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## Functionality and Speciation in Boolean Networks

Boolean Networks have been used to model Genetic Regulatory Networks since Stuart Kauffman proposed them as a model in the 1960s. Early work focused on how the topology of a network influenced its dynamics. We investigate the inverse problem asking which network topologies satisfy a specified dynamic. In earlier work by A. Wagner a biological function or cell process was specified by an initial condition  $v(0)$  and an end point  $v_1$  in the expression state space. By so specifying a biological function one can then ask which networks perform this function. Our view is that in many cases a more appropriate means for defining a biological function would be by specifying the entire path  $v(0), v(1), \dots, v(T)$ . We will report on how these two contrasting definitions of biological functionality lead to divergent results for their respective functional topologies, particularly regarding the implications for neutral evolution, multi-functionality and speciation.