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Global Dynamics of Extensions of Switching Models for Biological Systems

I present results related to a certain class of models called switching systems. For the past several decades these models have often been used to study biological systems. Part of my work involves placing a bound on the size of the parameter space of these models. This is an important result in regard to computation of the coarse global dynamics of switching systems, a key part of my mentors' research. In addition, I present results on a modification to the switching system. We seek such modifications because the switching model is incapable of accounting for the actions of all biochemicals in a given system; in particular, the model can represent proteins or mRNA but not both. Since fall 2015 I have studied an extension of this model which includes linear variables representing intermediaries between those of the switching system. This allows the extension to model both proteins and mRNA. I have proved many key results for this extension, in particular that my mentors' current methods for computing the switching system's coarse global dynamics carry over directly to the extension. In addition, the extension in general exhibits additional dynamic behavior not seen in the switching system.