

The Determination of Multiple Steady States in Two Families of Biological Systems

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The capacity of computational multiple steady states in two biological systems are determined by the Deficiency One Algorithm and the Subnetwork Analysis. One is a bacterial glycolysis model involving the generation of ATP, and the other one is an active membrane transport model, which is performed by pump proteins coupled to a source of metabolic energy. Mass action kinetics, is assumed and both models consist of eight coupled non-linear equations. A set of rate constants and two corresponding steady states are computed. The phenomena of bistability and hysteresis are discussed. The bifurcation of multiple steady states is also displayed. A signature of multiplicity is derived, which can be applied to mechanism identifications if steady state concentrations for some species are measured. The capacity of steady state multiplicity is extended to their families of reaction networks.

Key words: Multiple Steady States; Glycolysis; Active Membrane Transport; Bistability; Hysteresis; Bifurcation