



ALGORITHM FOR DETECTION OF PROTEIN COMPLEXES IN LARGE INTERACTION NETWORKS

Monday, December 26
3 P.M. Seminar Room,
1st Floor, Civil Engineering Building

This seminar will presents an algorithm for detection of protein complexes in large interaction networks. In a protein-protein interaction (PPI) network, a node represents a protein and an edge represents an interaction. The algorithm starts at a deterministic single node and then chooses and adds priority nodes one by one from the neighbors to the cluster. This goes on until two conditions are satisfied. A comparison between a PPI and a random network is also performed in the context of the proposed algorithm. The algorithm has been implemented in JAVA programming.

Md. Altaf-Ul-Amin, Assistant Professor, Comparative Genomics Lab of NAIST, Japan will present the seminar and it's implementation using JAVA programming. All of you are cordially invited.

ABSTRACT

This paper presents an algorithm for detection of protein complexes in large interaction networks. In a protein-protein interaction (PPI) network, a node represents a protein and an edge represents an interaction. The complexes are determined by way of finding clusters, i. e. the densely connected regions in the network. The algorithm starts at a deterministic single node and then chooses and adds priority nodes one by one from the neighbors to the cluster. This goes on until two conditions are satisfied. One of the conditions ensures the density of the cluster while the other keeps track of the periphery of the cluster. When a cluster is generated, it is removed from the network. The next cluster is then formed in the remaining network and the process goes on until no edge is left in the network. The timing complexity of the algorithm is polynomial of the order, where is the number of nodes in the network. We also show and analyze some protein complexes generated by the proposed algorithm from typical PPI networks of *Escherichia coli* and *Saccharomyces cerevisiae*. From the consistencies observed between predicted and known complexes, it can be concluded that proteins that form high-density clusters in PPI networks represent functional complexes. A comparison between a PPI and a random network is also performed in the context of the proposed algorithm. The algorithm has been implemented in JAVA programming.

About the Speaker

Md. Altaf-Ul-Amin received his B.Sc. degree in electrical and electronic engineering from Bangladesh University of Engineering and Technology (BUET), Dhaka, M.S. degree in electrical, electronic and systems engineering from Universiti Kebangsaan Malaysia (UKM) and PhD degree from Nara Institute of Science and Technology (NAIST), Japan. Currently he is working as an Assistant Professor in comparative Genomics Lab of NAIST, Japan.