

# **Perturbations in Boolean Networks as Model of Gene Regulatory Dynamics**

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## **Summary**

Boolean networks are coarse-grained models of the regulatory dynamics that controls the survival and proliferation of a living cell. The dynamics is time- and state-discrete. This Boolean abstraction assumes that small differences in concentration levels are irrelevant; and the binary distinction of a low or a high concentration of each biomolecule is sufficient to capture the dynamics. In this work, we briefly introduce the gene regulatory models, where with the advent of system-specific Boolean models, new conceptual questions and analytical and numerical challenges arise. In particular, the response of the system to external intervention presents a novel area of research.

Thus first we investigate how to quantify a node's individual impact on dynamics in a more detailed manner than an averaging against all eligible perturbations. Since each node now represents a specific biochemical entity, it is the subject of our interest. The prediction of node's dynamical impacts from the model may be compared to the empirical data from biological experiments.

Then we develop a hybrid model that incorporates both continuous and discrete random Boolean networks to compare the reaction of the dynamics against small as well as flip perturbations in different regimes. We show that the chaotic behaviour disappears in high sensitive Boolean ensembles with respect to continuous small fluctuations in contrast to the flipping.

Finally, we discuss the role of distributing delays in stabilizing of the Boolean dynamics against noise. These studies are expected to trigger additional experiments and lead to improvement of models in gene regulatory dynamics.