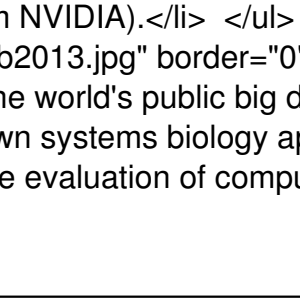
I participated in CAMDA Satellite Meeting on critical assessment of massive data analysis during 29th and 20th July at ISMB in Berlin, where I presented our matrix factorization-based data fusion approach to predicting drug-induced liver injury from toxicogenomics data sets and circumstantial evidence from related data sources. The outcome was positive and our work has been recognized as an excellent research. The main conference days of 21st Annual International Conference on Intelligent Systems for Molecular Biology (ISMB) and 12th European Conference on Computational Biology (ECCB) were in Berlin, 21st to 23rd July. Overall, the meeting was enjoyable and the talks there offered novel insights from both computational and biological perspectives. As a side note, in 2014 ISMB and ECCB will be organized separately, the ISMB conference will be in July in Boston and the ECCB meeting will be in September in Strasbourg. Here, I list some of the talks I attended at ISMB/ECCB. At some point it was difficult to pick the most interesting talk due to nine parallel sessions. Note that only the presenting authors are provided here. First day: <ul> Simple topological properties predict functional misannotations in a metabolic network (J. Pinney). Of men ad not mice. Comparative genome analysis of human diseases and mouse models (W. Xiao). Integration of heterogeneous -seq and -omics data sets: ongoing research and development projects at CLC bio (M. Lappe). Technology track. System based metatranscriptomic analysis (X. Xiong). Integrative analysis of large scale data (M. Spivakov, S. Menon). Workshop track. Multi-task learning for host-pathogen interactions (M. Kshirsagar). Integrative modelling coupled with mass spectrometry-based approaches reveals the structure and dynamics of protein assemblies (A. Politis). Synthetic lethality between gene defects affecting a single non-essential molecular pathway with reversible steps (I. Kupperstein). Second day: <ul> KeyPathwayMiner - extracting disease specific pathways by combining omics data and biological networks (J. Baumbach). Technology track. Compressive genomics (M. Baym). Predicting drug-target interactions using restricted Boltzmann machines (J. Zeng). Efficient network-guided multi locus associationmapping with graph cuts (C. Azencott). Differential genetic interactions of S. cerevisiae stress response pathways (P. Beltrao). Special session on dynamic interaction networks. Coordination of post-translational modifications in human protein interaction networks (J. Woodsmith). Special session on dynamic interaction networks. Prediction and analysis of protein interaction networks (A. Valencia). Special session on dynamic interaction networks. Characterizing the context of human protein-protein interactions for an improved understanding of drug mechanism of action (M. Kotlyar). Special session on dynamic interaction networks. GPU acceleration of bioinformatics pipeline (M. Berger and a team from NVIDIA). Third day:  Using the world's public big data to find novel uses for drugs (P. Bourne). A top-down systems biology approach to novel therapeutic strategies (P. Aloy). A large-scale evaluation of computational protein function prediction (P.

Radivojac). Deciphering the gene expression code via a combined synthetic computational biology approach (T. Tuller). Interplay of microRNAs, transcription factors and genes: linking dynamic expression changes to function (P. Nazarov). Visual analytics, the human back in the loop (J. Aerts). Turning networks into ontologies of gene function (J. Dutkowski). A method for integrating and ranking the evidence for biochemical pathways by mining reactions from text (S. Ananiadou).   I enjoyed the keynote talks: <ul> How chromatin organization and epigenetics talk with alternative splicing (G. Ast). Insights from sequencing thousands of human genomes (G. Abecasis). Sequencing based functional genomics (analysis) (L. Pachter). Searching for signals in sequences (G. Stormo). Results may vary. What is reproducible? Why do open science and who gets the credit? (C. A. Goble). Protein interactions in health and disease (D. Eisenberg). It has been quite lively on Twitter as well. The official hashtag was #ISMBECCB, at some point it was even a trending hashtag on Twitter.Check the archive, tweets captured important insights from the talks and take-away messages as well as some entertaining ideas such as theunofficial ISMB Bingo card by @jonathancairns.