Multistationarity in n-site mixed phosphorylation network model

BIOMATH 2024

Maya Mincheva[1], Suha Dajani[2]
Department of Mathematical Sciences
Northern Illinois University, USA
mmincheva@niu.edu

[2] Department of Mathematics
Lake Forrest College, USA
s_jay2001@hotmail.com

Multisite phosphorylation is an important mechanism in cellular biology associated with protein function and activity. Mathematical models of mono- and dual- site phosphorylation networks have been studied recently, while less research is available on multisite phosphorylation. Phosphorylation networks could be processive, distributive or mixed where the phosphorylation or dephosphorylation occurs through a combination of both mechanisms. Parametric dynamical systems modeling multisite phosphorylation networks are often multistationary, which means that they can have several positive steady states for some parameter values. We analyze a dynamical system of a mixed n-site phosphorylation network for multistationarity. A general algebraic condition in the form of a simple inequality which determines a multistationary parameter region is obtained.