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University of California, Berkeley, 970 Evans Hall, Berkeley, CA 94720. *Parametric inference of
biochemical network models.* Preliminary report.

A central problem in molecular systems biology is the inference of models for biochemical networks, such as gene regulatory
or metabolic networks from high-throughput data such as DNA microarrays. A wide range of methods is being developed
for this purpose, using a variety of modeling frameworks, from statistical models such as Bayesian networks, to discrete
dynamical systems such as Boolean networks and systems of ordinary differential equations. Here we present a method
using the framework of multistate discrete dynamical systems. The heart of the method is an evolutionary algorithm
that finds a model which is optimal with respect to dynamics and model complexity. It uses methods from computational
algebra to give a compact mathematical description of the entire model space to be searched. (Received September 20,
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