

Abstract Submitted  
for the MAR16 Meeting of  
The American Physical Society

**On the sufficiency of pairwise interactions in maximum entropy models of networks**<sup>1</sup> ILYA NEMENMAN, Emory University, LINA MERCHAN, Savannah State University — Biological information processing networks consist of many components, which are coupled by an even larger number of complex multivariate interactions. However, analyses of data sets from fields as diverse as neuroscience, molecular biology, and behavior have reported that observed statistics of states of some biological networks can be approximated well by maximum entropy models with only pairwise interactions among the components. Based on simulations of random Ising spin networks with  $p$ -spin ( $p \geq 2$ ) interactions, here we argue that this reduction in complexity can be thought of as a natural property of some densely interacting networks in certain regimes, and not necessarily as a special property of living systems.

<sup>1</sup>This work was supported in part by James S. McDonnell Foundation grant No. 220020321

Ilya Nemenman  
Emory University

Date submitted: 06 Nov 2015

Electronic form version 1.4