

Multistationarity in reaction networks models

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Mathematical models in biology are often available in the form of ordinary differential equations. Multistationarity or the existence of several steady states is an ubiquitous phenomenon in biochemical reaction models. We focus on providing an algorithm for the existence of several positive steady states that can be easily applied. The input is a system of ordinary differential equations whose behavior depends on a set of parameters and the output is a single polynomial. The sign of this polynomial decides the capacity for multiple (unique) steady states. Often we can obtain parameter inequalities that ensure the sign resulting in multiple (unique) steady states. These parameter inequalities in turn define parameter regions where multiple (unique) steady states exist.

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