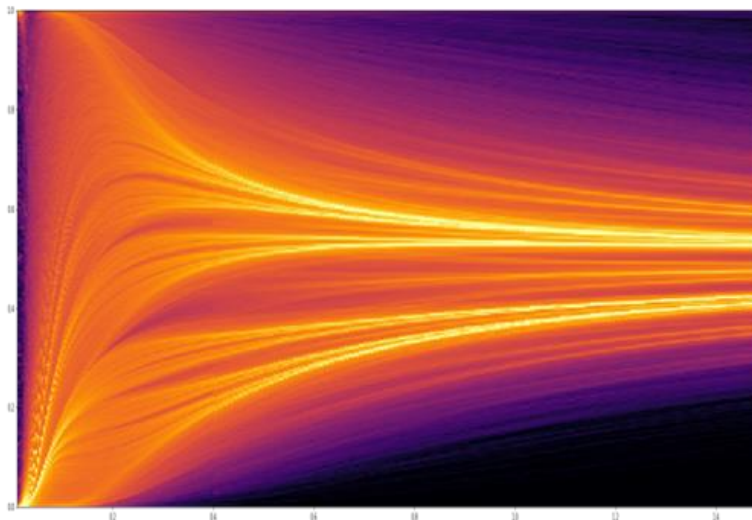# Dynamical analysis of sparse Boolean networks

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The dynamic cavity method provides an efficient way to evaluate probabilities of dynamic trajectories in systems of stochastic units with unidirectional sparse interactions. However, the complexity of the cavity approach grows exponentially with the in-degrees of the interacting units, which creates a de-facto barrier in systems with fat-tailed in-degree distributions. We present a dynamic programming algorithm that reduces the computational complexity from exponential to quadratic, whenever couplings are chosen randomly from a discrete set of equidistant values. As a case study, we analyse the heterogeneous statistics of single node activation in random Boolean networks with fat-tailed degree distribution and fully asymmetric binary couplings. In addition, we extend the dynamical cavity approach to calculate the pairwise correlations induced by different motifs in the network. Our results suggest that the statistics of observed correlations can be accurately described in terms of two basic motifs. We then investigate models with sparse, bi-directional interactions. Bi-directional links are known to add an extra layer of exponential complexity (in the time horizon considered) to the analysis, due to the presence of retarded self-interactions arising from feedback loops, however an ad-hoc approximation, called the One Time Approximation, has been introduced in recent years, which makes the analysis feasible. We observe that the stationary state associated with symmetric or anti-symmetric interactions is biased towards the active or inactive state respectively, even if independent interaction entries are drawn from a symmetric distribution. This phenomenon, which can be regarded as a form of symmetry-breaking, is peculiar to systems formulated in terms of Boolean variables, as opposed to Ising spins. Our study shows that a degree of bi-directionality in the interactions is conducive to having multiple attractors, when noise is sufficiently low, and the presence of multi-node interactions increases the diversity of attractors. These facts may hint at the mechanism with which gene regulatory networks sustain multi-cellular life.

References

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