GEORGE MASON UNIVERSITY

DEPARTMENT OF COMPUTER SCIENCE

TODAY
11:00-12:00
Student Union II Room 5 & 6

FACULTY RECRUITMENT SEMINAR

Xiaoning Qian

Electrical Engineering
Texas A & M University

BIOGRAPHY

Xiaoning Qian obtained his Bachelor and Master degrees in Electronic Engineering from Shanghai Jiao-Tong University in China in 1997 and 1999. After receiving his Ph.D. degree in Electrical Engineering for his work on shape-based indexing in medical image databases at Yale University in 2005, he worked as a postdoctoral associate in the Department of Diagnostic Radiology at Yale on several biomedical image analysis projects. In 2007, he joined the Bioinformatics Training Program at Texas A&M University as an associate research scientist in the Department of Electrical and Computer Engineering and a research assistant professor in the Department of Statistics. His current main research focus is to develop statistical and geometric models and relevant algorithms for the inference, analysis, and intervention of biological networks.

Analysis and Control for Biological Networks

The ultimate goal of studying the systems biology of biological networks is to apply intervention to living organisms for effective treatment of diseases. Starting with a project of comparing protein interaction networks of different organisms, I will present an efficient framework based on hidden Markov models (HMMs) to identify conserved homologous pathways in networks of interest. Finding these common interaction patterns across or within organisms can lead to a better understanding of the regulatory mechanisms underlying various cellular functions. With the regulatory relationship learned either from prior knowledge or interaction measurements, we further analyze long-run genome behavior based on its underlying Markov chain in the framework of the probabilistic Boolean network (PBN) model. The change of steady-state distribution of the Markov chain caused by possible perturbations to a network is the key measure for intervention. We derive analytic results for changes in the steady-state distributions of probabilistic Boolean networks resulting from modifications to the underlying regulatory rules. From these analytic results, we derive intervention strategies to obtain therapeutic benefits for future drug design or gene therapy design. The preliminary results in a network modeling melanoma cell line have shown that our methods can potentially serve as future intervention strategies to identify potential drug targets and design gene-based therapeutic strategies.