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Modeling of gene regulatory networks.

Gene regulatory networks (GRNs) represent the functional interactions between macromolecular compounds, such as DNA and proteins in a cell. Classically, various approaches are concerned with GRN modeling. In this presentation we will focus on an asynchronous multi-valued logical approach where genes have discrete expression levels depending on the state of the system. The qualitative analysis introduced by Thomas allows us to understand GRN dynamics via the logic parameters and to reason about the model. Biological properties, such as homeostasis, cyclic attractors and reachability can be expressed in temporal logic. We will show how model checking can be used to determine feasible models w.r.t. a temporal formula. Unfortunately, GRN modeling is limited by an incomplete knowledge about the system. Therefore, we will introduce a reverse-engineering method: constraints on logic parameters are deduced from a temporal formula and checked for satisfiability. (Received July 16, 2010)