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Global dynamics for switching systems and their extensions by linear differential equations

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Abstract

Switching systems use piecewise constant nonlinearities to model gene regulatory networks. This choice provides advantages in the analysis of behavior and allows the global description of dynamics in terms of Morse graphs associated to nodes of a parameter graph. The parameter graph captures spatial characteristics of a decomposition of parameter space into domains with identical Morse graphs. However, there are many cellular processes that do not exhibit threshold-like behavior and thus are not well described by a switching system. We consider a class of extensions of switching systems formed by a mixture of switching interactions and chains of variables governed by linear differential equations. We show that the parameter graphs associated to the switching system and any of its extensions are identical. For each parameter graph node, there is an order-preserving map from the Morse graph of the switching system to the Morse graph of any of its extensions. We provide counterexamples that show why possible stronger relationships between the Morse graphs are not valid.

Keywords. *switching systems, gene regulation, transcription/translation model, Morse graphs*

1 Introduction

While the last twenty years have brought unprecedented advances in experimental techniques allowing us to gather data on many cellular processes, the development of methods to combine this data into informative models is lagging behind [2, 33, 32]. Models of dynamic cellular processes based on ordinary differential equations require a choice of nonlinearities, parameters and initial conditions, and most of these are difficult to measure experimentally. Moreover, since the nonlinearities of multi-scale cellular processes are by necessity phenomenological, the measurement of the parameters depends on the model with which the data is interpreted. Changing the model leads to re-interpretation of the measurements, and often the need to remeasure all the parameters in the new model.

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