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Tailored graph ensembles as proxies or null models for real networks

There is a great demand, especially in cellular biology, for precise mathematical approaches to studying the observed topology of networks. We generate new tools with which to quantify the macroscopic topological structure of large directed networks, via a statistical mechanical analysis of constrained maximum entropy ensembles of directed random graphs. We look at prescribed joint distributions for in- and out-degrees and prescribed degree-degree correlation functions. We follow the approach pioneered in [1] for undirected networks. Applications of these tools include: comparing networks; distinguishing between meaningful and random structural features; and, defining and generating tailored random graphs as null models. We calculate exact and explicit formulae for the leading orders in the system size of the Shannon entropies and complexities of these ensembles. The results are applied to data on gene regulation networks.

References

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