Title

Gene Regulatory Network Reconstruction and Analysis

Abstract

Modeling and reconstruction of biological networks is a challenging inverse problem because of its nonlinearity, high dimensionality, non-uniqueness, sparse and noisy data, and significant computational cost. In this presentation, I will introduce a new Bayesian learning and optimization model (BLOM) developed in our Computational Biology and Bioinformatics Laboratory (CBBL) for inferring gene regulatory networks (GRNs) from time series microarray data. After extensive testing and validation using both synthetic and yeast cell cycle benchmark datasets, the BLOM was applied to reconstruction of GRNs related to neurological function of earthworms. It successfully identified hub genes and several important gene regulation relationships in the pathways and also addressed the dynamic change of biological networks in the course of the treatment and recovery of earthworm.

A Short Bio:

Dr. Joe Zhang has received his master degree in computer science and doctoral degree in computational analysis and modeling at the Louisiana Tech University. He was a research Assistant Professor in Computer Science at the University of Vermont. Now he is the Director and Associate Professor in the School of Computing at the University of Southern Mississippi. Dr. Zhang built the Computational Biology and Bioinformatics Lab at Southern Miss and has lead a research team consisting of three faculty members and six Ph.D. students and visiting scholars. Dr. Zhang has more than forty peer-reviewed publications and his research has been supported by National Science Foundation, National Institute of Health, Department of Defense and Department of Homeland Security. He is a Co-Founder and Program Committee Chair of the 2009 International Joint Conferences on Bioinformatics, System Biology and Intelligent Computing (IJCBS 09), Shanghai, China, August 3-5, 2009, and the Steering Committee Co-Chair of The ACM 2010 International Conference on Bioinformatics and Computing Biology (ACM-BCB 2010), Buffalo, NY, Aug 2-4, 2010. He helped found the ACM Special Interest Group – SIGBioinformatics in 2010 and serves as the Award Co-Chair.