Algebraic Framework for Discrete Models in Systems Biology

Franziska Hinkelmann
Virginia Tech

Discrete models are increasingly used in systems biology. They can reveal valuable insight about the qualitative behavior of a system when it is infeasible to estimate enough parameters accurately to build a continuous model. Many discrete models can be formulated as polynomial dynamical systems, that is state and time discrete dynamical systems described by polynomials over a finite field. This provides access to the algorithmic theory of computational algebra and the theoretical foundation of algebraic geometry, which helps with all aspects of the modeling process: construction, analysis, and usage of the model to generate new biological hypotheses.

Simulation is a common practice for analyzing discrete models, but many systems are far too large to capture all the relevant dynamical features through simulation alone. Converted to a polynomial dynamical systems, we can apply tools from computational algebra to analyze their dynamics. The key feature of biological systems that is exploited by our algorithms is their sparsity: while the number of nodes in a biological network may be quite large, each node is affected only by a small number of other nodes. In our experience with models arising in systems biology, this structure leads to fast computations when using algebraic models, and thus efficient analysis.

All welcome. Research students in particular are strongly encouraged to attend.

For further information, contact Elena Dimitrova, edimit@clemson.edu, 656-1524, Martin O-303 or Hui Xue, huixue@clemson.edu, 656-2332, Martin O-020.

Online: http://people.clemson.edu/~huixue/ADMSpring2011.html