

**ABSTRACT: A MEAN-FIELD STATISTICAL MECHANICS
MODEL FOR REGULATION NETWORKS**

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Let $\mathcal{G} = \{1, \dots, n\}$ represent the set of biochemical components interacting in a regulation network and denote by $x_i(t) \in \mathbb{R}$ the *density* of component i at time t . In its simpler version the *Interacting Markov Chains* (IMC) model approach associates N_i two-state Markov chains to each component i . These $N = \sum_{i=1}^n N_i$ chains interact in a mean-field manner as their flip-rates may depend on the global time-dependent probability distribution. The IMC model corresponds to a thermodynamic limit of a slightly unusual statistical mechanics model where the interaction among the N individual chains (*spins*) is associated to a directed graph, and therefore potentially asymmetric. This is important here as asymmetric interactions are natural in the biochemical setting, like, for instance, the enzyme/substrate interaction. Stochastic systems with this type of asymmetric interaction may exhibit highly non-trivial dynamical behavior like stable oscillating magnetizations. The important Piecewise-linear Differential Equations Method, recently introduced in the literature to analyze regulation networks, turns out to be a particular case of this model.

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