

# Seminar

## Fall 2011



THE UNIVERSITY OF  
SOUTHERN MISSISSIPPI  
SCHOOL OF COMPUTING

**Title:** Bayesian Learning and Optimization Approach to Gene Regulatory Network Analysis

**Time & Location:**

2:00pm, Friday, December 2, 2011  
Vislab (Tec 205)

**Speaker:** Dr. Joe Zhang, Ph.D.  
School of Computing, Southern Miss

**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 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.