

Abstract Submitted  
for the MAR10 Meeting of  
The American Physical Society

**Stochastic Polynomial Dynamic Models of the Yeast Cell Cycle**

INDRANIL MITRA, ELENA DIMITROVA, Clemson University, ABDUL S. JARRAH, Virginia Tech — In the last decade a new holistic approach for tackling biological problems, systems biology, which takes into account the study of the interactions between the components of a biological system to predict function and behavior has emerged. The reverse-engineering of biochemical networks from experimental data have increasingly become important in systems biology. Based on Boolean networks, we propose a time-discrete stochastic framework for the reverse engineering of the yeast cell cycle regulatory network from experimental data. With a suitable choice of state set, we have used powerful tools from computational algebra, that underlie the reverse-engineering algorithm, avoiding costly enumeration strategies. Stochasticity is introduced by choosing at each update step a random coordinate function for each variable, chosen from a probability space of update functions. The algorithm is based on a combinatorial structure known as the Gröbner fans of a polynomial ideal which identifies the underlying network structure and dynamics. The model depicts a correct dynamics of the yeast cell cycle network and reproduces the time sequence of expression patterns along the biological cell cycle. Our findings indicate that the methodology has high chance of success when applied to large and complex systems to determine the dynamical properties of corresponding networks.

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Date submitted: 07 Dec 2009

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