

FACULTY CANDIDATE SPRING 2007 SEMINAR

WHEN: April 17, 2007

WHERE: PGH 563

TIME: 11:00 AM

Host: Dr. Fofanov

SPEAKER: Dr. Hongwei Wu, University of Georgia

Multi-leveled Functional Classification of Genes and Prediction of Functional Modules for Bacterial Genomes

Since late eighties and early nineties when the Human Genome Project was initiated, a large volume of genomic data of different organisms have been made available thanks to the world-wide sequencing efforts; and, with the development of high-throughout experiment technologies, a lot of measurements about functional and structural properties of biological molecules have also been made available. In this post-genome era, the focuses of the field of computational biology and bioinformatics are to use computer-based methods to analyze and interpret these data.

Biological functions of genes can be described from two perspectives. One perspective is to describe the activities of genes and their products at the molecular level; and the other perspective is to describe the roles of genes and their products in the biological processes that they participate in. Accordingly, there are generally two kinds of methods to predict biological functions of newly sequenced genes. One is to identify the genes in those well investigated genomes that are similar to the unknown genes; and the other is to identify the genes that are functionally related to the unknown genes.

This talk will focus on my work on the multi-leveled functional classification of genes and the prediction of functional modules for bacterial genomes, which belong to the two different kinds of methods for the prediction of gene functions, respectively. Our studies on the multi-leveled functional classification of genes can not only be used to provide functional annotations of newly sequenced gene from multiple resolution levels, but can also be used to reveal evolutionary trace of genes and genomes. Whereas, our studies on the prediction of functional modules can not only be used to reveal the functional relatedness between genes, but also represent a key step towards deciphering biological networks/pathways in a systematic way.

BIO:

Hongwei Wu is currently a post-doctoral research associate with Computational System Biology Lab, Department of Biochemistry and Molecular Biology and Institute of Bioinformatics, University of Georgia. She received her Ph.D. and M.S. degrees in Electrical Engineering from the University of Southern California in 2004 and 2002, respectively, and her M.Eng and B.Eng from Tsinghua University of China in 1999 and 1997, respectively. Her current research interests are in the broad areas of computational

biology/bioinformatics with focuses on (1) comparative genomic analyses, (2) computationally reconstructing (modelling, estimating, simulating and predicting) gene pathways/networks, and (3) computational intelligence theories and applications to computational biology/bioinformatics, signal processing and machine learning.