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Hybrid approach for the modelling of gene regulatory networks

ABSTRACT

Gene regulatory networks (GRNs) have an important role in the field of synthetic biology as they make a realization of new cellular functions possible. Because the dynamics of GRNs are often complex, computer modeling and simulation are required. In this thesis, we present a new GRN modeling algorithm, called the hybrid discrete algorithm. It introduces stochasticity into an otherwise deterministic approach and is based on implicit rules that make modular modeling possible, without having to derive specific system equations. We describe a deterministic modeling approach based on probabilistic interpretation of gene regulation that uses ordinary differential equations. We also present stochastic modeling that takes stochasticity of gene expression into account and is based on chemical reactions. We use these three approaches to demonstrate modeling of three GRNs that have been experimentally verified - the repressilator and two bistable switches. All models successfully describe major characteristics of these GRNs.

Key words: gene regulatory networks, deterministic modeling, stochastic modeling, hybrid discrete algorithm, cooperativity, bistability