

Random graphs with specific degree distribution and giant component size

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Random networks are a powerful tool in the analytical modeling of complex networks as they allow us to write approximate mathematical models for diverse properties and behaviors of complex systems. These models are often used to study stochastic processes like percolation, where the giant connected component breaks down as edges are removed, yet they fail to properly account for the size of that component, even in a deterministic setting where all edges exist. Here, we introduce a simple conceptual step to account for such connectivity constraints in existing models. We distinguish between network neighbors based on two types of connections that can lead, or not, to the giant component, which we refer to as critical and subcritical degrees. The giant component is the largest unique component of a network that scales with the network's size under our model. It is analogous to many properties of interest, such as the largest epidemic possible on a contact network or the connectivity of an infrastructure network. Accounting explicitly for this component also allows us to capture important structural features of the network in a system of only one or two equations. When applied to sparse connected networks, we show that our approach compares favorably with the predictions of state-of-the-art models, like message passing, which require a number of equations that are linear in system size. We discuss potential applications of this simple framework for studying infrastructure networks where connectivity constraints are critical to the function of the system.

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Introduction: Models of networks. Random network models are a useful tool that allows simple mathematical analysis of the structure and properties of real complex networks [1]. Such models are typically parameterized with local connection rules enforcing structural constraints while leaving the rest of their structure random [2,3]. In theory, these rules should encode constraints that capture important features of real networks while the randomness reduces bias and preserves mathematical tractability. One of the most popular versions of this approach is the *Configuration Model* (CM), specified using the degree sequence of the network while assuming that edges are connected at random [4]. Many generalizations have been introduced over the years, including degree-degree correlations between neighbors [5], motifs [6,7], or more macroscopic structures like k -core or onion decomposition [8–11].

One notable use of this approach is the study of site or bond percolation on random networks, which is used to model the robustness of real networks to random failure or targeted attacks [12] and understand how they support dynamics such as the spread of epidemics or cascading failures [13]. In these

contexts, models can approximate the percolation threshold of real networks quite well [10,14–16], but typically fail to capture the actual size of the largest connected component far above the threshold. Given that the size of this component is related to the robustness against damage or small changes in edge functionality, it is unfortunate that most models dramatically fail in the regime where there is no damage or changes to the structure.

Here, we propose shifting the perspective on the information encoded in the stubs (i.e., the half-edges matched to generate the network)—from purely local to global—and illustrate how this can yield simple mathematical models that are more realistic at the global scale. Focusing on the problem of preserving the size of the largest connected component, we introduce a new computationally informed model based on the idea of critical connections. In a nutshell, our goal is to specify a critical substructure of interest identified computationally beforehand—like the largest connected component—and model edges that contribute to this critical substructure separately from other edges of the network. The resulting model can implicitly account for important network features, such as degree correlations or unknown statistics, that drive the connectivity of the substructure. By changing the perspective on the information encoded in stubs, thereby moving some of the complexity of the problem to computational preprocessing, we hope to provide a path toward rich yet simple new models that further the analytical study of complex networks.

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Random networks with a constrained giant component. The core idea of our approach builds upon the classic CM by considering two types of connections: tagging some connections as critically important and therefore following specific rules, and others as less important, subcritical connections. This tagging procedure can be arbitrarily complex, but must result in a joint degree distribution $P(s, c)$ over the “subcritical degree” (s) and “critical degree” (c) of every node. In a physical sense, only the latter will have the potential for supercritical effects under bond percolation, while subcritical connections can only contribute second-order effects.

The critical constraint we explore involves identifying connections that point toward the giant component of a network. Doing so will not only account for the size of that component but also for some of its structure. To see this, consider two nodes of degree 100, both in the giant component, but one has 99 neighbors of degree 1, while the other has none and is part of multiple loops over the giant component. Both nodes are connected to the giant component, but the second more robustly so, and our approach accounts for this difference.

Critical CM. We assume an undirected network where every connection between nodes i and j can be thought of as two directed edges (i, j) and (j, i) . In this case, critical connections are tagged through the following procedure:

- (1) Go over every directed edge (i, j) in the network.
- (2) Temporarily mask all edges pointing toward i , including (j, i) , to avoid backtracking.
- (3) Ask whether the component downstream from (i, j) —that is, the number of nodes k for which at least one path excluding i exists from j to k —is larger than some threshold value (we use 1% of the total number of nodes).
- (4) If yes, increase the critical degree c_i of i by 1. If not, increase the subcritical degree s_i of i by 1.
- (5) Restore all directed edges pointing toward i .
- (6) After going over all pairs, return a distribution $P(s, c)$.

Based on the joint critical-subcritical degree distribution $P(s, c)$, one can then construct a random network that is coherent with the tagging procedure, such that critical degrees in the original network data remain critical in a randomized version of the data. To do so, we rely on the concept of *excess degree*, that is, the number of *other* stubs available when one reaches a node through a given stub. We then define this Critical CM as follows:

- (1) A subcritical stub can only connect with the stub of a node whose excess critical degree is 0.
- (2) A critical stub can only connect with the stub of a node whose excess critical degree is at least 1.

Stubs are otherwise connected uniformly at random. Note that the second rule has a condition based on the excess critical degree of possible neighbors—that is, the number of critical stubs that leave that node—which assures that there exists a giant component that contains all nodes with at least one critical stub, therefore preserving the size of the giant component. The resulting model is illustrated in Fig. 1.

Size of the giant component. We now consider the infinite random network ensemble defined by the aforementioned connection rules and the joint distribution $P(s, c)$ (with everything else random), and compute the expected size of the giant component. We follow a standard approach based on probability-generating functions (PGFs) [17] which, while

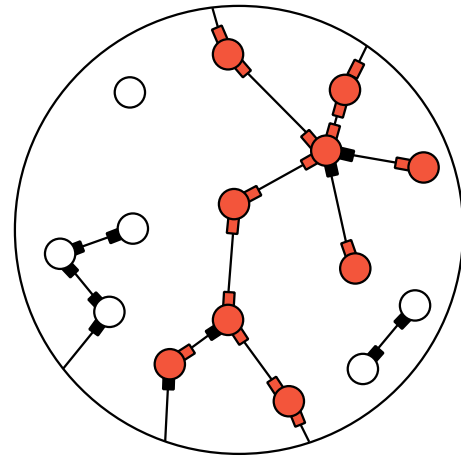


FIG. 1. Illustration of a Critical Configuration Model informed by the giant component of a network. Stubs are tagged as critical (red) and subcritical (black) based on whether they attach the node to the largest connected component. Nodes with a critical degree of at least 1 are then known to be in the giant component, but not all stubs in the giant component are critical, as some lead to dead ends.

very simple, give us an approximate solution to the problem. We highlight where the approximation comes into play and explain the slightly more involved formalism presented in the Supplemental Material [18].

When selecting a node at random in a random network drawn from the Critical CM, it will have a subcritical degree s and a critical degree c drawn from a joint distribution $P(s, c)$, which is generated by

$$G_0(x, y) = \sum_{s,c} P(s, c) x^s y^c. \quad (1)$$

When following any type of stubs, the type of stub through which we reach the neighboring node will be constrained by the excess degree of the reached node. Regardless, the joint degree pair of the reached node will be biased by either its subcritical degree s or critical degree c as per the *friendship paradox*, since a random edge is ten times more likely to reach a node of degree 10 than a node of degree 1. To that effect, we introduce the neighbor-generating function $f(x, y)$:

$$f(x, y) = \frac{\partial G_0(x, y)}{\partial x} + \frac{\partial G_0(x, y)}{\partial y}, \quad (2)$$

which is not normalized and therefore not a PGF.

More specifically, when following a subcritical stub, the connection rules defined previously state that we will reach a node proportionally to its number of subcritical stubs (s), or of critical stubs if it has only one ($c = 1$). The joint excess degree distribution of the reached node is therefore generated by $G_1^s(x, y)$ and written as

$$G_1^s(x, y) = \frac{\sum_{s,c} P(s, c) (\delta_{c,1} x^s + s \delta_{c,0} x^{s-1})}{\sum_{s,c} P(s, c) (\delta_{c,1} + s \delta_{c,0})} = \frac{f(x, 0)}{f(1, 0)}, \quad (3)$$

where $\delta_{a,b}$ is the Kronecker delta equal to 1 if a equals b and 0 otherwise. Note that $G_1^s(x, y)$ does not depend on y , since the critical excess degree of the reached node is 0, as per the connection rules. Similarly, when following a critical stub,

the connection rules state that we reach nodes proportionally to their total degree as long as they have an excess critical degree of at least 1. The joint excess degree distribution of these reached nodes is therefore generated by

$$\begin{aligned} G_1^c(x, y) &= \frac{\sum_{s,c} P(s, c)(c\bar{\delta}_{c,1}x^s y^{c-1} + s\bar{\delta}_{c,0}x^{s-1}y^c)}{\sum_{s,c} P(s, c)(c\bar{\delta}_{c,1} + s\bar{\delta}_{c,0})} \\ &= \frac{f(x, y) - f(x, 0)}{f(1, 1) - f(1, 0)}, \end{aligned} \quad (4)$$

where $\bar{\delta}_{a,b} \equiv 1 - \delta_{a,b}$.

These equations are, unfortunately, only an approximation. The excess degree of the node reached by a random edge depends not only on the type of stub we follow, but also on the type of the node to which that stub belongs. Indeed, while the model did not specify it directly, there are three types of nodes: nodes with zero critical stubs, nodes with a single critical stub, and nodes with more than one critical stub. We provide an exact treatment to account for their different structural roles in the Supplemental Material [18], where we show that the simpler description presented here provides an excellent approximation, nevertheless.

Once we know the distribution of nodes at the end of random stubs, we can then solve for the giant component of the network under a bond percolation process where every edge exists independently with probability p . We denote u_s and u_c the probabilities that a subcritical or critical stub (respectively) does not lead to the giant component. The first, u_s , is fixed to 1 by construction, whereas the second is the solution of the following self-consistent equation:

$$u_c = 1 - p + pG_1^c(1, u_c). \quad (5)$$

In other words, the probability that a critical stub does not lead to the giant component must be equal to the probability that the remaining stubs of the reached node do not lead to the giant component either. This occurs if the critical stub belongs to an edge that has been removed (probability $1 - p$), or, when the edge has not been removed, if none of the *other* critical stubs of the reached node lead to the giant component either (probability $pG_1^c(1, u_c)$). References [10,13,21] provide more details on this self-consistent argument.

Having solved Eq. (5), we may now compute the size of the giant component as the fraction of nodes for which at least one critical stub leads to it. Recalling that an individual critical stub does not lead to the giant component with probability u_c , we find:

$$S = \sum_{s,c} P(s, c)[1 - u_c^c] = 1 - G_0(1, u_c). \quad (6)$$

Notice that $u_c = 0$ is the only nontrivial solution to Eq. (5) when $p = 1$, meaning that the nodes with at least one critical stub will be connected to the giant component with probability 1 in the limit of infinite networks in the absence of damage, as expected. In other words, our model exactly preserves the size of the largest connected component perfectly when all edges exist, and approximates its size under a percolation process ($p < 1$).

Connections with other models. Most, if not all, random network models can be seen as mathematical frameworks used to compress complex network data based on some important

features or constraints. Our approach differs from common models in two ways.

First, instead of calibrating the model based on observed local properties from network data (e.g., degree distribution or degree-degree correlations) and validating the model by predicting the robustness of the corresponding network, the critical CM combines the calibration and validation steps. It uses information about how every node is embedded within the components found in the network data, thereby calibrating the model based on global information (i.e., the size of the largest connected component), and then attempts to extrapolate to the perturbed version of the same network.

Second, calibrating the critical CM requires more computational preprocessing than the CM. It does not merely count edges around every node as in the CM—an operation whose complexity scales as the number of edges E —but tags them all based on some criterion for “critical” connections, which can be costly to evaluate. A naive implementation of the procedure described would scale as E for every edge, and therefore as E^2 for the full preprocessing of a network of E edges.

There is therefore an important conceptual jump from the CM to the critical CM, since we now distinguish types of connections *and* have two different types of stubs informed by *global* connectivity patterns. This is similar to the difference between the CM and the popular Stochastic Block Model, which is meant to capture mesoscopic block or community structure in networks [25], which does not directly translate to a good description of dynamics like percolation [10]. For the critical CM, because we do not need a complicated inference procedure to tag stubs and because the role of one type of stub is fixed by construction (recall that $u_s = 1$), the resulting model is mathematically as complex as the CM, as we only need to solve for a single polynomial self-consistent quantity.

By contrast, state-of-the-art approaches rely on a similar conceptual jump but greatly increase the complexity of the resulting mathematics. The Message Passing Approach (MPA) is based on the idea that all stubs and all edges are distinguishable, and therefore tags the stub from node i leading to node j as a unique edge type $i \rightarrow j$ [22,26]. It then follows a similar calculation: Assuming an infinite number of nodes of any type (i.e., ignoring feedback through loops) whose degree sequence in types of stubs is explicitly given by the adjacency matrix of the true network, we can write a system of $2E$ -coupled self-consistent equations describing percolation on a network with E edges.

Also, depending on the joint distribution $P(s, c)$, the connection rules listed in Sec. II may enforce some level of degree correlation between neighbors. For instance, if only low-degree nodes have $c = 0$, then the critical CM will generate networks with degree correlations differing from that of the classic CM. In a sense, one could also view the critical CM as a crude version of the correlated configuration model [5] or of the Layered Correlated Configuration Model [10]. However, our preliminary investigation did not reveal any systematic relationship between the critical CM and these two models (see Supplemental Material [18]).

The critical CM therefore lies somewhere in between the CM and MPA. It can be seen as a fine-grained version of the CM where stubs are distinguished based on the structure of

the nonbacktracking component to which they lead. Alternatively, the critical CM can be seen as a coarse-graining of the MPA where we compress the $2E$ types of unique connections into only two, again based on the nonbacktracking component to which they lead. By comparing the critical CM to the CM and MPA, we hope to justify the development of more creative random network models. In other words, we can, in theory, efficiently compress mathematical models using network analysis as a preprocessing tool.

Results. We first compare the results of the critical CM to other models and simulations based on the giant component of a common corporate ownership dataset, shown in Fig. 2. This network was chosen because the CM completely fails to match simulations of a percolation process, in large part because the giant component contains a gigantic hub in its periphery. The CM completely overestimates the robustness of the giant component by underestimating the epidemic threshold, while conversely underestimating the final relative size of this giant component at $p = 1$. By comparing to simulations on a connected subset of the CM [20], we can show that by capturing the complete size of the giant component, one also captures the higher-than-expected percolation threshold due to the prevalence of negative degree correlations required for this connectivity (hubs have to connect multiple low-degree nodes). Interestingly, the critical CM does a much better job at capturing the unique structure of this network by accounting not only for the size of the giant component but also for implicit correlations between the degree of nodes and their role in the cohesion of the giant component (the so-called *critical degree*). This highlights how our analytical model differs from a uniform connected subset of the CM, but it is an effective model that captures how the degree sequence of the network interacts with its giant component through the correlations between the degree of a node and its critical degree. In fact, the critical CM mimics results from the MPA very closely while decreasing the number of equations by a factor equal to twice the number of edges (1 versus 9304 self-consistent equations).

We further compare the Critical CM to the classic CM and to simulations for four other connected networks in Fig. 3. These networks were chosen to highlight how the previous results hold in technological networks (e.g., the structure of the Internet) where the connectivity of the empirical networks might be surprising to the CM based on their degree distributions alone. However, in denser networks such as protein-protein interaction networks and social networks, the critical CM offers less of a gain and falls closer to the classic CM. The usefulness of our approach therefore relies on the structure of interest, in this case, the giant component, being surprising to classic random networks.

We can build on this intuition and look at the behavior of the critical CM on regular trees where all nodes have the same degree, up to a certain number of layers L where all nodes have degree one to close the tree. These structures are interesting for three reasons. First, our PGFs assume a treelike structure [most notably in Eq. (5), where we assume all stubs leaving a node are independent] but do not perform well on trees because of their highly constrained structure [10]. Second, the fact that trees are connected as a single component is surprising under the lens of most random net-

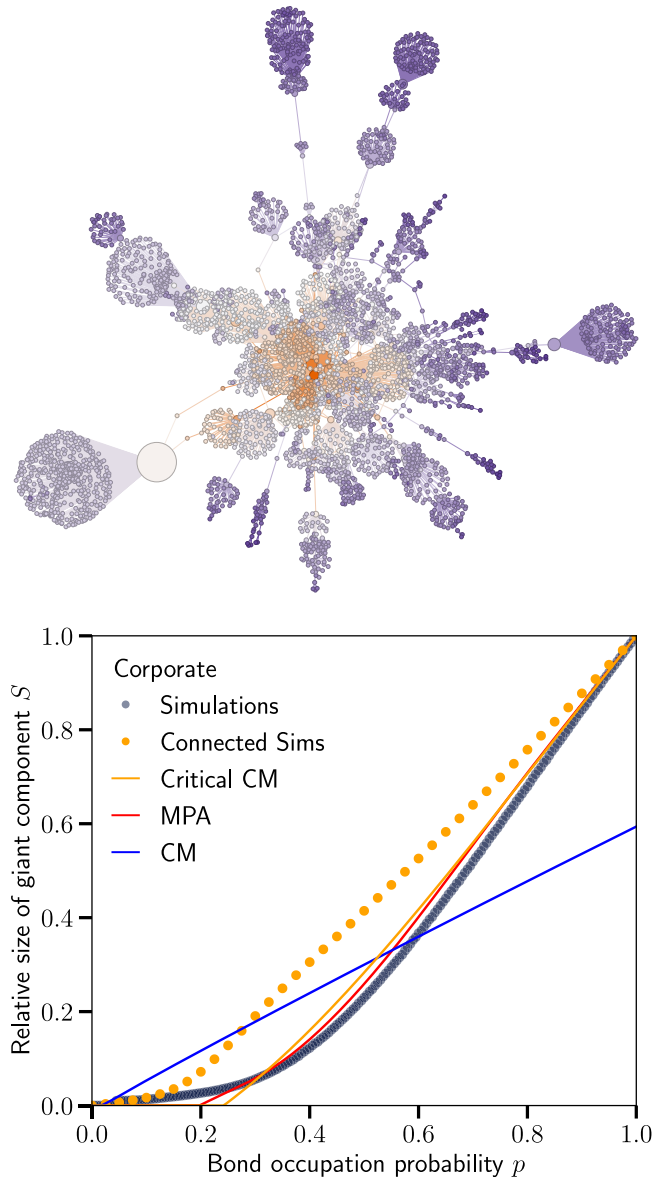


FIG. 2. (Top) The giant component of a corporate ownership network [19]. Node size corresponds to degree (linearly from 1 to 552) and node color corresponds to closeness centrality (inverse of the average distance to other nodes). This is an interesting network structure in part because of its extremely skewed degree distribution, and because its most connected node has a much higher degree than its second most connected (552 vs. 178), but the former is located in the periphery of the network while the latter is located in its core. (Bottom) We simulate bond percolation on this network (Simulations) and compare the results against three analytical models: the Message Passing Approach (MPA; 9304 self-consistent equations), the Configuration Model (CM; 1 self-consistent equation), and our Critical Configuration Model (Critical CM; 1 self-consistent equation). We also compare the results against simulations on a connected subset of the CM (Connected Sims [20]) to show that the critical CM does more than capture the size of the connected component at $p = 1$.

work models, given their high number of nodes of degree one (which explains why configuration models do not perform well on trees). Third, the MPA is exact on trees, where it will see the finite size of the system and exactly predict the

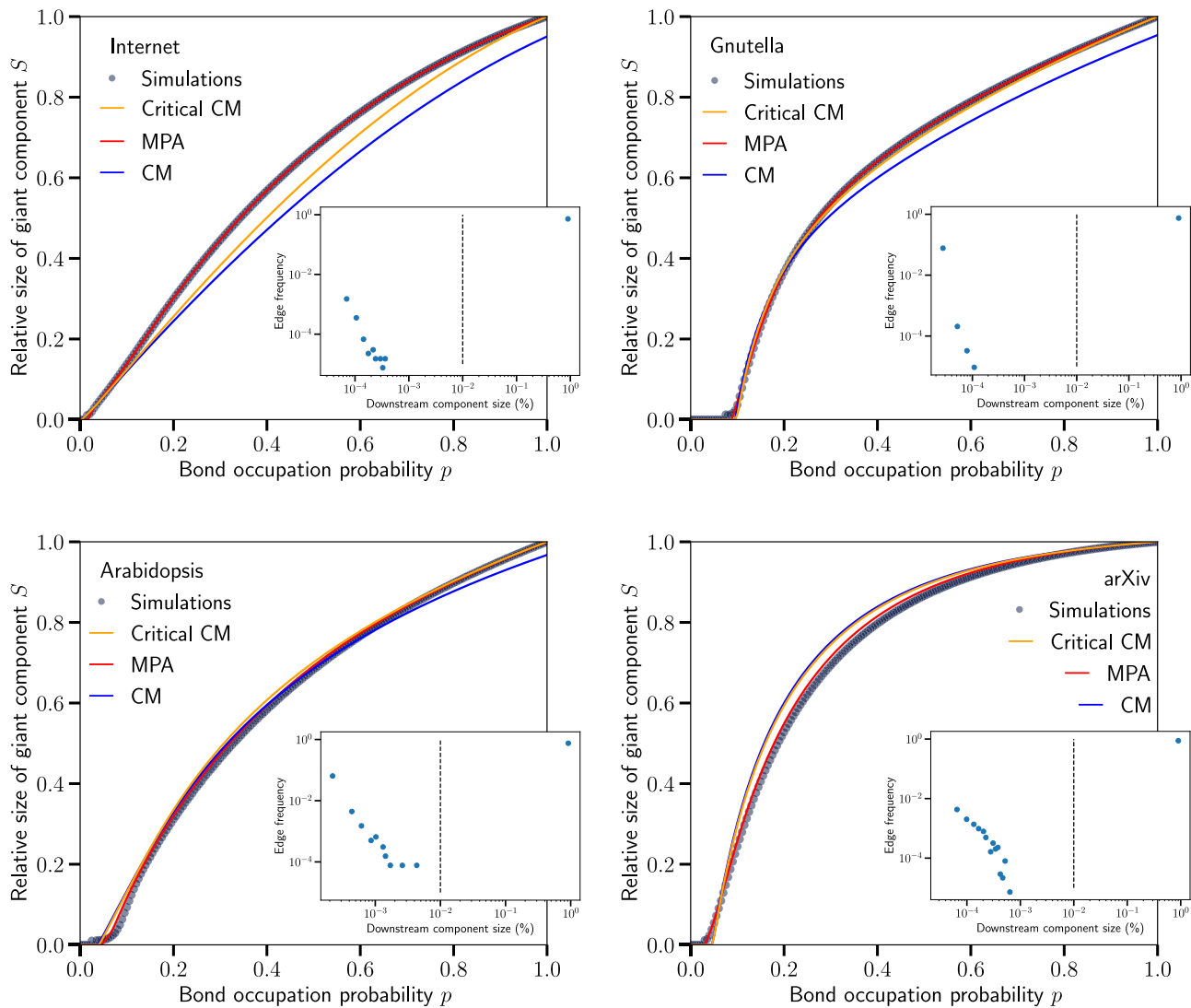


FIG. 3. Bond percolation on the Critical Configuration Model (Critical CM) and Configuration Model (CM) compared with simulations on the giant connected component of: (top left) the structure of the Internet at the level of autonomous systems [22], (top right) the peer-to-peer Gnutella network [23], (bottom left) the Arabidopsis protein-protein interaction network [24], and (bottom right) a coauthorship network from the arXiv preprint archive [17]. The insets show the (binned) distribution of downstream component sizes per directed edge. The distribution is highly bimodal, with edges either leading to a very large macroscopic fraction of the network or to a very small subset of the network. The critical CM is therefore highly robust to the choice of the threshold for criticality, as long as that threshold lies somewhere between 1% and 90% of the entire system.

distribution of small component sizes while predicting the lack of supercritical giant component [26].

The results of the critical CM on regular trees are shown in Fig. 4. As trees grow, only nodes in the first or second layer around the root will have more than one critical stub; all other nodes will have a single critical stub pointing toward the root of the tree. The critical CM therefore creates a very small core of central nodes around which we have directed chains of nodes, all with a single critical stub pointing toward the core. These chains make up the vast majority of nodes, and are always subcritical for $p < 1$ while only the small core can be supercritical. As the relative size of the core vanishes, the critical CM therefore converges to the same prediction as the MPA, but for a conceptually different reason. While MPA sees the finite size of the system, the critical CM instead sees

chains of critical stubs that are subcritical as soon as one edge is removed. Both predict the absence of a phase transition below $p = 1$.

Conclusion. Random network models are used for multiple reasons across network science and beyond. While many problems and dynamical systems are impossible to solve on a fixed network structure, they are often solvable on infinite random network ensembles. When these models work well, we build intuition about which structural constraints matter the most for the problems and dynamics of interest. This, in turn, also allows us to control for important features and therefore provide important null models for network analyses. Indeed, we often need to ask how surprising a network feature is given some other metrics. This is why modularity or even degree assortativity control for degree distribution, using

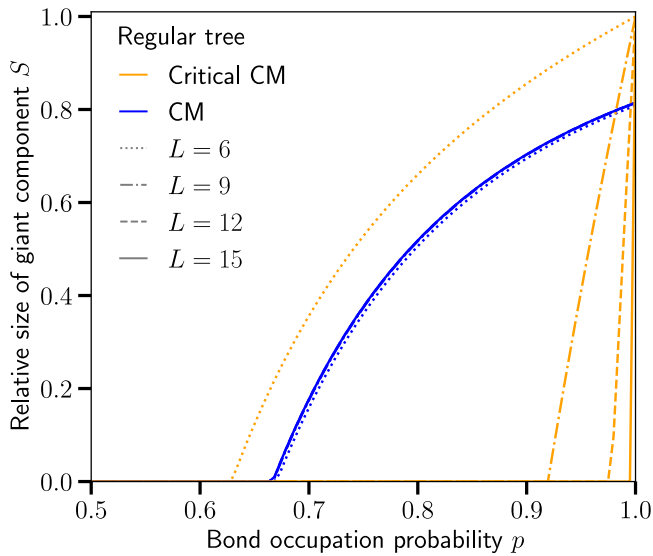


FIG. 4. Comparison of the behavior of the CM and critical CM parametrized by data coming from perfect trees of coordination number 3 and different depths L . As the trees grow, the critical CM converges to directed chains where all nodes have a single critical stub pointing toward the core of the tree. Those chains preserve the treelike structure of the original network and converge to a system of equations that predicts the absence of the giant component for any $T < 1$. This is the same prediction as the MPA, which effectively sees the finite size of the system and therefore does not predict any giant (infinite) connected component [26].

the CM as an underlying null model. Through this pipeline, improvements in random network models improve much of network science.

Given that network scientists often care about global properties of network structures, such as their connectivity and robustness, we need random network models that can control for these features. Unfortunately, most models are only built around simple local connection rules, leaving a significant gap in the network science toolbox. While we certainly do not claim that the critical CM introduced here should become a standard null model for network analyses and mathematical descriptions, it highlights the potential for rethinking the information encoded in the stubs to design models that reproduce ever more realistic network structures. As illustrated here, such a change in perspective may involve a more complicated parametrization requiring computational preprocessing, while nevertheless having a mathematical description that remains parsimonious [27].

Future variations of our approach could consider a parametrization of random networks based on statistics of their minimum spanning tree or dynamical features relevant to network control. Along these lines, we have explored similar models constrained by k -core decomposition in Refs. [8–10]. There remain many more models to explore. This line of research can be summarized as two simple questions: What features do we care about in a given network structure, and how can we best describe networks using these features? And when the answer to the first question is the global connectivity of a network, variations of the critical CM presented here should prove useful.

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