (BOSC 2012)

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The 13th Annual Bioinformatics Open Source Conference (BOSC 2012) will take place July 13-14, 2012, in Long Beach, CA, right before ISMB 2012.

The Bioinformatics Open Source Conference (BOSC) is sponsored by the Open Bioinformatics Foundation (O|B|F), a non-profit group dedicated to promoting the practice and philosophy of Open Source software development within the biological research community.

Open Source software has flourished in the bioinformatics community for well over a decade. When the first BOSC (Bioinformatics Open Source Conference) was held in 2000, there were already a number of popular open source bioinformatics packages, and the number and range of these projects has increased dramatically since then. Many open source bioinformatics packages are widely used by the research community across a wide variety of applications. Open source bioinformatics software has facilitated rapid innovation, dissemination, and wide adoption of new computational methods, reusable software components, and standards.

BOSC brings together bioinformatics open source developers from all over the world so they can forge connections each other (both within and across projects), increase the visibility of their work, and collaborate to build shared resources. Participants can work together to create use cases, prototype working code, or run hands-on tutorials in new software packages and emerging technologies. For those who are bioinformatics software users rather than developers, BOSC introduces or updates them on a wide array of projects that they might find useful.

Sessions

Cloud and Parallel Computing -- This session will cover cloud-based approaches to improving software and data accessibility. The emergence of cloud computing has made highly scalable cluster computing available to computational biologists. Services such as Amazon's Elastic Compute Cloud combined with publicly available datasets promise to lower the overhead to participate in large scale data analyses. Talks will focus on how the community can build up resources, datasets, and workflows for making the best use of cloud infrastructure. We will also include talks on data-parallel approaches to analyzing massive data sets, such as those resulting from next-generation sequencing and mass spec proteomics, and reports on the parallelization of bioinformatics algorithms in general.

Linked Data -- Linked Data is an emerging set of conventions on using basic Semantic Web standards (HTTP URIs and RDF in particular) to expose, share, and connect data, information, and knowledge online. Linked Data principles are increasingly being embraced by bioinformatics resources. For example, UniProt is now being made fully available in RDF

, and collaborative initiatives such as Bio2RDF aim to expose many commonly used database resources to data integration through RDF and its query language, SPARQL. This session is devoted to reports on software that works with such new data stores, or aids in their development, including technologies for interoperable web services, and tools for ontology building or maintenance.

Genome-scale Data Management -- This session will focus on processes and technologies that support the creating, managing and reporting of genomic data. This session is appropriate for discussion of systems that involve components such as (but not limited to) Ensembl and GMOD/Chado data stores, Taverna and Galaxy analysis workflows, and BioMart and InterMine warehouses.

Data Visualization and Imaging -- This session will address visualization techniques and tools that provide insight into large and highly complex biomedical data sets, as well as biological image processing, analysis and data management. Talks that address the development of frameworks and communities are particularly welcome.

Translational Bioinformatics -- This session will explore applications of biological and medical informatics to the development of personalized healthcare, therapies, and a better understanding of human health and disease. Topics include the analysis of human microarray and other 'omics data, bioinformatics methodologies for clinical research, and tools for discovering clinically useful associations in human databases.

Bioinformatics Open Source Project Updates -- This session will feature short talks from ongoing projects describing their recent progress. Abstracts will be solicited from open source projects affiliated with the O|B|F (see <http://www.open-bio.org/wiki/Projects>), including the Bio projects, DAS, BioMOBY, EMBOSS, and GMOD, but any other open-source project will be equally eligible to submit presentations for this session.

Panel: Interfacing with Industry -- Companies are more and more seeing the benefits of working with open source code and making their own code open; meanwhile, academics frequently partner with companies on their research projects. We encourage submissions from companies that work with open source software, as well as developers from non-commercial organizations who collaborate with companies. We anticipate a broadly useful conversation about the benefits and pitfalls of academic/commercial interaction.

Link: http://www.open-bio.org/wiki/BOSC_2012

Categories: Big Data, Bioinformatics, Biology, Computational Biology, Computer Science, Genomics, Informatics, Molecular and Cellular Biology, Research Methods, Translational Medicine

Audience: Bioinformatician, Biologist, Computer Scientist, Informatician, Molecular Biologist