New Problems and Methods in Computational Biology

Friday December 8, 2006

Gal Chechik, *Stanford University*
Christina Leslie, *Columbia University*
William Stafford Noble, *University of Washington*
Gunnar Rätsch, *Friedrich Miescher Laboratory of the Max Planck Society (Tübingen, Germany)*
Quaid Morris, *University of Toronto*
Koji Tsuda, *Max Planck Institute for biological Cybernetics (Tübingen, Germany)*

http://www.fml.tuebingen.mpg.de/nipscompbio

The field of computational biology has seen dramatic growth over the past few years, both in terms of available data, scientific questions and challenges for learning and inference. These new types of scientific and clinical problems require the development of novel supervised and unsupervised learning approaches.

In particular, the field is characterized by a diversity of heterogeneous data. The human genome sequence is accompanied by real-valued gene expression data, functional annotation of genes, genotyping information, a graph of interacting proteins, a set of equations describing the dynamics of a system, localization of proteins in a cell, a phylogenetic tree relating species, natural language text in the form of papers describing experiments, partial models that provide priors, and numerous other data sources.

The goal of this workshop is to present emerging problems and machine learning techniques in computational biology, with a particular emphasis on methods for computational learning from heterogeneous data. The workshop includes invited and submitted talks from experts in the fields of biology, bioinformatics and machine learning. The topics range from case studies of particular biological problems to novel learning approaches in computational biology.

New Problems and Methods in Computational Biology

Friday December 8, 2006

Organizers: G. Chechik, C. Leslie, W. S. Noble, G. Rätsch, Q. Morris & K. Tsuda

Morning session: 7:30am–10:30am

7:30am *opening remarks*

7:35am **Invited talk: Genetic variation and regulatory networks: mechanisms and complexity**, *Dana Pe'er*

8:15am **Prediction of tissue-specific cis-regulatory modules using Bayesian networks and probability trees**, *X. Chen and M. Blanchette*

8:30am **Metric learning pairwise kernel for graph inference**,
J.-P. Vert, J. Qiu and W. S. Noble

8:45am **Reverse engineering temporally rewiring gene networks**,
F. Guo, W. Fu, Y. Shi and E. P. Xing

9:10am *coffee break*

9:25am **Compact belief propagation: using symmetry properties in relational graphical models for efficient inference**, *A. Jaimovitch, O. Meshi and N. Friedman*

9:50am **Ab-initio gene finding using machine learning**,
G. Schweikert, A. Zien, G. Zeller, C.S. Ong, F. de Bona, S. Sonnenburg, P. Phillips, G. Rätsch

10:05am **The processing and analysis of in situ gene expression images of the mouse brain**,
M. N.Jagalur, C. Pal, E. L. Miller, R. T. Zoeller and D. Kulp

Afternoon session: 3:45pm–6:50pm

3:45pm **Invited talk: Analysis of heterogeneous microarray-based data**, *Terrence Furey*

4:25pm **Inferring active signaling pathways by boosting the phosphorylation network**,
S. Lianoglou, A. Kundaje and C. Leslie

4:40pm **Graph boosting for molecular QSAR analysis**,
H. Saigo, T. Kadowaki, T. Kudo and K. Tsuda

4:55pm **Stochastic integrative modeling of transcription regulation**,
N. Novershtern, A. Regev and N. Friedman

5:20pm *coffee break*

5:30pm **Improved prediction of HIV resistance in-vitro by biochemically-driven models**,
H. Neuvirth, M. Rosen-Zvi, N. Srebro, E. Aharoni, M. Zazzi and N. Tishby

5:55pm **Time-series alignment by non-negative multiple generalized CCA for quantitative proteomics**, *B. Fischer, V. Roth and J. M. Buhmann*

6:10pm **Reconstructing the phylogeny of mobile elements**,
S. O'Rourke, N. Zaitlen, N. Jojic and E. Eskin

6:25pm **Identifying the effects of human immune presure on the evolution of HIV**,
J. Carlson, C. Kadie, D. Heckerman