Report: International Workshop on Bioinformatics and Systems Biology (IBSB) 2011
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1) Overview

IBSB is a workshop held annually since 2000 as part of an international educational collaboration between several research in Japan, the United States and Germany: Boston University in the United States, Charité-Universitätsmedizin Berlin, Humboldt-Universität zu Berlin, Kyoto University, University of Tokyo. The workshop is forum for doctoral and post-doctoral researchers to present their current research and discuss their objectives with peers at a similar stage within their academic career.   This year was the 10th IBSB workshop and was held in Humboldt-Universität Berlin.

2) Conference Summary

The work I presented were methods developed during the past two years my of research in Japan. Specifically two optimization strategies for optimizing a network classifier – Boosted Expectation Propagation (BEP) and Boosted Message Passing (BMP).   These optimization strategies focus on efficiently combining local network information to construct a global network classifier. My presented work is in line with the a major conference theme of biological network analysis. Examples of complementary work presented at IBSB include "*Modeling Cancer Signaling: A Boolean Approach*" by Thomas Handorf who presented an approach to incorporate statistical and physical network models and "*Identifying key regulators in ovarian cancer by analysis of correlated transcription in context of a literature-derived causal network*" by Chia-Ling Huang who overlaid transcription information onto a potential disease mechanism network derived from literature sources.

3) Response and Feedback

My presentation generated several queries from both biological and machine learning areas.   The questions focused on the wider application of the presented method to different types networks, such as protein interaction networks. Specifically questions were on the assumption that local correlated structure is dictating global network performance and whether this is a valid assumption for other networks such as protein protein interaction networks (PPI) and the effect of network hubs on the model.   In response to these queries, it is possible we may shift the application of our method from PPI networks more towards evaluating the effect of proposed network edges to an otherwise known and validated network structure.   These discussion help put our proposed method into a more biologically applicable context and will certainly be taken into consideration in our future research plans.

4) Summer School

An additional event at this years IBSB was the opportunity to participate in a summer school. The topics covered at the summer school where quite broad ranging from physical approaches such as the use of bifurcation diagrams to track the stable solutions of non-linear differential equation systems and stochastic simulation methods for efficiently solving large systems of coupled differential equations; to statistical methodology such as using optimization strategies for Hidden Markov Models and their application to learning complex chemical structure and visualization of global metabolic networks. The topics taught in the summer school provided a wide view of the current research areas of interest in the fields of systems biology and bioinformatics.

5) Recreational Activities

The recreational activities of the conference involve a cruise along the Spree highlighting the history and architecture of Berlin and a Museum tour focusing on the history of Berlin.

Conference Site

Spree River Cruise

Spree River

View from the Top of the Berliner Dome