

SWITCHING NETWORKS DATABASE AS A PLATFORM FOR PARAMETER SEARCH IN GENE
REGULATORY NETWORKS

Tomas Gedeon

Montana State University, USA
gedeon@math.montana.edu

Experimental data on gene regulation and protein interaction is often very qualitative, with the only information available about pairwise interactions is the presence of either up- or down- regulation. Since majority of the parameters for any model in such a situation are not constrained by data, it is important to understand how different choices of parameters affect the dynamics and, therefore, the predictions of such a model. Continuous time Boolean networks, or switching networks, represent an attractive platform for qualitative studies of gene regulation, since the dynamics at fixed parameters is relatively easily to compute. However, it is quite difficult to analytically understand how changes of parameters affect dynamics. On the other hand, the Database for Dynamics is an numerical approach to study global dynamics over a parameter space. The results obtained by this method provably capture the dynamics a predetermined spatial scale. We combine these two approaches to present a method to study switching networks over parameter spaces. We apply our method to experimental data for cell cycle dynamics.

Joint work with Bree Cummins (Montana State University, USA), Bridget Fan (Montana State University, USA), Konstantin Mischaikow (Rutgers University, USA), Arnaud Goulet (Rutgers University, USA), Shaun Harker (Rutgers University, USA).