ABSTRACT:
The complex process of genetic control relies upon an elaborate network of interactions between genes. Our goal is to use simple mathematical models to understand the role of network structure in gene regulation. Here, we focus on Boolean systems, which have received extensive attention as useful models for genetic control. An important aspect of Boolean network models is the stability of their dynamics in response to small perturbations. Previous approaches to stability have assumed uncorrelated random network structure. Real gene networks typically have nontrivial topology significantly different from the random network paradigm. To address such situations, we present a general method for determining the stability of large networks of any specified network topology and predicting their steady-state behavior in response to small perturbations. Additionally, we generalize to the case where individual genes have a distribution of “expression biases,” and we consider a nonsynchronous update, as well as extension of our method to non-Boolean models in which there are more than two possible gene states. We find that stability is governed by the maximum eigenvalue of a modified adjacency matrix, and we test this result by comparison with numerical simulations. We also discuss the possible application of our work to experimentally inferred gene networks, and propose that a dynamical instability in the gene regulatory network may be a causal mechanism associated with some cancers.