Inferential Network Clustering with Hierarchical Bayesian Stochastic Blockmodels

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1 INTRODUCTION

Methods and models for network clustering have long been at the core of social network analysis (see Scott, McLevey, and Carrington 2024). Since the 1970s, network clustering has developed along two deeply intertwined conceptual paths: one focusing on cohesive subgroups and assortative community structure (e.g., see Moody and Mucha 2024), the other focusing on equivalence, social roles, and structural positions (e.g., see Dorien, Ferligoj, and Batagelj 2024).

Early research on social cohesion sought to identify fully connected subgroups in friendship networks (Festinger 1949; Luce and Perry 1949), while later work would focus more on social homophily or heterogeneity among closely connected groups (Friedkin 1984; Collins 1988; Erickson 1988). Increases in the size and complexity of network data has driven the development of many new methods for measuring social cohesion (Wasserman and Faust 1994), and for scaling up to large networks in reasonable timespans. The well-known and oft-employed Louvain algorithm for optimizing modularity (Blondel et al. 2008) and the improved Leiden algorithm (Traag, Waltman, and Van Eck 2019) are noteworthy contributions to this line of work.

The other path, which we are primarily concerned with in this chapter, seeks to cluster nodes based on a structural and/or probabilistic definition of node "equivalence," such as having identical sets of ties to other nodes. However defined, the concept of equivalence enables researchers to reduce complex networks into simplified representations of the relationships between positions, roles, or "blocks." We provide a brief high-level overview of this work below; interested readers can find more a more detailed account of role theory

and positional analysis in Dorien, Ferligoj, and Batagelj (2024), which focuses on generalized blockmodeling. In most of this chapter, we will focus on a probabilistic approach to blockmodeling: the hierarchical Bayesian stochastic blockmodel.

This chapter in organized in two parts. The purpose of the first is to introduce foundational ideas related to (a) equivalence and blockmodeling, (b) Bayesian inference and latent variable models, and finally (c) the synthesis of these ideas in the form of Bayesian stochastic blockmodels (BSBMs). In the second part of the chapter, we focus on two empirical examples that illustrate some important considerations when developing and interpreting BSBMs.

2 FOUNDATIONAL IDEAS

2.1 Equivalence and Blockmodels

Unlike network clustering methods that are primarily concerned with cohesion and connectivity, blockmodels are ultimately concerned with the concept of equivalence. In a classic paper, Lorrain and White (1971) introduced in the idea of "structural equivalence" as follows:

> *a* is structurally equivalent to *b* if a relates to every object *x* of [the set of nodes] *C* in exactly the same ways as *b* does. From the point of view of the logic of the structure, then, *a* and *b* are absolutely equivalent, they are substitutable (Lorrain and White 1971, 63).

From the start, this work has been highly influenced by anthropological role theory, specifically the work of SF Nadel ([1957] 2013), who emphasized the inherent complexity of measuring social roles and positions. The overarching goal of early work on blockmodels was to algorithmically reduce complex networks to simplified models of the relationships between structurally distinct social roles, or "positions." Any possible partition produced by a blockmodel could represent an imperfect proxy of the role structure. H. White, Boorman, and Breiger (1976) acknowledge this explicitly in their classic paper: "the blockmodels of this paper can be said to identify positions, but only in an elementary sense" (p. 734). With Nadel ([1957] 2013), they contend that data on many types of ties are needed to apprehend social structure, and it is therefore important to consider multiple models (H. White, Boorman, and Breiger 1976). Robins (2011) echoes this sentiment, suggesting that although social networks are "built by social processes that are ongoing and multiple," patterns in network data "provide evidence from which we may infer something of the social processes that build the network" (484). In short, it is not necessarily the case that structurally equivalent nodes perform the same social roles, and no single blockmodel can hope to capture the totality of a social dynamic within a given network.

The earliest blockmodels used a variety of deterministic approaches to partition empirical networks into clusters of equivalent nodes (Arabie, Boorman, et al. 1982; Arabie, Boorman, and Levitt 1978; Boorman and White 1976; Breiger, Boorman, and Arabie 1975; Light and

Mullins 1979; H. White, Boorman, and Breiger 1976; Wasserman and Faust 1994). However, the requirement that nodes be perfectly interchangeable was proven to be too strict in practice, especially given the complexity of social relationships and the imperfections of data collection and measurement. This led to further innovations in blockmodeling techniques (see Dorien, Ferligoj, and Batagelj 2024) as well as more relaxed criteria for equivalence, such as "regular equivalence" (D. White and Reitz 1983) and "stochastic equivalence." The latter is the basis of an approach that has come to be known as the "stochastic blockmodel" (SBM).

2.1.1 Stochastic Equivalence and Blockmodels

Unlike deterministic blockmodels, which require perfect or near-perfect interchangeability between nodes in a block, SBMs partition networks into blocks of stochastically equivalent nodes (Anderson, Wasserman, and Faust 1992; Holland, Laskey, and Leinhardt 1983; Nowicki and Snijders 2001; Snijders and Nowicki 1997; Wang and Wong 1987; Wasserman and Anderson 1987). In an SBM, blocks are organized so as to maximize the likelihood of block membership conditional on hypothesized edge probabilities, and therefore do not need to be perfectly uniform.

For a simple stochastic blockmodel to describe directed network A with N nodes, we need three pieces of information:

1. E, the total number of edges between nodes in A;
2. b, a vector of length N containing a block assignment for each node in the network where each $b_n \in 1...B$, where B is the number of distinct blocks;
3. p_{rs}, a B-by-B matrix where $r, s \in 1...B$, describing the probability of observing an edge from any node in group r to any node in group s.

Any two nodes in the same block are taken to be stochastically equivalent, which implies that any node in a given block will send ties to other nodes with the same probability as any other node in the same block. This is as true of the inter-block edges ($p_{rs}, r \neq s$) which is the probability that a node in one block sends an edge to a node in a different block, as it is of within-block edges ($p_{rs}, r = s$) where a node sends an edge to another node in the same block. It also implies that SBMs can identify blocks in which the nodes do not share any edges with one another, which is not the case for network clustering methods focused on cohesion (e.g., modularity-based algorithms such as Louvain and Leiden).

Fitting an SBM to an observed network requires determining the number of non-empty blocks to use and then partitioning the nodes (b) accordingly. Since the matrix of edge probabilities (p_{rs}) is determined by the block partition (b), each possible permutation of b can be viewed as a possible explanation of the data.[1] Each of these explanations is assigned a likelihood (i.e., a probability that it is the 'correct' explanation), with likelier explanations of the data being assigned more weight than less likely explanations.

1. The permutations of b must respect the model's constraints; in most cases, this means that b cannot contain any empty blocks.

With some empirical networks, an SBM may not initially appear to produce results that differ meaningfully from those produced by community detection algorithms based on notions of cohesion rather than equivalence. In fact, certain configurations of the SBM can be coaxed into producing plausible partitions along similar lines as cohesion-based methods (Zhang and Peixoto 2020). Closer inspection of the two should, however, dispel any notion that they are the same.

Consider the case of a random graph with an arbitrary number of nodes, a number of edges placed between nodes completely at random, and whose density falls somewhere between 'dense' and 'sparse' (such as an Edros-Renyi graph with a middling p (Erdös and Rényi 1959)). In most such generated networks, traditional modularity-based methods such as Louvain are prone to identifying 'communities' from random noise (Peixoto 2019). Blockmodel-based methods do not. The key point here is that 'traditional' community detection algorithms seek to understand networks *as they are observed*, whereas SBMs seek to understand *how networks came to be*, or *how they are generated*. In this sense, we can describe most traditional community detection techniques as descriptive (Peixoto 2023) and SBMs as inferential or generative.

Currently, descriptive approaches to network clustering are more widely used than inferential approaches. This is not necessarily a problem, as neither description nor inference enjoy any monopoly on the truth – in network science or otherwise – nor does one predominate the other in terms of applicability and utility. Descriptive forms of network clustering are invaluable for identifying certain features of an observed network, such as determining which edges are the most vital to community cohesion (e.g., Moody and Mucha 2024). However, inferential approaches should be used to answer inferential questions, and network analyses concerned with tie formation and other unobserved generative processes that generate those networks necessarily involve inference (Peixoto 2023).

Peixoto (2023) has proposed a 'litmus test' that is helpful in determining whether an inferential approach should be used. The idea is a simple one: after partitioning a network into groups, we learn that our network was generated randomly. Does this alter the utility of our partition? If so, then it is likely that an inferential approach is necessary and descriptive approaches are inappropriate. If not, then it is likely that an inferential approach is not necessary and descriptive approaches are appropriate. In other words, if the generative process that gave rise to the observed network is relevant, then we need an inferential approach; if not, description is likely to be as appropriate, if not moreso.

Bayesian approaches to blockmodeling are particularly effective at partitioning networks given some representation of unobserved generative processes and, unlike many other approaches to blockmodeling, can determine the most appropriate number of blocks to account for a given network. Before getting into the details of Bayesian stochastic blockmodels (BSBMs), we'll offer a brief overview of Bayesian inference and latent variable models for readers who are new to Bayesian statistics. Other readers should feel free to skip to the subsequent section.

2.2 The Logic of Bayesian Inference and Latent Variable Models

At its core, the Bayesian approach to inference uses data to update knowledge about one or more unobserved random variables (McElreath 2020). This is accomplished via Bayes' ubiquitous theorem, which states that the probability of an event A conditional on another event B is equal to the probability of B conditional on A multiplied by the unconditional probability of A divided by the unconditional probability of B. The foregoing can be encapsulated as such:

$$P(A|B) = \frac{P(B|A)P(A)}{P(B)}$$

While Bayes' theorem is widely accepted and applied across all statistical paradigms and disciplines, Bayesian inference distinguishes itself by using probability to describe logically-informed states of belief with respect to a given proposition. By way of contrast: the other major statistical paradigm, Frequentism, only permits the use of probability for events that can be sampled from among a population or repeated a theoretically infinite number of times, and thus does not view probability as compatible with statements about hypotheses, propositions, or states of belief (Clayton 2021).

Readers familiar with Frequentist inference will know that the standard approach to ordinary least-squares (OLS) regression modelling, for example, stipulates that the relationship between a dependent variable (y) and one or more independent variables (X) is governed by a commensurate number of 'parameters.' In the simplest case, there is one parameter for each independent variable (β) plus one parameter for the intercept (α), and the value of each is considered 'fixed' but unknown. Frequentist doctrine demands this; since parameter values cannot be sampled from, they do not have a frequency. They are true, or they are not. As such, Frequentist tests of statistical significance are configured to assess the plausibility of the observed data assuming the 'null' hypothesis (indicating 'no difference' or 'no correlation') is true. If the data is deemed unlikely enough (with the threshold, α, set pre-experimentally), the null is 'rejected' in favour of the data-determined 'alternative' hypothesis.

In the Bayesian paradigm, unobserved random variables in a model are conceptualized as latent variables, information about which can be encoded using probability distributions.[2] Rather than treating unobserved variables as fully unknown but with an assumed fixed value (as the Frequentist paradigm does for its parameters), Bayesian inference generally

2. It should be noted that Bayesian inference also uses parameters, but generally reserves the moniker for a specific class of model setting that is both fixed and known. Prior probability distributions almost always take the form of parameterized distributions, such as the Gaussian, Poisson, Binomial, or Exponential distributions. In the context of a model, a Gaussian distribution with μ=1 (location) and σ=2 (scale) represents a perfectly valid prior probability for an unobserved latent variable: in this way, Bayesian models frequently use parameters to describe prior uncertainty, despite the parameters themselves being known and fixed.

places 'weakly informative' distributions over its latent variables and then updates them using observed data.[3]

These distributions (known as 'priors', see below) are designed to be consistent with the knowledge researchers have about the latent variables before confronting them (and the rest of the model) with empirical data.

Each of the possible values a latent variable can take can be thought of as an individual 'hypothesis' about the value of that variable (e.g. the hypothesis that β=0.59).[4] Bayesian inference seeks to describe the relative plausibility of all such hypotheses (which we'll represent using H) conditional upon a model and observed evidence (the latter of which we'll represent with E). This can be accomplished via Bayes' theorem, which in this setting establishes that the probability of a hypothesis (H) given some evidence (E) is equal to the likelihood of that evidence given some hypothesis, multiplied by the unconditional probability of the hypothesis, divided by the unconditional probability of the evidence. Returning to Bayes' theorem, but with the new symbols subbed in, we get:

$$P(H|E) = \frac{P(E|H)P(H)}{P(E)}$$

Each of the components in the forgoing expression is individually named:

- $P(H|E)$ is the probability of a given hypothesis conditional upon the observed evidence. This is our quantity of interest, and it is known as the 'Posterior Probability' or 'Inferential Probability' (Clayton 2021).
- $P(E|H)$ is referred to as the 'Likelihood' or 'Sampling Probability' of the data (Clayton 2021). Likelihood in the Bayesian context is generally identical to that employed in the classical or Frequentist paradigms. It measures the probability of observing the evidence we did observe under the assumption that the hypothesis is true.
- $P(H)$ is called the 'Prior', and it represents our extant knowledge about the hypothesis before observing the data. Bayesian models treat priors as latent variables whose probability distributions are logically determined by the information available to the researcher (Cox 1946; Jaynes 2003). While some may baulk at the inclusion of prior information, the use of a prior is essential for producing a posterior probability.
- $P(E)$ stands for the unconditional probability of the evidence and is sometimes referred to as the "Bayes Denominator" or the "Marginal Probability of the Data." In many applied settings, this value is difficult to conceptualize and impossible to compute analytically. Fortunately, it only serves to normalize the product in the numerator (ensuring that all posterior probabilities sum to 1), and sampling-based techniques such as MCMC largely obviate the need to know it directly (McElreath 2020).

3. This is not always the case, as some models/applications are better served by wholly uninformative priors, such as a flat prior, or an improper prior such as Jeffries' prior. Conversely, some models may use strongly informative priors, which may constrain model behaviour (Zondervan-Zwijnenburg et al. 2017).

4. The number of hypotheses contained in a discrete latent variable is countable, whereas the number of hypotheses in a continuous latent variable is un-countably infinite.

The Bayesian use of latent variables confers a great many advantages over the Frequentist adherence to parameter values. For the purposes of this chapter, the most salient advantage is that Bayesian latent variables are never reduced to a single point estimate: at all times, they are configured so as to contain complete descriptions of their probability mass (in the case of discrete variables) or probability density (in the case of continuous variable). This permits Bayesian inference to sustain consideration of multiple plausible values for any given latent variable, weighted proportionally to their posterior probability. The Frequentist approach, conversely, identifies a single value that uniquely maximizes likelihood and discards all others.

Latent variables also permit Bayesian models to run as well 'forwards' as they do 'backwards.' What we mean by this is that any well-specified Bayesian model is as well-suited for inferential purposes ('backwards') as it is for simulation ('forwards').[5] The inferential mode – as discussed above – uses data to update prior distributions over a model's latent variables using the likelihood of the data, which produces a posterior distribution for each latent variable. The simulative mode draws samples from the joint distribution of the model's latent variables to produce a synthetic dataset – this can be done using prior information alone (before observing data), or with the latent variables' posterior distributions.[6]

Some, in fact, have gone as far as to use latent variables as a sort of grand unifying principle, arguing that even observed data is simply a special case of a probability distribution (McElreath 2020).[7] This view is consistent with the Bayesian paradigm's treatment of measurement error and missing data: the former uses the observed value as a parameter for a distribution representing uncertainty, and the latter treats the missing value as a latent variable with a weakly informative distribution determined by observed values from the same case (McElreath 2020). In this sense, almost all aspects of a Bayesian model – priors, posteriors, data, and parameters – take the form of latent variables with differing degrees of uncertainty encoded in their distributions.

2.3 The Synthesis: Hierarchical Bayesian Stochastic Blockmodels

Now that we are armed with the foundational ideas motivating blockmodeling and the Bayesian estimation of latent variables, we may proceed to their synthesis. As this is intended to be an accessible introduction, we have opted to minimize the technical details

5. The term 'well-specified', here, is left intentionally ambiguous. Not all prior distributions lend themselves to meaningful output in the simulative mode, and flat/improper priors tend to dramatically limit the utility of a Bayesian model (McElreath 2020). As such, the merit of Bayesian model simulation depends on good prior specification, a topic that is well beyond the scope of this chapter. Interested readers are encouraged to consult the 'Prior Choice Recommendations' page in the stan GitHub repository.

6. Bayesian model invertability is made more intuitive, we find, when considered in light of the fact that one model's posterior is another model's prior – the only distinction is the amount of information encoded.

7. Namely, one that has all of its probability mass or density on the observed value.

and encourage those interested in developing a deeper understanding of SMB-family models to consult foundational and cutting-edge texts on the subject (e.g., Snijders and Nowicki 1997; Nowicki and Snijders 2001; Peixoto 2019, 2023; Zhang and Peixoto 2020).

The Bayesian approach to blockmodeling involves building a generative model and using it to assess the likelihood of the observed network (A) conditional on the range of possible hypotheses about the latent variables (Peixoto 2019). By constraining our generative model so that it adheres to the observed network's node and inter-block degree counts, the number of latent variables estimated shrinks from several to just one: b.

Fundamentally, we are interested in determining the probability that a given node partition vector b of length N – which partitions the nodes of network A into a number of blocks (B), with each block consisting of stochastically equivalent nodes – was responsible for generating network A. In the now-familiar language of Bayes' theorem, we arrive at the following:

$$P(b|A) = \frac{P(A|b)P(b)}{P(A)}$$

Where:

- A: an N-by-N adjacency matrix, where each entry $A_{i,j}$ indicates the presence or absence of an edge between node i and j (in an undirected network, A is symmetric. In a network without self-loops, the diagonal of A is 0).
- N: the number of nodes in network A.
- B: the number of blocks in a given partition b.
- b: a vector of length N that indexes the nodes in the network, where $b_i \in 1...B$ and $i \in 1...N$. Each permutation of b represents one possible partition of the network.
- $P(b|A)$: the posterior probability, or – equivalently – the probability of a partition b given the observed network A. This is our value of interest.
- $P(b)$: the prior probability of partition b. Since observed network data is generally unique, it makes little sense to introduce information to an BSBM via the prior; the priors, thus, are derived from the observed network.[8]
- $P(A|b)$: the likelihood of observing network A given partition b.
- $P(A)$: the marginal probability of the observed network A. Direct calculation thereof is intractable; the need for knowledge of this value is obviated via sampling.

The likelihood term can be expanded further:[9]

8. For more detail on this aspect of specifying BSBMs, see Peixoto (2019).

9. Since we are only interested in modelling block membership, we are able to greatly simplify our task through the use of a 'microcanonical model' (Peixoto 2019). Borrowed from the field of physics, microcanonical modelling permits models to sort their parameters into those with 'hard' constraints, and those with 'soft' constraints. By treating invariant aspects of the network – such as inter-block edge counts – as fixed parameters, we can avoid (potentially intractable) summation and integration signs in our model specification.

$$P(A|b) = P(A|e, b)P(e|b)$$

where e is a B-by-B matrix and entry e_{rs} contains the number of edges shared between group r and group s.[10]

With the model specified, all that remains is to estimate the posterior probability distribution $P(b|A)$. It should be stressed that BSBMs do not identify the single best-fitting partition (b) to the exclusion of all others, but rather provide the probability of all plausible partitions.[11] This is accomplished via Markov Chain Monte Carlo (MCMC) sampling, which draws samples from the joint distribution of the model and data proportional to each combination's posterior probability (Peixoto 2019). An extremely efficient MCMC algorithm for sampling from BSBMs can be found in Peixoto's Python package `graph-tool` (Peixoto 2014b).

2.3.1 Model Selection using Minimum Description Length

As is the case with many other unsupervised learning techniques, BSBMs require users to either pre-specify the number of non-empty blocks (B) or infer the optimal number of blocks from data. Unless an appropriate number of blocks is known a priori, pre-specification of B is a fraught endeavour. Setting B too low paves over the nuances of the data and using a principle such as likelihood maximization imbues blockmodels with a concerning propensity for overfitting the observed network by favouring excessively large numbers of blocks (Peixoto 2019).

Standard practice urges the use of information criteria that reward model likelihood (as a measure of overall fit) but punish model complexity to guard against overfitting. Most of the well-known and widely used criteria are not, however, applicable to SBMs. Field mainstays such as the Akiake Information Criterion (AIC) and the Bayesian Information Criterion (BIC) make invalid assumptions about SBM likelihood functions (Peixoto 2023). Fortunately, Bayesian posterior probability happens to be a 'universal code' for an information theoretic concept known as 'description length' (Grünwald 2007), which can be exploited to provide a principled choice of B.

A model's 'description length' refers to the amount of information it encodes. It can be measured using a variety of scales, the most common of which is the 'bit' or 'Shannon' (Shannon 1948), written using capital sigma (Σ). The concept of Occam's Razor guides information theory towards the principle of 'minimum description length', which holds that models should balance providing the best possible explanation of the data with the

10. At this stage, the mathematical model is not yet complete, as the statement of likelihood is not yet directly computable. Since the purpose of this chapter is to introduce readers to BSBMs, we have elided the model's grittier mathematical detail. See Peixoto (2019) for the full specification.

11. One or two explanations of the data may predominate over the others, but a Bayesian model never formally discards any hypothesis with a posterior probability greater than 0.

complexity of the model used to do so.[12] Peixoto's (2019) derivation takes the following steps:

We start from the previous equation describing the BSBM's likelihood:

$$P(A|b) = P(A|e,b)P(e|b)$$

Multiplying both sides by $P(b)$ gives us:

$$P(A|b)P(b) = P(A|e,b)P(e,b)$$

The above step places the 'Bayes Numerator' on the left-hand side of the equation, which trivially implies that both sides of the equation above are now proportional to the posterior probability. We can then establish a proportional relationship with description length via the bit/Shannon:

$$P(A|e,b)P(e,b) = 2^{-\Sigma}$$

Which can be rearranged thus:

$$log_2 P(A|e,b)P(e,b) = log_2(2^{-\Sigma})$$
$$log_2 P(A|e,b) + log_2 P(e,b) = -\Sigma log_2(2)$$
$$-log_2 P(A|e,b) - log_2 P(e,b) = \Sigma$$

The final expression in the above sequence highlights how MDL encodes the trade-off between model complexity and model fit: with higher values of B (more blocks total), the model does a better job of retrodicting the data, which increases the likelihood ($P(A|e,b)$), decreasing description length. As B increases, however, so too does the model complexity, which increases the entropy of the priors ($P(e,b)$), which increases description length.

Because the description length of a model is measured in binary bits/Shannons, it can be thought of as the number of 'yes-or-no' questions one would need to ask to specify and perfectly recreate the observed data in light of the model (MacKay 2003). The core idea here is that a model with a lower overall description length will have almost certainly done a better job of capturing the 'true' model, compared to other models with higher description lengths. In the context of BSBMs, we can think of each different choice of $B \in 1...N$ as representing a different model; MDL provides us with a principled means of determining which model to select. The best choice of B, then, is the one that produces the lowest description length of any $B \in 1...N$.

Most BSBMs can be improved by performing node reassignments via MCMC sampling. The process of reassigning nodes takes advantage of the fully-specified Bayesian probability

12. The same principle can be found in the other information criteria briefly discussed in the previous paragraph, AIC and BIC.

model and its ability to provide full distributions as answers to inferential queries such as our own. Rather than provide the single most likely partition, any BSBM's posterior can be sampled from to recover each node's probability of belonging to each block (for a given B). The end result is a distribution of nodewise block memberships, wherein each node's probability of belonging to a given block is proportional to the likelihood of the partition that assigned the node to the block in question.

Finally, while the BSBM approach described above is effective at avoiding overfitting, it is still prone to underfitting: it can mistake network structure as being the product of random noise when the structure is, in fact, inferentially meaningful. The solution to this conundrum, as proposed by Peixoto (2019), is to situate the node-level BSBM (which has been the focus of our chapter to this point) at the bottom rung of a potentially infinite series of hierarchical BSBM models. In essence, the solution involves modelling the blocks of a node-level BSBM as a network wherein each node represents a block, the edges between which are weighted according to the observed edge counts in the lowest-level model. This 'network of blocks' can itself be partitioned using a higher-level BSBM using similar logic, procedure, and model selection techniques as the node-level BSBM.[13] The resulting blocks-of-blocks can themselves be modelled in yet another layer of partitioning, and so on *ad infinitium*. This layered approach to the BSMB permits the effective recovery of nested network structures without sacrificing the model's ability to learn from data in the absence of strongly informative prior information (which would be required to recover complex structure in a single-layer BSBM). Unless otherwise noted, the Hierarchical Bayesian Stochastic Blockmodel will be our model of choice throughout the following empirical analyses.

3 EMPIRICAL EXAMPLES

In the second part of this chapter, we present two empirical examples that illustrate the use of BSBMs and speak more generally to the use of inferential approaches to network clustering. Our primary goals in this part of the chapter are to (1) illustrate some important considerations when developing a BSBM, (2) clarify what to expect in terms of results, and (3) suggest some ways of further interrogating results. To that end, we have selected two networks that differ in useful and interesting ways. The first is constructed from Enron email data, the other from data about disinformation campaigns on Twitter.

3.1 The Enron Email Network

Our first example uses a network derived from the ubiquitous Enron email corpus (Klimt and Yang 2004), which has been used in a wide variety of research contexts, including classification, agent-based models of communication (Matsuyama and Terano 2008; VanBuren et al. 2009), and social network analysis (Aven 2015; Corneli et al. 2019; Leskovec et al. 2009).

13. In what should be a familiar refrain by now, readers who are interested in the technical aspects of Hierarchical BSBMs should consult Peixoto (2019, 2023).

The versions of the Enron email dataset available from Stanford's SNAP database and from graph-tool's built-in network repository are both undirected and binary (Leskovec et al. 2009), but we consider the network to be directed and weighted. Our reasoning for this is conceptually grounded – in a corporate hierarchy, the direction and volume of email exchanges might be important. The CEO of a corporation, for example, would receive more emails from subordinates than vice versa. We include only the 'core' employees who were implicated in the legal proceedings and for whom complete email data and identifying information is available, forming a more-or-less complete network. For the rest of the employees, there are no records of their emails amongst each other – only to and from the core, which the Stanford SNAP database terms "sinks or sources" (Leskovec et al. 2009). The resulting network consists of 149 nodes with 2582 edges weighted by volume of emails exchanged (total: 65,143).

In what follows, we use the Python package graph-tool (Peixoto 2014b) to develop BSBMs that partition the network into blocks that mirror the actual job titles held by employees. In other words, we will consider the job titles to be a kind of partial "ground truth" for social roles and see whether our BSBMs can approximate those roles using nothing other than the relational data. However, despite how integral this dataset is reported to be (Hardin, Sarkis, and Urc 2015; Wilson and Banzhaf 2009), it lacks definitive metadata about the job titles of the included employees (Diesner and Carley 2005). We added employee job title information to the dataset ourselves, building on a version of the dataset with other corrections made by Ruhe (2016). From there, we attempted to reconcile as many available versions of the data as we could find. Where there were disagreements between many versions, or remaining vague job titles, we turned to cached online data from the Internet Archive and from Google's web caches. Finally, we used any available LinkedIn profiles of former Enron employees to further enhance the accuracy of the position labels. We also decided to work with the raw emails in the data, rather than choosing any single version of the Enron network to trust.[14]

Figures 1-4 show results from different BSBMs fit to the Enron email network. Figure 1 and Figure 2 are based on BSBMs that have not been refined through cycles of MCMC node reassignments. The first uses binary data whereas the second is weighted. Figure 3 and Figure 4 are refined through MCMC node reassignments. Again, the third is based on binary data and the fourth is weighted.

In these figures, and most others in this chapter, we can see the original complex network with circular nodes, labelled with each job title. The hierarchical BSBM is superimposed with square blue nodes, except for Figure 4 and Figure 5, which we clustered using Traag, Waltman, and Van Eck's (2019) Leiden algorithm rather than a BSBM for the sake of comparison. The original nodes are positioned and coloured according to their block assign-

14. Our investigation left us reasonably confident that our corrections were sound, but also surprised us with the discovery of job titles that have not appeared in any other dataset to date. We wound up with only five completely uninformative "employee" titles remaining, as compared to the best case of 25 in the other datasets that we found. Nonetheless, we by no means claim to have achieved 100% accuracy, given how many other researchers have had a chance to do the same. The authors welcome and encourage any suggested corrections to this dataset. The Enron email corpus is still one of the only public datasets of corporate emails, in a world increasingly rich with such email data – most of latter will never be seen by academic network analysts.

ments. In cases where there is more uncertainty about the block assignment, the nodes can be represented as small pie charts that give a rough sense of other plausible block assignments. High resolution colour images are available in the online supplement.

Figure 1 shows results for an unweighted BSBM using only Peixoto's (2014a) highly performative clustering heuristic. Inspecting the job titles clustered together in each block, we can identify a number of blocks that look intuitively homogenous. The CEOs are divided into different clusters, but they share a block one step up the hierarchy. Two of the three blocks in this cluster – the ones with the CEOs and COO – are primarily senior management and executives, while the third has a number of in-house lawyers and more senior management. Figure 2 shows results a model that uses edge weights (volume of emails) as a covariate but is otherwise identical.[15] Although there is some consistency with the results in the first model, as well as a fair share of intuitive clustering, the CEO blocks are now clustered with a very large block that includes many traders.

Figure 3 and Figure 4 show the result of BSBMs that have been refined through a relatively modest 10,000 cycles of MCMC node reassignments, after which we assessed the minimum description length to see whether the model improved.[16] The cycles of reassignment can be tracked and the frequency that a node was placed in a given block provides the marginal posterior distribution, which serves as an estimate of the probability that this was the best choice.

Here, 'best choice' is meant to imply that some latent social dynamic (i.e., not in the model) had the most influence on the observed network. A purely hypothetical explanation might be that certain administrative assistants act as proxies for the CEOs they were grouped with, sending some portion of the emails that the CEOs would have otherwise sent. This could just as easily be driven by social steering of staff barbecue plans as it is by work-related emails. It could also be something as complex as deliberate instruction, meant to make operations appear "business-as-usual" despite the fraudulent activity happening behind the scenes.

In the refined unweighted SBM shown in Figure 3, there are some significant changes that stand out. The two blocks of CEOs and executive management are now clustered together in the hierarchy, with the other executive block now joining a block of primarily non-executive employees. Changes in the refined weighted SBM are less visibly apparent but there is a great deal of information available here for further comparison.

As mentioned previously, we should not be too certain about block assignments where nodes are colored by pie charts, which indicate the plausibility of some other block assignment. One example is the director on the right side of the unweighted network (see

15. The implementation of BSBMs in Python's graph-tool can incorporate as many edge covariates as you like into the Bayesian process, beyond the standard edge weights. Including too many covariates does tend to considerably increase both computation time and the number of blocks. The weighted results for Enron tend to be a bit less visibly intuitive on most model runs, but this might mean that they are better representing some process not determined by job title.

16. This refinement process tends to consistently improve the MDL of a model by some amount, however small, but of course this doesn't tell us whether the model is good; it merely tells us that it has outperformed its compatriots.

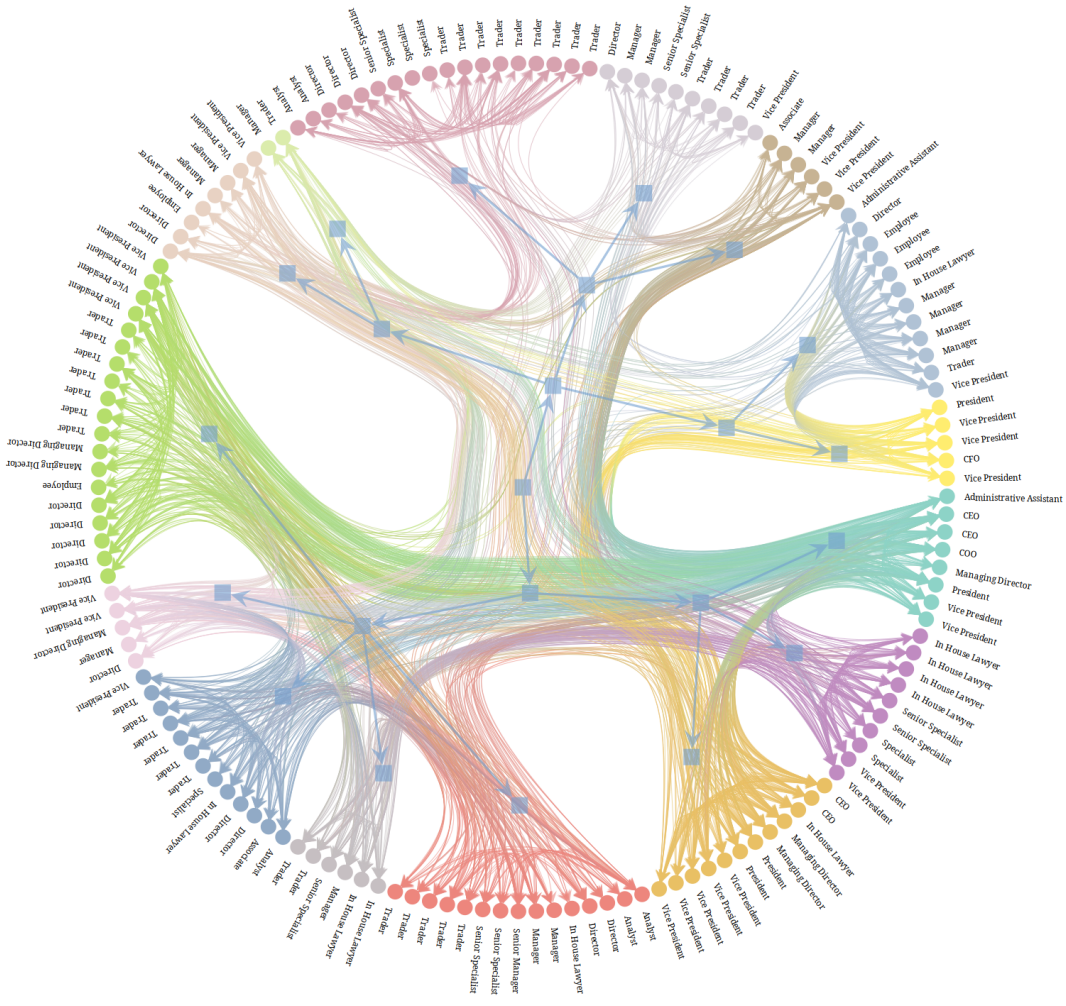


Figure 1: The Enron network with job labels, as partitioned using an unweighted BSBM.

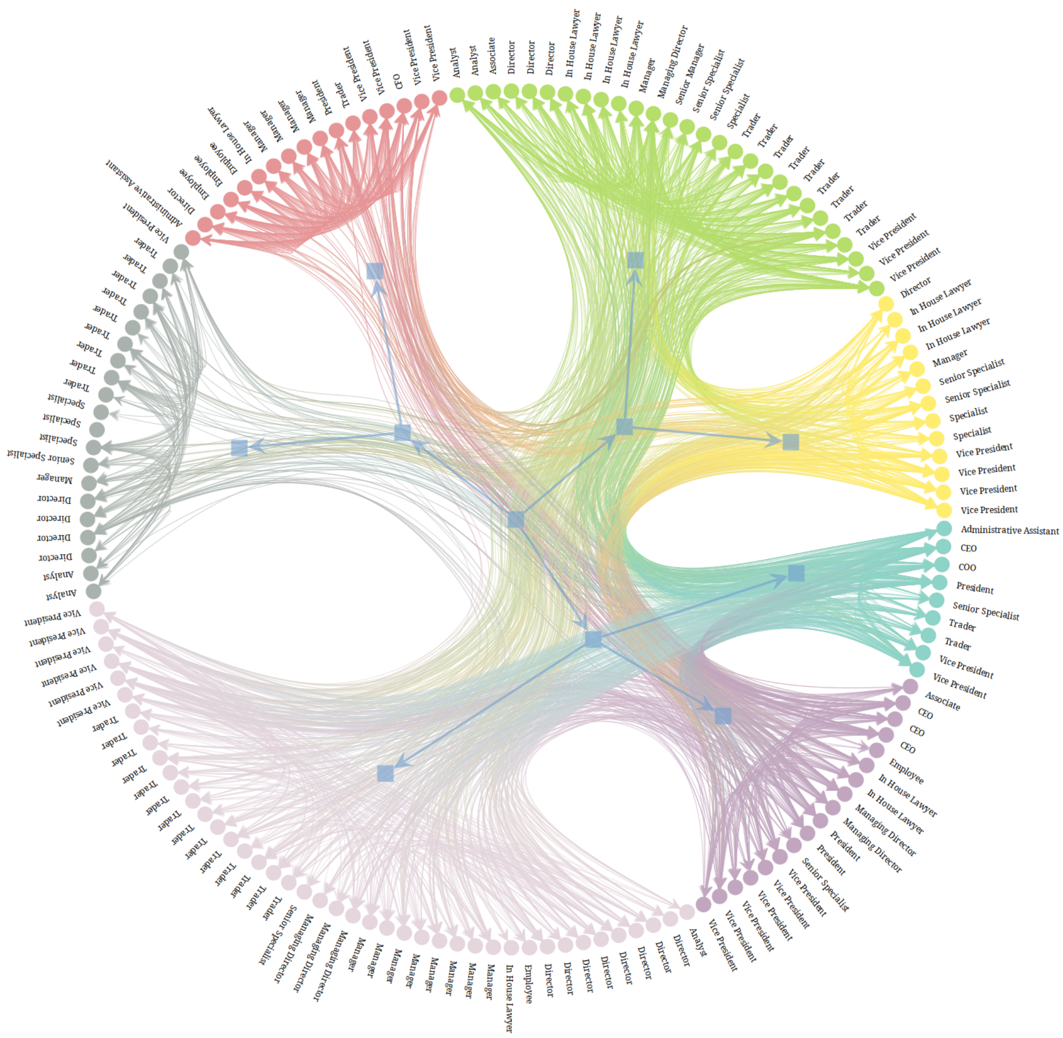


Figure 2: The Enron network with job labels, as partitioned using a weighted BSBM.

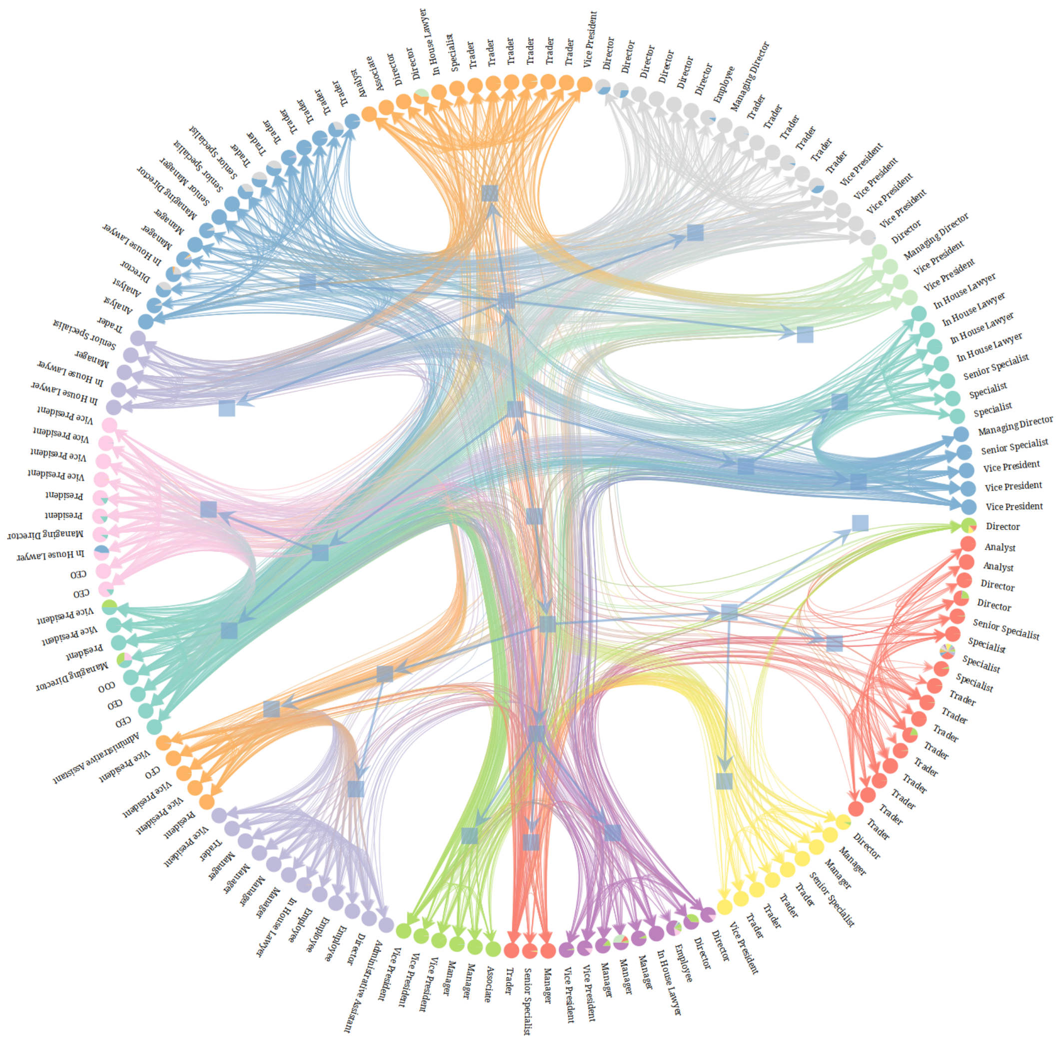


Figure 3: The Enron network with job labels, as partitioned using an unweighted BSBM, refined through MCMC.

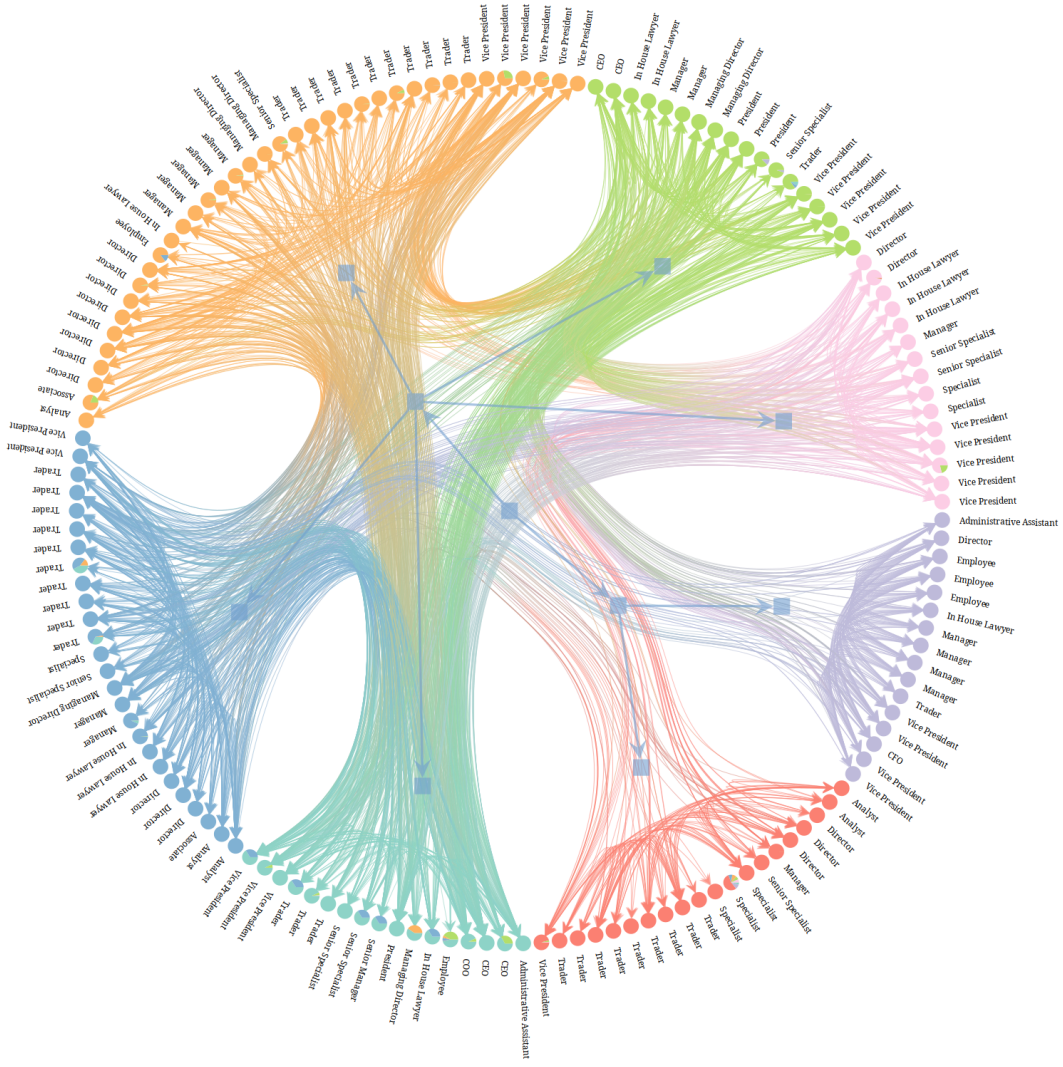


Figure 4: The Enron network with job labels, as partitioned using a weighted BSBM, refined through MCMC.

Figure 2), who was placed alone in a block, but with the possibility of being assigned to either of the two blocks below. Multiple plausible block assignments like this could mean that an employee has a diverse set of behaviours in the company, that the model or data do a poor job of representing their behaviours, or that more than one model is needed to infer the particular social dynamic where they are more consistent.

Peixoto (2021) has recently implemented a model clustering function in graph-tool that can help researchers get a sense of whether there are different generative stories consistent with the data. For each cluster of models, an overall likelihood contribution to the data can be calculated as a proportion to the other models, out of 100. In the case of the Enron models, only two clusters ever turn up and the second with less than 0.001 likelihood, so is not worth exploring here. The uncertainty of some of the individual node assignments, often seen in directors and managers, would be a better place to look.

For the sake of comparison, we provide unweighted and weighted assortative cluster results from the Leiden algorithm, using the respective network layouts from the refined SBM models. The results are shown in Figure 5 and Figure 6, and in Table 1 and Table 2. In both cases, the Leiden algorithm was run with the additional refinement iterations that ensure modularity has been maximized to full model resolution (Traag, Waltman, and Van Eck 2019).

Table 1 compares the MDL (i.e., how successfully the model has condensed the information required to recreate the network) for the six analyses so far (4 partitioned with BSBMs, 2 with Leiden). We can see that the three models with edge weights have significantly longer description lengths. This is to be expected because MDL compares different ways of modeling the same data. As soon as edge weights or other covariates are added to the network, the data used to represent with the model has increased. MDL cannot indicate whether the weighted or unweighted model is preferable. However, for both weighted and unweighted networks, we can see that the SBMs we refined with 10,000 MCMC runs both slightly outperform the unrefined SBMs, and moderately outperform the Leiden algorithm.

Table 1: Minimum Description Length (MDL) comparison for the six Enron analyses.

	BSBM	BSBM, refined with MCMC	Leiden
unweighted	6350.47	6336.73	6660.11
weighted	16763.89	16754.96	16941.6

We can also evaluate our models using another metric from information theory – mutual information. Mutual information is widely used to evaluate cluster and classification models by comparing the consensus between a ground-truth label of datapoints and the labels produced by a model. There have been a number of variants of mutual information introduced to improve on different aspects of the measure, often for different applications. Here, we use Newman, Cantwell, and Young's (2020) reduced mutual information (RMI) score, which was developed with particular attention to evaluating community detection methods in networks. We can use RMI to calculate the agreement between any clustering

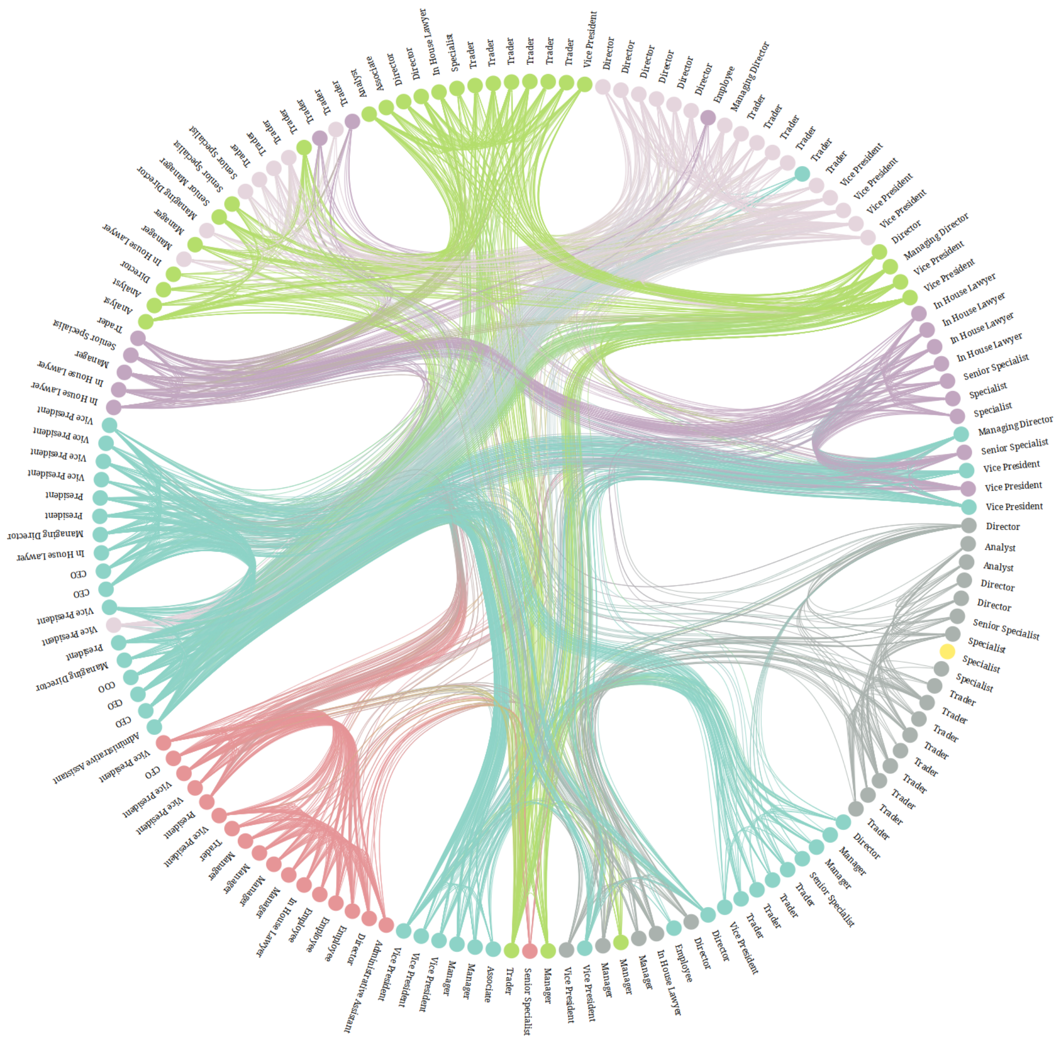


Figure 5: The Enron network with job labels, as partitioned using an unweighted Leiden algorithm.

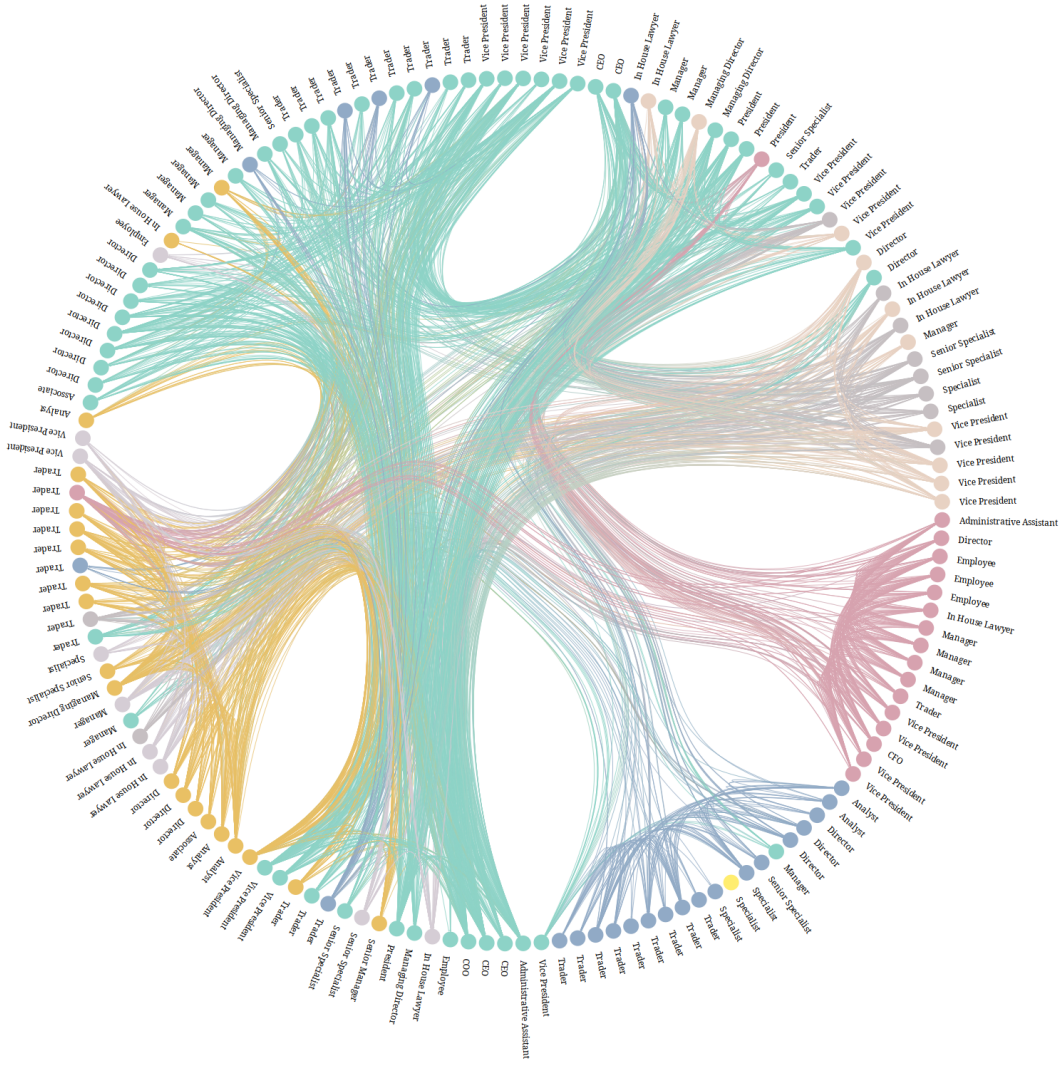


Figure 6: The Enron network with job labels, as partitioned using a weighted Leiden algorithm.

– "ground-truth" or not. Our focus, however, will be on how each model performs relative to the 'Job Title' classifications we added to the dataset.

Table 2 shows the RMI scores of pairwise comparisons between the six model examples above and the employee job titles, with a score of 1 indicating perfect agreement. Contrary to the MDL measure, the unrefined variants of the SBM perform better here than the refined ones, with the weighted unrefined SBM score doubling the second-best score of the weighted Leiden algorithm.

Table 2: Reduced mutual information (RMI) scores for pairwise comparisons of the six Enron analyses and the employees official job titles.

Job Title	SBM unweighted	SBM weighted	SBM refined unweighted	SBM refined weighted	Leiden unweighted	Leiden weighted
Job Title	1					
SBM unweighted	0.004363	1				
SBM weighted	0.042249	0.557893	1			
SBM refined unweighted	-0.01196	0.866441	0.54449 1			
SBM refined weighted	0.01394	0.484362	0.74883	0.482392	1	
Leiden unweighted	-0.00021	0.61373	0.547643	0.595718	0.465708	1
Leiden weighted	0.020552	0.4696	0.534218	0.478979	0.437218	0.56049 1

What explains the apparent contradiction between MDL and RMI? Overfitting is a likely explanation: recall the results of the unrefined weighted SBM (Figure 2), where the two executive blocks were clustered with a higher-order block containing many traders. Traders are the most common employee label (there are 35 of them), so placing them together in clusters will disproportionately impact a mutual information score. In this case, the RMI score is 0.44 when placing all of the traders in one group when every other employee is in a second group. In this sense, models that cluster the most common label ('Trader', in this case) together will score well on RMI whilst not necessarily featuring a comparatively laudable MDL score.

The conceptual caveats here are multiple. We rarely have a "ground truth" available, but it is also worth stressing the fact that the job titles in this example are only one part of the "ground truth" – or are, perhaps, a product of a more general "ground truth" that jointly gives rise to the observed network structure and the job titles. Various norms of corporate hierarchical structure – such as proscribed efficiency guidelines, proximity, and social taboos – are also likely to have been influential. Without more information, the only sure inference to make here is that workplace roles have had some form of influence on who sent emails to whom.

3.2 Disinformation on Twitter: IRA Tweets

In our second empirical example, we analyze networks derived from a corpus of Tweets that Twitter determined were the work of Russia's Internet Research Agency (IRA) as part of their election interference research initiative.[17] In 2018, Twitter began releasing datasets of activity by accounts that they had identified as state-backed operations (Roeder, n.d.). Data attributed to Russia's infamous Internet Research Agency (IRA) was the centerpiece of these releases, containing information on roughly 10 million tweets from 4,611 accounts.

There are two distinct approaches to forming network edges from Twitter: using metadata (e.g. followers and followees) and using activity data (e.g. mentions, retweets, or replies). In this case, we aggregated all three forms of activity data. Since the full IRA network is too large and complex to give a proper treatment in this brief example, we filter the network to retain only the 1,000 most heavily weighted edges. This leaves 777 nodes in the network, with 555 identified as affiliated with the IRA and 222 accounts not identified as affiliated with the IRA. The combined weight of these 1,000 edges is 423,911 – so, a lot of activity. This network represents the source and target accounts involved in the heaviest amount of Twitter interaction surrounding the IRA actors. Notably, the data only includes Tweets made by the IRA accounts, forming a directed network that can still be blockmodeled.

Unlike the Enron data, we know next-to-nothing about the identity of the individuals responsible – it is likely that each IRA worker was responsible for many such accounts. Insofar as Twitter's undisclosed method for detecting state actors can be trusted as accurate, we do know that the Twitter accounts in question were acting under the guidance of some authority. It is also reasonable to assume that the behavior of these accounts is much more singularly focused than that of corporate employees; if a state-employed Twitter operative wanted to plan a barbeque with their co-workers, they would do it somewhere other than in public Tweets from their 'sock puppet' accounts. Given what we know about the generative processes giving rise to this network, one place to start might be to look for evidence of any coordination at all.

In the four subplots of Figure 7, we show the top 1,000 edges from the IRA network at a few key time points from a day-by-day tie formation animation. These edges are displayed in the animation when first established, so although they eventually have the largest edge

17. See https://github.com/fivethirtyeight/russian-troll-tweets/.

weights, they are drawn on the day when the edge weight was 1 or more. Source nodes are circled in black if they first interacted with their target on the day of the image. Similarly, in the online color versions of these figures, the IRA accounts are shown in red, non-IRA in blue, and deleted accounts in orange. Edges directed to each of those account categories are coloured in the same scheme.

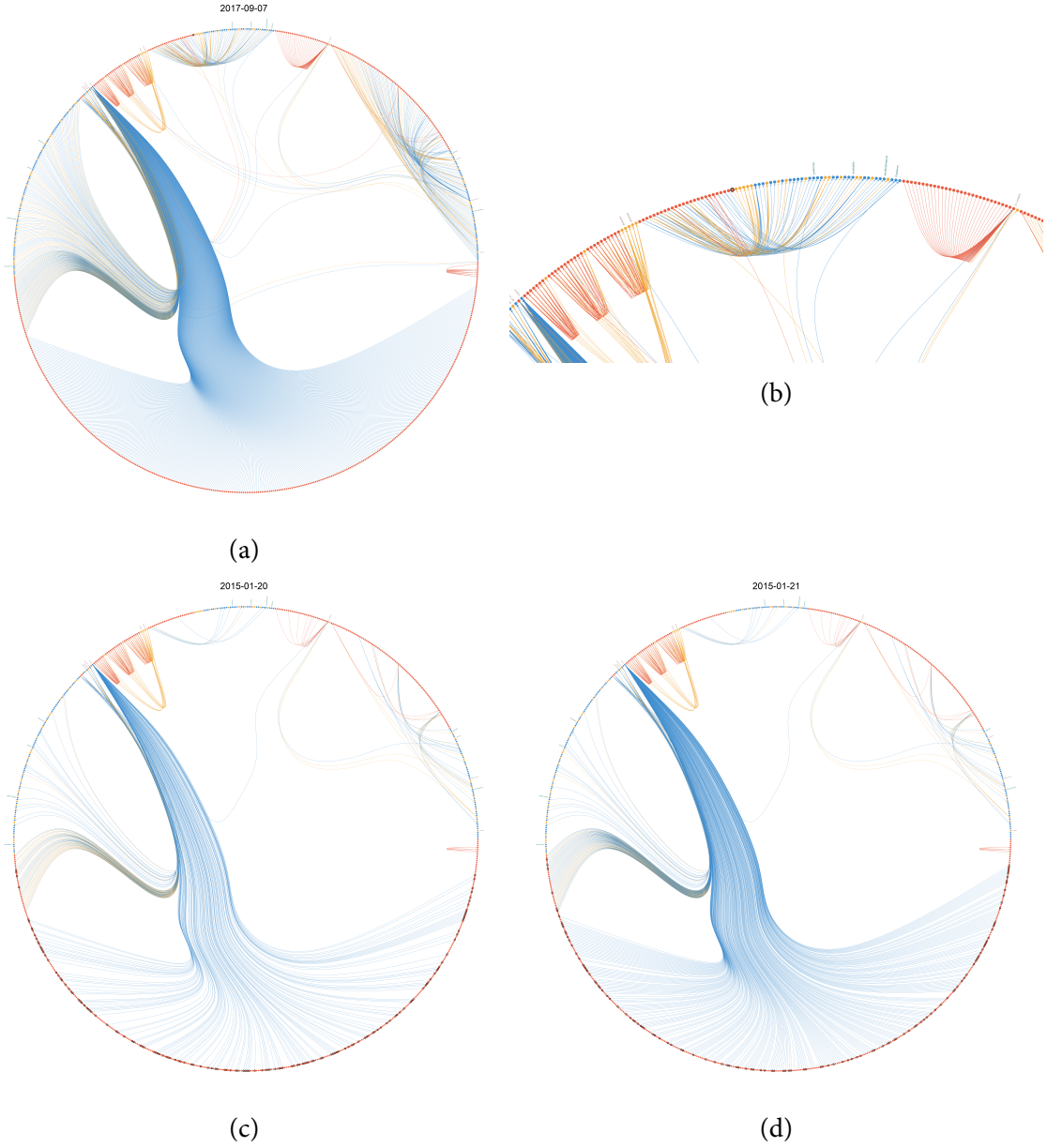


Figure 7: Activity in the IRA network at four points in time. Subplots B-D show December 12th, 20th, and 21st of 2015, respectively. Subplot A shows the network on September 7th, 2017, when the last IRA Tweet in the dataset was sent.

Subplot A in Figure 7 shows the network on September 7th, 2017, when the last IRA Tweet in the dataset was sent. The large swath of edges from the bottom occurred primarily in the span of two days. They all originated from the same block of IRA accounts, and they

all targeted the same account, rianru, which is the account of state-owned Russian news agency RIA Novosti. It would be reasonable to say here that there is evidence of some form of coordinated action. The other blocks display less dramatic but still distinguishable patterns.

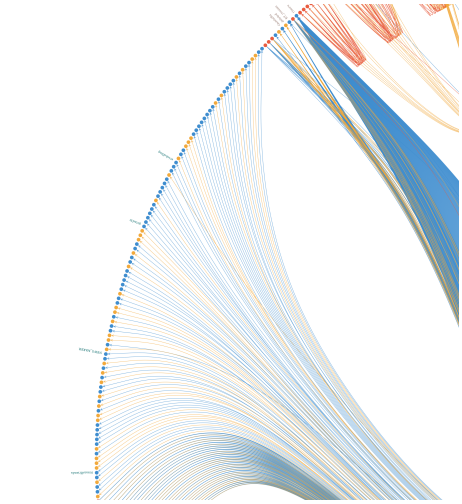
The IRA Twitter blockmodel might suggest the presence of marked distinctions between different sets of behaviours, each guided by sets of strategies from senior decision makers. On the other hand, there is no way to analyze the available data to distinguish between five distinct blocks of Twitter accounts, each belonging to sets of state employees with official orders and, for example, five state employees each running multiple accounts as they see fit – in other words, we can't easily distinguish top-down coordination from simultaneous autonomous activity. Likewise, the media focus that surrounded online state-backed behaviour during the US election cycle might make it tempting, and legitimately compelling, to conclude that any identified organized behaviour is supportive evidence of foreign influence operations. This conclusion is exactly what Twitter suggested when releasing the data. In reality, disinformation researchers increasingly find that a large portion of online disinformation is targeted domestically (Grace 2022; Somerville and Heerin 2020).

The network visualizations in Figure 8 show an enlarged view of some key distinct patterns in the network. Subplot A shows a small number of IRA accounts targeting Twitter accounts of non-descript origin, and primarily spreading conspiracy theories of the time.[18] The second image shows activity focused on popular US media organizations, like *Mashable*, *The Washington Post*, and *Fox News*. In the third image is a mix, with *Al Jazeera*, the *Financial Times*, and a popular Russia-based satire account as targets. There is a great deal of in-depth analysis that could be undertaken here, but it does seem evident that the activity of these accounts was not solely focused on the US election, especially given the attention paid to *RIA Novosti* (*rianru*).

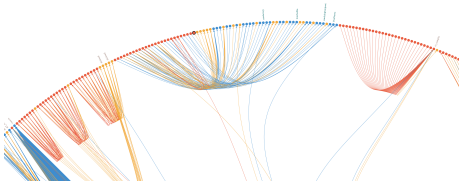
Inference about the goals behind these Twitter strategies might be possible, but not without care – how would a foreign influence objective be distinguishable from purposefully crafting the *impression* of foreign influence, for other purposes? And how would the intended audience be identified? When 100 accounts send 10,000 Tweets each at the *New York Times*, they are almost certainly not banking on the producers of that newspaper to consider their statements. In still other settings, it turns out that none of these considerations even matter, where the reality is that bots are just tweeting amongst each other (Thread 2021).

As the two foregoing analyses have made abundantly clear, BSBMs are powerful tools for drawing inferences about the processes that give rise to social structure in networks. What should be equally clear, however, is that researchers must exercise caution when interpreting said inferences. In our analysis of the Enron email network, we saw that BSBMs admirably retrodict some of the structures we might expect to see in a hierarchical network of corporate communications, but were equally made aware of the fact that BSBMs do not necessarily measure any particular kind of 'ground truth' – or if they do, that it may not be the same ground truth researchers expect to draw inferences about. As H. White,

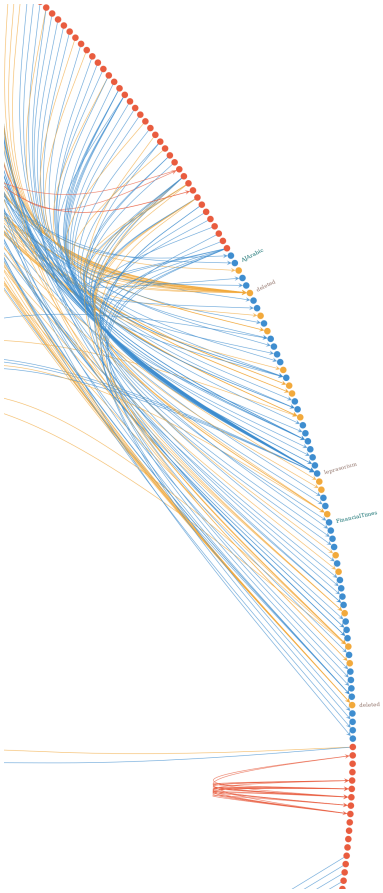
18. Such as Barack Obama being born in Kenya. More recently, these accounts post about Covid-19 conspiracies.



(a)



(b)



(c)

Figure 8: Three different enlarged views of the filtered IRA Network.

Boorman, and Breiger (1976), Robins (2011); and Nadel ([1957] 2013) are wont to emphasize: social roles are complex, embedded, and multifaceted: researchers cannot hope to apprehend the totality of a social role through the analysis of one kind of social tie. In our analysis of the IRA disinformation campaign on Twitter, we encountered the pitfalls of ascribing a causal story to the patterns of behaviour hinted at by the results of a BSBM: the same results can be easily re-interpreted to support conclusions that emphasize the foreign influence role of IRA activity, the domestic influence role of IRA activity, or the seemingly impotent bot-on-bot IRA activity.

4 CONCLUSION

In this chapter, we introduced readers to the Bayesian Stochastic Blockmodel – which is a powerful inferential counterpart to prevailing descriptive approaches to community detection and network clustering – and demonstrated the process of applying and interpreting BSBMs in two very different contexts. As with all unsupervised learning, great care is required when specifying and drawing inferences from the graph partitions we obtain by developing and fitting BSBMs. This is not because SBMs are uniquely prone to misapplication or are otherwise unwieldy. BSBMs open many exciting research opportunities for network scientists by combining decades of insightful work on equivalence, blockmodels, and network clustering (see Dorien, this volume) with probabilistic thinking and generative modelling. But, as with all other approaches, we need careful and deliberate analysis to make inferences about meaningful human behaviour.

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