1038-92-84 **Gheorghe Craciun*** (craciun@math.wisc.edu), Department of Mathematics, University of Wisconsin-Madison, Madison, WI 53706. *Mathematical and computational methods for understanding the dynamics of biochemical networks.*

Biochemical reaction network models give rise to polynomial dynamical systems that are usually high dimensional, nonlinear, and have many unknown parameters. Due to the presence of these unknown parameters (such as reaction rate constants) direct numerical simulation of the chemical dynamics is practically impossible. On the other hand, we will show that important properties of these systems are determined only by the network structure, and do not depend on the unknown parameters. Also, we will point out connections with classical problems in algebraic geometry, such as the real Jacobian conjecture. (Received January 29, 2008)