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Automating Manifold Boundary Model Reduction in Michaelis-Menten Reaction Networks MERRILL ASP, MARK TRANSTRUM, Brigham Young University – Provo — One of the major issues in understanding complex systems, such as those in systems biology, is the large number of parameters to be fit to data. Methods to approximate and reduce complex models are therefore an important problem. Recent advances in information theory have led to a new method of identifying limiting approximations in complex models known as the Manifold Boundary Approximation Method. I apply this method to systems modeled as coupled differential equations describing networks of Michaelis-Menten reactions. Such models are common in biochemical systems such as developmental biology and cancer. I discuss how this approximation method when applied to such networks can be automated.

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