Report: International Workshop on Bioinformatics and Systems Biology (IWBSB)

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1) Overview

IWBSB 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 9th IWBSB workshop and was held in Boston University.

2) Conference Summary

The work I presented were methods developed during the past two years my of research in Japan. Specifically I presented a network pathways classifier – Hierarchical Mixture of Markov Experts (HME3M). HME3M searches for frequently traversed network pathways by using real biological observations of the network from microarray expression data. This work is in line with the machine learning and statistical strands of IWBSB and similar work was also presented by: "*Network-based Function Discrimination" (*Nils Christian), "*A State-Space Representation of VAR Models with Sparse Learning for Dynamic Gene Networks" (*Kaname Kojima), and "*Annotating Gene Functions with Integrative Spectral Clustering on Microarray Expressions and Sequences" (*Motoki Shiga). These presentations also focused analyzing the key features of metabolic networks that determine different biological functions. Christian et al. is aimed at identifying particular graph properties of metabolic networks that determine "essential" compounds which are required for specific network functions. Kojima et al. focused on defining an efficient EM algorithm for analyzing dynamic gene networks that change over time and Shiga et al. proposed a clustering method for combining metabolic and gene sequence networks with microarray data. All of these methods share the goal of analyzing the structure of biological networks and seek to identify their response to certain influences such as local structure, time and genetic dependencies.

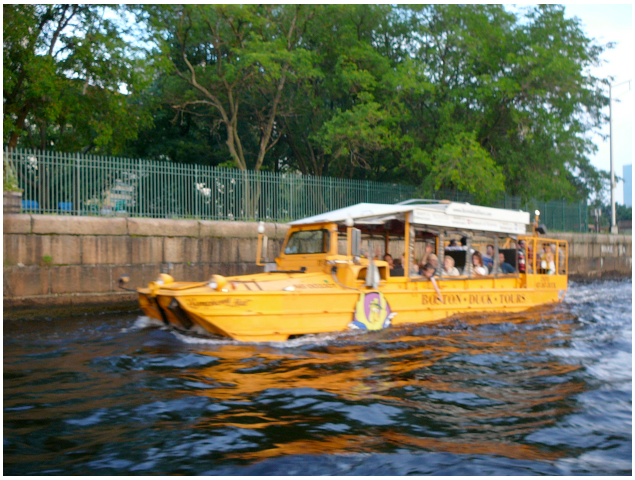
3) Response and Feedback

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 and categories of data such as protein class and function information. Specifically questions were on the assumption that HME3M considers each reaction in the network have the same single gene dependency. HME3M does not consider multiple gene dependency or specific reaction types. However a certain degree of this information can be included by consider

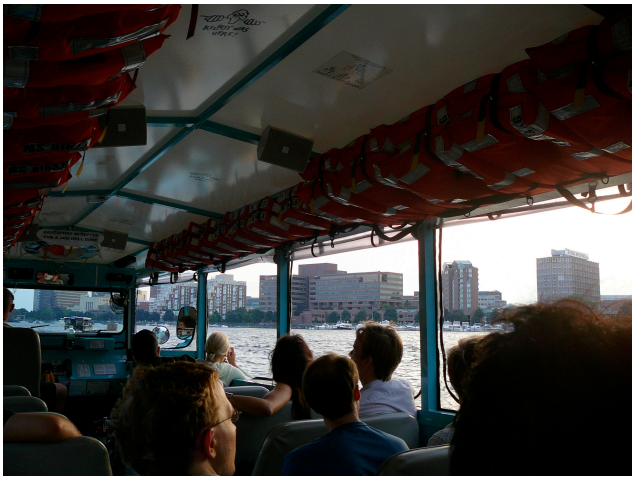
hierarchical extension to the underlying 3M pathway clustering model (Mamitsuka et al. 2003, SIGKDD). Another query of HME3M was if it could be improved if gene expression information was known exactly. HME3M, however does not consider the precision of gene expression information but focuses on a binary discretization indicating over expression. We are currently investigating ways of overcoming this limitation of HME3M to improve our model. The questions I received helped to position my method within the wider bioinformatics literature and gave me several ideas for future research directions.

4) Recreational Activities

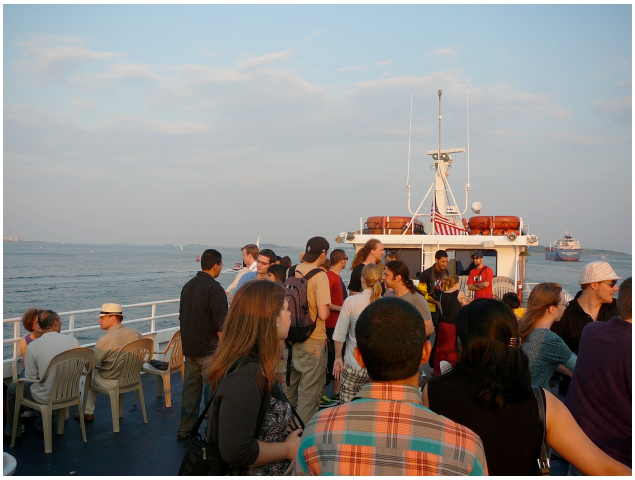
The recreational activities of the conference involved two key events. Firstly a “duck tour” highlighting the history of Boston on both land and water in an amphibious vehicle. Secondly a harbor cruise with quintessential Boston cuisine such as clam chowder and Boston lobster was provided. Below are photos from each event.



Boston “Duck” tours.



View from inside the “Duck”



Top deck of the Boston Harbor Cruise

Sunset over Boson Harbor