Algebraic models in systems biology

Reinhard Laubenbacher

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Progress in systems biology relies on the use of mathematical and statistical models for system level studies of biological processes. Several different modeling frameworks have been used successfully, including traditional differential equations based models, a variety of stochastic models, agent-based models, and Boolean networks, to name some common ones. This talk will focus on several types of discrete models, and will describe a common mathematical approach to their comparison and analysis, which relies on computational algebraic geometry. Several software packages will be discussed.