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Role of Combinatorial Complexity in Genetic Networks

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ABSTRACT

A common motif found in genetic networks is the formation of large complexes. One difficulty in modeling this motif is the large number of possible intermediate complexes that can form. For instance, if a complex could contain up to 10 different proteins, 210 possible intermediate complexes can form. Keeping track of all complexes is difficult and often ignored in mathematical models. Here we present an algorithm to code ordinary differential equations (ODEs) to model genetic networks with combinatorial complexity. In these routines, the general binding rules, which counts for the majority of the reactions, are implemented automatically, thus the users only need to code a few specific reaction rules. Using this algorithm, we find that the behavior of these models depends greatly on the specific rules of complex formation. Through simulating three generic models for complex formation, we find that these models show widely different timescales, distribution of intermediate states, and ability to promote oscillations within feedback loops. These results provide tools for the incorporation of combinatorial complexity of genetic networks and show how this incorporation may be vital to accurately predict the network dynamics.

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