Department of Electrical and Computer Engineering

TEXAS TECH UNIVERSITY
Edward E. Whitacre Jr.
College *of* Engineering

Fall 2011 Seminar Series

Seminar Title: Uncover context-specific co-regulations by transcription factors and microRNAs using Bayesian factor model

Time: October 21, 2011, 3:00 - 4:00 PM

Location: Lankford Lab ECE 101

Speaker:
Prof. **Yufei Huang**
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Abstract:

In multicellular organisms, transcription factors (TFs) and microRNAs (miRNAs) embody two largest families of molecules that regulate gene mRNA transcription. The study of gene transcription requires the understanding of cooperative regulations by TFs and miRNAs, which however have not been extensively studied. A novel Bayesian sparse non-negative factor regression (BSNFR) model is proposed for joint transcriptional regulations by TFs and miRNAs. The model admits multiple data including gene expression data, miRNA expression data, TF targets, and miRNA targets. BSNFR not only identifies potential TF/miRNA-mediated regulations but also estimates the regulatory impacts by TFs/miRNAs and the unknown TF activities. BSNFR also includes a nonparametric Bayesian structure to the latent factors to enable the discovery of the clustering effects among biological samples due to (disease) subtypes. The proposed BSNFR model and the developed Gibbs sampling solution were validated on simulated data and applied to glioblastoma multiforme (GBM) dataset. A GBM specific TF-miRNA co-regulated transcriptional network was reconstructed. This GBM network includes 107 regulations recorded in the existing databases and 16 new regulations. Functional analysis suggests that the regulated genes are enriched in many cancer related pathways. In addition, BSNFR also identified 3 clusters among GBM patient samples, two of which demonstrates significant survival differences (p = 0:004). Finally, the estimated TF activities imply that EGR-1 is significantly correlated with patient survivals (p = 0:004) and can be used as a potential biomarker.

Speaker Bio:

Yufei Huang received his Ph.D. degree in electrical engineering from the State University of New York at Stony Brook in 2001. Since 2002, he has been with the Department of Electrical and Computer Engineering at the University of Texas at San Antonio (UTSA), where he is now Associate Professor. He has been a visiting professor at the Center of Bioinformatics, Harvard Center for Neurodegeneration & Repair. He is now also an adjunct professor of the Greehey Children's Cancer Institute and Dept. of Epidemiology and Biostatistics at the University of Texas Health Science Center at San Antonio.

Dr. Huang's expertise is in the area of computational biology, statistical modeling, and Bayesian methods. His current focus is on high throughput biomedical data integration, gene regulatory networks discovery, microRNA target identification, and LC-MS proteomics data analysis. He was a recipient of US National Science Foundation (NSF) Early CAREER Award in 2005, Best Paper Award of 2006 Artificial Neural Networks in Engineering Conference, and 2007 Best Paper Award of IEEE Signal Processing Magazine. His research has been supported by NSF, National Institute of Health, Air Force Office of Scientific Research, Army Research Lab and Qatar National Research Fund. He has been an organizer of workshops and special sessions including the IEEE Workshop on Genomic Signal Processing and Statistics (GENSIPS), and Workshop on Systems Biology and Medicine, and IEEE Bioinformatics and Biomedicine Conference. He is the co-chair of IEEE Genomic Signal Processing and Statistics, 2011. He is an Associate Editor of IEEE Transactions on Signal Processing, EURASIP Journal on Bioinformatics and Computational Biology, and Int. Journal of Data Mining & Bioinformatics.