



## **IEEE Student Branch at LIU-Brooklyn & Cybernetics Study Association (CSA)**

**October 26, Friday, 6~ 8:00 PM**

**LIU-Brooklyn, Center for Entrepreneurship & Innovation  
Pratt Building Room 110**

### **Distinguished Lecture - Using Networks to Study Relationships between Metabolic Processes and Disease**

Joint Lecture by **Prof. Aaron Kershenbaum**, IEEE Life Fellow, Drexel School of Medicine  
and **Prof. Robert Schiaffino**, Iona College

#### **ABSTRACT:**

Metabolic processes in the human body form interacting networks and can be analyzed as such. This includes biochemical reactions, gene expression, brain function and all other processes that keep us alive. The malfunction of any of these processes can result in disease. The diagnosis and treatment of disease can be improved by analyzing such networks. These networks are large and complex. The fact that they interact makes the problem of analyzing them even more challenging. But as computer processing power and memory have grown and the internet has become a resource for collecting and sharing medical and biological data, it has become possible to carry out meaningful analysis of even large human biological networks. The key to this is the development of network models and algorithms to work with them.

A network is a graph with nodes and edges that have properties associated with them. These properties include capacity, reaction time, failure probability, and functionality. The nodes represent components of a (biological) process; the edges represent relationships among the nodes.

A network that describes a process is called a network model. In this talk we will present several network models for relationships among diseases and metabolic functions, including both chemical and genetic processes. We will then describe algorithms and data structures that we have used to analyze specific problems. If a graph contains two distinct types of nodes and all edges go between nodes in one set and nodes in the other, it is a bipartite graph. If there is an edge between every pair of nodes in a part of the graph (subgraph), we call this subgraph a clique. If, furthermore, the graph is bipartite, we refer to the subgraph as a biclique. Cliques represent a very strong relationship among its nodes. In the worst case it is computationally very difficult to identify all cliques or bicliques in a network. We present an efficient algorithm for finding all bicliques in a real network and show results on a network with roughly 2000 nodes where the two sets of nodes represent diseases and metabolic functions.

A graph may contain subgraphs with identical structures; i.e. the nodes in one subgraph are connected in the same way as the nodes in another. Such collections of subgraphs are called motifs. Motifs indicate similarities in the relationships among the nodes in one set with relationships in the other. The motifs may match only topologically; i.e., we can match the nodes in one set to the nodes in the other set and the connectivity among the nodes is the same in both cases. If properties of the nodes and edges involved also match, then there is a functional similarity as well as a structural one. Again, in the worst case, it is computationally difficult to find all motifs in a network or collection of networks. We present an algorithm for finding motifs in actual networks representing gene interactions that take place in different organisms. This allows us to identify biological similarities among the organisms involved.



**Prof. Aaron Kershenbaum** earned a Ph.D. in Electrical Engineering at the Polytechnic Institute of Brooklyn. He started his professional career at Network Analysis Corporation (NAC), an organization that did pioneering work in the field of digital communications, including the design and analysis of ARPANET (the first computer network), NASDAQ, and many of the first CATV networks. He then joined the faculty at Polytechnic Institute of Brooklyn where he helped found the New York State Center for Advanced Technology in Telecommunications and supervised 34 PhD theses. He then joined IBM Research where he worked on projects in network optimization, software security, and natural language processing, retiring 2008. After retiring from IBM, he was part of teams doing research in medicine and epidemiology at the Columbia University School of Public Health and the University of Pennsylvania Center for Clinical Epidemiology and Biostatistics. Together with Dr. Schiaffino, he did research analyzing large scale data and text corpora at Iona College. He is currently a Part Time Research Professor at the Drexel School of Medicine working with clinical faculty there on analysis of clinical data for medical research, genetic interactions and the diagnosis and treatment of disease. He enjoys solving mathematical problems with his grandchildren.



**Prof. Bob Schiaffino** earned a Ph.D. in Computer Science at Polytechnic Institute of Brooklyn under the mentorship of Dr. Aaron Kershenbaum. His research interests include applications of graph algorithms to a variety of problems including text categorization, authorship attribution, and genetic interactions. He and Dr. Kershenbaum have coauthored papers in these areas. His current interest is in applying graph algorithms in the analysis of “big data” of various types such as financial data, political data, and astronomical data. For the last thirty years he has been a faculty member of the Computer Science Department of Iona College. He has primarily taught courses in Algorithms, Data Structures, and Operating Systems. During his time at Iona he has served as department chair and coordinator of graduate programs.

**Agenda: 6:00 ~ 6:30 PM (Refreshments), 6:30 ~ 6:45 PM, (Opening Remarks by Dean Ray Pullaro, School of Business, LIU Brooklyn), 6:45~ 8:00PM (Distinguished Lecture Presentation), 8:00 ~8:15 PM (Q/A).**

**Directions: <http://www.liu.edu/Brooklyn/About/Visit/Directions.aspx>**

**ALL ARE WELCOME**