An effective network reduction approach to find the dynamical repertoire of discrete dynamic networks

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***Short Abstract* — Despite all the progress in developing analysis tools for discrete dynamic models, there is still a need to find approaches that can directly relate the network structure to its stable patterns of activity. Here we present a novel network reduction approach that can be efficiently applied to large network sizes (up to size 1000). This method is based on a topological criterion to find network motifs that will stabilize in a fixed state. In most cases our method goes beyond reducing the network and can predict the dynamical repertoire of the nodes (fixed states or oscillations) in the system's attractors.**

***Keywords* — Biological networks, discrete dynamic models, Boolean networks, complex networks, attractors.**

THERE is a great interest in understanding how complex cellular behaviors emerge from the underlying network of interactions inside living organisms. Informative dynamic models give insight into the processes involved, offer new predictions and guide further experiments. The qualitative dynamics of these systems can be reproduced using discrete dynamic models [1-3]. In discrete dynamic models the elements of the system can only take a discrete number of states, with the simplest case being the Boolean scenario, in which only 2 states are allowed: 1 (ON) or 0 (OFF). Discrete dynamic models have the advantage of requiring only the combinatorial activating or inhibiting nature of the interactions, and not the kinetic details [3].

Despite the simplicity of the discrete-state assumption, combinatorial complexity still obstructs the modeling of large cellular networks. This is especially problematic because one is commonly interested in the stable patterns of activity of a cellular network, which should correspond to the attractors of the discrete dynamic model.

In this work we offer a solution to this problem by introducing a novel network reduction approach that uses a topological criterion to identify network motifs that will stabilize in a fixed state [4]. Specifically, these network motifs correspond to certain types of strongly connected components in a suitably expanded representation of the network. We have found that our method goes beyond reducing the network and in most cases can actually predict the dynamical repertoire of the nodes (fixed states or oscillations) in the attractors of the system. It is also noteworthy that our method can be applied to large network sizes (up to 1000 nodes and possibly beyond) and has been shown to preserve both fixed points and complex attractors [4].

In order to illustrate the generality of our network reduction method, we apply it to a previously developed biological network model, and also to an ensemble of random Boolean networks. Our chosen biological network is the signaling and regulatory network involved in a type of white blood cell cancer (T cell large granular lymphocyte leukemia or T-LGL leukemia) [5]. Interestingly, we find that the network motifs identified during our reduction method play a significant role in the biology of T-LGL leukemia.

Overall, our method adds a powerful technique to find the dynamical repertoire of a discrete dynamic network model and opens up the possibility of finding the whole attractor landscape of large biological networks.

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