1051-14-92 **Elena S Dimitrova*** (edimit@clemson.edu), 0-303 Martin Hall, Clemson University, Clemson, SC 29634-0975, and **Abdul S Jarrah** (ajarrah@vbi.vt.edu), Virginia Bioinformatics Institute, Washington Street (0477), Virginia Tech, Blacksburg, VA 24061. *Probabilistic dynamical systems for reverse engineering of the yeast cell cycle network.*

We introduce probabilistic polynomial systems (PPS) for the reverse engineering of gene regulatory networks from data that are discretized into a finite number of expression levels. A PPS is a function-stochastic system over a finite field whose functions are polynomials. Given a data set of discretized time series, we present a method for generating a PPS model that contains all minimal data-fitting polynomials and for determining their chance of being selected to participate in the system evolution. We use the method to model the yeast cell-cycle network which is known to have a stochastic nature. (Received August 17, 2009)