

Report on the annual Intelligent Systems for Molecular Biology conference
Fortaleza, Brazil, 6 – 10.8.06

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Introduction and Motivation:

The conference on Intelligent Systems for Molecular Biology (ISMB) is visited by researchers from many fields of computational biology. The presented scientific work covers many bioinformatics fields as genomic, phylogenetic, text mining, structural biology etc. In regard to my PhD thesis, I was especially interested in the proteomics and systems biology section of the ISMB conference

Highlights

Clearly the keynote speakers were my personal highlight of the ISMB meeting. I enjoyed the very interesting talk of Elena Conti about molecular mechanism of RNA degradation, which offered the otherwise algorithmic focused conference very exciting biological insights. Mathieu Blanchette gave an exciting talk about the reconstruction and learning content of mammalian genomes to illustrate another example of new results from the post-sequencing area.

Unfortunately, several keynotes speaker were not able to join the meeting in Fortaleza due to recent grounding of the VARIG airline. It would have been very interesting to hear the talk of Charles Delisi about new approaches in the detection of biomarkers, which is very close related work to research efforts in my scientific group. Also noble price winner Kurt Wütherich was not able to join ISMB, leaving a missing talk on the use of bioinformatics on protein structure determination.

Interesting Side sessions and Posters

Beside the keynote lectures, there were numerous sessions on a wide range of bioinformatics topics. I mainly focused on proteomics, network analysis, molecular interaction studies and systems biology.

An interesting talk was performed by the group of Prof. Buhmann, which presented their pairwise LC/MS alignment tool, dealing with retention time calibration issues. This touches closely my work since I am developing a multi dimensional alignment software for the analysis of LC/MS data. Beside, the group of Prof. Reinert presented in a software demo session their open source software C++ library OpenMS, which offers functionality for the analysis of LC/MS data.

Otherwise, many efforts are ongoing in developing databases and data representations for molecular interaction data. Since we are working with protein-protein interaction, I was interested in finding existing tools to store, visualize and share such data. The PSI standard is a new XML schema at the EBI, which offers a common way to archive interaction data. Also they are developing and maintaining a database InterPro where interaction data can be stored and retrieved. This data is manually annotated to offer a collection of high quality molecular interaction data. In addition, IntAct is also a new data exploration system developed among others by the group of Rolf Apweiler, which allows to view and analyze different types of molecular interactions as for example to join metabolomic with molecular interaction data.

Own scientific exchanges

I presented my work in a poster, where I illustrated a novel tool to assess pairwise correlations of LC/MS runs using only MS1 information. I had several discussions with people interested in my program, especially since it is based on a label free quantification and does not require MS2 information or labeling methods.