THE UNIVERSITY   **OF HONG KONG**

Department of Mathematics

Numerical Mathematics and Applied Analysis Group Seminar (NMAA)

Computational Analysis and Inference of Protein-Protein Interactions from Domain Information

Professor Morihiro Hayashida

Bioinformatics Center, Institute for Chemical Research
Kyoto University, Japan

on Thursday, May 25, 2006 at 2:30 – 4:00p.m.
in Room 309, Run Run Shaw Building, HKU

Abstract

Several computational methods have been proposed for inferring protein-protein interactions. Deng et al. proposed a probabilistic model of protein-protein interactions based on domain-domain interactions, and developed an inferring method using an EM algorithm from this model. They found some biologically significant novel interactions. However, the classification accuracy of their method is not so high. Therefore, we propose new methods based on linear programming, and improve the accuracy. In order to understand how proteins have obtained various functions, we analyze a network of proteins using domain information. We consider differences of domain compositions between proteins, and introduce a protein domain network. This network also shows a scale-free behavior. We propose a model of protein evolution using domains, and show that the model can reconstruct the protein domain network.

All are welcome