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Ising models of strongly coupled biological networks with multivariate interactions[1] LINA MERCHAN, Department of Physics, Emory University, Atlanta, GA 30322, USA, ILYA NEMENMAN, Departments of Physics and Biology, Computational and Life Sciences Initiative, Emory University, Atlanta, GA 30322, USA — Biological networks consist of a large number of variables that can be coupled by complex multivariate interactions. However, several neuroscience and cell biology experiments have reported that observed statistics of network states can be approximated surprisingly well by maximum entropy models that constrain correlations only within pairs of variables. We would like to verify if this reduction in complexity results from intricacies of biological organization, or if it is a more general attribute of these networks. We generate random networks with p-spin ($p > 2$) interactions, with N spins and M interaction terms. The probability distribution of the network states is then calculated and approximated with a maximum entropy model based on constraining pairwise spin correlations. Depending on the M/N ratio and the strength of the interaction terms, we observe a transition where the pairwise approximation is very good to a region where it fails. This resembles the sat-unsat transition in constraint satisfaction problems. We argue that the pairwise model works when the number of highly probable states is small. We argue that many biological systems must operate in a strongly constrained regime, and hence we expect the pairwise approximation to be accurate for a wide class of problems.

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