



"Surfing on Complex
Biological Networks:
The Next
Generation of
Bioinformatics
Research"



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Abstract. In this post-genomic era, biological networks are promising resources for the next generation of Bioinformatics research. The systematic analysis of biological networks, such as genetic interaction networks, gene regulatory networks, signal transduction networks and protein interaction networks, becomes a new paradigm for characterization of functional behaviors of bio-molecules. Various graph-theoretic algorithms have been applied to the biological network analysis. However, they have been challenging because of a significant amount of erroneous data and complex connectivity of the networks. In this talk, I present two novel approaches for functional knowledge discovery from protein interaction networks. As the first topic, I introduce a functional influence model and a dynamic flow simulation algorithm based on random walks. The functional flow patterns generated by this algorithm are used to identify functional modules, groups of proteins that participate in the same biological functions. The other subject is to restructure protein interaction networks for revealing hierarchical organizations. Based on the concepts of path strength and centrality, this algorithm converts the complex connectivity of the network into a hub-oriented tree structure. The selected hubs are interpreted as functionally essential proteins. The efficiency and scalability of these approaches demonstrate that they are well-applicable to high-level organisms.

Bio. Young-Rae Cho is an assistant professor in Department of Computer Science at Baylor University. He received his Ph.D. degree from Department of Computer Science at State University of New York at Buffalo in 2009, and Master of Computer Science degree at University of Illinois at Urbana-Champaign in 2003. He had worked as a senior researcher at Samsung Electronics in Korea from 1994 to 1999. His current research interests include Bioinformatics, Computational Systems Biology and Biological Data Mining. He is an author of over twenty publications in journals, conference proceedings and book chapters. He is a professional member of ACM and a member of IEEE Computer Society and ISCB (International Society for Computational Biology).