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Many biological systems are modeled qualitatively with discrete models. Several different modeling types have established communities in the biological sciences, including probabilistic Boolean networks, logical models, bounded petri-nets, and agent-based models. These and other discrete model types can be translated into algebraic models. Using algebraic models as a representation for discrete models allows one to apply theory from algebraic geometry and tools from computational algebra to analyze the dynamic features of such systems. Simulation has become common practice for analyzing discrete models, but most real world biological systems are far too complex to be analyzed by simulation alone. We use various abstract algebra techniques to develop algorithms and software to analyze discrete models for key dynamic features of biological relevance. All algorithms and methods are available through a web-interface <<http://adam.vbi.vt.edu/>>. Analysis of Dynamic Algebraic Models (ADAM) has a ‘modeler friendly’ interface that allows for fast analysis of large models while requiring no understanding of the underlying mathematics or installing software. By providing a user-friendly interface to fast analysis tools, we promote the use of discrete models to model large complex systems. (Received September 21, 2010)