Thresholding normally distributed data creates complex networks

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Network data sets are often constructed by some kind of thresholding procedure. The resulting networks frequently possess properties such as heavy-tailed degree distributions, clustering, large connected components and short average shortest path lengths. These properties are considered typical of complex networks and appear in many contexts, prompting consideration of their universality. Here we introduce a simple generative model for continuous valued relational data and study the network ensemble obtained by thresholding it. We find that some, but not all, of the properties associated with complex networks can be seen after thresholding, even though the underlying data is not “complex”. In particular, we observe heavy-tailed degree distributions, large numbers of triangles, and short path lengths, while we do not observe non-vanishing clustering or community structure.

I. INTRODUCTION

Networks are a popular tool for representing and analyzing real-world systems consisting of entities and their relationships. However, nature does not directly hand us networks. Instead, researchers create them from real-world data—knowingly simplifying the situation—in the hope of gaining insight. In the most basic incarnation, networks are simple graphs—undirected and unweighted with only one type of node and one type of edge. The usual picture is that nodes represent some group of objects (people, neurons, proteins, etc.), and edges represent some kind of interaction between them (friendship, synapses, binding, etc.) [1–8].

In the real world interactions are seldom binary, and so creating a simple network requires thresholding, which may take several forms [4–10]. The most obvious case is when a continuous valued data set is explicitly thresholded by deciding what level of interaction is sufficiently strong to count as an edge in the network. A more subtle case is that of experimental limitation: interactions that exist but are very weak or rare may not be observed. Even for binary valued data sets the sampling method may hide an implicit thresholding mechanism. Consider a friendship network. Most everyday interactions between people are presumably not strong enough to constitute friendship. At what point does a casual acquaintance cross over to the category of friend? When people list their friends, in a survey for instance, they will implicitly apply some criteria to filter the friends from the acquaintances. However, an understanding of the properties one should expect to observe from thresholded relational data is currently lacking.

In this paper we examine the properties of networks created by thresholding relational data. To do this we introduce a basic model of the underlying relational data, which is then thresholded to produce edges in the network. The model is derived from three assumptions:

1. all nodes are statistically identical;
2. any correlations are local;
3. the underlying relational data is normally distributed.

All three of these assumptions—which are no doubt violated in real-world systems—are quite natural for a null model. Assumption 1, that all nodes are identical, severely constrains what correlation structures are admissible. In fact, only two free parameters remain in the covariance matrix once this assumption is made. Assumption 2 sets one of those parameters to zero—edges that are not directly joined to each other are uncorrelated. The other parameter, the local correlation strength, we call $\rho$. Our remaining freedom is to pick a distribution that is consistent with the required correlation matrix. The most obvious and simple choice is assumption 3, the multivariate normal (Gaussian) distribution. We believe this to be the simplest non-trivial model for relational data.

The thresholding procedure will also be very simple: any of the relational data that falls above some threshold, $t$, will be said to constitute an edge in the network, and any that falls below will not. The threshold value $t$ will be a parameter of the model.

Our network ensemble on $n$ nodes is thus defined by two parameters: the threshold, $t$, and a local correlation coefficient, $\rho$. Despite the simplicity of the model—all the underlying relational data is normally distributed—we nonetheless find that the thresholding procedure reproduces a number of the behaviours typically observed in complex networks, such as heavy-tailed degree distributions, short average path lengths,
and large numbers of triangles. It does not, however, yield non-vanishing clustering or community structure in the large $n$ limit and so cannot account for this observation in real-world data sets.

This paper has two main parts. In Sec. [II] we define and justify the network model. Then, in Sec. [III] we study the properties of the network ensemble. We look at the density of edges, triangles and clustering, the degree distributions, shortest path lengths, and the giant component.

II. MODEL SPECIFICATION

A. Thresholding locally correlated data

A network can be represented by its adjacency matrix, $A$, where $A_{ij} = 1$ if node $i$ and $j$ are connected and $A_{ij} = 0$ otherwise. We consider networks created by thresholding underlying relational data, $X$, adding an edge between $i$ and $j$ if

$$X_{ij} \geq t. \quad (1)$$

To specify a model we need to pick a distribution for $X$. Assuming that all nodes are statistically identical—exchangeable in the parlance of statistics—constrains our choice of distribution.

If nodes are identical then the marginal distribution for $X_{ij}$ must be the same for all (distinct) pairs $i$ and $j$. Further, by a linear transform we can always set $E[X_{ij}] = 0$ and $\text{Var}[X_{ij}] = 1$, and so long as the appropriate transformation is made to $t$, this shift will have no effect on the thresholded network. For this reason we will always assume $X_{ij}$ has mean 0 and variance 1. Exchangeability puts further constraints on the covariance matrix, whose entries can take only three values. For $i, j, k, l$ all distinct, these are

$$\text{Var}[X_{ij}] = \Sigma_{(i,j),(i,j)} = 1,$$
$$\text{Cov}[X_{ij}, X_{kl}] = \Sigma_{(i,j),(k,l)} = \rho,$$
$$\text{Cov}[X_{ij}, X_{kl}] = \Sigma_{(i,j),(k,l)} = \gamma, \quad (2)$$

where $\text{Cov}[X, Y]$ denotes covariance. We will assume that $\gamma = 0$ since this quantifies the correlation between two edges that do not share a node, i.e. two edges that do not “touch”. So far we have two free parameters, $t$ and $\rho$. The remaining task is to pick a distribution with the required covariance matrix, $\Sigma$.

In principle any distribution could be used, but the obvious choice is a multivariate normal distribution. The normal distribution has many points in its favour. Famously it arises in the central limit theorem, which makes it a plausible model for many random processes. Further, it is the maximum entropy distribution with the required covariance matrix, and so could be justified as the “least informative distribution”—the model that makes the fewest extra assumptions. But perhaps of equal importance is the fact that it’s well-studied and has convenient mathematical properties.

In standard notation a multivariate normal distribution (MVN) is denoted $N(\mu, \Sigma)$. The probability density function of an $N$-dimensional MVN is

$$P(x) = \frac{e^{-\frac{1}{2}(x-\mu)^T \Sigma^{-1} (x-\mu)}}{\sqrt{(2\pi)^N \text{det}(\Sigma)}}. \quad (3)$$

A concise statement of the model is: given the freely chosen parameters $t \in \mathbb{R}, \rho \in [0, \frac{1}{2}]$, and the number of nodes $n$, draw a random variable $X$ with

$$X \sim N(0, \Sigma), \quad (4)$$

where

$$\Sigma_{(i,j),(i,j)} = 1,$$
$$\Sigma_{(i,j),(k,l)} = \rho,$$
$$\Sigma_{(i,j),(k,l)} = 0. \quad (5)$$

Then create the network by thresholding $X$,

$$A_{ij} = \begin{cases} 1 & \text{if } X_{ij} \geq t, \\ 0 & \text{otherwise}. \end{cases} \quad (6)$$

Note, we constrain $0 \leq \rho \leq \frac{1}{2}$ so that $\Sigma$ is positive semi-definite [II].

B. Sampling from the model

We now describe a simple algorithm to sample from the model. This algorithm also provides an intuitive model interpretation.

Let $Z_i$ be $n$ i.i.d. variables, $N(0, 1)$. Let $Y_{ij}$ be $\binom{n}{2}$ i.i.d. variables, $N(0, 1)$. Then let

$$W_{ij} = \sqrt{1 - 2\rho Y_{ij} + \sqrt{\rho} (Z_i + Z_j)}. \quad (7)$$

Note that $W_{ij}$ is normally distributed with mean zero and further

$$\text{Var}[W_{ij}] = 1,$$
$$\text{Cov}[W_{ij}, W_{ik}] = \rho,$$
$$\text{Cov}[W_{ij}, W_{kl}] = 0. \quad (8)$$

Hence, $W$ is distributed identically to $X$. So, to sample from the model:

1. Sample $z$, a length $n$ vector of i.i.d. standard normal variables.

2. For $i < j$, generate $y \sim N(0, 1)$, and if

$$y > \frac{t - \sqrt{\rho} (z_i + z_j)}{\sqrt{1 - 2\rho}}, \quad (9)$$

add edge $(i, j)$ to the network.
FIG. 1. Thresholding relational data to obtain networks. Panel (a) shows a general procedure to obtain unweighted networks from edge weights. Each edge weight is hypothesized to have been drawn from a specific distribution, generating an undirected weighted network. An unweighted network is then produced by assigning an edge whenever an edge weight $X_{ij}$ is greater than a threshold $t$. In panel (b) we show how edge weights are correlated in the model of Sec. II by covariance matrix $\Sigma$ (Eq. (5)). Edge weights for edges which connect through a node have covariance $\text{Cov}[X_{ij}, X_{ik}] = \rho$, while edge weights not connected by a node have zero covariance. If $\rho = \frac{1}{2}$, generating $y$ is unnecessary and one can simply add edge $(i, j)$ if $\sqrt{1/2}(z_i + z_j) \geq t$.

A Python package to generate networks along with scripts for the figures in this paper is publicly available [12].

In order to achieve the required correlations, the algorithm above separates $X_{ij}$ into node and edge effects. Each node is given a value $Z_i$. Then $X_{ij}$ is created by a linear combination of $Z_i$ and $Z_j$ plus i.i.d. random noise $Y_{ij}$. We can interpret the $Z$’s as latent variables that control the propensity for individual nodes to have edges and $\rho$ controls the relative strength of the noise process. Note that when $\rho = 1/2$ edges are entirely determined by the values of $Z$, while at $\rho = 0$ edges are entirely random and independent. Although the normal model is equivalent to a latent variable model it was not derived by assuming the existence of latent variables.

III. NETWORK PROPERTIES

We now turn our attention to properties of the networks created by the model.

A. Edge density

Edges in the network exist whenever the corresponding weight $X_{ij}$ is greater than $t$. The marginal distribution for $X_{ij}$ is simply a standard normal distribution. Thus,

$$E[A_{ij}] = P[A_{ij} = 1] = P[X_{ij} \geq t] = 1 - \Phi(t),$$

(10)

where $\Phi(x)$ is the cumulative distribution function for the standard normal distribution $N(0, 1)$. When $\rho = 0$ all edges exist independently and the model is equivalent to the random graph, $G_{n,p}$, with $p = 1 - \Phi(t)$.

The mean degree is equally simple to compute. For all $\rho$

$$E[k_i] = \sum_{j \neq i} E[A_{ij}] = (n - 1)(1 - \Phi(t)),$$

(11)

If we want to pick $t$ for a desired mean degree $\langle k \rangle$, it is easy to invert this to obtain

$$t = \Phi^{-1}\left(1 - \frac{\langle k \rangle}{n - 1}\right).$$

(12)

B. Triangles, clustering, and degree variance

Many complex networks are observed to have large numbers of triangles. The clustering coefficient or transitivity is one way to quantify this. We can quantify the clustering with the probability that a triangle is closed, given that two of its edges already exist,

$$C = P[A_{ik} = 1 | A_{ij}, A_{jk} = 1] = \frac{P[A_{ik}, A_{ij}, A_{jk} = 1]}{P[A_{ij}, A_{jk} = 1]}.$$

(13)
The numerator of this equation corresponds to the density of triangles while the denominator corresponds to the density of two-stars (which also determines the variance of the degree distribution). Note that for simplicity we shorten the logical connective “and” (or “\(\land\)”) using commas, e.g. \(P[A_{ij} = 1 \land A_{jk} = 1] \equiv P[A_{ij}, A_{jk} = 1]\).

The marginal distributions of an MVN are themselves MVN, and are found by simply dropping the unwanted rows and columns in the correlation matrix \(\Sigma\). Thus, \((X_{ij}, X_{ik}, X_{jk})^T\) will be bivariate normally distributed and \((X_{ij}, X_{ik}, X_{jk})^T\) will be trivariate normally distributed, both with correlation coefficient \(\rho\). Introducing the Hermite polynomials \(H_N(x)\) as defined in Appendix [A], one finds that

\[
P[X_{ij}, X_{ik}, X_{jk} \geq t] = \sum_{N=0}^{\infty} \frac{\rho^N}{N!} [\phi(t)H_{N-1}(t)]^2
\]  

(14)

dependent on the number of stars and

\[
P[X_{ij}, X_{ik}, X_{jk} \geq t]
= \sum_{N=0}^{\infty} \sum_{i=0}^{N} \sum_{j=0}^{N-i} \frac{\rho^N}{N!j!} H_{N-i-j}(t) H_{N-1-i}(t) H_{N-1-j}(t)
\]  

(15)

\[
\text{for two-stars, and}
\]

\[
P[X_{ij}, X_{ik}, X_{jk} \geq t]
= \sum_{N=0}^{\infty} \frac{\rho^N}{N!} [\phi(t)H_{N-1}(t)]^2
\]

(14)

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P[X_{ij}, X_{ik}, X_{jk} \geq t]
= \sum_{N=0}^{\infty} \sum_{i=0}^{N} \sum_{j=0}^{N-i} \frac{\rho^N}{N!j!} H_{N-i-j}(t) H_{N-1-i}(t) H_{N-1-j}(t)
\]

(15)

for triangles. Both sums converge for \(\rho \leq 0.5\), and we can estimate them accurately with a finite number of terms [13]. Noting that there are \(\binom{n-1}{2}\) potential triangles for each node, the expected number of triangles per node is simply \(\binom{n}{2}\) times their density

\[
T = \frac{(n-1)}{2} P[X_{ij}, X_{ik}, X_{jk} \geq t].
\]  

(16)

Plots of these functions are shown in Fig. 1. We find that \(T\) is much larger in these networks than in the random graph \(G_{n,p}\)—larger by multiple orders of magnitude. In fact, while \(T\) goes to zero in the large \(n\) limit for the random graph, in this model we find that \(T\) increases with \(n\) for large values of \(\rho\). On the other hand, the clustering coefficient \(C\) decreases with growing number of nodes for all parameter values. This leads to a slightly paradoxical result for large \(\rho\): in the limit \(n \to \infty\) the expected number of triangles at each node goes to infinity, and the clustering coefficient still goes to zero! The reason for this is that the number of two-stars diverges faster than the number of triangles.

Equation (14) can also be used to compute the variance of the degree distribution. To see this note that a node of degree \(k\) has \(\binom{k}{2}\) two-stars. Further, noting that there are \(\binom{n-2}{k}\) potential two-stars (the same number of potential triangles, noted above) we find

\[
\frac{1}{2} \langle k^2 \rangle = \frac{(n-1)}{2} P[X_{ij}, X_{ik}, X_{jk} \geq t].
\]  

(17)

Combining this with Eq. (11) the variance of the node degree \(k\) can be written

\[
\text{Var}[k] = (n-1)\phi(t) [1-\Phi(t)]
+ (n-1)(n+2) \sum_{N=1}^{\infty} \frac{\rho^N}{N!} \phi(t) H_{N-1}(t) \right]^2.
\]  

(18)

The first term is simply the variance of a binomial distribution. For \(\rho = 0\) the second term vanishes and we recover the correct result for the random graph \(G_{n,p}\). For \(\rho > 0\) the sum is positive and monotonically increases with \(\rho\) as illustrated in Fig. 3.

C. Degree distribution

In the previous two subsections we gave expressions for the mean and variance of the degrees. Here we give expressions for the full distribution of degrees.

The degree distribution \(p_k\) is the probability that a node has \(k\) edges. For this model the degree distribution can be written

\[
p_k = \frac{(n-1)}{k} \frac{1}{2\pi \rho} \int_{-\infty}^{\infty} e^{k(y)} dy
\]  

(19)

where

\[
f_k(y) = k \ln[1-\Phi(y)] + (n-k-1) \ln[\Phi(y)]
- \frac{1}{2} \left( \frac{t-\sqrt{1-\rho t}}{\sqrt{\rho}} \right)^2.
\]  

(20)

This result is derived in Appendix [B].

The integral in Eq. (19) can be computed numerically to high precision using Gauss-Hermite quadrature, centred at the maximum of \(f_k(y)\). Increasing the order of Gauss-Hermite quadrature (i.e. incorporating more points) increases the accuracy. The full details are in Appendix [B].

We can also approximate the integral using Laplace’s method [14], an asymptotic approximation for integrals of this form (equivalent to a first order Gauss-Hermite quadrature). The idea of the method is to replace the function \(f_k(y)\) by a second order Taylor series around its maximum. For large \(n\), the last (quadratic) term in \(f_k\) will be negligible and for \(0 < k < n-1\), the maximum will be at

\[
y_{0,k} = \Phi^{-1}\left(1 - \frac{k}{n-1}\right).
\]  

(21)

Combining this with Stirling’s approximation for the binomial coefficient, we find

\[
p_k \sim \frac{1}{n-1} \frac{1-\rho}{\rho} \exp\left[-\frac{(1-2\rho)(n-1)}{2\rho} \right] \frac{n}{n-1} \left[ \frac{(n-1)}{2} \right]^{y_{0,k} - k^2}
\]  

(22)

Together with the closed form approximation for \(\Phi^{-1}\), given in Appendix [C], Eq. (22) provides a closed form approximation for the degree distribution.

Figure 5 shows some example degree distributions, computed to high precision using Eq. (19) along with the asymptotic approximation, Eq. (22), where we chose \(n = 100000\) and \(k = 100\).

To illustrate how the threshold model compares to real networks, we chose three network data sets from different domains, and fit the model. The first data set is a network of friendships between students at a U.S. high school.
FIG. 2. Clustering $C$ and triangles per node $T$ as computed in Sec. III B. Clustering decreases with increasing number of nodes, however the number of triangles per node increases with growing number of nodes $n$ for large values of $\rho$. Clustering increases both with increasing mean degree $\langle k \rangle$ and local edge weight correlation $\rho$. In panel (a) and (c) we chose $n = 100000$ and in panel (b) and (d), we fixed $\langle k \rangle = 4$.

FIG. 3. The variance of degree, Eq. (18), increases with $\rho$, the local edge weight correlation. With increasing mean degree $\langle k \rangle$, even small correlations $\rho$ produce networks of significantly broader degree distribution than the random graph $G_{n,p}$.

$(n = 2587)$ [13], the second data set is a co-authorship network of researchers $(n = 16726)$ [16], and the third network describes interactions between proteins $(n = 6327)$ [17].

Given a number of nodes $n$ the model studied in this paper has two free parameters, $t$ and $\rho$. A simple procedure to fit the model to the data introduced above is to choose $t$ and $\rho$ so that the mean and variance of the model’s degree distribution match the observed values. We use Eq. (12) to fix $t$ and subsequently Newton’s method to solve Eq. (18) for $\rho$.

The results of this exercise are shown in Fig. 5. The networks were chosen for their different degree distributions—note the different scales on the axes: linear, log-linear, and log-log. Nonetheless, the threshold model seems to provide plausible fits in each case. A more rigorous fitting procedure, along with statistical tests (e.g. goodness of fit tests) could be developed but we leave this to future work.

Note, while the degrees in the thresholded networks, $k_i = \sum_j A_{ij}$, follow a heavy-tailed distribution, the underlying degrees $d_i = \sum_j X_{ij}$ are normally distributed. The interesting properties of these degree distributions arise due to thresholding.

D. Giant component

A well studied problem in the theory of random graphs is the formation of a large connected (giant) component. At very low densities only a handful of nodes can be reached from any other node but at some critical point a macroscopic number of nodes will be connected. For the random graph this transition occurs at a mean degree of $\langle k \rangle = 1$ [1] [18] [19].

To explore the effects of $\rho > 0$ we sampled from the model as described in Sec. II B and measured the size of the second largest component as a susceptibility parameter for the phase transition. The maximum of this susceptibility parameter is used to find the transition lines in Fig. 6.

We find that as $\rho$ or $n$ increases, the transition occurs at lower values of the mean degree. This result is in line with the configuration model for which the transition point decreases with increasing variance in the degree distribution. For $\rho = 0$ we recover the standard result for the random graph.

For the other limit case, $\rho = 1/2$, recall that all edge weights can be considered to arise from node “propensities”, $Z_i$, with $X_{ij} = \sqrt{1/2}(Z_i + Z_j)$. This implies that all nodes that are connected to any other nodes must also be connected to the node with maximum propensity $Z_{\text{max}}$. The size of the largest component is then given by this node’s degree plus one, $k_{\text{max}} + 1$. The second largest component is then always of size 1. We therefore omit $\rho = 1/2$ in the numerical analysis.

E. Shortest path lengths

Another phenomenon well established in the complex networks literature is that randomly chosen nodes often have surprisingly short paths between them. This is often referred to as the “six degrees of separation” or “small-world” phenomenon [1] [20]. By a common definition, network models are considered to demonstrate this property if the average shortest path length $\langle d_{ij} \rangle$ between nodes grows logarithmically (or slower) as the number of nodes increases [1].

Using the method described in Sec. II B we sampled from the threshold model to verify that it displays this property. We looked at networks with between 100 and 30000 nodes, with
FIG. 4. We show degree distributions computed using Eq. (19) for $n = 100000$ and $\langle k \rangle = 100$ for increasing local edge weight correlation $\rho$ in log-log (a) and linear scales (b). We also compare them to the asymptotic approximation Eq. (22). Note that large values of $\rho$ produce broad degree distributions which could be easily mistaken for log-normal or power-law distributions.

FIG. 5. Degree histograms for the three real-world networks introduced in Sec. III C along with fitted distributions from the thresholded normal model. We show (a) a high school friendship network, (b) a co-authorship network between scientists, and (c) a protein–protein interaction network.

FIG. 6. Simulations with $1000 \leq n \leq 30000$, mean degree $10^{-3} \leq \langle k \rangle \leq 10$, $0 \leq \rho \leq 0.45$. 1000 samples were taken for each of the parameter combinations. Panel (a) shows the points of transitions for increasing number of nodes $n$. To the left of the line the network does not posses a giant component, while to the right it does. The transition point was computed using the mean size of the second largest component as a susceptibility parameter. Panel (b) shows an example of the susceptibility parameter for $n = 10000$. 
FIG. 7. Panel (a) shows the scaling of the average shortest path in the largest connected component with the number of nodes, \( n \). We fix the mean degree \( \langle k \rangle = 5 \) and each point is averaged over 200 samples. For \( \rho = 0 \) we recover the result for the random graph \( G_{n,p} \) where \( \langle d_{ij} \rangle \propto \log n \). For non-zero correlation, the average shortest path length increases slower than logarithmically. In panel (b) we show the average shortest path length for different mean degrees and values of \( \rho \) for networks with \( n = 10000 \), again sampled 200 times for each parameter combination.

mean degree \( \langle k \rangle = 5 \), and investigated the influence of increasing edge weight correlation \( \rho \). After sampling a network from the model we computed the average shortest path length \( \langle d_{ij} \rangle \) on the largest (giant) component. For each parameter combination we computed the mean by averaging 200 sampled networks.

The results are shown in Fig. 7. Since it is well known that the random graph \( G_{n,p} \) has short shortest paths \(^{21}\) it is unsurprising that the threshold model does also (recall, for \( \rho = 0 \) they are equivalent, and we see the standard \( \langle d_{ij} \rangle \propto \log n \) scaling behaviour). For \( \rho > 0 \) we see that average shortest path lengths grow significantly slower than logarithmically, a behaviour sometimes referred to as “ultra small-world” and often related to networks with power-law degree distribution \(^{22, 23}\). In our model, the effect appears despite the fact that the degree distribution does not follow a power-law.

As discussed, when \( \rho = 1/2 \) all edge weights can be considered to arise from node propensities \( Z_i \), such that \( X_{ij} = \sqrt{1/2}(Z_i + Z_j) \). All nodes are then either disconnected or part of the giant component, and the node with maximum propensity \( Z_{\text{max}} \) is connected to all nodes in the giant component. Hence, all nodes in the giant component are either directly connected or can reach each other in two steps through the maximum-degree node. So, when \( \rho = 1/2 \) the average shortest path length must be \( 1 \leq \langle d_{ij} \rangle < 2 \).

IV. DISCUSSION

In this paper we studied the effects of thresholding relational data. We started with a simple model of normally distributed data, with only one free parameter, \( \rho \), controlling local correlations in the data. We then demonstrated that thresholding this normally distributed relational data reproduces many of the properties commonly associated with complex networks. In particular, we find this model has a heavy-tailed degree distribution, relatively large numbers of triangles, and short average path lengths.

The underlying relational data \( X \) in the model we introduce would not usually be considered complex. One could think of \( X \) itself as a weighted network. Thought of in this way, the underlying network is a complete graph. Further, all edge weights (and linear combinations thereof) are normally distributed. For example, the “degrees”, \( d_i = \sum_j X_{ij} \), are normally distributed. And yet, after thresholding the networks look considerably more complex—the thresholding procedure itself is responsible for this. Future empirical work on complex networks should consider this. When one finds a supposedly complex network it could be an artifact of some thresholding process.

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[11] To see why $\rho > \frac{1}{2}$ is problematic, consider the marginal distribution for four edges, say $X_{ij}, X_{jk}, X_{kl}, X_{il}$. A simple calculation shows that the covariance matrix has a negative eigenvalue for $\rho > \frac{1}{2}$. Similarly, since $\text{Var} \left[ \Sigma_{ij} \right]$ must be greater than zero, $\rho$ must be greater than $-1/(n-2)$ and so negative correlations can be vanishingly weak at most.

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Appendix A: Multivariate normal integrals and Hermite polynomials

The probability of a two-star existing with nodes $i, j$ and $k$ as constituents is given by

$$P[X_{ij} X_{ik} \geq t] = \frac{1}{2\pi \sqrt{1-\rho^2}} \int_{t}^{\infty} \int_{t}^{\infty} e^{-\frac{1}{2} \left( \frac{x^2 + y^2 - 2\rho xy}{1-\rho^2} \right)} dx dy.$$  \hspace{1cm} (A1)

Direct computation of the integral is not straightforward but we can compute it quickly using the Hermite polynomials \[\text{[13]}\]. A quick outline of this method: for $n \geq 0$, define the Hermite polynomials as

$$H_n(x) = (-1)^n e^{\frac{x^2}{2}} \frac{d^n}{dx^n} e^{-\frac{x^2}{2}}. \hspace{1cm} (A2)$$

As the name suggests, the Hermite polynomials are in fact polynomials, for example $H_0(x) = 1$, $H_1(x) = x$, $H_2(x) = x^2 - 1$, and so on. For notational convenience also define

$$H_{-1}(x) = \frac{1 - \Phi(x)}{\phi(x)}. \hspace{1cm} (A3)$$

Using the Hermite polynomials, we can expand Eq. \[\text{[A1]}\] as an infinite sum and integrate term by term. The final result is given by Eq. \[\text{[14]}\]. The same trick is used for the 3-dimensional integral to give Eq. \[\text{[15]}\].

Appendix B: Degree distribution

Since, by assumption, all nodes in this model are equivalent, we will simply consider the one-node marginal to compute the degree distribution. Let $U$ be all the terms in $X$ that
are associated with node 0, i.e. \( U_j = X_{0j} \). Then, \( U \) is multivariate normally distributed, \( \mathcal{N}(0, \Sigma^{(0)}) \), where \( \Sigma^{(0)} \) has ones along the diagonal and \( \rho \) everywhere else

\[
\Sigma^{(0)}_{jk} = \begin{cases} 
1 & \text{for } j = k, \\
\rho & \text{otherwise}.
\end{cases}
\]

The focal node will have degree \( k \) when exactly \( k \) terms in \( U \) are larger than the threshold \( t \). There are \( \binom{n-1}{k} \) different ways this can happen and each is equally likely. So, to compute \( p_k \) we can compute the probability that the first \( k \) terms in \( U \) are larger than \( t \) and all others are smaller, and then multiply by \( \binom{n-1}{k} \) to obtain

\[
p_k = \binom{n-1}{k} P[U_1, \ldots, U_k \geq t; U_{k+1}, \ldots, U_{n-1} < t]. \tag{B1}
\]

To solve this integral we use a standard trick [24]. First, we note that if \( Z_0, Z_1, \ldots, Z_{n-1} \) are i.i.d. \( \mathcal{N}(0, 1) \) then

\[
((\sqrt{1-\rho}Z_1 + \sqrt{\rho}Z_0), \ldots, (\sqrt{1-\rho}Z_{n-1} + \sqrt{\rho}Z_0))^T \tag{B2}
\]

will be distributed identically to \( U \). Further, once we know the value of \( Z_0 \) then all the terms are independent, and the probability that any one of them is greater than \( t \) is the probability that \( Z_1 \geq \frac{t - \sqrt{\rho}z}{\sqrt{1-\rho}} \). Given \( Z_0 = 0 \), the probability that exactly \( k \) values will greater than \( t \) and the rest less than \( t \) is

\[
\binom{n-1}{k} (1 - \Phi \left( \frac{t - \sqrt{\rho}z}{\sqrt{1-\rho}} \right) )^k \Phi \left( \frac{t - \sqrt{\rho}z}{\sqrt{1-\rho}} \right)^{n-1-k}. \tag{B3}
\]

Averaging this quantity over \( z \) then provides us with the correct expression,

\[
p_k = \binom{n-1}{k} \int_{-\infty}^{\infty} \left( 1 - \Phi \left( \frac{t - \sqrt{\rho}z}{\sqrt{1-\rho}} \right) \right)^k \Phi \left( \frac{t - \sqrt{\rho}z}{\sqrt{1-\rho}} \right)^{n-1-k} \phi(z) \, dz = I_{n,k} \tag{B4}
\]

where \( I_{n,k} \) is the integral. A change of variables allows us to write

\[
I_{n,k} = \sqrt{\frac{1 - \rho}{2\pi\rho}} \int_{-\infty}^{\infty} e^{k(y)} \, dy \tag{B5}
\]

where

\[
f_k(y) = k \ln [1 - \Phi(y)] + (n - k - 1) \ln [\Phi(y)] - \frac{1}{2} \left( \frac{t - \sqrt{1-\rho}y}{\sqrt{\rho}} \right)^2. \tag{B6}
\]

A standard approach to approximate such an integral is to use Laplace’s method. In this approach one expands \( f \) about its maximum and then neglects higher order terms, \( f(y) \approx f(\bar{y}) - \frac{f''(\bar{y})}{2} (y - \bar{y})^2 \). Having done this, the integral reduces to a standard Gaussian integral. While this approach is asymptotically correct (in the large \( n \) and \( k \) limit), we can improve the approximation by including more terms using Gauss-Hermite quadrature. Re-writing the integral again, and making another change of variables:

\[
I_{n,k} = \sqrt{\frac{1 - \rho}{2\pi\rho}} e^{k(\bar{y})} \int_{-\infty}^{\infty} e^{-z^2 + R_k \left( \frac{x}{\sqrt{f''(\bar{y})}} + \bar{y} \right) } \, dx \tag{B7}
\]

where \( R_k \) is the remaining terms of \( f_k \) after expansion:

\[
R_k(y) = f_k(y) - f_k(\bar{y}) + \frac{|f''(\bar{y})|}{2} (y - \bar{y})^2. \tag{B8}
\]

Now we can approximate the integral using Gauss-Hermite quadrature:

\[
I_{n,k}(N) = \sqrt{\frac{1 - \rho}{2\pi\rho}} e^{k(\bar{y})} \sum_{i=1}^{N} w_i e^{R_k \left( \frac{x_i}{\sqrt{f''(\bar{y})}} + \bar{y} \right) }, \tag{B9}
\]

where \( x_i \) are the points for which \( H_N(x_i) = 0 \) and the weights \( w_i \) are

\[
w_i = \frac{N! \sqrt{2\pi}}{N^2 [H_{N-1}(x_i)]^2}. \tag{B10}
\]

Note that \( I_{n,k}(1) \) is Laplace’s approximation, i.e. Laplace’s approximation is a first order Gauss-Hermite quadrature at the maximum of \( f_k \), while \( I_{n,k}(N) \) approximates the remainder terms with increasingly higher order polynomials and so we expect \( I_{n,k}(N) \to I_{n,k} \) as \( N \) increases.

**Appendix C: Approximation of inverse cdf**

The normal distribution’s inverse CDF, \( \Phi^{-1}(x) \), can be approximated [25] for \( 0 < x \leq 0.5 \) as

\[
\Phi^{-1}(x) \approx \frac{a_0 + a_1 s}{1 + b_1 s + b_2 s^2} - s, \quad s = \sqrt{-2 \ln(x)} \tag{C1}
\]

with

\[
a_0 = 2.30753, \quad b_1 = 0.99229, \tag{C2a}
\]

\[
a_1 = 0.27061, \quad b_2 = 0.04481. \tag{C2b}
\]

For \( 0.5 < x \leq 1 \) we use \( \Phi^{-1}(x) = -\Phi^{-1}(1-x) \).