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Identifying and controlling the dynamical repertoire of intracellular networks JORGE G.T. ZAÑUDO, RÉKA ALBERT, The Pennsylvania State University — An important challenge when modeling large intracellular networks is to relate the network structure and function to its stable patterns of activity (attractors). Here we present an approach that can be efficiently applied to large network sizes (up to size 1000 and possibly beyond). Formulated in a discrete dynamic framework, this method is based on a topological criterion to find network motifs that stabilize in a fixed state. Combining these network motifs with network reduction techniques, our method predicts the dynamical repertoire of the network elements (fixed states or oscillations) in the model's attractors, and has also been shown to find all of the model's attractors. To illustrate the applicability of our method, we apply it to two different intracellular network models: the network involved in a type of T cell cancer (T cell large granular lymphocytic leukemia), and the network involved in the metastasis of a type of liver cancer (hepatocellular carcinoma). Interestingly, we find that the network motifs identified during our reduction method play a significant role in the cell fate decision mechanisms in both systems, and also provide insights into how to control the dynamics of the system.

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