综合报告会

Lecture

国家数学与交叉科学中心

Time: 2:00-3:00 pm, May 29, 2014

Venue: N219 （南楼）

Computational Approaches for Metagenomics Data Analysis

Speaker: Prof. Fengzhu Sun

University of Southern California

Abstract:

Metagenomics studies apply sequencing technologies to study the composition and function of microbes within their natural environments. Accurate estimations of alpha diversity, the composition of different organisms within a community and beta diversity, the comparison of different communities, based on enormous amount of sequence data from new sequencing technologies are essential problems in molecular ecology. I will talk about our collaborations with marine biologists to develop computational approaches and applied them to the analysis of metagenomics data from the marine communities. I will introduce three programs developed in our group.

1. Identify local time delayed associations between microbial organisms (LSA),
2. Estimating abundance levels of organisms based on whole metagenome shotgun reads,
3. Comparing metagenomic communities based on k-tuples.

Brief CV:

Dr. Fengzhu Sun is Professor and Head of Computational Biology and Bioinformatics within the Molecular and Computational Biology Program at USC.

Professor Sun works in the area of Computational Biology and Bioinformatics, Statistical Genetics, and Mathematical Modeling. His research interests include protein interaction networks, gene expression, single nucleotide polymorphisms (SNP), linkage disequilibrium (LD) and their applications in predicting protein functions, gene regulation networks, and disease gene identification. He is also interested in metagenomics, in particular, marine genomics, and alignment-free sequence analysis. His previous research accomplishments include: 1) protein domain interaction and protein function prediction integrating multiple data sources, 2) dynamic programming algorithms for haplotype block partition and tag SNP selection, 3) 1-TDT: transmission disequilibrium test when one parent is available, and 4) theoretical studies of polymerase chain reaction (PCR) related biotechnologies.