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The technological revolution in molecular biology has provided data that allow the study of large-scale molecular networks through mathematical models. Algebraic models, such as Boolean networks, cellular automata, and more general types of models, are being used increasingly for this purpose. They have the advantage of being intuitive and accessible to a broad range of researchers in the life sciences. At the same time, they lead to many interesting and deep mathematical problems in algebra, combinatorics, dynamical systems theory, and stochastic processes. This talk will introduce algebraic models and their application to biological networks. It will also describe mathematical results and open problems related to them. (Received April 10, 2008)