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Modeling the Dynamics of Feed-Forward Biological Networks.

Many important biological pathways, including apoptosis and glycolysis, are feed-forward in the sense that they can be rendered as directed graphs without any directed cycles. The structure of such networks may vary from organism to organism, and it is of great interest to determine (i) the effect of network topology on the overall speed/efficiency of the network and (ii) whether speed may convey evolutionary advantages. Modeling the dynamics of feed forward networks typically involves solving systems of ordinary differential equations.

As a first step toward ranking the efficiency of various network topologies, we seek classes of non-isomorphic networks which, nonetheless, exhibit the same dynamics; such networks are called isodynamic. In this talk, we shall present several theoretical results, proving that certain classes of networks are isodynamic. For example, consider the class of all feed-forward networks with (i) no isolated vertices; (ii) precisely one "source" vertex (i.e., indegree zero); and (iii) precisely one "target" vertex with indegree $n - 1$ and outdegree zero. We prove that, if all reaction rate constants are identical, then all such networks are pairwise isodynamic. (Received July 22, 2008)