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In the study of networked systems such as biological, technological, and social networks the available data are often uncertain. Rather than knowing the structure of a network exactly, we know the connections between nodes only with a certain probability. In this paper we develop methods for the analysis of such uncertain data, focusing particularly on the problem of community detection. We give a principled maximum-likelihood method for inferring community structure and demonstrate how the results can be used to make improved estimates of the true structure of the network. Using computer-generated benchmark networks we demonstrate that our methods are able to reconstruct known communities more accurately than previous approaches based on data thresholding. We also give an example application to the detection of communities in a protein-protein interaction network.

I. INTRODUCTION

Many systems of scientific interest can be usefully represented as networks and the last few years have seen a surge of interest in the study of networks, due in part to the fruitful application of a range of techniques drawn from physics [1]. Most current techniques for the analysis of networks begin with the assumption that the network data available to us are reliable, a faithful representation of the true structure of the network. But many real-world data sets, perhaps most of them, in fact contain errors and inaccuracies. Thus, rather than representing a network by a set of nodes joined by binary yes-or-no edges, as is commonly done, a more realistic approach would be to specify a probability or likelihood of connection between every pair of nodes, representing our certainty (or uncertainty) about the existence of the corresponding edge. If most of the probabilities are close to zero or one then the data are reliable—for every node pair we are close to being certain that it either is or is not connected by an edge. But if a significant fraction of pairs have a probability that is neither close to zero nor close to one then we are uncertain about the network structure. In recent years an increasing number of network studies have started to provide probabilistic estimates of uncertainty in this way, particularly in the biological sciences.

One simple method for dealing with uncertain networks is *thresholding*: we assume that edges exist whenever their probability exceeds a certain threshold that we choose. In work on protein-protein interaction networks, for example, Krogan *et al.* [2] assembled a sophisticated interaction data set that includes explicit estimates of the likelihood of interaction between every pair of proteins studied. To analyze their data set, however, they then converted it into a conventional binary network by thresholding the likelihoods, followed by traditional network analyses. While this technique can certainly reveal useful information, it has some drawbacks. First, there is the issue of the choice of the threshold level. Krogan *et al.* used a value of 0.273 for their threshold, but there is little doubt that their results would be different if they had chosen a different value and little known about how to choose the value correctly. Second, thresholding throws away potentially useful information. There is a substantial difference between an edge with probability 0.3 and an edge with probability 0.9, but the distinction is lost if one applies a threshold at 0.273—both fall above the threshold and so are considered to be edges. Third, and more subtly, thresholded probability values fail to satisfy certain basic mathematical requirements, meaning that thresholded networks are essentially guaranteed to be wrong, often by a wide margin. If, for instance, we have 100 node pairs connected with probability 0.5 each, then on average we expect 50 of those pairs to be connected by edges. If we place a threshold on the probability values at, say, 0.273, however, then all 100 of them will be converted into edges, a result sufficiently far from the expected value of 50 as to have a very low chance of being correct.

In this paper we develop an alternative and principled approach to the analysis of uncertain network data. We focus in particular on the problem of community detection in networks, one of the best studied analysis tasks. We make use of maximum-likelihood inference techniques, whose application to networks with definite edges is well developed [3–6]. Here we extend those developments to uncertain networks and show that the resulting analyses give significantly better results in controlled tests than thresholding methods. As a corollary, our methods also allow us to estimate which of the uncertain edges in a data set is mostly likely to be a true edge and hence reconstruct, in a probabilistic fashion, the true structure of the underlying network.

A number of authors have looked at related questions in the past. There exists a substantial literature on the analysis of weighted networks, meaning networks in which the positions of the edges are exactly known but the edges carry varying weights, such as strengths, lengths, or volumes of traffic. Such weighted networks are somewhat similar to the uncertain networks studied in this paper—edges can be either strong or weak in a certain sense—but at a deeper level they are different. For instance, the data sets we consider include probabilities of connection for every node pair, whereas weighted networks have weights only for node pairs that are known to be connected by an edge. More importantly, in our uncertain networks we imagine that there is a definite underlying network but that it is not observed; all we see are noisy measurements of the underlying truth. In weighted networks the data are considered to be exact and true and the variation of edge weights represents an actual physical variation in the properties of connections.

Methods for analyzing weighted networks include simple mappings to unweighted networks and generalizations of standard methods to the weighted case [7]. Inference methods, akin to those we use here, have also been applied to the weighted case [8] and to the case of affinity matrices, as used for example in computer vision for image segmentation [9]. A little further afield, Harris and Srinivasan [10] have looked at network failures in a noisy network model in which edges are deleted with uniform probability, while Saade *et al.* [11] use spectral techniques to detect node properties, but not community affiliations, when the underlying network is known but the node properties depend on noisy edge labels. Guimer and Sales-Pardo [12] similarly give a framework for network inference in the presence of noise, but their model assumes one can observe only an unweighted network with possibly erroneous edges. In related work, Xu *et al.* [13] have studied the prediction of edge labels using inference methods and Kurihara *et al.* [14] have applied inference to a case where the data give the frequency of interaction between nodes. Lastly, Bassett *et al.* [15] have studied correlation matrices, which can be view as a type of weighted network, and give a technique for computing the probability that correlations are the result of chance, though this type of data is quite distinct from the edge probabilities studied in this manuscript.

II. METHODS

We focus on the problem of community detection in networks whose structure is uncertain. We suppose that we have data which, rather than specifying with certainty whether there is an edge between two nodes i and j, gives us only a likelihood or probability Q_{ij} that there is an edge. We will assume that the probabilities are independent. Correlated probabilities are certainly possible, but the simple case of independent probabilities already gives many interesting results, as we will see.

At the most basic level our goal is to classify the nodes of the network into non-overlapping communities—groups of nodes with dense connections within groups and sparser connections between groups, also known as "assortative" structure. More generally we may also be interested in disassortative structures in which there are more connections between groups than within them, or mixed structures in which different groups may be either assortative or disassortative within the same network. Conceptually, we assume that even though our knowledge of the network is uncertain, there is a definite underlying network in which each edge either exists or does not, but we cannot see this network. The underlying network is assumed to be undirected and simple (i.e., it has no multi-edges or self-edges). The edge probabilities we observe are a noisy representation of the true network, but they nonetheless can contain information about structure—enough information, as we will see, to make possible the accurate detection of communities in many situations.

Our approach to the detection problem takes the classic form of a statistical inference algorithm. We propose a generative model for uncertain community-structured networks, then fit that model to our observed data. The parameters of the fit tell us about the community structure.

A. The model

The model we use is an extension to the case of uncertain networks of the standard stochastic block model, a random graph model widely used for community structure analyses [3, 16, 17]. In the conventional definition of the stochastic block model, a number n of nodes are distributed at random among k groups, with a probability γ_r of being assigned to group r, where $\sum_{r=1}^{k} \gamma_r = 1$. Then undirected edges are placed independently at random between node pairs with probabilities ω_{rs} that depend only on the groups r, s that a pair belongs to and nothing else. If the diagonal elements ω_{rr} of the probability matrix are significantly larger than the off-diagonal entries then one has traditional assortative community structure, with a higher density of connections within groups than between them. But one can also make the diagonal entries smaller to generate disassortative structure or mixed structure types.

Given the parameters γ_r and ω_{rs}, one can write down the probability, or likelihood, that we generate a particular network in which node i is assigned to group g_i and the placement of the edges is described by an adjacency matrix $\mathbf{A}$ with elements $A_{ij} = 1$ if there is an edge between nodes i and j and 0 otherwise:

$$\begin{aligned} P(\mathbf{A}, \mathbf{g}|\boldsymbol{\gamma}, \boldsymbol{\omega}) &= P(\mathbf{g}|\boldsymbol{\gamma}) P(\mathbf{A}|\mathbf{g}, \boldsymbol{\omega}) \\ &= \prod_i \gamma_{g_i} \prod_{i<j} \omega_{g_i g_j}^{A_{ij}} (1 - \omega_{g_i g_j})^{1-A_{ij}}. \end{aligned} \tag{1}$$

Here $\boldsymbol{\gamma}$ represents the vector of group probabilities γ_r and $\boldsymbol{\omega}$ represents the matrix of probabilities ω_{rs}.

In extending the stochastic block model to uncertain networks we imagine a multi-step process, illustrated in Figs. 1 and 2, in which the network is first generated using the standard stochastic block model and then the definite edges and non-edges are replaced by probabilities, effectively adding noise to the network data. The exact shape of the noise will depend on the detailed effects of the experimental procedure used to measure the network, which we assume to be unknown. We assume only that the edge likelihoods are true probabilities in a sense defined below (see Eq. (4)). Remarkably, however, it still turns out to be possible to perform precise inference on the data.

We represent the noise process by two unknown functions. The function $\beta_1(Q)$ represents the probability density on the interval from 0 to 1 that a true edge between two nodes in the original (unobserved) network gives rise to a measured probability Q of connection between the same nodes in the observed (probabilistic) data. Conversely, the function $\beta_0(Q)$ represents the probability density that a non-edge gives rise to probability Q.

Given these two functions, we can write an expression for the probability (technically, probability density) that a true network represented by adjacency matrix $\mathbf{A}$ gives rise to a matrix of observed edge probabilities $\mathbf{Q} = \{Q_{ij}\}$ thus:

$$P(\mathbf{Q}|\mathbf{A}) = \prod_{i<j} \bigl[\beta_1(Q_{ij})\bigr]^{A_{ij}} \bigl[\beta_0(Q_{ij})\bigr]^{1-A_{ij}}. \tag{2}$$

The crucial observation that makes our calculations possible is that the functions β_0 and β_1 are not independent, because the numbers Q_{ij} that they generate are not just any edge weights but are specifically probabilities and are assumed to be independent. If we were to gather together all node pairs that have probability Q of being connected by an edge, the independence assumption implies that a fraction Q of them on average should in fact be connected by edges and the remainder should be non-edges. For example, 90% of all node pairs with $Q_{ij} = 0.9$ should, in expectation, be connected by edges.

If there are m edges in total in our underlying true network, then there are $m\beta_1(Q)\,\mathrm{d}Q$ edges with observed probability lying between Q and $Q + \mathrm{d}Q$ and $[\binom{n}{2} - m]\beta_0(Q)\,\mathrm{d}Q$ non-edges in the same interval. Hence for every possible value of Q we must have

$$\frac{m\beta_1(Q)\,\mathrm{d}Q}{m\beta_1(Q)\,\mathrm{d}Q + (\binom{n}{2} - m)\beta_0(Q)\,\mathrm{d}Q} = Q. \tag{3}$$

Rearranging, we then find that

$$\frac{\beta_1(Q)}{\beta_0(Q)} = \frac{Q/\rho}{(1-Q)/(1-\rho)}, \tag{4}$$

where

$$\rho = \frac{m}{\binom{n}{2}} \tag{5}$$

is the so-called *density* of the network, the fraction of possible edges that are in fact present. Since we don't know the true network, we don't normally know the value of m, but it can be approximated by the expected number of edges $\sum_{i<j} Q_{ij}$, which becomes an increasingly good estimate as the network gets larger, and from this figure we can calculate ρ.

Note that Eq. (4) implies that $\beta_0(1) = 0$ and $\beta_1(0) = 0$. The equation is also compatible with the choice $\beta_0(Q) = \delta(Q)$, $\beta_1(Q) = \delta(Q-1)$, where $\delta(x)$ is the Dirac delta function, which corresponds to the conventional case of a perfectly certain network with $Q_{ij} = A_{ij}$.

Using Eq. (4) we can now write Eq. (2) as

$$P(\mathbf{Q}|\mathbf{A}) = \prod_{i<j} \frac{1-\rho}{1-Q_{ij}} \beta_0(Q_{ij}) \times \prod_{i<j} \biggl(\frac{Q_{ij}}{\rho}\biggr)^{A_{ij}} \biggl(\frac{1-Q_{ij}}{1-\rho}\biggr)^{1-A_{ij}}. \tag{6}$$

The first product is a constant for any given set of observed probabilities $\mathbf{Q}$ and hence will have no effect on our maximum-likelihood calculations (which depend only on the position of the likelihood maximum and not on its absolute value). Henceforth, we will neglect this factor. Then we combine Eqs. (1) and (6) to get an expression for the likelihood of the data $\mathbf{Q}$ and the community assignments $\mathbf{g}$, neglecting constants and given the model parameters $\boldsymbol{\gamma}$ and $\boldsymbol{\omega}$:

$$\begin{aligned} P(\mathbf{Q},\mathbf{g}|\boldsymbol{\gamma},\boldsymbol{\omega}) &= \sum_{\mathbf{A}} P(\mathbf{Q}|\mathbf{A}) P(\mathbf{A},\mathbf{g}|\boldsymbol{\gamma},\boldsymbol{\omega}) \\ &= \prod_i \gamma_{g_i} \prod_{i<j} \sum_{A_{ij}=0,1} \biggl[\frac{Q_{ij}\omega_{g_i g_j}}{\rho}\biggr]^{A_{ij}} \biggl[\frac{(1-Q_{ij})(1-\omega_{g_i g_j})}{1-\rho}\biggr]^{1-A_{ij}} \\ &= \prod_i \gamma_{g_i} \prod_{i<j} \biggl[\frac{Q_{ij}\omega_{g_i g_j}}{\rho} + \frac{(1-Q_{ij})(1-\omega_{g_i g_j})}{1-\rho}\biggr]. \end{aligned} \tag{7}$$

Our goal is now, given a particular set of observed data $\mathbf{Q}$, to maximize this likelihood to find the best-fit parameters $\boldsymbol{\gamma}$ and $\boldsymbol{\omega}$. In the process we will determine the community assignments $\mathbf{g}$ as well (which are frequently the primary objects of interest).

B. Fitting to empirical data

Fitting the model to an observed but uncertain network, represented by the probabilities Q_{ij}, means determining the values of the parameters $\boldsymbol{\gamma}$ and $\boldsymbol{\omega}$ that maximize the probability of generating the particular data we see. In other words, we want to maximize the *marginal likelihood* of the data given the parameters:

$$P(\mathbf{Q}|\boldsymbol{\gamma},\boldsymbol{\omega}) = \sum_{\mathbf{g}} P(\mathbf{Q},\mathbf{g}|\boldsymbol{\gamma},\boldsymbol{\omega}). \tag{8}$$

Equivalently, we can maximize the logarithm of this quantity, which gives the same result (since the logarithm is a monotone function) but is often easier.

Direct maximization by differentiation gives rise to a set of implicit equations that have no simple solution, so

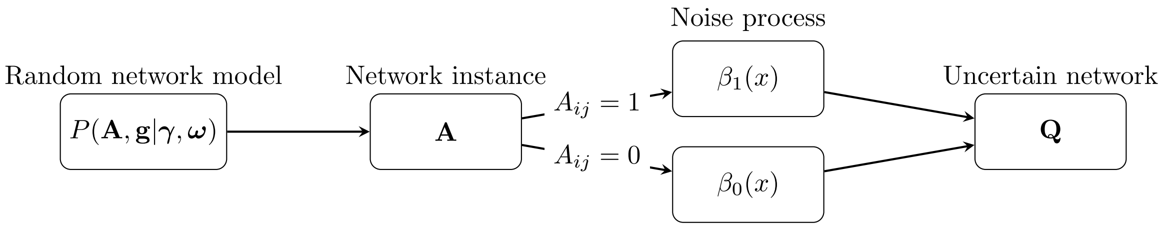


FIG. 1: The model of uncertain network generation used in our calculations. A community assignment **g** and network **A** are drawn from a random network model such as the stochastic blockmodel. The experimental uncertainty is represented by giving each pair of nodes i, j a probability Q_{ij} of being connected by an edge, drawn from different distributions for edges $A_{ij} = 1$ and non-edges $A_{ij} = 0$.

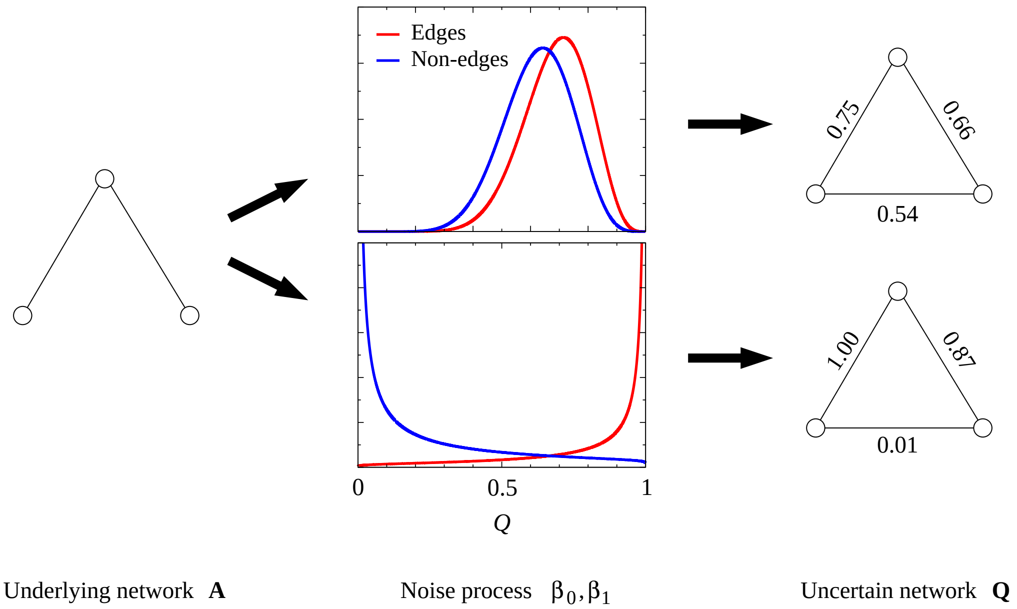


FIG. 2: Simple example of the generation of two uncertain networks from an initial network with three nodes. The two networks generated (right-hand side) differ only in their noise distributions, $\beta_0(Q)$ and $\beta_1(Q)$, whose probability density functions (PDFs) are shown in the center. The upper pair of distributions corresponds to a low-noise setting in which the PDFs for edges and non-edges are quite distinct and the resulting probability matrix **Q** retains most of the information from the original adjacency matrix **A**. The lower pair of distributions corresponds to a high-noise setting in which the two PDFs are almost the same and the final matrix **Q** retains little of the original network structure.

instead we employ a standard trick from the statistics toolbox and apply *Jensen's inequality*, which says that for any set of positive-definite quantities x_i, the log of their sum satisfies

$$\log\sum_i x_i \geq \sum_i q_i \log\frac{x_i}{q_i}, \tag{9}$$

where q_i is any probability distribution over i satisfying the normalization condition $\sum_i q_i = 1$. One can easily verify that the exact equality is achieved by choosing

$$q_i = \frac{x_i}{\sum_i x_i}. \tag{10}$$

Applying Jensen's inequality to (8), we get

$$\begin{aligned}\log P(\mathbf{Q}|\boldsymbol{\gamma},\boldsymbol{\omega}) &\geq \sum_{\mathbf{g}} q(\mathbf{g}) \log \frac{P(\mathbf{Q},\mathbf{g}|\boldsymbol{\gamma},\boldsymbol{\omega})}{q(\mathbf{g})} \\ &= \sum_{\mathbf{g}} q(\mathbf{g}) \sum_i \log \gamma_{g_i} + \tfrac{1}{2} \sum_{\mathbf{g}} q(\mathbf{g}) \sum_{ij} \log\biggl[\frac{Q_{ij}\omega_{g_ig_j}}{\rho} + \frac{(1-Q_{ij})(1-\omega_{g_ig_j})}{1-\rho}\biggr] - \sum_{\mathbf{g}} q(\mathbf{g}) \log q(\mathbf{g}) \\ &= \sum_i \sum_r q_r^i \log \gamma_r + \tfrac{1}{2} \sum_{ij} \sum_{rs} q_{rs}^{ij} \log\biggl[\frac{Q_{ij}\omega_{rs}}{\rho} + \frac{(1-Q_{ij})(1-\omega_{rs})}{1-\rho}\biggr] - \sum_{\mathbf{g}} q(\mathbf{g}) \log q(\mathbf{g}), \qquad (11)\end{aligned}$$

where q_r^i is the marginal probability within the probability distribution $q(\mathbf{g})$ that node i belongs to community r:

$$q_r^i = \sum_{\mathbf{g}} q(\mathbf{g}) \delta_{g_i,r}, \qquad (12)$$

and q_{rs}^{ij} is the joint marginal probability that nodes i and j belong to communities r and s respectively:

$$q_{rs}^{ij} = \sum_{\mathbf{g}} q(\mathbf{g}) \delta_{g_i,r} \delta_{g_j,s}, \qquad (13)$$

with δ_{ij} being the Kronecker delta.

Following Eq. (10), the exact equality in (11), and hence the maximum of the right-hand side, is achieved when

$$\begin{aligned} q(\mathbf{g}) &= \frac{P(\mathbf{Q},\mathbf{g}|\boldsymbol{\gamma},\boldsymbol{\omega})}{\sum_{\mathbf{g}} P(\mathbf{Q},\mathbf{g}|\boldsymbol{\gamma},\boldsymbol{\omega})} \\ &= \frac{\prod_i \gamma_{g_i} \prod_{i<j} \Bigl[\frac{Q_{ij}\omega_{g_ig_j}}{\rho} + \frac{(1-Q_{ij})(1-\omega_{g_ig_j})}{1-\rho}\Bigr]}{\sum_{\mathbf{g}} \prod_i \gamma_{g_i} \prod_{i<j} \Bigl[\frac{Q_{ij}\omega_{g_ig_j}}{\rho} + \frac{(1-Q_{ij})(1-\omega_{g_ig_j})}{1-\rho}\Bigr]}. \end{aligned} \qquad (14)$$

Thus, calculating the maximum of the left-hand side of (11) with respect to the parameters $\boldsymbol{\gamma}, \boldsymbol{\omega}$ is equivalent to a double maximization of the right-hand side with respect to $q(\mathbf{g})$ (by choosing the value above) so as to make the two sides equal, and then with respect to the parameters. At first sight, this seems to make the problem more complex, but numerically it is in fact easier—the double maximization can be achieved in a relatively straightforward manner by alternately maximizing with respect to $q(\mathbf{g})$ using Eq. (14) and then with respect to the parameters. Such alternate maximizations can trivially be shown always to converge to a local maximum of the log-likelihood. They are not guaranteed to find the global maximum, however, so commonly we repeat the entire calculation several times from different starting points and choose among the results the one which gives the highest value of the likelihood.

Once we have converged to the maximum, the final value of the probability distribution $q(\mathbf{g})$ is given by Eq. (14) to be

$$q(\mathbf{g}) = \frac{P(\mathbf{Q},\mathbf{g}|\boldsymbol{\gamma},\boldsymbol{\omega})}{P(\mathbf{Q}|\boldsymbol{\gamma},\boldsymbol{\omega})} = P(\mathbf{g}|\mathbf{Q},\boldsymbol{\gamma},\boldsymbol{\omega}). \qquad (15)$$

In other words, $q(\mathbf{g})$ is the posterior distribution over community assignments $\mathbf{g}$ given the observed data $\mathbf{Q}$ and the model parameters. Thus, in addition to telling us the values of the parameters, our calculation tells us the probability of any assignment of nodes to communities. Specifically, the one-node marginal probability q_r^i, Eq. (12), tells us the probability that node i belongs to community r and, armed with this information, we can calculate the most probable community that each node belongs to, which is the primary goal of our calculation. These marginals also allow us to assess the strength of our community structure, as when the data poorly support community structure the posterior distribution simply becomes uniform.

We still need to perform the maximization of (11) over the parameters. We note first that the final sum is independent of either $\boldsymbol{\gamma}$ or $\boldsymbol{\omega}$ and hence can be neglected. Maximization of the remaining terms with respect to $\boldsymbol{\gamma}$ is straightforward. Differentiating with respect to γ_r, subject to the normalization condition $\sum_r \gamma_r = 1$, gives

$$\gamma_r = \frac{1}{n} \sum_i q_r^i. \qquad (16)$$

Maximization with respect to $\boldsymbol{\omega}$ is a little more tricky. Only the second term in (11) depends on $\boldsymbol{\omega}$, but direct differentiation of this term yields a difficult equation, so instead we apply Jensen's inequality (9) again, giving

$$\sum_{ij} \sum_{rs} q_{rs}^{ij} \log\biggl[\frac{Q_{ij}\omega_{rs}}{\rho} + \frac{(1-Q_{ij})(1-\omega_{rs})}{1-\rho}\biggr] \geq \sum_{ij} \sum_{rs} q_{rs}^{ij} \biggl[t_{rs}^{ij} \log \frac{Q_{ij}\omega_{rs}}{\rho t_{rs}^{ij}} + (1-t_{rs}^{ij}) \log \frac{(1-Q_{ij})(1-\omega_{rs})}{(1-\rho)(1-t_{rs}^{ij})}\biggr], \qquad (17)$$

where t_{rs}^{ij} is any number between zero and one.

The exact equality, and hence the maximum of the right-hand side, is achieved when

$$t_{rs}^{ij} = \frac{Q_{ij}\omega_{rs}/\rho}{Q_{ij}\omega_{rs}/\rho + (1-Q_{ij})(1-\omega_{rs})/(1-\rho)}. \tag{18}$$

Thus, by the same argument as previously, we can maximize the left-hand side of (17) by repeatedly maximizing the right-hand side with respect to t_{rs}^{ij} using Eq. (18) and with respect to ω_{rs} by differentiation. Performing the derivative and setting the result to zero, we find that the maximum with respect to ω_{rs} falls at

$$\omega_{rs} = \frac{\sum_{ij} q_{rs}^{ij} t_{rs}^{ij}}{\sum_{ij} q_{rs}^{ij}}. \tag{19}$$

The optimal values of the ω_{rs} can now be calculated by iterating Eqs. (18) and (19) alternately to convergence from a suitable initial condition.

The quantity t_{rs}^{ij} has a simple physical interpretation, as we can see by applying Eq. (4) to (18), giving

$$t_{rs}^{ij} = \frac{\omega_{rs}\beta_1(Q_{ij})}{\omega_{rs}\beta_1(Q_{ij}) + (1-\omega_{rs})\beta_0(Q_{ij})}. \tag{20}$$

But by definition

$$\omega_{rs} = P(A_{ij}=1|g_i=r, g_j=s), \tag{21}$$

$$\beta_1(Q_{ij}) = P(Q_{ij}|A_{ij}=1), \tag{22}$$

$$\beta_0(Q_{ij}) = P(Q_{ij}|A_{ij}=0), \tag{23}$$

and hence

$$\begin{aligned} t_{rs}^{ij} &= \frac{P(A_{ij}=1|g_i=r,g_j=s)P(Q_{ij}|A_{ij}=1)}{P(Q_{ij}|g_i=r,g_j=s)} \\ &= P(A_{ij}=1|Q_{ij},g_i=r,g_j=s). \end{aligned} \tag{24}$$

In other words, t_{rs}^{ij} is the posterior probability that there is an edge between nodes i and j, given that they are in groups r and s respectively. This quantity will be useful shortly when we consider the problem of reconstructing a network from uncertain observations.

We now have a complete algorithm for fitting our model to the observed data. The steps of the algorithm are as follows:

1. Make an initial guess (for instance at random) for the values of the parameters $\boldsymbol{\gamma}$ and $\boldsymbol{\omega}$.

2. Calculate the distribution $q(\mathbf{g})$ from Eq. (14).

3. Calculate the one- and two-node marginal probabilities q_r^i and q_{rs}^{ij} from Eqs. (12) and (13).

4. From these quantities calculate updated values of $\boldsymbol{\gamma}$ from Eq. (16) and $\boldsymbol{\omega}$ by iterating Eqs. (18) and (19) to convergence starting from the current estimate of $\boldsymbol{\omega}$.

5. Repeat from step 2 until $q(\mathbf{g})$ and the model parameters converge.

Algorithms of this type are known as expectation–maximization or EM algorithms [18, 19]. The end result is a maximum likelihood estimate of the parameters $\boldsymbol{\gamma}$ and $\boldsymbol{\omega}$ along with the posterior distribution over community assignments $q(\mathbf{g})$ and the probability t_{rs}^{ij} of an edge between any pair of nodes.

Equation (19) can usefully be simplified a little further, in two ways. First, note that Eq. (18) implies that $t_{rs}^{ij} = 0$ whenever $Q_{ij} = 0$. All of the real-world data sets we have examined are *sparse*, meaning that a large majority of the probabilities Q_{ij} are zero. This means that most of the terms in the numerator of (19) vanish and can be dropped from the sum, which speeds up the calculation considerably. Indeed t_{rs}^{ij} need not be evaluated at all for node pairs i, j such that $Q_{ij} = 0$, since this sum is the only place that t_{rs}^{ij} appears in our calculation. Moreover it turns out that we need not evaluate q_{rs}^{ij} for such node pairs either. The only other place that q_{rs}^{ij} appears is in the denominator of Eq. (19), which can be simplified by using Eq. (13) to rewrite it thus:

$$\sum_{ij} q_{rs}^{ij} = \sum_{g} q(\mathbf{g}) \sum_i \delta_{g_i,r} \sum_j \delta_{g_j,s} = \langle n_r n_s \rangle, \tag{25}$$

where $\langle \ldots \rangle$ indicates an average over $q(\mathbf{g})$ and $n_r = \sum_i \delta_{g_i,r}$ is the number of nodes in group r, for community assignment $\mathbf{g}$. For large networks the number of nodes in a group becomes tightly peaked about its mean value so that $\langle n_r n_s \rangle \simeq \langle n_r \rangle \langle n_s \rangle$ where $\langle n_r \rangle = \sum_{\mathbf{g}} q(\mathbf{g}) \sum_i \delta_{g_i,r} = \sum_i q_r^i$. Hence

$$\omega_{rs} = \frac{\sum_{ij} q_{rs}^{ij} t_{rs}^{ij}}{\sum_i q_r^i \sum_j q_s^j}. \tag{26}$$

This obviates the need to calculate q_{rs}^{ij} for node pairs such that $Q_{ij} = 0$ (which is most node pairs), and in addition speeds the calculation further because the denominator can now be evaluated in time proportional to the number of nodes in the network, rather than the number of nodes squared, as in Eq. (19). (And the numerator can be evaluated in time proportional to the number of nonzero Q_{ij}, which is small.)

C. Belief propagation

In principle, the methods of the previous section constitute a complete algorithm for fitting our model to observed network data. In practice, however, it is an impractical one because it's unreasonably slow. The bottleneck is the sum in the denominator of Eq. (14), which is a sum over all possible assignments $\mathbf{g}$ of nodes to communities. If there are n nodes and k communities then there are k^n possible assignments, a number that grows with n so rapidly as to prohibit explicit numerical evaluation of the sum for all but the smallest of networks.

This is not a new problem. It is common to most EM algorithms, not only for network applications but for statistics in general. The traditional way around it is to approximate the distribution $q(\mathbf{g})$ by importance sampling using Markov chain Monte Carlo. In this paper, however, we use a different method, proposed recently by Decelle *et al.* [6, 20] and specific to networks, namely belief propagation.

Originally developed in physics and computer science for the probabilistic solution of problems on graphs and lattices [21, 22], belief propagation is a message passing method in which the nodes of a network exchange messages or "beliefs," which are probabilities representing the current best estimate of the solution to the problem of interest. In the present case we define a message $\eta_r^{i\to j}$ which is equal to the probability that node i belongs to community r if node j is removed from the network. The removal of a node is crucial, since it allows us to write a self-consistent set of equations satisfied by the messages, whose solution gives us the distribution $q(\mathbf{g})$ over group assignments. Although the equations can without difficulty be written exactly and in full, we will here approximate them to leading order only in the small quantities ω_{rs}. We find this approximation to give excellent results in our applications and the equations are considerably simpler, as well as giving a faster final algorithm.

Within this approximation, the belief propagation equation for the message $\eta_r^{i\to j}$ is:

$$\eta_r^{i\to j} = \frac{\gamma_r}{Z_{i\to j}} \exp\biggl(-\sum_{k,s} q_s^k \omega_{rs}\biggr) \prod_{\substack{k(\neq j)\\ Q_{ik}\neq 0}} \sum_s \eta_s^{k\to i} \biggl[\frac{Q_{ik}\omega_{rs}}{\rho} + \frac{(1-Q_{ik})(1-\omega_{rs})}{1-\rho}\biggr], \tag{27}$$

where $Z_{i\to j}$ is a normalization coefficient that ensures $\sum_r \eta_r^{i\to j} = 1$, having value

$$Z_{i\to j} = \sum_r \gamma_r \exp\biggl(-\sum_{k,s} q_s^k \omega_{rs}\biggr) \prod_{\substack{k(\neq j)\\ Q_{ik}\neq 0}} \sum_s \eta_s^{k\to i} \biggl[\frac{Q_{ik}\omega_{rs}}{\rho} + \frac{(1-Q_{ik})(1-\omega_{rs})}{1-\rho}\biggr], \tag{28}$$

and q_r^i is, as before, the one-node marginal probability of Eq. (12), which can itself be conveniently calculated directly from the messages $\eta_r^{i\to j}$ via

$$q_r^i = \frac{\gamma_r}{Z_i} \exp\biggl(-\sum_{j,s} q_s^j \omega_{rs}\biggr) \prod_{\substack{j\\ Q_{ij}\neq 0}} \sum_s \eta_s^{j\to i} \biggl[\frac{Q_{ij}\omega_{rs}}{\rho} + \frac{(1-Q_{ij})(1-\omega_{rs})}{1-\rho}\biggr], \tag{29}$$

with

$$Z_i = \sum_r \gamma_r \exp\biggl(-\sum_{j,s} q_s^j \omega_{rs}\biggr) \prod_{\substack{j\\ Q_{ij}\neq 0}} \sum_s \eta_s^{j\to i} \biggl[\frac{Q_{ij}\omega_{rs}}{\rho} + \frac{(1-Q_{ij})(1-\omega_{rs})}{1-\rho}\biggr]. \tag{30}$$

These equations are exact if the set of node pairs i, j with edge probabilities $Q_{ij} > 0$ forms a tree or is at least locally tree-like (meaning that arbitrarily large local neighborhoods take the form of trees in the limit of large network size). For non-trees, which includes most real-world networks, they are only approximate, but previous results from a number of studies show the approximation to be a good one in practice [6, 20, 22–25]. Probability data of the kind we consider might further deviate from a strict tree-like form if they include a large number of low-probability edges, but nonetheless we find the belief propagation method to work well.

Solution of the equations is by iteration. Typically we start from the current best estimate of the values of the beliefs and iterate to convergence, then from the converged values we calculate the crucial two-node marginal probability q_{rs}^{ij} by noting that

$$\begin{aligned} q_{rs}^{ij} &= P(g_i = r, g_j = s|Q_{ij}) \\ &= \frac{P(g_i = r, g_j = s)P(Q_{ij}|g_i = r, g_j = s)}{\sum_{rs} P(g_i = r, g_j = s)P(Q_{ij}|g_i = r, g_j = s)}. \end{aligned} \tag{31}$$

where all data $\mathbf{Q}$ other than Q_{ij} are assumed given in each probability. The probabilities in these expressions are equal to

$$P(g_i = r, g_j = s) = \eta_r^{i\to j}\eta_s^{j\to i}, \tag{32}$$

$$\begin{aligned} P(Q_{ij}|g_i = r, g_j = s) &= \beta_0(Q_{ij}) \frac{1-\rho}{1-Q_{ij}} \\ &\quad \times \biggl[\frac{Q_{ij}\omega_{rs}}{\rho} + \frac{(1-Q_{ij})(1-\omega_{rs})}{1-\rho}\biggr]. \end{aligned} \tag{33}$$

Substituting these into (31), we get

$$q_{rs}^{ij} = \frac{\eta_r^{i\to j}\eta_s^{j\to i}\left[\frac{Q_{ij}\omega_{rs}}{\rho} + \frac{(1-Q_{ij})(1-\omega_{rs})}{1-\rho}\right]}{\sum_{rs}\eta_r^{i\to j}\eta_s^{j\to i}\left[\frac{Q_{ij}\omega_{rs}}{\rho} + \frac{(1-Q_{ij})(1-\omega_{rs})}{1-\rho}\right]}. \tag{34}$$

Our final algorithm then consists of alternately (a) iterating the belief propagation equations (27) to convergence and using the results to calculate the marginal probabilities q_r^i and q_{rs}^{ij} from Eqs. (29) and (34), and (b) iterating Eqs. (18) and (26) to convergence to calculate new values of the ω_{rs} and using Eq. (16) to calculate new values of γ_r. In practice the algorithm is efficient—in other tests of belief propagation it has been found fast enough for applications to networks of a million nodes or more.

D. Degree-corrected model

Our method gives a complete algorithm for fitting the standard stochastic block model to uncertain network data represented by the matrix $\mathbf{Q}$ of edge probabilities. As pointed out previously by Karrer and Newman [17], however, the stochastic block model gives poor performance for community detection on many real-world networks because the model assumes a Poisson degree distribution, which is strongly in conflict with the broad, frequently fat-tailed degree distributions seen in real-world networks. Because of this conflict it is often not possible to find a good fit of the stochastic block model to observed network data, for any parameter values, and in such cases the model can return poor performance on community detection tasks.

The fix for this problem is straightforward. The *degree-corrected stochastic block model* is identical to the standard block model except that the probability of an edge between nodes i, j that fall in groups r, s is $d_i d_j \omega_{rs}$ (instead of just ω_{rs}), where d_i is the observed degree of node i in the network. This modification allows the model to accurately fit arbitrary degree distributions, and community detection algorithms that perform fits to the degree-corrected model are found to return excellent results in real-world applications [17].

We can make the same modification to our methods as well. The developments follow exactly the same lines as for the ordinary (uncorrected) stochastic block model. The crucial equations (18) and (26) become

$$t_{rs}^{ij} = \frac{Q_{ij}d_i d_j\omega_{rs}/\rho}{Q_{ij}d_i d_j\omega_{rs}/\rho + (1-Q_{ij})(1-d_i d_j\omega_{rs})/(1-\rho)} \tag{35}$$

and

$$\omega_{rs} = \frac{\sum_{ij} q_{rs}^{ij} t_{rs}^{ij}}{\sum_i d_i q_r^i \sum_j d_j q_s^j}, \tag{36}$$

while the belief propagation equation (27) becomes

$$\eta_r^{i\to j} = \frac{\gamma_r}{Z_{i\to j}}\exp\biggl(-d_i d_j \sum_{k,s} q_s^k \omega_{rs}\biggr) \times \prod_{\substack{k(\neq j)\\ Q_{ik}\neq 0}} \sum_s \eta_s^{k\to i}\biggl[\frac{Q_{ik}d_i d_j\omega_{rs}}{\rho} + \frac{(1-Q_{ik})(1-d_i d_j\omega_{rs})}{1-\rho}\biggr], \tag{37}$$

with corresponding modifications to Eqs. (28) to (30) and Eq. (34).

In the following sections we describe a number of example applications of our methods. Among these, the tests on synthetic networks (Section III A) are performed using the standard stochastic block model, without degree-correction, while the tests on real-world networks (Section III B) use the degree-corrected version.

III. RESULTS

We have tested the methods described in the previous sections both on computer-generated benchmark networks with known structure and on real-world examples.

A. Synthetic networks

Computer-generated or “synthetic” networks provide a controlled test of the performance of our algorithm. We generate networks with known community structure planted within them and then test whether the algorithm is able accurately to detect that structure.

For the tests reported here, we generate networks using the standard (not degree-corrected) stochastic block model and then add noise to them to represent the network uncertainty, using functions β_0 and β_1 as defined in Section II A. We use networks of size $n = 4000$ nodes, divided into two equally-size communities, and as the noise function $\beta_1(Q)$ for the edges we use a beta distribution:

$$\beta_1(Q) = \frac{Q^{a_1-1}(1-Q)^{b_1-1}}{\mathrm{B}(a_1,b_1)}, \tag{38}$$

where $\mathrm{B}(a,b)$ is Euler's beta function. As the noise function $\beta_0(Q)$ for the non-edges we use a beta function plus an additional delta-function spike at zero:

$$\beta_0(Q) = c\frac{Q^{a_0-1}(1-Q)^{b_0-1}}{\mathrm{B}(a_0,b_0)} + (1-c)\delta(Q). \tag{39}$$

The delta function makes the matrix $\mathbf{Q}$ of edge probabilities realistically sparse, in keeping with the structure of real-world data sets, with a fraction $1-c$ of non-edges having exactly zero probability in the observed data, on average.

Thus there are a total of five parameters in our noise functions: a_0, b_0, a_1, b_1, and c. Not all of these parameters are independent, however, because our functions still have to satisfy the constraint (4). Substituting Eqs. (38) and (39) into (4), we see that for the constraint to be satisfied for all $Q > 0$ we must have $a_0 = a_1 - 1$, $b_0 = b_1 + 1$, and

$$c = \frac{1-\rho}{\rho}\,\frac{\mathrm{B}(a_1,b_1)}{\mathrm{B}(a_0,b_0)} = \frac{1-\rho}{\rho}\,\frac{\mathrm{B}(a_1,b_1)}{\mathrm{B}(a_1-1,b_1+1)} = \frac{1-\rho}{\rho}\,\frac{a_1-1}{b_1}. \tag{40}$$

Thus there are really just two degrees of freedom in the choice of the noise functions. Once we fix the parameters a_1 and b_1, everything else is fixed also. Alternatively, we can fix the parameter c, thereby fixing the density of the data matrix $\mathbf{Q}$, plus one or other of the parameters a_1 and b_1.

The networks we generate are now analyzed using the non-degree-corrected algorithm of Sections II A to II C. To quantify performance we assign each node i to the community r for which its probability q_r^i of membership, Eq. (12), as computed by the algorithm, is greatest, then compare the result to the known true community assignments from which the network was generated. Success (or lack of it) is quantified by computing the fraction of nodes placed by the algorithm in the correct groups. We also compare the results against the naive (but common) thresholding method discussed in the introduction [2], in which edge probabilities Q_{ij} are turned into binary yes-or-no edges by cutting them off at some fixed threshold τ, so that the adjacency matrix element A_{ij} is 1 if and only if $Q_{ij} > \tau$. Community structure in the thresholded network is analyzed using the standard stochastic block model algorithm described in, for example, Refs. [6] and [20].

As we vary the parameters of the underlying network and noise functions the performance of both algorithms varies. When the community structure is strong and the noise is weak both algorithms (not surprisingly) do well, recovering the community structure nearly perfectly, while for weak enough community structure or strong noise neither algorithm does better than chance. But, as shown in Fig. 3a, there is a regime of intermediate structure and noise in which our algorithm does significantly better than the naive technique. The figure shows the fraction of correctly classified nodes in the naive algorithm as a function of the threshold τ (data points in the figure) compared against the performance of the algorithm of this paper (dashed line) and, as we can see, the latter outperforms the former no matter what value of τ is used. Note that the worst possible performance still classifies a half of the nodes correctly—even a random coin toss would get this many right—so this is the minimum value on the plot. For high threshold values τ approaching one, the threshold method throws away essentially all edges, leaving itself no data to work with, and hence does little better than chance. Conversely for low thresholds the threshold method treats any node pair with a nonzero connection probability Q_{ij} as having an edge, even when an edge is wildly unlikely, thereby introducing large amounts of noise into the calculation that again reduce performance to a level little better than chance. The optimal performance falls somewhere between these two extremes, around $\tau = 0.25$ in this case, but even at this optimal point the thresholding method's performance falls far short of the algorithm of this paper.

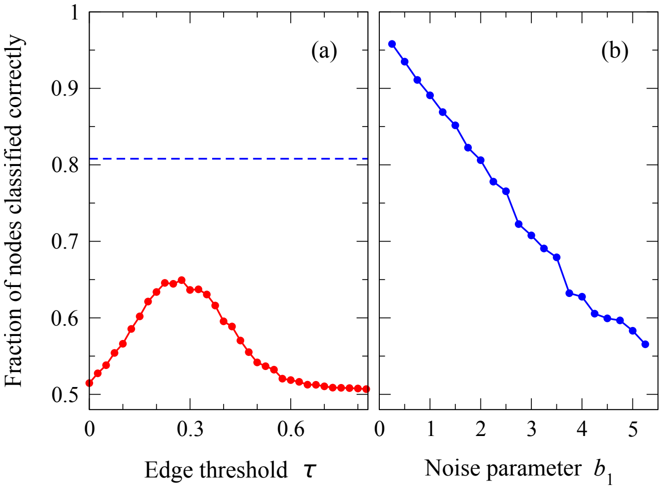


FIG. 3: (Color online) Tests of the method described in this paper on synthetic benchmark networks. (a) Fraction of nodes placed in the correct community for uncertain networks generated using a stochastic block model with $n = 4000$ nodes, two groups of equal size, edge probabilities $\omega_{11} = \omega_{22} = 0.02$, $\omega_{12} = \omega_{21} = 0.014$, and noise parameters $a_1 = 1.4$ and $b_1 = 2$ (see Eq. (38)). The horizontal dashed line shows the performance of the algorithm described in this paper. The points show the performance of a naive algorithm in which the uncertain network is first converted to a binary network by thresholding the edge probabilities and the result then fed into a standard community detection algorithm. The results for each algorithm are averaged over 20 repetitions of the experiment with different networks. Statistical errors are comparable in size to the data points. (b) Fraction of nodes classified into their correct communities for stochastic block model networks with varying amounts of noise in the data. The parameters are the same as for (a) but with the sparsity parameter c fixed at $1/4n$ (see Eq. (39) and the ensuing discussion) and varying the parameter b_1, which controls the level of noise in the data.

Figure 3b shows a different test of the method. Again we use networks generated from a stochastic block model with two groups and calculate the fraction of correctly classified nodes. Now, however, we vary the amount of noise introduced into the network to test the algorithm's ability to recover structure in data of varying quality. The parameters of the underlying network are held constant, as is the parameter c that controls the sparsity of the data matrix $\mathbf{Q}$. This leaves only one degree of freedom, which we take to be the parameter b_1 of the noise process (see Eq. (38)).

A network with little noise in the data is one in which true edges in the underlying network are represented by probabilities Q_{ij} close to 1, in other words by a noise distribution $\beta_1(Q)$ with most of its weight close to 1. Such distributions correspond to small values of the parameter b_1. Noisier data are those in which the values of the Q_{ij} are smaller, approaching the values for the non-edges, thereby making it difficult to distinguish between edges and non-edges. These networks are generated by larger values of b_1. Figure 3b shows the fraction of correctly classified nodes as a function of b_1, so the noise level is increasing, and the quality of the simulated data decreasing, from left to right in the figure.

As we can see, the algorithm returns close to perfect results when b_1 is small—meaning that the quality of the data is high and the algorithm almost sees the true underlying structure of the network. Performance degrades as the noise level increases, although the algorithm continues to do significantly better than chance even for high levels of noise, indicating that there is still useful information to be extracted even from rather poor data sets.

B. Protein interaction network

As a real-world example of our methods we have applied them to protein-protein interaction networks from the STRING database [26]. This database contains protein interaction information for 1133 species drawn from a large body of research literature covering a range of different techniques, including direct interaction experiments, genomic information, and cross-species comparisons. The resulting networks are of exactly the form considered in this paper. For each network there is assumed to be a true underlying network in which every pair of proteins either interacts or doesn't, but, given the uncertainty in the data on which they are based, STRING provides only probabilistic estimates of the presence of each interaction. Thus the data we have for each species consists of a set of proteins—the nodes—plus a likelihood of interaction for each protein pair. A significant majority of protein pairs in each of the networks are recorded as having zero probability of interaction, so the network is sparse in the sense assumed by our analysis and conducive to fast computation.

In the STRING database as well as the work of Krogan *et al.* [2], protein pairs are recorded as having zero interaction probability when they never bind in high throughput experiments. Though a true zero probability of interaction is unlikely due to the possibility of human or equipment error, proteins which do not bind are most likely to have a value of zero. In principle one could add a small estimate of error to every cell of the matrix, but a small enough error would make no difference in the final outcome.

We analyze the data using the degree-corrected version of our algorithm described in Section II D, which is appropriate because the networks in the STRING database, like most real-world networks, have broad degree distributions.

Figure 4a shows the communities found in a three-way split of the protein-protein interaction network of the bacterium *Borrelia hermsii* HS1. Node colors denote the strongest community affiliation for each node, as quantified by the one-node marginal probability q_r^i, with node size being proportional to the probability a node is in its most likely community (so that larger nodes are more certain). In practice, most nodes belong wholly to just one community.

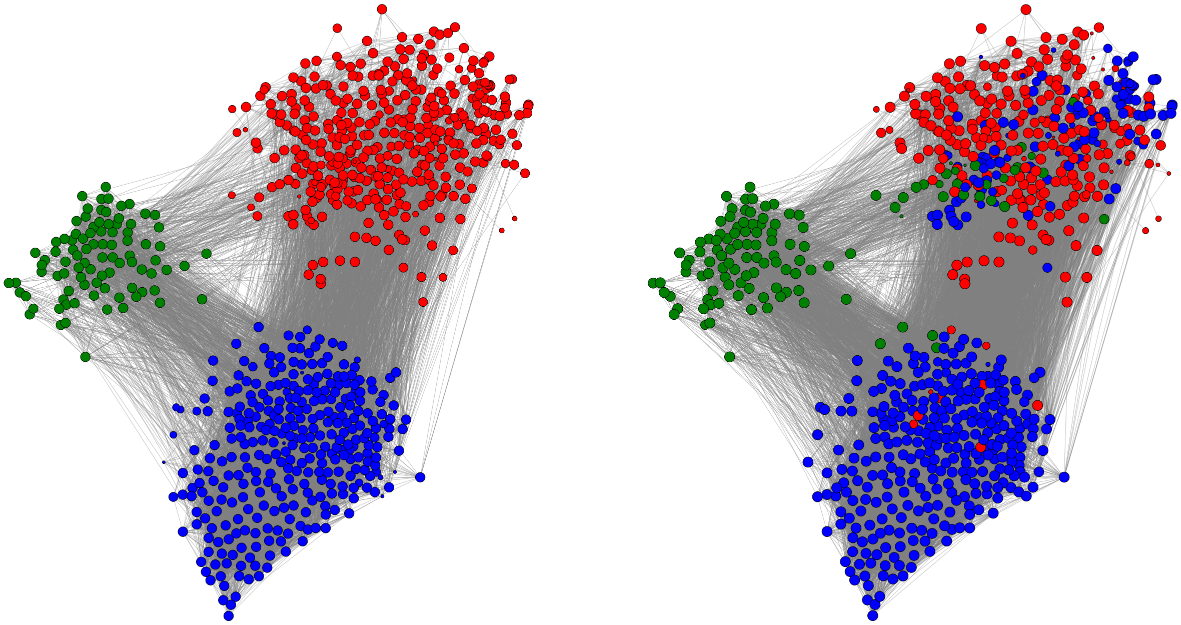
For comparison, we also show in Fig. 4b the communities found in the same network by the naive thresholding algorithm discussed earlier in which a node pair i, j is considered connected by an edge if and only if the probability Q_{ij} exceeds a certain threshold, which here is set at 0.25, though other thresholds gave similar results. By contrast with the synthetic networks of the previous section, we do not know the true underlying communities for this network and so cannot calculate the fraction of correctly classified nodes, but it is clear from the figures that the new technique gives significantly different results from the thresholding method, particularly for the community that appears in the upper right of the figure.

A closer examination of the data reveals a possible explanation. The communities at the left and bottom in both panels of Fig. 4 consist primarily of high-probability edges and are easily identified in the data, so it is perhaps not surprising that both algorithms identify these communities readily and are largely in agreement. However, the third community, in the upper right of the figure, consists largely of edges of relatively low probability and the thresholding method has more difficulty with this case because many edges fall below the threshold value and so are lost, which may explain why the thresholding method divides the nodes of this community among the three groups.

To give a simple picture, imagine a community whose nodes are connected by very many internal edges, but all of those edges have low probability. Because there are so many of them, the total expected number of true internal edges in the underlying network—the number of node pairs times the average probability of connection—could be quite high, high enough to create a cohesive network community. Our algorithm, which takes edge probabilities into account, will allow for this. The thresholding algorithm on the other hand can fail because the edges all have low probability, below the threshold used by the algorithm, and hence are discarded. The result is that the thresholding algorithm sees no edges at all and hence no community. The fundamental problem is that thresholding is just too crude a tool to see subtle patterns in noisy data.

IV. EDGE RECOVERY

A secondary goal in our analysis of uncertain networks is to deduce the structure of the (unobserved) underlying network from the uncertain data. That is, given the



(a) Method of this paper

(b) Thresholding method

FIG. 4: (Color online) Communities found by (a) the algorithm described in this paper and (b) the thresholding algorithm, in a three-way split of the protein interaction network of the bacterium *Borrelia hermsii* HS1, taken from the STRING database. Nodes are laid out according to the communities in (a) and the layout is the same in both panels.

matrix $\mathbf{Q}$ of edge probabilities, can we make an informed guess about the adjacency matrix $\mathbf{A}$? We call this the *edge recovery* problem. It is related to, but distinct from, the well studied *link prediction* problem [27], in which one is given a binary network of edges and non-edges but some of the data may be erroneous and the problem is to guess which ones. In the problem we consider, by contrast, the data given are assumed to be correct, but they are incomplete in the sense of being only the probabilities of the edges, rather the edges themselves.

The simplest approach in the present case is simply to use the edge probabilities Q_{ij} themselves to predict the edges—those node pairs i, j with the highest probabilities are assumed most likely to be connected by edges. But if we know, or believe, that our network contains community structure, then we can do a better job. If we know where the communities in the network lie, at least approximately, then given two pairs of nodes with similar values of Q_{ij}, the pair that are in the same community should be more likely to be connected by an edge than the pair that are not (assuming "assortative" mixing in which edge probabilities are higher inside communities).

It turns out that our EM algorithm gives us precisely the information we need to perform edge recovery. The (posterior) probability of having an edge between any pair of nodes i, j can be written as

$$\begin{aligned} P(A_{ij} = 1) \\ &= \sum_{rs} P(A_{ij} = 1 | g_i = r, g_j = s) P(g_i = r, g_j = s) \\ &= \sum_{rs} t_{rs}^{ij} q_{rs}^{ij}, \end{aligned} \tag{41}$$

where the data $\mathbf{Q}$ and the parameters $\boldsymbol{\gamma}, \boldsymbol{\omega}$ are assumed given in each probability and we have made use of Eq. (24) and the definition of q_{rs}^{ij}. Both t_{rs}^{ij} and q_{rs}^{ij} are calculated in the course of running the EM algorithm, so we already have these quantities available to us and calculating $P(A_{ij} = 1)$ is a small extra step.

Figure 5 shows a test of the accuracy of our edge predictions using synthetic test networks once again. In these tests we generate networks with community structure using the standard stochastic block model, as previously, then run the network through the EM algorithm and calculate the posterior edge probabilities of Eq. (41) above. We compare the results against competing predictions based on the prior edge probabilities Q_{ij} alone.

The figure shows *receiver operating characteristic* (ROC) curves of the results. To construct an ROC curve, one asks how many edges we would get right, and how many wrong, if we were to simply predict that the fraction x of node pairs with the highest probabilities of connection are in fact connected by edges. The ROC curve is the plot of the fraction of such predictions that turn out right (true positives) against the fraction wrong (false positives) for values of x from zero to one. By definition

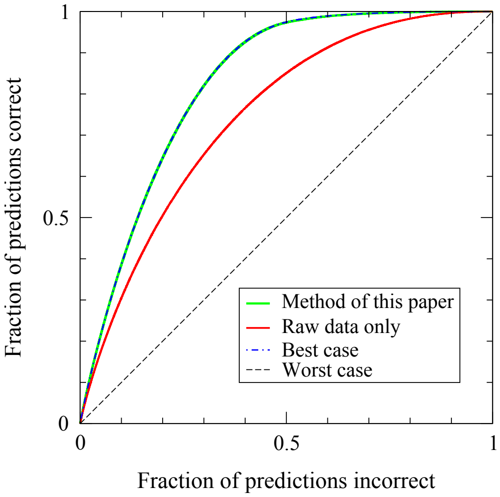


FIG. 5: (Color online) Receiver operating characteristic (ROC) curves for the edge recovery problem on a synthetic network generated using a two-group stochastic block model with $n = 4000$ nodes, $\omega_{11} = \omega_{22} = 0.05$, $\omega_{12} = \omega_{21} = 0.001$, and noise parameters $b_1 = 4$ and $c = 1/4n$. The three curves show the performance of the algorithm of this paper, the naive algorithm based on the raw probabilities Q_{ij} alone, and a hypothetical "ideal" algorithm that knows the values of the parameters used to generate the model (so that one does not have to run the EM algorithm at all). The diagonal dashed line represents is curve generated by an algorithm that does no better than chance.

the curve always lies on or above the 45-degree line and the higher the curve the better the results, since a higher curve implies more true positives and fewer false ones.

Figure 5 shows the ROC curves both for our method and for the naive method based on the raw probabilities Q_{ij} alone and we can see that, for the particular networks studied here, the additional information revealed by fitting the block model results in a substantial improvement in our ability to identify the edges of the network correctly. One common way to summarize the information contained in an ROC curve is to calculate the area under the curve, where an area of 0.5 corresponds to the poorest possible results—no better than a random guess—and an area of 1 corresponds to perfect edge recovery. For the example shown in Fig. 5, the area under the curve for our algorithm is 0.89 while that for the naive algorithm is significantly lower at 0.80.

Also shown in the figure is a third curve representing performance on the edge recovery task if we assume we know the exact parameters of the stochastic block model that were used to generate the network, i.e., that we don't need to run the EM algorithm to learn the parameter values. This is an unrealistic situation—we very rarely know such parameters in the real world—but it represents the best possible prediction we could hope to make under any circumstances. And, as the figure shows, this best possible performance is in this case indistinguishable from the performance of our EM algorithm, indicating that the EM algorithm is performing the edge recovery task essentially optimally in this case.

V. CONCLUSIONS

In this paper we have described methods for the analysis of networks represented by uncertain measurements of their edges. In particular we have described a method for performing the common task of community detection on such networks by fitting a generative network model to the data using a combination of an expectation–maximization (EM) algorithm and belief propagation. We have also shown how the resulting fit can be used to reconstruct the true underlying network by making predictions of which nodes are connected by edges. Using controlled tests on computer-generated benchmark networks, we have shown that our methods give better results than previously used techniques that rely on simple thresholding of probabilities to turn indefinite networks into definite ones. And we have given an example application of our methods to a bacterial protein interaction network taken from the STRING database.

The methods described in this paper could be extended to the detection of other types of structure in networks. If one can define a generative model for a structure of interest then the developments of Section II can be applied, simply replacing the likelihood $P(\mathbf{A}, \mathbf{g}|\boldsymbol{\gamma}, \boldsymbol{\omega})$ in Eq. (7) with the appropriate probability of generation. Generative models have been recently proposed for hierarchical structure in networks [4], overlapping communities [28], ranking or stratified structure [29], and others. In principle, our methods could be extended to any of these structure types in uncertain networks.

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