1048-92-131 **Jeremy Gunawardena*** (jeremy@hms.harvard.edu), Department of Systems Biology, Harvard Medical School, 200 Longwood Avenue, Boston, MA 02139. *Algebraic geometric approaches to biological complexity.*

Biomolecular systems often give rise to polynomial dynamical systems and have to be studied by simulation. This requires specification of parameter values, which are often unknown. Furthermore, mechanisms like post-translational modification (PTM) lead to combinatorial explosion, since a protein with n sites may occupy 2^n states. Simulation makes it hard to discern biological principles amidst these details. The steady states of a polynomial dynamical system form an algebraic variety but this has not previously been exploited. Here we show that for certain kinds of PTM systems, algebraic geometric methods provide two important advantages. First, they reduce the complexity of finding steady states from integrating an exponentially large number of differential equations to solving a small number of algebraic equations. Second, they allow parameters to be treated as symbols, rather than as numbers. These results enable the first estimate of the information storage capacity of PTM systems. Underlying these results is the surprising finding that the steady state variety is rational and that its geometry can be biologically significant. If these methods can be extended to a broader class of systems, they would provide powerful tools for analysing biological complexity. (Received February 03, 2009)