
Hidden slow-fast dynamics in biochemical models

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Abstract

The analysis of the global dynamics of biochemical systems can be a challenging task even for systems of small or moderate size. Often these difficulties are related to the occurrence of variables and parameters of vastly different orders of magnitudes. Hence, very different mechanisms may dominate the dynamics in certain regions of phase- and/or parameter-space. Identifying and analysing these regimes and the resulting decompositions into subsystems can be utilized in the analysis of the global dynamics. In suitably scaled variables the dynamics within individual regimes may be organized by lower-dimensional slow manifolds. However, often crucial dynamical effects take place at non-hyperbolic parts of these slow-manifolds which prevents the application of standard methods from geometric singular perturbation theory. The blow-up method can be used to overcome these difficulties and to match the individual regimes. In the talk this approach is presented in the context of selected models describing metabolic or signalling processes in cellular biology.

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