

Abstract Submitted  
for the MAR13 Meeting of  
The American Physical Society

**Automated adaptive model inference to predict biological network dynamics**<sup>1</sup> BRYAN DANIELS, University of Wisconsin-Madison, ILYA NEMENMAN, Emory University — Dynamical models of cellular regulation often consist of large and intricate networks of interactions at the molecular scale. Since individual interaction parameters are usually difficult to measure, these parameters are often estimated implicitly, using statistical fits. This can lead to overfitting and degradation in the quality of models' predictions. Here we study phenomenological models that adapt their level of detail to the amount of available data, leading to accurate predictions even when microscopic details are not well understood. The model search is made computationally efficient by testing an ordered, nested set of models and by using a model class that can be solved using linear regression in log-space. We test the method on synthetic data and find that phenomenological models inferred this way often outperform detailed, “correct” molecular models in making predictions about responses of the system to signals yet unseen.

<sup>1</sup>This research has been partially supported by Los Alamos LDRD Program and by the James S McDonnell Foundation grant No. 220020321.

Bryan Daniels  
University of Wisconsin-Madison

Date submitted: 11 Dec 2012

Electronic form version 1.4