Public Abstract
Avanthi Mummaneni
M.S.
Computer Science
Analysis of the Enzymatic Network
Advisor: Dr. Toni Kazic
Graduation Term: Winter, 2005

PUBLIC ABSTRACT

Studying large networks of biochemical reactions is the best means to understand the relationships between the structure of the network and its functions. In order to study the behavior of networks, the first step is to study their architecture.

Studying network architecture raises many basic questions about its connectivity. How are the compounds and reactive conjunction nodes connected to each other? What is the correlation in frequencies of compounds and reactions? What reactions have the same reactants and the same number of reactants? Are there repeated architectural features? Is the network really composed of the canonical pathways of biochemistry books, or is its architecture more complex?

I addressed these questions by building a database of systematically classified enzymatic reactions (END). I gathered the input for the Enzyme Nomenclature Database (END) from IUBMB/IUPAC Enzyme Nomenclature website.

The data of END represent a basic notion of a biochemical network. I did various calculations and implemented several algorithms to study the architecture of the network of these enzymatic reactions in END. Most of the reactions in the network have reactive conjunction degrees of four and five and most compounds are connected to only one reaction. The network can be connected into a single large component by compounds of low degree. There are more branched regions in the network than simple straight paths. There are many more regions densely connected internally than their immediate context.