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A combinatorial/algebraic topological approach to dynamics of regulatory networks.

Models of multiscale systems, such as those encountered in systems biology, are often characterized by heuristic nonlinearities and poorly defined parameters. Furthermore, it is typically not possible to obtain precise experimental data for these systems. Nevertheless, verification of the models requires the ability to obtain meaningful dynamical structures that can be compared quantitatively with the experimental data. With this in mind we present an approach to modeling dynamics that is based on a purely topological approach to dynamics. We will describe these ideas in the context of models for gene regulatory networks.