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A Logic-Based Technique that Charaterizes the Class of Boolean Networks Producing a Given Biological Pathway GUANYU WANG, CHEN ZENG, George Washington University — A central theme in biophysics is the relationship between structure and function. The question becomes especially intricate at the systems level in which the objects of study are biological networks composed of large numbers of interacting molecules. To what extent does the requirement of carrying out a specific function constrain the structural and more general dynamical properties of a network? Does the biological network optimally designed? Here we present an efficient logic-based technique that captures the ensemble of all the networks that realize the same biological function. The biological function is first represented by a dynamical trajectory in the state space, which impose constraints to the network space. Through some Boolean reasoning we can discover the fundamental building blocks of the network space, namely the irreducible edges and minimal networks. The approach is applied to a cell cycle model and reveals some interesting properties. The full network has 34 edges, but only 23 edges are essential for the cell cycle function. Moreover, this 23 edge minimal network alone can guarantee the robustness of the cell cycle function. In total there exists 40320 such minimal networks, but the naturally occurring one is specially selected by nature, because it has many good properties: high robustness, large designability, etc.

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