Detecting Morse decompositions of the global attractor of regulatory networks by time series data

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Complex network structure frequently appear in biological systems such as gene regulatory networks, circadian rhythm models, signal transduction circuits, etc. As a mathematical formulation of such biological complex network systems, Fiedler, Mochizuki and their collaborators (JDDE 2013) recently defined a class of ODEs associated with a finite digraph called a regulatory network, and proved that its dynamics on the global attractor can in principle be faithfully monitored by information from a (potentially much) fewer number of nodes called the feedback vertex set of the graph.

In this talk, I will use their theory to give a method for detecting a more detailed information on the dynamics of regulatorynetworks, namely the Morse decomposition of its global attractor. The main idea is to take time series data from the feedback vertex set of a regulatory network, and construct a combinatorial multi-valued map, to which we apply the so-called Conley-Morse Database method.

As a test example, we study Mirsky's mathematical model for mammalian circadian rhythm which can be represented as aregulatory network with 21 nodes, and show that numerically generated time series data from its feedback vertex set consisting of 7 nodes correctly detect a Morse decomposition in the global attractor, including 1 stable periodic orbit, 2 unstable periodic orbits, and 1 unstable fixed point.

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