1035-92-554 **Elena S Dimitrova*** (edimit@clemson.edu), O-303 Martin Hall, Clemson, VA 29634, **Reinhard Laubenbacher** (reinhard@vbi.vt.edu), Washington St. (0477), Blacksburg, VA 24061, and **Abdul Salam Jarrah** (ajarrah@vbi.vt.edu), Washington St. (0477), Blacksburg, 24061. *A Computational Algebra Method for Biochemical Network Modeling.* Preliminary report.

Polynomial dynamical systems have been used successfully as a framework for the reconstruction, or reverse engineering, of biochemical networks from experimental data. Within this modeling space, using different monomial orders for the polynomial model computation may result in different models. We present a systematic method for selecting the most likely polynomial models for a given data set, using a combinatorial structure known as the Gröbner fan of the ideal of the input data. We illustrate the method by applying it to reconstruct the yeast cell-cycle network. (Received September 10, 2007)