Bias and variance in the social structure of gender

Kristen M. Altenburger *  
Johan Ugander †

Abstract

The observation that individuals tend to be friends with people who are similar to themselves, commonly known as homophily, is a prominent and well-studied feature of social networks. Many machine learning methods exploit homophily to predict attributes of individuals based on the attributes of their friends. Meanwhile, recent work has shown that gender homophily can be weak or nonexistent in practice, making gender prediction particularly challenging. In this work, we identify another useful structural feature for predicting gender, an overdispersion of gender preferences introduced by individuals who have extreme preferences for a particular gender, regardless of their own gender. We call this property monophily for “love of one,” and jointly characterize the statistical structure of homophily and monophily in social networks in terms of preference bias and preference variance. For prediction, we find that this pattern of extreme gender preferences introduces friend-of-friend correlations, where individuals are similar to their friends-of-friends without necessarily being similar to their friends. We analyze a population of online friendship networks in U.S. colleges and offline friendship networks in U.S. high schools and observe a fundamental difference between the success of prediction methods based on friends, “the company you keep,” compared to methods based on friends-of-friends, “the company you’re kept in.” These findings offer an alternative perspective on attribute prediction in general and gender in particular, complicating the already difficult task of protecting attribute privacy.

Homophily is the observed phenomenon in social networks whereby friendships form frequently among similar individuals [29, 34]. Homophily can originate from an individual’s personal preference to become friends with similar others (choice homophily), structural opportunities to interact with similar others (induced homophily), or a combination of both [26]. An important consequence of homophily is that even if an individual does not disclose attribute information about themselves (such as their gender, age, or race), methods for relational learning [37, 22, 31, 45, 3, 48] can often leverage attributes disclosed by that individual’s friends to predict their private attributes. Gender prediction, however, is a difficult relational learning problem, as gender homophily can be weak or non-existent in both online and offline settings [53, 49, 46, 36, 27]. Weak gender homophily motivates us to examine alternative network structures useful for attribute prediction [13].

In this work, we focus on gender prediction and document the presence of individuals in social networks with extreme gender preferences for a particular gender, regardless of their own gender. We call this overdispersion of preferences “monophily” to indicate it as distinct from the preference bias introduced by homophily, and observe that monophily is nearly ubiquitous across the population of online and offline friendship networks that we study. The presence of these individuals with extreme preferences introduces similarity among friends-of-friends or along 2-hop relations. For the practical problem of attribute prediction, being friends with an individual with extreme gender preferences is a strong signal of one’s own gender and is therefore useful for gender prediction.

In order to model these empirical observations, as part of this work we also introduce an overdispersed stochastic block model that enables us to separately simulate homophily and monophily in social networks. We show how the 2-hop structural relationship induced by overdispersion (monophily) can exist in the complete absence of any 1-hop bias (homophily), and find that overdispersed friendship preferences can drive successful classification algorithms in settings with weak or even no homophily. Therefore, in networks with weak homophily but strong monophily, your friends-of-friends (“the company you’re kept in”) can then be responsible for disclosing private attribute information, as opposed to your friends (“the company you keep”). These findings extend the importance of privacy policies that protect relational data, while also proposing an intuitive structural property of social networks of independent interest.

*Department of Management Science & Engineering, Stanford University. Email: kaltenb@stanford.edu.
†Department of Management Science & Engineering, Stanford University. Email: jugander@stanford.edu.
In the spirit of a solution-oriented science [55], our analysis addresses the practical problem of inferring gender on social networks by revisiting the social theory of homophily and introducing alternative considerations for heterogeneity in friendship preferences. In addition to improving prediction, we also present monophily as an independent structure of interest when studying “gender as a social structure” [42] by explicitly quantifying the variability in gender preferences beyond the bias captured by homophily. Only recently has the role of variability in general and overdispersion in particular been studied on social networks where classic perspectives have prioritized analyzing aggregate patterns of interaction [40]. This work follows other advances in incorporating variance and overdispersion in social data analysis including understanding the consequences of overdispersion when estimating the size of sub-populations [60], documenting variations in the homophily of political ideology [1], assessing gender variation in linguistic patterns [2], and inferring social structure based on indirectly observed data [32].

The paper proceeds by first establishing how we measure the bias (homophily) and excess variance (monophily) of gender preferences. We then examine how relational inference methods for node classification relate to the presence of homophily and/or monophily. While previous models of homophily have shown its statistical significance in network data [58, 17], we highlight that the statistical significance of monophily does not necessarily imply predictive power when the task is to infer private attributes. Following the empirical analysis, we introduce a network model of overdispersed preferences that generalizes the well-studied stochastic block model [21]. Throughout this work we view gender as a binary attribute and aim to measure homophily in a manner that encompasses all sources of preference due to both choice and induced homophily. While we focus on gender, the methods developed in this work contribute a broad statistical toolkit for the general study of variability in social group interactions across a wide range of attributes or traits.

We begin by showing how the conventional homophily index can be interpreted as the maximum likelihood estimate of a parameter within a simple generalized linear model. We then extend this model to capture overdispersed preferences using a quasi-likelihood approach, introducing an overdispersed model with additional parameters that concisely measure the overdispersion of gender preferences among females (F) and males (M), respectively. We propose estimates of these parameters as our measures of monophily among females and males in network data.

The homophily index of a graph [7, 10] characterizes the aggregate pattern of individuals’ biases or preferences in forming friendships with people of their own attribute class relative to people from other classes. For a generic attribute class r and assuming there are k = 2 classes, the homophily index with respect to class r is defined as

\[
\hat{h}_r = \frac{\sum_{i \in r} d_{i,\text{in}}}{\sum_{i \in r} d_{i,\text{in}} + \sum_{i \in r} d_{i,\text{out}}} = \frac{\sum_{i \in r} d_{i,\text{in}}}{\sum_{i \in r} d_{i}},
\]

where \(d_{i,\text{in}}\) denotes node \(i\)’s observed in-class degree with similar others, \(d_{i,\text{out}}\) denotes its observed out-class degree with different others, \(d_i\) denotes its observed total degree, and \(n_r\) will represent the total number of nodes with attribute \(r\) such that \(N = \sum_{r=1}^{k} n_r\). For notational simplicity, we use \(i \in r\) to refer to the set of all nodes with attribute value \(r\).

In measuring binary gender homophily (i.e. \(r = F\) or \(r = M\)), we first illustrate how to measure homophily among females. We assume that each individual \(i \in F\) in a network forms in-class connections with the other \(n_F\) individuals at a rate \(p_{\text{in},F}\) and out-class ties with the other \(n_M\) individuals at a rate \(p_{\text{out}}\) (and similarly for each individual \(i \in M\) that a connection with males form at a rate \(p_{\text{in},M}\) and with females form at a rate \(p_{\text{out}}\)). We therefore expect for each individual \(i \in F\) that their class-specific degrees obey the following distributions (permitting self-loops):

\[
D_{i,\text{in}}|p_{\text{in},F} \sim \text{Binom}(n_F, p_{\text{in},F}), \tag{2}
\]

\[
D_{i,\text{out}}|p_{\text{out}} \sim \text{Binom}(n_M, p_{\text{out}}), \tag{3}
\]

\[
D_i|p_{\text{in},F}, p_{\text{out}} = D_{i,\text{in}}|p_{\text{in},F} + D_{i,\text{out}}|p_{\text{out}}, \tag{4}
\]

where \(D_{i,\text{in}}\) is a random variable describing the in-class degree, \(D_{i,\text{out}}\) describes the out-class degree, and \(D_i\) describes the total degree of node \(i\) in class \(F\). We explicitly condition these random variables on the parameters \(p_{\text{in},F}\) and \(p_{\text{out}}\) to make clear that these parameters are, for now, fixed and constant.

The nodes \(i \in M\) have the same binomial degree distribution specified by in-class degrees formed among the \(n_M\) nodes at a rate \(p_{\text{in},M}\) and out-class degrees formed among the \(n_F\) nodes at a rate \(p_{\text{out}}\). With only \(k = 2\) classes, for simplicity we use the notation \(p_{\text{out}}\) in place of e.g. \(p_{\text{out},r,s}\), highlighting that the rates could depend on the specific in- and out-classes \(r\) and \(s\) in the most general directed multi-class case. Note that the random variables in equations (2-4) are approximately independent,
Figure 1: Evidence of overdispersion in gender preferences. On the Amherst College network we compute the empirical distribution (filled bars) of in-class preferences for females (Left) and males (Right). We compare these distributions to a null distribution (solid lines) based on preferences with binomial variation (for details of null model sampling, see Methods). We observe overdispersion of in-class gender bias in friendship formation for females and males as the observed empirical variance is greater than under the null.

but not completely: constraints on the joint distribution of the degrees corresponding to the constraints of the Erdős-Gallai theorem (since the degrees must correspond to a graph) create a dependence, but this dependence is small for graphs of modest size or larger [54] and we safely ignore it here.

To show how the homophily index can be estimated using a generalized linear model (GLM) [33] of in- versus out-class degrees, let the observed degree data be \( \{(d_i, n_i, d_i), i \in F\} \), where the set-up is analogous for \( i \in M \). Among the \( F \) individuals, their in-class degree distribution conditional on their total observed degree is approximately distributed as

\[
D_{i,\text{in}}|d_i, n_{i,F,F}, n_{i,F,out} \sim \text{Binom}(d_i, n_F p_{i,F}/(n_F p_{i,F} + n_M p_{i,out}))
\]

in the case of two attribute classes (Supplementary Note 1). By applying a logistic-binomial model [16, 1], an adaptation of the logistic regression model for count data, the logistic link function of the binomial logistic regression model is then specified as

\[
\frac{n_F p_{i,F}}{n_F p_{i,F} + n_M p_{i,out}} = \logit^{-1}(\beta_0 F) = e^{\beta_0 F}/(1 + e^{\beta_0 F})
\]

assuming there are no additional covariates (which could otherwise be incorporated). For this model we can then derive the maximum likelihood estimate of \( \beta_0 F \) as:

\[
\hat{\beta}^{\text{MLE}}_0 F = \logit\left(\sum_{i \in F} d_{i,\text{in}}/\sum_{i \in F} d_i\right) = \logit(\hat{h}_F),
\]

or equivalently \( e^{\hat{\beta}^{\text{MLE}}_0 F}/(1 + e^{\hat{\beta}^{\text{MLE}}_0 F}) = \hat{h}_F \) (Supplementary Note 2). Here \( \hat{h}_F \) is exactly the homophily index specified in equation (1) above, and hence the homophily index can be interpreted as the intercept term estimated from a GLM applied to the observed degree data.

Given this interpretation of the homophily index within a GLM framework, it is useful to refer to the quantity \( n_r p_{i,r}/(n_r p_{i,r} + (N - n_r) p_{i,out}) = h_r = \log^{-1}(\beta_{0r}) \) as the “homophily parameter” for each class \( r \), letting the “homophily index” for each class embody the corresponding maximum likelihood estimate, \( \hat{h}_r \). The homophily index is focused on assessing whether \( h_r \) is different from the in-class’ relative proportion in the population, \( n_r/N \). Meanwhile, this model gives a poor assessment of the variance of the data due to the constrained relationship between mean and variance [16]. More specifically, in this model of in-class degrees for class \( r \), the variance of the in-class degrees is constrained to be

\[
\text{Var}[D_{i,\text{in}}|d_i] = d_i h_r (1 - h_r) \quad \text{(Supplementary Note 3)}.
\]

We observe that across the full population of 97 co-educational college online social networks from the Facebook100 dataset (FB100), the distribution of gender preferences are overdispersed, with a variance larger than the above model predicts (for details on the FB100 dataset, see Methods). As seen in Figure 1 for the Amherst College network, the empirical distributions of the gender preferences are more dispersed (less concentrated) than the homophily-only null distributions (for details of null model sampling, see Methods). Across the females and males at Amherst College, there is clear evidence that the variance of the distribution of in-class preferences is greater than what would be expected given the homophily-only null model.
A quasi-likelihood set-up allows each node $i$ compared to alternative methods, in order to adapt the GLM to accommodate this overdispersion. The data [56, 57, 33, 35]. We employ a quasi-likelihood approach [57], the least presumptive approach (Methods).

Equivalent evidence of overdispersion in a directed setting (for details on the Add Health dataset, see Note 4). We consistently observe the variance of degrees of freedom since the model features only a single intercept parameter [57, 16] (Supplementary Note 3). This set-up does not specify a distribution on $h_r$ to be constant across all nodes in the class. Letting $\hat{h}_r$ to measure bias and the estimates $\hat{\phi}_r$ in $r$-class versus out-class friendships.

We formally test the statistical significance of overdispersion of in-degrees relative to out-degrees among nodes with attribute class value $r$ given the fitted GLM with $\hat{\beta}^{MLE}_F$ and the nominal variance of individual $i$'s in-class degree count under this model. The standard test for overdispersion compares the sum of squared standardized residuals $\sum_{i\in r} \frac{(d_{i,r}-d_i)^2}{d_i \hat{h}_r (1-h_r)}$ to $\chi^2_{n_r-1}$, where there are $n_r - 1$ degrees of freedom since the model features only a single intercept parameter [57, 16] (Supplementary Note 4).

A variety of modeling methods have been proposed to measure and model extra variation in count data [56, 57, 33, 35]. We employ a quasi-likelihood approach [57], the least presumptive approach compared to alternative methods, in order to adapt the GLM to accommodate this overdispersion. The quasi-likelihood set-up allows each node $i$ in class $r$ to have an individual latent preference for in-class friendships, $h_{i,r}$, such that $\mathbb{E}[h_{i,r}] = h_r$ and $\text{Var}[h_{i,r}] = \phi_r h_r (1-h_r)$ for some $\phi_r \geq 0$. The parameter $\phi_r$ is introduced to incorporate the extra variation, and the variance is parameterized as such for notational convenience (Supplementary Note 3). This set-up does not specify a distribution on $h_{i,r}$ but instead uses $\phi_r$ to quantify how much nodes in class $r$ vary in allocating their in-class versus out-class friendships.

The case when $\phi_r = 0$ corresponds to the typical homophily-only model (Williams’ Model I), which restricts $h_{i,r}$ to be constant across all nodes in the class. Letting $\phi_r > 0$ (Williams’ Model II) captures variation beyond the conventional model (Supplementary Note 3). Through an iterative procedure due to Williams that maximizes a quasi-likelihood function (Supplementary Note 4), we jointly estimate $\hat{\beta}^{MQE}_F$, $\hat{\phi}_F$ among female nodes and $\hat{\beta}^{MQE}_M$, $\hat{\phi}_M$ among male nodes, allowing us to use $\hat{\phi}_F$ and $\hat{\phi}_M$ as measures of preference overdispersion in the data. Note that the homophily measures estimated under Williams’ Model II, $\hat{\beta}^{MQE}_F$ and $\hat{\beta}^{MQE}_M$, are slightly different than the traditional homophily indices, $\hat{\beta}_F^{MLE}$ and $\hat{\beta}_M^{MLE}$, but the estimates $\hat{\phi}_F^{MLE}$ and $\hat{\phi}_M^{MLE}$ are highly correlated (Supplementary Note 5), and we focus our characterization of homophily on $\hat{\beta}_F^{MLE}$ and $\hat{\beta}_M^{MLE}$ given the direct connection to the homophily index.

In Figure 2, we evaluate both bias (homophily) and overdispersion (monophily) in gender preferences, using the conventional homophily index $\hat{h}_r$ to measure bias and the estimates $\hat{\phi}_r$ to measure overdispersion across the populations of college networks in the FB100 dataset. We see that across these networks the homophily measures $\hat{h}_r$ closely follow the class proportion $n_r/N$, whereas the monophily measures $\hat{\phi}_r$ depart significantly from zero and show no sign of varying with class proportion. We next show how overdispersed preferences help explain the “predictability” of gender in relational trait inference in settings with weak or nonexistent gender homophily.

Having established $\hat{\phi}_F$ and $\hat{\phi}_M$ as our measures of overdispersion, we now illustrate the key role
overdispersion can play in the success of some but not all methods for relational inference. Our specific focus is to understand how the efficacy of different relational inference methods varies in the presence or absence of homophily and/or monophily, building on the challenge of predicting gender on large-scale social networks with minimal gender homophily. We explore a typical setting where individuals reveal information completely at random \cite{18, 31, 44, 19} (i.e. uniformly), meaning that the likelihood to be labeled or to provide public information does not depend on other attributes. The prediction task is then to infer private gender attributes using public gender attributes and the social network relationships. We address this prediction problem through the lens of homophily and monophily. While historically the social sciences have placed a strong emphasis on explanation at the expense of prediction \cite{20}, this work reverses this traditional focus by showing how statistically significant homophily does not necessarily imply high predictability of attributes. Instead, we highlight the role of variation in relational inference methods, especially in applications when the bias introduced by homophily is weak or nonexistent.

Relational inference methods can be categorized based on the neighborhood relationships they exploit for classification, either learning from 1-hop (immediate friends) or 2-hop (friend-of-friend) relations. This distinction in relational learning is not often considered, but we note that it is a direct analog of a common distinction between the PageRank \cite{38} and Hubs and Authorities \cite{24} algorithms in graph ranking. PageRank is based on the principle that “a node is important if it is linked to by other important nodes,” while Hubs and Authorities is based on the principle that “a node is important if it is linked to by nodes that link to important nodes.” These differing principles can extract very different notions of importance in graph ranking; the latter is motivated by web ranking problems where, e.g., car companies don’t link to other car companies but should still appear high in search results for “cars.” Analogously, we observe that 2-hop and 1-hop methods are differently well-suited for different node classification problems. We compare these classification methods relative to a baseline model that assigns scores based on the relative class proportions observed in the training sample.

Classification methods based on a node’s 1-hop (immediate) neighbors include:

- The 1-hop Majority Vote (1-hop MV) classifier, also called the weighted-vote relational neighbor (wvRN) classifier \cite{31}, builds directly on similarities between connected nodes where unlabeled nodes are scored based on the proportion of labels among their neighbors. When a node does not have any labeled neighbors, the relative class proportions in the training data are used (Supplementary Note 6).

- The ZGL method \cite{61} scores unlabeled nodes by computing the relative probabilities of reaching each node in a graph under a random walk originating at the labeled node sets. The ZGL method can be characterized as an iterated/semi-supervised adaptation of 1-hop MV \cite{3}.

Methods that exploit 2-hop (neighbor-of-neighbor) relations include:

- The 2-hop Majority Vote (2-hop MV) classifier uses the relationship between a node and its 2-hop neighbors weighted by the number of length-2 paths. Unlabeled nodes are scored based on the weighted proportion of labels among their 2-hop neighbors.

- LINK-Logistic Regression \cite{59} uses labeled nodes to fit a regularized logistic regression model (Supplementary Note 7) that interprets rows of the adjacency matrix as sparse binary feature vectors, striving to predict labels from these features. The trained model is then applied to the feature vectors (adjacency matrix rows) of unlabeled nodes, which are scored based on the probability estimates from the model. Small variations that use the same feature set but employ e.g. SVMs or Random Forests instead of Logistic Regression give qualitatively similar performance. Employing the LINK feature set as part of a Naive Bayes classifier gives a clear view of LINK as a family of 2-hop methods (Supplementary Note 8).

We observe only slight gender homophily across the population of college networks in the FB100 dataset, and accordingly in Figure 3A we observe limited performance using 1-hop methods (1-hop MV and ZGL) to predict gender in a single representative network. Meanwhile, we see that 2-hop methods (2-hop MV and LINK) have higher performance, corroborating our intuition for 2-hop methods being able to surface structural signals for classification in the presence of overdispersed preferences. As illustrated in Figure 3B, classification for 2-hop Majority Vote considerably outperforms classification based on 1-hop Majority Vote across the population of FB100 schools, and we attribute this performance difference to the monophily in the network. In addition to the undirected FB100 networks, we also examined node classification on the directed Add Health school networks (Supplementary Note 9), where we observe similar results.
Figure 3: Comparison of 1-hop versus 2-hop classifiers and the relationship between classification performance and homophily versus monophily. (Top) A comparison of the performance of classification methods for gender inference on the Amherst College network with $n_F=1015$ and $n_M=1017$, measured by AUC, varying the percentage of nodes that are given as labeled (for details on the cross-validation, see Methods). Homophily and monophily measured for the Amherst College give $\hat{h}_F = 0.55$, $\hat{\phi}_F = 0.04$ and $\hat{h}_M = 0.51$, $\hat{\phi}_M = 0.04$. We observe strong classification performance from the LINK method, which we attribute to the overdispersed gender preferences. (Bottom) Across FB100 networks we compare the correlation between 1-hop and 2-hop Majority Vote (with 50% initially labeled nodes) versus gender homophily and gender monophily. We observe that homophily has high explanatory power for the 1-hop Majority Vote AUC across schools while monophily has very little. Meanwhile, homophily has weak explanatory power of the 2-hop Majority Vote AUC across schools while monophily has strong explanatory power for that method.
In order to generalize these empirical observations on the impact of homophily versus monophily on 1-hop and 2-hop inference methods, we generate synthetic graphs with extra-binomial variation by introducing a variant on the stochastic block model (SBM) [21], also known as the planted partition model [8], a well-studied statistical distribution over graphs with desired block structure commonly employed to study network association patterns. An SBM models association preferences among $k$ node classes by specifying a set of block sizes $n_1, \ldots, n_k$ and a preference matrix $P$ where $P_{a_i a_j}$ denotes the independent probability of an edge between nodes $i$ and $j$ in attribute classes $a_i$ and $a_j$. For modeling associations between two genders using SBMs, the matrix $P$ is simply a $2 \times 2$ matrix denoting the edge probabilities within and between the two genders. Assortative block structure is present when $in$-class probabilities are greater than $out$-class probabilities.

We propose an overdispersed extension of the stochastic block model to additionally capture monophily (extra-binomial heterogeneity in preferences) by relaxing this restriction of fixed class probabilities among all nodes in a given class and assuming a latent distribution on gender preferences [57]. We specifically employ a latent Beta distributions on preferences [9] applied to graphs, though other latent distributions or other means of incorporating overdispersion [12, 17] could be just as reasonable; note that the measure of monophily $\phi_r$ developed earlier in this work (that uses a quasi-likelihood approach) is agnostic to the choice of latent distribution.

The proposed overdispersed stochastic block model (oSBM) is defined by the block sizes $n_1, \ldots, n_k$, $k \times k$ preference matrix $P$, and additional overdispersion parameters $\phi_{in} > 0$ and $\phi_{out} > 0$. Here $\phi_{in}$ and $\phi_{out}$ are concrete parameters of a generative model, while we will continue to use $\phi_r$ to describe generic overdispersion in preferences (when $\phi_r > 0$). Networks are generated from the model via a multi-level approach, where first each node’s $in$- and $out$-class degrees are created by sampling class preference parameters $(p_{in} in$ and $p_{out} out$) from an appropriate latent Beta distribution with specified means $p_{in}$ and $p_{out}$ for $in$- and $out$- class probabilities respectively. We assume the same mean across all attribute classes $r$, so we denote this mean by $p_{in}$ instead of $p_{in,r}$ for a given class $r$. Given the resulting individual preferences, a graph is generated analogously to how the degree-corrected SBM [23] attains prescribed degrees using a Chung-Lu construction [6], with expected $in$-degrees $d_{i,in} = n_r p_{in}$ and expected $out$-degrees $d_{i,out} = (N - n_r) p_{out}$ (Supplementary Note 10). We note that this overdispersed stochastic block model complements related work on overdispersion in social network surveys [60] where an individual’s degree to a class is taken to be distributed Gamma-Poisson. Under an oSBM, the number of individuals from a specific class that a given node is connected to will approximately follow a Beta-Binomial distribution, a close relative of the Gamma-Poisson distribution [5].

The oSBM allows us to validate and explore the relative performance of node inference methods on graphs with and without homophily and/or monophily. Figure 4A illustrates the distribution in gender preferences from four settings of the oSBM that vary the homophily and monophily parameters. In Figure 4B, we then compare the relative performance of 1-hop Majority Vote, ZGL, 2-hop Majority Vote, and LINK when attempting node classification on graphs from each of the four settings. We observe in the homophily-only setting ($p_{in} > p_{out}, \phi_r = 0$) that all inference methods perform well, while in the monophily-only setting ($p_{in} = p_{out}, \phi_r > 0$), 1-hop MV and ZGL have no predictive power while LINK-Logistic Regression and 2-hop MV show impressive performance despite the complete lack of homophily. We conclude that the presence of monophily can be sufficient, even in the complete absence of homophily, for accurate trait inference in networks.

The overarching bias-variance framework we develop for group preferences is highly interpretable, broadly enriching the tools available for studying prediction and explanation in social systems [20] and helps support the continued growth of studying variation in homophily. By adapting a quasi-likelihood approach, we can simultaneously estimate both bias and overdispersion in group preferences, where the traditional homophily index and our monophily index can be interpreted as parameters within a single extra-binomial generalized linear model. This model also offers straightforward techniques for testing the statistical significance of homophily and monophily in social networks.

The networks we study largely exhibit minimal gender homophily, and we attribute the success in gender prediction of the previously introduced LINK algorithm [59] to the presence of strongly overdispersed gender preferences in these networks. We verify and generalize these empirical observations by introducing overdispersion into a stochastic block model via a multi-level approach. We use this model to demonstrate how homophily is a sufficient but not necessary condition for gender inference, and that overdispersion provides an alternative sufficient condition. This model should be of independent interest to researchers looking to create realistic models of social data that can replicate the overdispersed preferences we observe.

These findings provide a new perspective on social network trait classification in general and gender
Figure 4: Four different overdispersed stochastic block models and the associated performance of 1-hop and 2-hop classifiers. (Top) Trait preference distributions for four instances of oSBMs (filled bars) varying $p_{in}$, $p_{out}$, and $\phi_r$ parameters: no homophily and no monophily ($p_{in} = p_{out}, \phi_r = 0$), monophily but no homophily ($p_{in} = p_{out}, \phi_r > 0$), homophily but no monophily ($p_{in} > p_{out}, \phi_r = 0$), and both homophily and monophily ($p_{in} > p_{out}, \phi_r > 0$). We then compute a null distribution (solid lines) based on affinities with binomial variation (for details of null model sampling, see Methods). (Bottom) Across the same corresponding oSBM settings, we compare the relative classification performance for different inference methods and observe a clear bifurcation of performance in the case of monophily but no homophily.
in particular, as well as further complicating the already difficult task of preserving privacy in social networks. The overdispersion of preferences documented in this work motivates a re-examination of 2-hop network structure in network analysis very broadly, e.g. developing label-dependent inference methods [14] or community detection methods [11] that engage with relations among friends-of-friends, rather than only friends. Methods for studying privacy in bipartite affiliation networks [25] should also be revisited. We ultimately believe that the overdispersion of preferences deserves study as a social structure in its own right, and encourage investigations into social correlates of preference overdispersion. While preference biases have long been the predominant focus of group structure in social networks, this work highlights the need to simultaneously give serious parallel consideration to variability.

Methods

Description of Data

We analyze populations of networks from two sources, the Facebook100 (FB100) network dataset [52] (Supplementary Note 5) and the Add Health in-school friendship nomination dataset [41] (Supplementary Note 9). For all networks in both datasets, we restrict the analysis to only nodes that disclose their gender, completely removing those with missing gender labels. We also restrict to nodes in the largest (weakly) connected component in order to benchmark against classification methods [61] that assume a connected graph. The Facebook100 dataset (FB100), analyzed in the main paper, consists of online friendship networks from Facebook that was collected in September 2005 from 100 U.S. colleges, primarily consisting of college-aged individuals [51]. We exclude Wellesley College, Smith College, and Simmons College from our analysis, which all have > 98% female nodes in the original network dataset.

Null distribution of gender preferences

In order to assess whether gender preferences are overdispersed in empirical networks, we compare the variance of the empirical distribution of $d_{i,in}/d_i$ across all nodes $i$ in the same class $r$ to the variance of a Binomial null distribution without overdispersion. Since the basic model assumes that $(D_i, d_i | D_i = d_i) \sim \text{Binom}(d_i, \hat{h}_r)$, we simulate draws from this distribution by repeatedly sampling from Binom$(d_i, \hat{h}_r)$ for each node $i$ to produce a distribution of samples under the null.

Description of cross-validation

We vary the percentage of initially labeled nodes by selecting a labeled sample uniformly at random [31]. We train our models on the $x\%$ labeled individuals (training dataset), and measure classification performance on the remaining unlabeled nodes (testing dataset), using the same train/test splits across the different inference methods. We evaluate performance for 10 different random samples of initially labeled nodes, reporting the mean weighted Area Under the Curve (AUC) for each $x\%$ of initially labeled nodes where the weights are based on the relative number of true class training labels. The vertical error bars denote the standard deviation in AUC scores across the 10 samples.

Data availability

The Facebook100 (FB100) dataset is publicly available from the Internet Archive at https://archive.org/details/oxford-2005-facebook-matrix and other public repositories. The Add Health dataset can be obtained from the Carolina Population Center at the University of North Carolina by contacting addhealth_contracts@unc.edu.

Code availability

IPython notebooks are available at https://github.com/kaltenburger/gender_graph_code, documenting all results and figures.

Acknowledgements

We thank Bailey Fosdick, Jon Kleinberg, Isabel Kloumann, Daniel Larremore, Joel Nishimura, Mason Porter, Matthew Salganik, Sam Way, and attendees of the 2016 International Conference on Computa-
tional Social Science and the 2016 SIAM Workshop on Network Science for comments. Supported in part by an National Defense Science and Engineering Graduate (NDSEG) Fellowship, the Akiko Yamazaki and Jerry Yang Engineering Fellowship, and a David Morgenthaler II Faculty Fellowship.

References

[1] Alan Agresti and Maria Kateri. *Categorical Data Analysis*. Springer, 2011.

[2] David Bamman, Jacob Eisenstein, and Tyler Schnoebelen. Gender identity and lexical variation in social media. *Journal of Sociolinguistics*, 18(2):135–160, 2014.

[3] Smriti Bhagat, Graham Cormode, and S Muthukrishnan. Node classification in social networks. In *Social Network Data Analytics*, pages 115–148. Springer, 2011.

[4] Andrei Boutyline and Robb Willer. The social structure of political echo chambers: Variation in ideological homophily in online networks. *Political Psychology*, 2016.

[5] Christopher Chatfield and Gerald J Goodhardt. The beta-binomial model for consumer purchasing behaviour. In *Mathematical Models in Marketing*, pages 53–57. Springer, 1976.

[6] Fan Chung and Linyuan Lu. Connected components in random graphs with given expected degree sequences. *Annals of Combinatorics*, 6(2):125–145, 2002.

[7] James Coleman. Relational analysis: the study of social organizations with survey methods. *Human Organization*, 17(4):28–36, 1958.

[8] Anne Condon and Richard M Karp. Algorithms for graph partitioning on the planted partition model. *Random Structures and Algorithms*, 18(2):116–140, 2001.

[9] Martin J Crowder. Beta-binomial anova for proportions. *Applied Statistics*, pages 34–37, 1978.

[10] Sergio Currarini, Matthew O Jackson, and Paolo Pin. An economic model of friendship: Homophily, minorities, and segregation. *Econometrica*, 77(4):1003–1045, 2009.

[11] Aurelien Decelle, Florent Krzakala, Cristopher Moore, and Lenka Zdeborová. Asymptotic analysis of the stochastic block model for modular networks and its algorithmic applications. *Physical Review E*, 84(6):066106, 2011.

[12] Thomas A DiPrete and Jerry D Forristal. Multilevel models: methods and substance. *Annual Review of Sociology*, pages 331–357, 1994.

[13] George T Duncan and Diane Lambert. Disclosure-limited data dissemination. *Journal of the American Statistical Association*, 81(393):10–18, 1986.

[14] Brian Gallagher and Tina Eliassi-Rad. Leveraging label-independent features for classification in sparsely labeled networks: An empirical study. In *Advances in Social Network Mining and Analysis*, pages 1–19. Springer, 2010.

[15] Paul H Garthwaite, Ian T Jolliffe, and Byron Jones. *Statistical Inference*. Oxford University Press on Demand, 2002.

[16] Andrew Gelman and Jennifer Hill. *Data Analysis Using Regression and Multilevel/Hierarchical Models*. Cambridge University Press, 2006.

[17] Guang Guo and Hongxin Zhao. Multilevel modeling for binary data. *Annual Review of Sociology*, pages 441–462, 2000.

[18] Jianming He, Wesley W Chu, and Zhenyu Victor Liu. Inferring privacy information from social networks. In *International Conference on Intelligence and Security Informatics*, pages 154–165. Springer, 2006.

[19] Daniel F Heitjan and Srabashi Basu. Distinguishing “missing at random” and “missing completely at random”. *The American Statistician*, 50(3):207–213, 1996.
[20] Jake M Hofman, Amit Sharma, and Duncan J Watts. Prediction and explanation in social systems. *Science*, 355(6324):486–488, 2017.

[21] Paul W Holland, Kathryn Blackmond Laskey, and Samuel Leinhardt. Stochastic blockmodels: First steps. *Social Networks*, 5(2):109–137, 1983.

[22] David Jensen, Jennifer Neville, and Brian Gallagher. Why collective inference improves relational classification. In *Proceedings of the Tenth ACM SIGKDD International Conference on Knowledge Discovery and Data Mining*, pages 593–598. ACM, 2004.

[23] Brian Karrer and Mark EJ Newman. Stochastic blockmodels and community structure in networks. *Physical Review E*, 83(1):016107, 2011.

[24] Jon M Kleinberg. Authoritative sources in a hyperlinked environment. In *SODA*, pages 668–677, 1998.

[25] Michal Kosinski, David Stillwell, and Thore Graepel. Private traits and attributes are predictable from digital records of human behavior. *Proceedings of the National Academy of Sciences*, 110(15):5802–5805, 2013.

[26] Gueorgi Kossinets and Duncan J Watts. Origins of homophily in an evolving social network. *American Journal of Sociology*, 115(2):405–450, 2009.

[27] David Laniado, Yana Volkovich, Karolin Kappler, and Andreas Kaltenbrunner. Gender homophily in online dyadic and triadic relationships. *EPJ Data Science*, 5(1):19, 2016.

[28] Daniel B Larremore, Aaron Clauset, and Abigail Z Jacobs. Efficiently inferring community structure in bipartite networks. *Physical Review E*, 90(1):012805, 2014.

[29] Paul F Lazarsfeld and Robert K Merton. Friendship as a social process: A substantive and methodological analysis. *Freedom and Control in Modern Society*, 18(1):18–66, 1954.

[30] Saskia Le Cessie and Johannes C Van Houwelingen. Ridge estimators in logistic regression. *Applied Statistics*, pages 191–201, 1992.

[31] Sofus A Macskassy and Foster Provost. Classification in networked data: A toolkit and a univariate case study. *Journal of Machine Learning Research*, 8:935–983, 2007.

[32] Tyler H McCormick, Amal Moussa, Johannes Ruf, Thomas A DiPrete, Andrew Gelman, Julien Teitler, and Tian Zheng. A practical guide to measuring social structure using indirectly observed network data. *Journal of Statistical Theory and Practice*, 7(1):120–132, 2013.

[33] Peter McCullagh and John A Nelder. *Generalized Linear Models*, volume 37. CRC press, 1989.

[34] Miller McPherson, Lynn Smith-Lovin, and James M Cook. Birds of a feather: Homophily in social networks. *Annual Review of Sociology*, pages 415–444, 2001.

[35] Jorge G Morel and Neerchal K Nagaraj. A finite mixture distribution for modelling multinomial extra variation. *Biometrika*, 80(2):363–371, 1993.

[36] Jennifer Watling Neal. Hanging out: Features of urban children’s peer social networks. *Journal of Social and Personal Relationships*, 2010.

[37] Jennifer Neville and David Jensen. Supporting relational knowledge discovery: Lessons in architecture and algorithm design. In *Proceedings of the Data Mining Lessons Learned Workshop, 19th International Conference on Machine Learning*, 2002.

[38] Lawrence Page, Sergey Brin, Rajeev Motwani, and Terry Winograd. The pagerank citation ranking: Bringing order to the web. Technical report, Stanford InfoLab, 1999.

[39] Ross L Prentice. Binary regression using an extended beta-binomial distribution, with discussion of correlation induced by covariate measurement errors. *Journal of the American Statistical Association*, 81(394):321–327, 1986.

[40] Adrian E Raftery. Statistics in sociology, 1950–2000: A selective review. *Sociological Methodology*, 31(1):1–45, 2001.
[41] Michael D Resnick, Peter S Bearman, Robert Wm Blum, Karl E Bauman, Kathleen M Harris, Jo Jones, Joyce Tabor, Trish Beuhring, Renee E Sieving, Marcia Shew, et al. Protecting adolescents from harm: findings from the national longitudinal study on adolescent health. *JAMA*, 278(10):823–832, 1997.

[42] Barbara J Risman. Gender as a social structure theory wrestling with activism. *Gender & Society*, 18(4):429–450, 2004.

[43] Saharon Rosset, Ji Zhu, and Trevor Hastie. Boosting as a regularized path to a maximum margin classifier. *Journal of Machine Learning Research*, 5(Aug):941–973, 2004.

[44] Donald B Rubin. Inference and missing data. *Biometrika*, 63(3):581–592, 1976.

[45] Prithviraj Sen, Galileo Namata, Mustafa Bilgic, Lise Getoor, Brian Galligher, and Tina Eliassi-Rad. Collective classification in network data. *AI Magazine*, 29(3):93, 2008.

[46] Wesley Shrum, Neil H Cheek, and Saundra Hunter. Friendship in school: Gender and racial homophily. *Sociology of Education*, pages 227–239, 1988.

[47] Jeffrey A Smith, Miller McPherson, and Lynn Smith-Lovin. Social distance in the united states: Sex, race, religion, age, and education homophily among confidants, 1985 to 2004. *American Sociological Review*, 79(3):432–456, 2014.

[48] Ben Taskar, Pieter Abbeel, and Daphne Koller. Discriminative probabilistic models for relational data. In *Proceedings of the Eighteenth Conference on Uncertainty in Artificial Intelligence*, pages 485–492. Morgan Kaufmann Publishers Inc., 2002.

[49] Mike Thelwall. Homophily in myspace. *Journal of the American Society for Information Science and Technology*, 60(2):219–231, 2009.

[50] Robert Tibshirani. Regression shrinkage and selection via the lasso. *Journal of the Royal Statistical Society. Series B (Methodological)*, pages 267–288, 1996.

[51] Amanda L Traud, Eric D Kelsic, Peter J Mucha, and Mason A Porter. Comparing community structure to characteristics in online collegiate social networks. *SIAM Review*, 53(3):526–543, 2011.

[52] Amanda L Traud, Peter J Mucha, and Mason A Porter. Social structure of facebook networks. *Physica A: Statistical Mechanics and its Applications*, 391(16):4165–4180, 2012.

[53] Johan Ugander, Brian Karrer, Lars Backstrom, and Cameron Marlow. The anatomy of the facebook social graph. *arXiv preprint arXiv:1111.4503*, 2011.

[54] Remco Van Der Hofstad. *Random Graphs and Complex Networks*, volume 1. Cambridge University Press, 2016.

[55] Duncan J Watts. Should social science be more solution-oriented? *Nature Human Behaviour*, 1:0015, 2017.

[56] Robert WM Wedderburn. Quasi-likelihood functions, generalized linear models, and the gauss—newton method. *Biometrika*, 61(3):439–447, 1974.

[57] David A Williams. Extra-binomial variation in logistic linear models. *Applied Statistics*, pages 144–148, 1982.

[58] Andreas Wimmer and Kevin Lewis. Beyond and below racial homophily: Erg models of a friendship network documented on facebook. *American Journal of Sociology*, 116(2):583–642, 2010.

[59] Elena Zheleva and Lise Getoor. To join or not to join: the illusion of privacy in social networks with mixed public and private user profiles. In *Proceedings of the 18th International Conference on World Wide Web*, pages 531–540, 2009.

[60] Tian Zheng, Matthew J Salganik, and Andrew Gelman. How many people do you know in prison? using overdispersion in count data to estimate social structure in networks. *Journal of the American Statistical Association*, 101(474):409–423, 2006.

[61] Xiaojin Zhu, Zoubin Ghahramani, John Lafferty, et al. Semi-supervised learning using gaussian fields and harmonic functions. In *ICML*, volume 3, pages 912–919, 2003.
Supplementary Information

Contents

1 Distribution of in-class Degrees 15
2 Homophily Index as Intercept Term 15
3 Properties of Binomial Degree Data 16
   3.1 Without overdispersion (Model I) .................................................. 17
   3.2 With overdispersion (Model II) ....................................................... 17
4 Algorithm for Estimating Overdispersion Parameter $\phi_r$ 19
5 Facebook Data Pre-processing 20
6 Majority Vote Classification 23
7 Regularization for LINK 23
8 Interpretation of LINK as a 2-hop Method 25
9 Add Health Analysis 27
10 Sampling graphs from the Overdispersed Stochastic Block Model (oSBM) 30
   10.1 Properties based on oSBM parameterization .................................... 31
   10.2 Confirm mean attribute affinity is preserved ................................... 31
   10.3 Confirm variance of attribute affinity is preserved .......................... 31
   10.4 Confirm that expected degrees are approximately preserved .............. 32
The notation is explained in the main paper, and we repeat it here for clarity. Note that we use the terminology “nodes” and “individuals” interchangeably. For notational simplicity, we will use \(i \in r\) to mean the set of all nodes \(i\) with attribute value \(r\), \(n_r\) to be the number of nodes with attribute value \(r\), and \((N - n_r) = n_s\) to be the number of nodes with attribute value \(s \neq r\) (where we focus primarily on a \(k = 2\) class set-up). The \(in\)-class degree \(d_{i,in}\) denotes the observed number of friendships node \(i\) has with individuals that also have the same attribute value \(r\), and the \(out\)-class degree \(d_{i,out}\) denotes the observed number of friendships node \(i\) has with those that do not have attribute value \(r\). We use capital letters \((D_{i,in}, D_{i,out})\) when treating the \(in-/out\)-class degrees as random variables. Finally, we represent the probability of an \(in\)-class link forming as \(p_{in,r}\) for nodes in class \(r\) and represent the probability of \(out\)-class forming as \(p_{out}\), where we are assuming \(k = 2\) classes in which case \(p_{out}\) is necessarily equivalent for both classes.

1 Distribution of \(in\)-class Degrees

We analyze a 2-class set-up divided into attribute classes \(r\) and \(s\), where we give derivations for all nodes \(i \in r\) and the set-up is similar for \(i \in s\). For all nodes \(i \in r\), node \(i\)'s total observed degree \(d_i\) is partitioned between \(in\)-class degrees \(d_{i,in}\) and \(out\)-class degrees \(d_{i,out}\). We observe first that the conditional random variable \((D_{i,in}|D_i = d_i)\) is approximately binomially distributed, for all \(i\) in a particular class, according to the following argument: for large populations (where \(n_r\) and \(N - n_r = n_s\) are large with \(p_{in,r} n_r\) and \(p_{out} n_s\) constant), then \(D_{i,in}\) and \(D_{i,out}\), which are binomial distributed, can be viewed as approximately Poisson distributed. Under this Poisson approximation, the conditional distribution \((D_{i,in} = k|D_{i,in} + D_{i,out} = d_i)\) is distributed Bin \(\left(\frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}}\right)\). In full formalism:

\[
\Pr(D_{i,in} = k|D_i = d_i) = \frac{\Pr(D_{i,in} = k|D_{i,in} + D_{i,out} = d_i)}{\Pr(D_{i,in} + D_{i,out} = d_i)}
\]

\[
= \frac{\left[ e^{-n_r p_{in,r}} \frac{\left(n_r p_{in,r}\right)^k}{k!} + o(e^{-n_r}) \right] \left[ e^{-n_s p_{out}} \frac{(n_s p_{out})^{d_i-k}}{(d_i-k)!} + o(e^{-n_s}) \right]} \left[ e^{-n_r p_{in,r} - n_s p_{out}} \frac{(n_r p_{in,r} + n_s p_{out})^{d_i}}{d_i!} + o(e^{-n_r - n_s}) \right]
\]

\[
= \left(\frac{d_i}{k}\right) \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \left(\frac{n_s p_{out}}{n_r p_{in,r} + n_s p_{out}}\right)^{d_i-k} + o(1),
\]

where \(o(1)\) captures an error term that is asymptotically small when \(n_r\) and \(n_s\) are both large. These steps allow us to identify the conditional distribution \((D_{i,in}|D_i = d_i)\) as approximately Bin \(\left(\frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}}\right)\). When \(n_r = n_s\), this distribution reduces to simply Bin \(\left(\frac{p_{in,r}}{p_{in,r} + p_{out}}\right)\), and when \(p_{in,r} = p_{out}\), this distribution reduces simply to Bin \(\left(\frac{p_{in,r}}{p_{in,r} + p_{out}}\right)\).

2 Homophily Index as Intercept Term

Here we show that the maximum likelihood estimate of the intercept term in the logistic regression model applied to the \(in\)- and \(out\)-degree counts among nodes in a particular class \(r\) can be interpreted as the conventional homophily index \(h_r\). This result is derived specifically for a two-class setting.

Consider \(D_{i,in}|D_i, p_{in,r}, p_{out} \sim \text{Bin} \left(\frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}}\right)\) for nodes \(i \in r\), as derived above with \(p_{in,r}\) and \(p_{out}\) explicitly shown as fixed for clarity and where we define the homophily parameter \(h_r = \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}}\). Then since the binomial distribution is a member of the exponential dispersion family and can therefore be modeled using a generalized linear model (GLM) with a logit link function, we have that

\[
\logit \left(\frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}}\right) = \log \left(\frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}}\right) = \log \left(\frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}}\right) = \beta_0 r \quad \text{or equivalently} \quad \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} = \logit^{-1}(\beta_0 r) = \logit^{-1}(h_r).
\]

Given the observed degree counts for nodes with attribute value \(r\) represented as \(\{d_{i,in}, d_i\}, i \in r\), which are approximately independent (but weakly dependent due to combinatorial constraints on the joint distribution of degrees), we derive the maximum likelihood estimate \(h_r\), and show its connection with the homophily index \(h_r = \sum_{i \in r} d_{i,in}/\sum_{i \in r} d_i\). First consider the likelihood function:
\[ L(\beta_{0r}) = P(D_{1,\text{in}} = d_{1,\text{in}}, D_{2,\text{in}} = d_{2,\text{in}}, \ldots, D_{n_r,\text{in}} = d_{n_r,\text{in}}) \]
\[ = \prod_{i \in r} \left( \frac{d_i}{d_i,\text{in}} \right) \cdot \left( \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right)^{d_i,\text{in}} \cdot \left( 1 - \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right)^{d_i,\text{out}} \]
\[ = \prod_{i \in r} \left( \frac{\beta_0}{1 + e^{\beta_0}} \right)^{d_i,\text{in}} \cdot \left( 1 - \frac{\beta_0}{1 + e^{\beta_0}} \right)^{d_i,\text{out}} \]
\[ \propto \left( \frac{e^{\beta_0}}{1 + e^{\beta_0}} \right)^{\sum_{i \in r, i,\text{in}} d_i,\text{in}} \cdot \left( 1 - \frac{e^{\beta_0}}{1 + e^{\beta_0}} \right)^{\sum_{i \in r} d_i,\text{out}}. \]

We transform this likelihood function to a log-likelihood function:
\[ l(\beta_{0r}) = \log \left( \frac{e^{\beta_0}}{1 + e^{\beta_0}} \right)^{\sum_{i \in r, i,\text{in}} d_i,\text{in}} + \log \left( 1 - \frac{e^{\beta_0}}{1 + e^{\beta_0}} \right)^{\sum_{i \in r} d_i,\text{out}} \]
\[ = \beta_0 \cdot \sum_{i \in r} d_i,\text{in} \cdot \left( 1 + e^{\beta_0} \right) \cdot \sum_{i \in r} d_i,\text{in} + \log \left( 1 - \frac{e^{\beta_0}}{1 + e^{\beta_0}} \right) \cdot \sum_{i \in r} d_i,\text{out} \]
\[ = \beta_0 \cdot \sum_{i \in r} d_i,\text{in} \cdot \left( 1 + e^{\beta_0} \right) \cdot \sum_{i \in r} d_i,\text{in} - \log \left( 1 + e^{\beta_0} \right) \cdot \sum_{i \in r} d_i,\text{out}. \]

and from here we set \( \frac{d(\beta_{0r})}{d\beta_{0r}} = 0 \) and solve for \( \beta_{0r} \):
\[ 0 = \sum_{i \in r} d_i,\text{in} - \sum_{i \in r} d_i,\text{in} \cdot \frac{\beta_0}{1 + e^{\beta_0}} \cdot \sum_{i \in r} d_i,\text{in} \cdot \frac{\beta_0}{1 + e^{\beta_0}} \cdot \sum_{i \in r} d_i,\text{in} \]
\[ 0 = \sum_{i \in r} d_i,\text{in} + \frac{\beta_0}{1 + e^{\beta_0}} \cdot \left( -\sum_{i \in r} d_i,\text{in} - \sum_{i \in r} d_i,\text{out} \right) \]
\[ \frac{\beta_0}{1 + e^{\beta_0}} = \sum_{i \in r} d_i,\text{in} + \sum_{i \in r} d_i,\text{out} = \sum_{i \in r} d_i. \]

Here \( \hat{\beta}_{0r} \) is the maximum likelihood estimator, and we use the superscript “MLE” to make this clear. Thus when using binomial logistic regression applied to the in-degrees \( D_{i,\text{in}} \), \( p_{in,r}, p_{out} \), we obtain that
\[ \log^{-1}(\hat{\beta}_{0r}) = \frac{\hat{\beta}_{0r}}{1 + e^{\hat{\beta}_{0r}}} = \sum_{i \in r} d_i,\text{in} \cdot \sum_{i \in r} d_i \cdot \hat{h}_r, \text{ the conventional homophily index.} \]

### 3 Properties of Binomial Degree Data

For a realized expected degree sequence \( (d_i) \) among nodes \( i \) in class \( r \), the conditional distribution in in-class degrees is (asymptotically, per Section 2): \( D_{i,\text{in}} | d_i, p_{in,r}, p_{out} \sim \text{Binom} \left( d_i, \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right) \) as previously derived. In this section, we assess the unconditional expectation and variance of the in-class degree sequence in settings where \( \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \) is assumed to be constant for all nodes (Model I below) and when \( \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \) is assumed to be random (Model II below). The derivations of Model I and Model II follow those presented in Chapter 10 of [15] and are adapted to this context in terms of in- and out-class degrees.
3.1 Without overdispersion (Model I)

The expectation of $D_{i,in}$ when there is no overdispersion (when $\frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}}$ is constant for all nodes) is:

$$
\mathbb{E}[D_{i,in}|d_i] = \mathbb{E}\left[ \mathbb{E}\left[ (D_{i,in}|d_i) \left| \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right. \right] \right]
$$

(21)

$$
= \mathbb{E}\left[ \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right]
$$

(22)

$$
= d_i \cdot \mathbb{E}\left[ \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right]
$$

(23)

$$
= d_i \cdot \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}}
$$

(24)

$$
= d_i \cdot \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}}.
$$

(25)

The variance (again with $\frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}}$ known) is:

$$
\text{Var}[D_{i,in}|d_i] = \mathbb{E}\left[ \text{Var}\left[ (D_{i,in}|d_i) \left| \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right. \right] \right] + \text{Var}\left[ \mathbb{E}\left[ (D_{i,in}|d_i) \left| \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right. \right] \right]
$$

(26)

$$
= \mathbb{E}\left[ d_i \cdot \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right] \cdot \left( 1 - \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right) + \text{Var}\left[ \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right] \cdot \left( 1 - \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right)
$$

(27)

Considering each of these two terms, we have:

$$
\mathbb{E}\left[ d_i \cdot \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right] \cdot \left( 1 - \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right) = d_i \cdot \mathbb{E}\left[ \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right] - \mathbb{E}\left[ \left( \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right)^2 \right]
$$

(28)

$$
= d_i \cdot \mathbb{E}\left[ \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right] - \text{Var}\left[ \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right] - \mathbb{E}\left[ \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right]^2
$$

(29)

$$
= d_i \cdot \mathbb{E}\left[ \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right] - 0 - \left( \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right)^2
$$

(30)

$$
= d_i \cdot \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \cdot \left( 1 - \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right)
$$

(31)

$$
\text{Var}\left[ \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right] = d_i^2 \cdot \text{Var}\left[ \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right] = d_i^2 \cdot 0 = 0.
$$

(32)

As a result, we obtain that $\text{Var}[D_{i,in}|d_i] = d_i \cdot \mathbb{E}[D_{i,in}|d_i] = d_i \cdot \left( 1 - h_r \right)$, where $h_r$ is:

$$
h_r = \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}}.
$$

If the expectation and variance are rewritten in terms of $h_r$, then they are: $\mathbb{E}[D_{i,in}|d_i] = d_i \cdot h_r$ and $\text{Var}[D_{i,in}|d_i] = d_i \cdot h_r \cdot (1 - h_r)$, respectively.

3.2 With overdispersion (Model II)

Following previous notational set-ups, we introduce overdispersion by allowing $\frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}}$ to vary across nodes such that $\mathbb{E}\left[ \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right] = \mathbb{E}[h_r] = \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} = h_r$ and (for notational convenience as will be clearer later) that $\text{Var}\left[ \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right] = \text{Var}[h_r] = \phi_r \cdot \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \cdot \left( 1 - \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right) = \phi_r \cdot \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \cdot \left( 1 - \frac{n_r p_{out}}{n_r p_{in,r} + n_s p_{out}} \right) = \phi_r \cdot \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \cdot \left( 1 - h_r \right) = \phi_r \cdot \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \cdot \left( 1 - \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \right) = \phi_r \cdot \frac{n_r p_{in,r}}{n_r p_{in,r} + n_s p_{out}} \cdot \left( 1 - h_r \right)$.
\( \phi_r \cdot h_r \cdot (1 - h_r) \). Note that the only assumption we’re making is that \( \phi_r \) is constant across nodes in a given class but we are not making any distributional assumptions on \( n_r p_{i,in} \).

Then, the unconditional expectation of \( D_{i,in} \) (unconditional on \( n_r p_{i,in} + n_s p_{i,out} \) when there is overdispersion (when \( n_r p_{i,in} + n_s p_{i,out} \) is random across all nodes) is:

\[
E[D_{i,in}|d_i] = E \left[ \left( D_{i,in}|d_i \right) \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \right] = E \left[ d_i \cdot \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \right] = E \left[ d_i \cdot E \left[ \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \right] \right] = E \left[ d_i \cdot \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \right] = \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}}
\]

And the unconditional variance (unconditional on \( n_r p_{i,in} + n_s p_{i,out} \) is:

\[
Var[D_{i,in}|d_i] = E \left[ Var \left( D_{i,in}|d_i \right) \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \right] + Var \left[ E \left( D_{i,in}|d_i \right) \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \right] = E \left[ d_i \cdot \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \cdot \left( 1 - \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \right) \right] + Var \left[ d_i \cdot \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \right]
\]

Considering each part, we have:

\[
E \left[ d_i \cdot \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \cdot \left( 1 - \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \right) \right] = d_i \cdot E \left[ \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \right] - E \left[ \left( \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \right)^2 \right]
\]

\[
= d_i \cdot E \left[ \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \right] - Var \left[ \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \right] - E \left[ \left( \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \right)^2 \right]
\]

\[
= d_i \cdot \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} - \phi_r \cdot \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \cdot \left( 1 - \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \right) - \left( \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \right)^2
\]

\[
= d_i \cdot \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \cdot \left( 1 - \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \right) \cdot (1 - \phi_r)
\]

and

\[
Var \left[ d_i \cdot \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \right] = d_i^2 \cdot Var \left[ \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \right] = d_i^2 \cdot \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \cdot \left( 1 - \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \right) \cdot \phi_r
\]

This derivation means that \( Var[D_{i,in}|d_i] = d_i \cdot \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \cdot \left( 1 - \frac{n_r p_{i,in}}{n_r p_{i,in} + n_s p_{out}} \right) \cdot (1 - \phi_r) + d_i^2 \cdot \phi_r \).
\[
\frac{n_r \cdot p_{in,r}}{n_r \cdot p_{in,r} + n_s \cdot p_{out}} \cdot \left(1 - \frac{n_r \cdot p_{in,r}}{n_r \cdot p_{in,r} + n_s \cdot p_{out}}\right),
\]

which simplifies to

\[
\begin{align*}
\text{Var}[D_{i,in} | d_i] &= d_i \cdot \frac{n_r \cdot p_{in,r}}{n_r \cdot p_{in,r} + n_s \cdot p_{out}} \cdot \left(1 - \frac{n_r \cdot p_{in,r}}{n_r \cdot p_{in,r} + n_s \cdot p_{out}}\right) \cdot (1 - \phi_r + d_i \cdot \phi_r) \\
&= d_i \cdot \frac{n_r \cdot p_{in,r}}{n_r \cdot p_{in,r} + n_s \cdot p_{out}} \cdot \left(1 - \frac{n_r \cdot p_{in,r}}{n_r \cdot p_{in,r} + n_s \cdot p_{out}}\right) \cdot (1 + (d_i - 1) \cdot \phi_r).
\end{align*}
\]

Therefore, when \(\phi_r > 0\) then the dispersion in \(D_{i,in} | d_i\) is greater than what would be expected in the setting where \(\phi_r = 0\). If the expectation and variance are rewritten in terms of \(h_r\), then they are:

\[
\begin{align*}
\mathbb{E}[D_{i,in} | d_i] &= d_i \cdot h_r \quad \text{and} \quad \text{Var}[D_{i,in} | d_i] = d_i \cdot h_r \cdot (1 - h_r) \cdot (1 + (d_i - 1) \cdot \phi_r),
\end{align*}
\]

4 Algorithm for Estimating Overdispersion Parameter \(\phi_r\)

This section describes the iterative procedure for estimating the overdispersion (\(\phi_r\)) among nodes \(i\) in class \(r\) by restating the procedure due to Williams [57] using our class-degree notation. The procedure initially assumes the null model without overdispersion (Model I) is true and then iteratively assesses the resulting residual variation via a goodness of fit statistic (\(X^2\)) based on the sum of squared residuals, allowing \(\phi_r > 0\) and then updating the estimates \(\hat{\beta}_0\) and \(\hat{\phi}_r\) until convergence. The final \(\hat{\phi}_r\) at the end of this process is the estimated overdispersion. Note that testing the goodness of fit statistic (\(X^2\)) relies on a predetermined significance parameter (\(\alpha\)), which in the main paper we test the statistical significance of overdispersion in the networks we study at the \(\alpha = 0.001\) significance level. For clarity on the notational differences between our work and that of Williams, we provide the following table that’s explained in more detail below:

| Table S1: Conversion between our notation and Williams’ notation[57]. |
|---------------------------------------------|
| **Our notation** | **Williams’ notation** |
| \(d_i\) | \(m_i\) |
| \(d_{i,in}\) | \(R_i\) |
| \(\bar{h}_r\) | \(\theta = \frac{1 + \exp(-\beta_0)}{1 + \exp(-\lambda)}\) |
| \(\text{Var}(h_{i,r}) = \phi_r \cdot h_r \cdot (1 - h_r)\) | \(\text{Var}([P_i] = \phi \cdot \theta_1 \cdot (1 - \theta_1)\) |
| \(v_i = d_i \cdot h_r \cdot (1 - h_r)\) | \(v_i = m_i \cdot \theta_1 \cdot (1 - \theta_1)\) |
| \(w_i^{-1} = 1 + \phi_r \cdot (d_i - 1)\) | \(w_i^{-1} = 1 + \phi \cdot (m_i - 1)\) |

Given the observed degree data \(\{(d_{i,in}, d_i), i \in r\}\) and assuming the underlying generative process is \(D_{i,in} | d_{i,in}, p_{in,r}, p_{out} \sim \text{Binom}(d_i, \frac{n_r \cdot p_{in,r}}{n_r \cdot p_{in,r} + n_s \cdot p_{out}})\) where \(d_i\) is assumed to vary across nodes, the distinguishing feature between the initial Model I (no overdispersion) and the subsequent Model II (overdispersion) is the variance. \(\text{Var}[D_{i,in} | d_i] = d_i \cdot h_r \cdot (1 - h_r) \cdot (1 + (d_i - 1) \cdot \phi_r)\). For notational convenience by allowing \(v_i = d_i \cdot h_r \cdot (1 - h_r)\) and \(w_i^{-1} = 1 + (d_i - 1) \cdot \phi_r\), then \(\text{Var}[D_{i,in} | d_i] = v_i \cdot w_i^{-1}\) where Model I strictly enforces \(\phi_r = 0\) or equivalently \(w_i^{-1} = w_i = 1\). Meanwhile for Model II we allow \(\phi_r > 0\) or equivalently \(0 < w_i^{-1} < 1\).

The steps of Williams’ iterative algorithm for jointly estimating \(\hat{\beta}_0\) and \(\hat{\phi}_r\) are then as follows. Viewed as an iterated algorithm, the iteration is in earnest only over the variables \(\hat{\beta}_0\) and \(\hat{\phi}_r\) given the input data \((d_i)\) and \((d_{i,in})\), but a number of auxiliary variables (e.g. \(w_i, v_i, q\)) greatly simplify the notation.

1. First assume there’s no overdispersion (\(\phi_r = 0\)) and test for the significance of overdispersion being present (\(\phi_r > 0\)) by fitting Model I assuming there are no additional explanatory variables. Then \(\hat{\beta}_0^\text{MLE} = \logit(\sum_{i \in r} d_{i,in} / \sum_{i \in r} d_i)\). Evaluate the model fit by computing a goodness-of-fit statistic (\(X^2\)) or the sum of squared residuals as

\[
X^2 = \sum_{i \in r} \left[(d_{i,in} - d_i \cdot h_r)^2/(d_i \cdot h_r \cdot (1 - h_r))\right],
\]

which under the null should be distributed \(\chi^2_{n_r - 1}\). Note as is illustrated in the main paper, we use \(w_i = 1\) for this initial goodness-of-fit test, a direct consequence of \(\phi_r = 0\) under the initial null model.

2. Compare \(X^2\) with the \(\chi^2_{n_r - 1}\) distribution which is valid under the null \(\phi_r = 0\) being true. Then assuming the null model is true, we compute the statistical significance of \(X^2\) by computing the
It shows that these nodes comprise the majority of individuals in each graph, so subsetting is a minimal
methods. Figure S2 illustrates the relative proportion of nodes in the largest connected component, and
completely remove them in this work since our goal is to compare the relative performance of inference
Vote, but given that we are not able to include them in a training/testing cross-validation set-up, we
unknown individuals can be useful for revealing the gender of others using e.g. LINK or 2-hop Majority
Figure S1 shows that across the Facebook schools there’s a very small percentage of individuals with
5 Facebook Data Pre-processing

\begin{align*}
\hat{h}_r^0 &= \frac{1}{1 + \exp(-\hat{\beta}_{0r}^{\text{MLE}})} \\
\phi_r^0 &= \frac{d_i \cdot \hat{h}_r^0}{\sum_{i \in r} v_i^0} \\
q_r^0 &= \frac{1}{\sum_{i \in r} v_i^0} X^2 - (n_r - 1) (d_i - 1) (1 - \hat{\phi}_r^0 \cdot q_r^0) \tag{54}
\end{align*}

3. Update the weights \( \hat{w}_i^t \), re-estimate \( \hat{\beta}_{0r}^{t+1} \), and update \( \hat{h}_r^t \) and \( \hat{\phi}_r^t \):

\begin{align*}
\hat{w}_i^{t+1} &= \frac{1}{1 + \phi_r^{t+1} (d_i - 1)} \\
\hat{\beta}_{0r}^{t+1} &= \frac{\sum_{i \in r} w_i^{t+1} \cdot [v_i^t \cdot \hat{\beta}_{0r}^t + d_i \cdot \hat{h}_r^t - d_i \cdot \hat{h}_r^t]}{\sum_{i \in r} w_i^{t+1} v_i^t} \tag{56}
\hat{h}_r^{t+1} &= \frac{1}{1 + \exp(-\hat{\beta}_{0r}^{t+1})} \\
v_i^{t+1} &= d_i \cdot \hat{h}_r^{t+1} \cdot (1 - \hat{h}_r^{t+1}) \tag{58}
\end{align*}

4. Compute the new sum of squared residuals \( X^2 \):

\begin{align*}
X^2(t+1) = \sum_{i \in r} \frac{(w_i^{t+1} \cdot [d_i \cdot \hat{h}_r^{t+1}]^2)}{v_i^{t+1}} \tag{59}
\end{align*}

sand if this updated value is close to the degrees of freedom \( n_r - 1 \), then \( \hat{\phi}_r = \hat{\phi}_r^{t} \) is the dispersion estimate and the procedure stops. Otherwise, update

\begin{align*}
q_r^{t+1} &= \frac{1}{\sum_{i \in r} w_i^{t+1} v_i^{t+1}} \\
\hat{\phi}_r^{t+1} &= \frac{X^2(t+1) - \sum_{i \in r} w_i^{t+1} \cdot (1 - w_i^{t+1} \cdot v_i^{t+1} \cdot q_r^{t+1})}{\sum_{i \in r} w_i^{t+1} \cdot (d_i - 1) \cdot (1 - w_i^{t+1} \cdot v_i^{t+1} \cdot q_r^{t+1})} \tag{61}
\end{align*}

and return to 3 with \( t \leftarrow t + 1 \).

We use the R package \texttt{dispmod} to compute \( \hat{\phi}_r \). The code snippet below assumes that the vectors \texttt{deg\_same} and \texttt{deg\_different} contains the degrees \( d_{i,\text{in}} \) and \( d_{i,\text{out}} \), respectively:

```r
compute_monophily_phi <- function(deg_same, deg_different){
  mod <- glm(cbind(deg_same, deg_different) ~ 1, family=binomial(logit))
  mod.disp <- glm.binomial.disp(mod, maxit = 50, verbose = F)
  return(mod.disp$dispersion)
}
```

5 Facebook Data Pre-processing

Figure S1 shows that across the Facebook schools there’s a very small percentage of individuals with
true unknown gender labels, always less than 16% with an average of 8.4%. We acknowledge that these
unknown individuals can be useful for revealing the gender of others using e.g. LINK or 2-hop Majority
Vote, but given that we are not able to include them in a training/testing cross-validation set-up, we
completely remove them in this work since our goal is to compare the relative performance of inference
methods. Figure S2 illustrates the relative proportion of nodes in the largest connected component, and
shows that these nodes comprise the majority of individuals in each graph, so subsetting is a minimal
change compared to the original dataset. Figure S3 illustrates that across the population of schools, males and females have comparable average degrees. The mean average degree is 71.35 for males and 79.22 for females.

Figure S4 compares the original $\hat{\beta}^{MLE}_0, \hat{\beta}^{MLE}_F$ to the updated $\hat{\beta}^{MQE}_0, \hat{\beta}^{MQE}_F$ under the iterative Williams Method. We observe that the estimates strongly correlate, which is not surprising given that the average degree between males and females is similar and as noted in [57] that “...the difference between the maximum likelihood estimate of $\beta$ under Model I and the maximum quasi-likelihood estimate of $\beta$ under Model II is expected to be small when the $m_i$ are of a similar magnitude.”

Figure S1: The proportion of nodes with missing gender labels in the original network dataset across the 97 schools from the FB100 schools.

Figure S2: The relative proportion of the original nodes preserved after subsetting to the largest connected component across the 97 schools from the FB100 schools.
Figure S3: The average node degree among nodes in the largest connected component across the 97 schools from the FB100 schools.

Figure S4: (Top) Confirmation that $\hat{\beta}_0^{MLE}$ and the homophily index $\hat{h}_r$ are equivalent, seen here for female (red) and male (black) classes across the 97 colleges from the FB100 networks. (Bottom) Comparison of the maximum likelihood estimate $\hat{\beta}_0^{MLE}$ versus the Williams estimate $\hat{\beta}_0^{MQE}$ obtained from maximizing the quasi-likelihood for the same data, confirming that the difference between the estimates is small in practice, as noted by Williams [57].
6 Majority Vote Classification

The aim of the 1-hop (immediate friends) and 2-hop (friends-of-friends) Majority Vote classifiers is to aggregate the known labels among an unknown node’s friendship network in order to assign classification scores. Given the vector of training labels $a_1, \ldots, a_n$, where $a_i = +1$ for female training label, $a_i = -1$ for Male training label, and $a_i = NA$ is a testing label, we implement the following procedures:

- For the 1-hop Majority Vote, we use the portion of the adjacency matrix corresponding to the unknown testing labels, which we’ll refer to as $A_{test}$ and for a specific unknown node $u$ as $A_{u,test} = A_{test}[u,\cdot]$. Then the classification score assigned to unknown node $u$ is based on the relative difference in the proportion of labeled male friends versus labeled female friends:

$$\frac{A_{u,test} \cdot \|a = -1\| - A_{u,test} \cdot \|a = +1\|}{A_{u,test} \cdot \|a = -1\| + A_{u,test} \cdot \|a = +1\|}.$$  \hspace{1cm} (62)

If node $u$ does not have any labeled neighbors meaning that $A_{u,test} \cdot \|a = -1\|+A_{u,test} \cdot \|a = +1\| = 0$, then we assign a score based on the relative proportions in the training sample:

$$\frac{\sum \|a = -1\| - \sum \|a = +1\|}{\sum \|a = -1\| + \sum \|a = +1\|}.$$  \hspace{1cm} (63)

- For the 2-hop Majority Vote, we implement a similar procedure as the 1-hop Majority Vote except now weights are based on $A_{test}^2$, weighted by the number of length-2 paths to labeled friends-of-friends.

- Note that in the case of ties or when an individual has an equal number of female and male friends, then we still assign this relative class proportion since we compare relational inference methods based on their AUC.

7 Regularization for LINK

The LINK model introduced by Zheleva and Getoor [59] learns a binary logistic regression classifier where the features are the entire row of the adjacency matrix among users who reveal their attribute and the outcome variable is the user’s revealed attribute value. We examine these model fitting issues in this section as they pertain to binary gender inference on the datasets we study, where regularization should be given careful consideration given the large number of predictors and small number of training observations (e.g. $p \gg n_{train}$) where $n_{train}$ denotes the size of the training sample. The method of $\ell_2$-regularized logistic regression minimizes the following cost function where $\beta$ represents the parameter vector corresponding to each of the $N$ nodes in the graph with $\beta_0$ intercept, observed gender values $y_i \in \{-1, 1\}$, gain parameter $C$, and $X_i$ corresponding to the $i$th row of the adjacency matrix for user $i$:

$$\min_{\beta_0, \beta} \frac{1}{2} \beta^T \beta + C \cdot \sum_{i \in \text{train}} \log(\exp(- y_i (X_i^T \beta + \beta_0)) + 1).$$  \hspace{1cm} (64)

Here $C$ captures the inverse of the regularization strength, where for concreteness small (large) values of $C$ correspond with large (small) amounts of regularization. After exploring the sensitivity of the $C$ parameter on classification performance, we find minimal improvement from incorporating $\ell_2$-regularization. To minimize this cost function we use the implementation in Python’s scikit-learn library.

We evaluated several different optimization methods for minimizing the regularized loss across a wide range of gains $C$; in these evaluations we focus on the Amherst College network from the FB100 dataset, the same network featured in the individual network analyses in the main paper. We evaluate scikit-learn’s lbfgs, newton-cg, and liblinear solvers, all with their default parameter settings, as illustrated in Figures S5 and S6 across varying regularization gains. Note that only the liblinear solver is evaluated with $\ell_2$-regularization and $\ell_1$-regularization in Python, while lbfgs and newton-cg are only evaluated with $\ell_2$-regularization. These different solvers sometimes choose rather different models, as seen in the sometimes large differences in AUC. But ultimately across all three solvers we observe robust evidence that $\ell_2$-regularization does not help the AUC, and therefore choose to learn the LINK models throughout this paper (outside this section) using a very large regularization gain $C$ with the lbfgs solver, effectively disabling regularization.

23
On the subject of $\ell_1$-regularization within LINK, we briefly note that such a regularization would in a sense be trying to find a small subset of individuals to use as features for the entire graph, an insight motivated by the “subset selection” interpretation of $\ell_1$-regularization \cite{10}. Since each of the $n$ nodes is only connected to a small fraction of the graph, there's a formal sense to which we require some $O(n)$ fraction of the nodes to have non-zero weights, not $o(n)$, contradicting the subset selection motivation. As a result, the lack of improvement from $\ell_1$-regularization is expected, and indeed this is what we see in Figure S6.

We observe, as has been previously noted \cite{30}, that this unregularized model with a very large number parameters is still empirically good at distinguishing between classes. We also observe a tendency toward separability in Amherst, as seen in Figure S7. Then, as noted in \cite{43}, behavior with a large gain $C$ is similar to choosing an $\ell_2$ max-margin classifier.

**Figure S5**: Evaluate sensitivity to regularization parameter, $C$, on Amherst College, for 1 fold, for $\ell_2$-regularization.

**Figure S6**: Evaluate sensitivity to regularization parameter, $C$, on Amherst College, for 1 fold, for $\ell_1$-regularization.
8 Interpretation of LINK as a 2-hop Method

We claim that the LINK family of linear classifiers (based on linear weights applied the the columns of the adjacency matrix as feature vectors), which include LINK-Logistic Regression, LINK-SVM, and LINK-Naive Bayes, obtain their predictive power from 2-hop paths to individuals friends-of-friends. This section establishes this 2-hop connection explicitly by deriving the weights used by LINK in a Naive Bayes classifier. We demonstrate the Naive Bayes classifier reduces to a linear aggregation over a nodes friends of a nonlinear aggregation over those nodes’ friends (the friends of friends of the classification subject).

Note that we employ a Laplace smoothing factor (“+1”) to handle the case when a node does not have any male or female friends in the training sample.

Suppose that for our training data we observe labels $y_{\text{train}} \in \{ M, F \}$ with the corresponding observed features $x_i \in \{ 0, 1 \}$ and random variable $X \in \{ 0, 1 \}^N$ where $N$ is the total number of nodes in the graph. This set-up represents the observed gender labels, $y_{\text{train}}$, and the observed friendships that all nodes in the network have with these training data. From this information, we construct the Naive Bayes classification rule by making the standard conditional independence assumption and studying the likelihood ratio:

$$LR(x) = \frac{P(y_{\text{train}} = F) \cdot P(X|y_{\text{train}} = F)}{P(y_{\text{train}} = M) \cdot P(X|y_{\text{train}} = M)}$$

(65)

$$= \frac{P(y_{\text{train}} = F) \cdot \prod_{i=1}^{N} P(X_i = x_i|y_{\text{train}} = F)}{P(y_{\text{train}} = M) \cdot \prod_{i=1}^{N} P(X_i = x_i|y_{\text{train}} = M)}$$

(66)

$$= \frac{P(y_{\text{train}} = F)}{P(y_{\text{train}} = M)} \cdot \prod_{i:x_i=0} P(X_i = x_i|y_{\text{train}} = F) \cdot \prod_{i:x_i=1} P(X_i = x_i|y_{\text{train}} = F)$$

(67)

Note that in this expression we’ve separated the non-neighbors and neighbors of a test node by the restriction ($i : x_i = 0$ and $i : x_i = 1$), to be considered separately.

We now have the following empirical estimates, where $n_{F,\text{train}}$ ($n_{M,\text{train}}$) denotes the number of females (males) in the training sample, $d_{i,F,\text{train}}$ ($d_{i,M,\text{train}}$) denotes node $i$’s degree with $F$ ($M$) nodes in the training sample, and we finally assume $d_{i,F,\text{train}} + d_{i,M,\text{train}} = d_{i,\text{train}}$. For simplicity in notation, we’ll remove the $\text{train}$ subscript for the rest of this section. Including +1 Laplace smoothing we have
the following standard maximum likelihood estimates for the “parameters” of the Naive Bayes model:

\[
P(Y_{\text{train}} = F) = \frac{n_F}{n_F + n_M} \quad (68)
\]

\[
P(Y_{\text{train}} = M) = \frac{n_M}{n_F + n_M} \quad (69)
\]

\[
P(X_i = 1|Y_{\text{train}} = F) = \frac{d_i,F + 1}{n_F + 2} \quad (70)
\]

\[
P(X_i = 1|Y_{\text{train}} = M) = \frac{d_i,M + 1}{n_M + 2} \quad (71)
\]

\[
P(X_i = 0|Y_{\text{train}} = F) = \frac{n_F - d_i,F + 1}{n_F + 2} \quad (72)
\]

\[
P(X_i = 0|Y_{\text{train}} = M) = \frac{n_M - d_i,M + 1}{n_M + 2} \quad (73)
\]

Substituting these empirical estimates into the earlier likelihood ratio, we obtain the following likelihood ratio for classifying a test node as belonging to class \( F \):

\[
LR(x) = \frac{n_F}{n_M} \prod_{i:x_i=0} \left( \frac{n_F - d_i,F + 1}{n_F + 2} \right) \prod_{i:x_i=1} \left( \frac{d_i,F + 1}{d_i,M + 1} \right) \quad (74)
\]

\[
= \frac{n_F}{n_M} \prod_{i:x_i=0} \left( \frac{n_F - d_i,F + 1}{n_M - d_i,M + 1} + 1 \right) \prod_{i:x_i=1} \left( \frac{d_i,F + 1}{d_i,M + 1} \right) \quad (75)
\]

\[
= \frac{n_F}{n_M} \left( \frac{n_M + 2}{n_F + 2} \right)^N \prod_{i:x_i=0} \left( \frac{n_F - d_i,F + 1}{n_M - d_i,M + 1} \right) \prod_{i:x_i=1} \left( \frac{d_i,F + 1}{d_i,M + 1} \right) \quad (76)
\]

\[
= \frac{n_F}{n_M} \left( \frac{n_M + 2}{n_F + 2} \right)^N \prod_{i=1}^N \left( \frac{d_i,F + 1}{d_i,M + 1} \right)^{x_i} \left( \frac{n_F - d_i,F + 1}{n_M - d_i,M + 1} \right)^{1-x_i} \quad (77)
\]

Then considering the log of the likelihood-ratio, where

\[
C = \log(n_F/n_M) + N \log((n_M + 2)/(n_F + 2))
\]

is a constant:

\[
\log(LR(x)) = C + \log \left( \prod_{i=1}^N \left( \frac{d_i,F + 1}{d_i,M + 1} \right)^{x_i} \left( \frac{n_F - d_i,F + 1}{n_M - d_i,M + 1} \right)^{1-x_i} \right) \quad (78)
\]

\[
= C + \sum_{i=1}^N x_i \cdot \log \left( \frac{d_i,F + 1}{d_i,M + 1} \right) + \sum_{i=1}^N (1 - x_i) \cdot \log \left( \frac{n_F - d_i,F + 1}{n_M - d_i,M + 1} \right) \quad (79)
\]

\[
= C + \sum_{i=1}^N \log \left( \frac{n_F - d_i,F + 1}{n_M - d_i,M + 1} \right) + \sum_{i=1}^N x_i \cdot \left( \log \left[ \frac{d_i,F + 1}{d_i,M + 1} \right] - \log \left[ \frac{n_F - d_i,F + 1}{n_M - d_i,M + 1} \right] \right) \quad (80)
\]

\[
= C + \sum_{i=1}^N \log \left[ \frac{n_F - d_i,F + 1}{n_M - d_i,M + 1} \right] + \sum_{i=1}^N x_i \cdot \log \left[ \left( \frac{d_i,F + 1}{d_i,M + 1} \right) \cdot \left( \frac{n_M - d_i,M + 1}{n_F - d_i,F + 1} \right) \right] \quad (81)
\]

If we assume that the network is sparse we have that \( n_F, n_M \gg d_i,F, d_i,M \) and can therefore simplify:

\[
\log(LR(x)) \approx C + \sum_{i=1}^N \log \left[ \frac{n_F}{n_M} \right] + \sum_{i=1}^N x_i \cdot \log \left[ \left( \frac{d_i,F + 1}{d_i,M + 1} \right) \cdot \left( \frac{n_M}{n_F} \right) \right] \quad (82)
\]

\[
= C' + \sum_{i=1}^N x_i \cdot \log \left[ \left( \frac{d_i,F + 1}{d_i,M + 1} \right) \cdot \left( \frac{n_M}{n_F} \right) \right] \quad (83)
\]
Thus, we see that LINK-Naive Bayes in particular (and the LINK method in general) is a 2-hop method since the classification procedure relies on the degrees $d_{i,F}$ and $d_{i,M}$ of an unlabeled test node’s neighbor, effectively incorporating information about the labels of nodes two hops away. In the case when $n_M = n_F$, then we can directly observe this 2-hop relation as the log-likelihood ratio $\log(LR(x))$ reduces to $C' + \sum_{i=1}^{N} x_i \cdot \log \left( \frac{d_{i,F} + 1}{d_{i,M} + 1} \right)$. Ignoring the +1 (which comes from the use of Laplacian smoothing), the likelihood a test node is $F$ is scored based on the relative tendency of the test node’s neighbors to form friendships with $F$ nodes relative to $M$ nodes. Note that the scoring is not based on the neighbor’s labels but rather on the neighbor-of-neighbor’s labels in the training data.

9 Add Health Analysis

This section provides an analysis of gender inference on the Add Health dataset [41]. We evaluate homophily and monophily on the undirected and directed degree sequences, where the measures generalize cleanly to the directed setting. We follow the same data pre-processing steps as we did for the FB100, restricting the analysis to only nodes that disclose their gender and restricting to nodes in the largest (weakly) connected component.

A particularly remarkable property of the Add Health networks is that they result from a directed friendship nomination survey that limited the number of male and female friends that each person could nominate, up to five of each. While a survey under such constraints strongly limits the presence of homophily, it does not limit monophily in the in-directed network. For instance, if all females nominate person $u$, then “having $u$ as a friend” would be a key feature for inferring the gender of individuals who have kept that information private. We observe that it is therefore still possible to achieve high classification accuracy in the directed Add Health networks collected with constrained surveys using methods that can harness monophily, a clear demonstration that constrained surveys cannot guarantee privacy. We leave as an open question how to limit the predictive performance of directed network surveys for inferring private attributes.

The out-directed graph is described by an adjacency matrix $A_{ij} = 1$ if student $i$ nominated student $j$. The data collection was restricted such that $\sum_j A_{ij} \leq 10$, $\sum_{j \in M} A_{ij} \leq 5$, and $\sum_{j \in F} A_{ij} \leq 5$. The in-directed graph is defined by an adjacency matrix $A_{ij} = 1$ if student $i$ was nominated by student $j$ and is not restricted as $0 \leq \sum_j A_{ij} \leq N$. Due to the restriction on the out-directed degree sequences, we expect the gender preferences to be underdispersed, which is evident in Figure S9. Lastly, we drop one school (School #27) due to the high proportion of male students (99.8%) at that school.

Focusing on a single representative school, School #23, we evaluate the variance of the empirical distributions for individuals to nominate same-gender friends relative to a null model as shown in Figure S8 which compare to Figure 1 (for the Amherst College Facebook network) in the main paper. Then evaluating the relative performance of LINK-logistic regression [59] on the undirected versus directed degree sequences, we observe that overdispersion again drives the improved performance of LINK in the directed setting.

The classification performance of LINK is driven by in-nominations. That is, a machine learning model based on the feature that user $i$ is nominated by all females will be more useful than a model based on the feature on who user $i$ nominates. Therefore, in Figure S10 we observe that the “in features” created based on a model fit on the out-directed adjacency matrix is the most useful in learning the relationship of correlating received nominations from particular genders. We attribute LINK’s limited performance on the undirected graph as shown in Figure S10 to the underdispersion inherent in the Add Health data collection process.
Figure S8: For Add Health School #23, we compare the variance of the empirical in-class preference distribution (filled bars) relative to the simulated null distribution (solid lines) for the undirected network, out-link network, and in-link network. We observe that the out-link network is underdispersed, which is in part due to the restriction on nominating male and female friends. Meanwhile, we observe the in-link network to be overdispersed which seems to be due to a larger than expected number of individuals nominating all male or all female friends.

Figure S9: (Left) Homophily index $\hat{h}_r$, (Middle) monophily index $\hat{\phi}_r$, and (Right) statistically significant monophily index values at the 0.001 level across Add Health schools, in three different arrangements: (Top) undirected, (Center) out-directed, and (Bottom) in-directed.
Figure S10: Gender classification on school #23 in Add Health with \( n_F = (309, 302, 291) \) and \( n_M = (369, 337, 324) \) for the different (undirected, in-directed, and out-directed) graph versions, respectively.
10 Sampling graphs from the Overdispersed Stochastic Block Model (oSBM)

This section introduces an algorithm for sampling graphs from an overdispersed stochastic block model on \( k \) blocks assuming a latent Beta distribution on friendship preferences and adopting the Beta parameterization in [39]. The algorithm takes as input parameters to control the block structure, \( p_{in} \) and \( p_{out} \), as well as parameters to control the dispersion, \( \phi_{in}^* \) and \( \phi_{out}^* \). Note we assume the same parameter value for \( p_{in,r} \) across all attribute classes \( r \), so denote this by \( p_{in} \) instead of \( p_{in,r} \) for a given class \( r \). In settings where one wants to preserve a given overall average node degree \( \lambda = \frac{1}{N} \sum_{i=1}^{N} d_i \), we give the following parameterization for \( p_{in} \) and \( p_{out} \) that relies on a block structure parameter \( \lambda \geq 1 \) and assumes \( k > 1 \) blocks:

\[
\frac{\lambda}{N} = p_{in} d \quad \Longrightarrow \quad p_{in} = \frac{d \cdot \lambda}{N}
\]

(84)

\[
d = \frac{1}{N} \sum_{i=1}^{k} n_i \cdot (p_{in} n_i + p_{out} \sum_{j=1, j \neq i}^{k} n_j)) \quad \Longrightarrow \quad p_{out} = \frac{d \cdot N - p_{in} \sum_{i=1}^{k} n_i^2}{\sum_{i=1}^{k} n_i \cdot (\sum_{j=1, j \neq i}^{k} n_j)}
\]

(85)

Algorithm 1 Sample from Overdispersed Block Model

1: procedure SAMPLE FROM OVERDISPersed BLOCK Model
2: Input: Given \( k \geq 2 \) mutually exclusive attribute class labels \( \{a_1, \ldots, a_k\} \) for unique class blocks of size \( n_1, \ldots, n_k \) nodes, respectively, let \( N = \sum_{j=1}^{k} n_j \). Also given: block structure \( p_{in}, p_{out} \), dispersion parameters \( \phi_{in}^*, \phi_{out}^* \).
3: Model affinity probabilities for \( in- \) and \( out- \) class degree distributions using latent Beta distribution [39] with parameters \( 0 < p_{in} < 1 \) and \( 0 < p_{out} < 1 \):
4: Create \( in- \) class parameters:
5: \( \alpha_{in} = p_{in} \cdot (\frac{1}{p_{in}}) \cdot (1 - \phi_{in}^*) \)
6: \( \beta_{in} = (1 - p_{in}) \cdot (\frac{1}{p_{in}}) \cdot (1 - \phi_{in}^*) \)
7: Create \( out- \) class parameters:
8: \( \alpha_{out} = p_{out} \cdot (\frac{1}{p_{out}}) \cdot (1 - \phi_{out}^*) \)
9: \( \beta_{out} = (1 - p_{out}) \cdot (\frac{1}{p_{out}}) \cdot (1 - \phi_{out}^*) \)
10: for each attribute class \( \{1, \ldots, k\} \) do
11: \( for \) each node \( i \) in specific class \( r \) do
12: \( p_{i,in} \sim \text{Beta}(\alpha_{in}, \beta_{in}) \)
13: \( d_{i,in} = p_{i,in} \cdot n_r \)
14: \( p_{i,out} \sim \text{Beta}(\alpha_{out}, \beta_{out}) \)
15: \( d_{i,out} = p_{i,out} \cdot \sum_{j=1, j \neq r}^{k} n_j = p_{i,out} \cdot (N - n_r) \)
16: for each affiliation pair \( a_i, a_j \) s.t. \( a_i \leq a_j \) do
17: if \( a_i = a_j = r \) then
18: Create Chung-Lu graph with expected degree sequence \( (d_{i,in}) \) \( \forall i \in r \):
19: \( for \) each node pair \( i, j \in r, i < j \) do
20: \( A_{ij} | p_{i,in}, p_{j,in} \sim \text{Bern} \left( \frac{d_{i,in} d_{j,in}}{n_r^2 p_{in}} \right) \)
21: Set \( A_{ij} := A_{ij} \)
22: if \( a_i = r \neq a_j = s \) then
23: Create bipartite Chung-Lu graph (adopting [28]) with expected degree sequence \( (d_{i,out}) \) and \( (d_{j,out}) \) \( \forall i \in r, \forall j \in s \):
24: \( for \) each node pair \( i \in r, j \in s \) do
25: \( A_{ij} | p_{i,out}, p_{j,out} \sim \text{Bern} \left( \frac{d_{i,out} d_{j,out}}{(N-n_r)(N-n_s) p_{out}} \right) \)
26: Set \( A_{ij} := A_{ij} \)
27: Output: Symmetric adjacency matrix \( A \).
10.1 Properties based on oSBM parameterization.

We assume an underlying model where nodes have an individual affinity for in- and out-class friends where the mean in-class affinity is $p_{\text{in}}$ and the mean out-class affinity is $p_{\text{out}}$. For all nodes $i$ in class $r$, we draw in- and out-class affinity probabilities from a Beta distribution with the following parameterization to preserve the mean in- and out- affinities and the given dispersion parameters $\phi_{\text{in}}$ and $\phi_{\text{out}}$:

$$p_{i,\text{in}} \sim \text{Beta}(\alpha_{\text{in}}, \beta_{\text{in}})$$

where

$$\alpha_{\text{in}} = p_{\text{in}} \cdot \left(\frac{1}{\phi_{\text{in}}}\right) \cdot (1 - \phi_{\text{in}})$$

$$\beta_{\text{in}} = (1 - p_{\text{in}}) \cdot \left(\frac{1}{\phi_{\text{in}}}\right) \cdot (1 - \phi_{\text{in}}) = \left(\frac{1}{\phi_{\text{in}}}\right) \cdot (1 - \phi_{\text{in}}) - \alpha_{\text{in}}, \quad (86)$$

$$p_{i,\text{out}} \sim \text{Beta}(\alpha_{\text{out}}, \beta_{\text{out}})$$

where

$$\alpha_{\text{out}} = p_{\text{out}} \cdot \left(\frac{1}{\phi_{\text{out}}}\right) \cdot (1 - \phi_{\text{out}})$$

$$\beta_{\text{out}} = (1 - p_{\text{out}}) \cdot \left(\frac{1}{\phi_{\text{out}}}\right) \cdot (1 - \phi_{\text{out}}) = \left(\frac{1}{\phi_{\text{out}}}\right) \cdot (1 - \phi_{\text{out}}) - \alpha_{\text{out}}, \quad (87)$$

10.2 Confirm mean attribute affinity is preserved.

For in-class attribute affinity probabilities, we confirm that the above parameterization of the latent Beta distribution is such that $E[p_{i,\text{in}}] = p_{\text{in}}$:

$$E[p_{i,\text{in}}] = \frac{\alpha_{\text{in}}}{\alpha_{\text{in}} + \beta_{\text{in}}} = \frac{p_{\text{in}} \cdot \left(\frac{1}{\phi_{\text{in}}}\right) \cdot (1 - \phi_{\text{in}})}{\left(\frac{1}{\phi_{\text{in}}}\right) \cdot (1 - \phi_{\text{in}})} = p_{\text{in}}, \quad (90)$$

A similar check shows that the out-community affinity probability is such that $E[p_{i,\text{out}}] = p_{\text{out}}$.

10.3 Confirm variance of attribute affinity is preserved.

For in-class affinity probabilities, we confirm that the above parameterization is such that $\phi_{\text{in}}$ introduces extra binomial variation such that $\text{Var}[p_{i,\text{in}}] = \phi_{\text{in}} \cdot p_{\text{in}} \cdot (1 - p_{\text{in}})$:

$$\text{Var}[p_{i,\text{in}}] = \frac{\alpha_{\text{in}} \beta_{\text{in}}}{(\alpha_{\text{in}} + \beta_{\text{in}})^2(\alpha_{\text{in}} + \beta_{\text{in}} + 1)}$$

$$= \frac{\alpha_{\text{in}} \beta_{\text{in}}}{\alpha_{\text{in}} + \beta_{\text{in}} \alpha_{\text{in}} + \beta_{\text{in}} \alpha_{\text{in}} + \beta_{\text{in}} + 1} \cdot \frac{1}{\alpha_{\text{in}} + \beta_{\text{in}} + 1}$$

$$= \frac{p_{\text{in}} \cdot (1 - p_{\text{in}}) \cdot \frac{1}{\phi_{\text{in}} \cdot (1 - \phi_{\text{in}}) + 1}}{\alpha_{\text{in}} + \beta_{\text{in}} + 1}$$

$$= \frac{p_{\text{in}} \cdot (1 - p_{\text{in}}) \cdot \frac{1}{\phi_{\text{in}} - 1 + 1}}{\phi_{\text{in}}}$$

$$= \frac{p_{\text{in}} \cdot (1 - p_{\text{in}})}{\phi_{\text{in}}} \cdot \phi_{\text{in}}. \quad (95)$$

A similar check for the out-community affinity probability shows that $\text{Var}[p_{i,\text{out}}] = \phi_{\text{out}} \cdot p_{\text{out}} \cdot (1 - p_{\text{out}})$. 

31
10.4 Confirm that expected degrees are approximately preserved.

We confirm the oSBM parameterization for edge probabilities, outlined in Algorithm 1 such that $P(A_{ij} = 1 | d_{i,in}, d_{j,in})$ for in-class edges or $P(A_{ij} = 1 | d_{i,out}, d_{j,out})$ for out-class edges, approximately preserves $(d_{i,in})$ and $(d_{i,out})$ as the class-specific expected degrees, and will therefore also approximately preserve $(d_i)$ as the overall expected degrees.

Let node $i$ be in class $r$, and we want to show that $E\left[\sum_{j \in r} A_{ij} | p_{i,in}, p_{j,in}\right] = d_{i,in}$. We have:

$$E\left[\sum_{j \in r} A_{ij} | p_{i,in}, p_{j,in}\right] = \sum_{j \in r} E[A_{ij} | p_{i,in}, p_{j,in}]$$

$$= \sum_{j \in r} d_{i,in} \cdot d_{j,in} / n_r^2 \cdot p_{in}$$

$$= \frac{d_{i,in}}{n_r \cdot p_{in}} \sum_{j \in r} p_{j,in} \cdot n_r$$

$$= \frac{d_{i,in}}{n_r \cdot p_{in}} \sum_{j \in r} p_{j,in}$$

$$\approx \frac{d_{i,in}}{n_r \cdot p_{in}} (n_r \cdot p_{in})$$

$$= d_{i,in}.$$ 

Let node $i$ be in class $r$ and $E\left[\sum_{j \in s \neq r} A_{ij} | p_{i,out}, p_{j,out}\right] = d_{i,out}$, then we have the following:

$$E\left[\sum_{j \in s \neq r} A_{ij} | p_{i,out}, p_{j,out}\right] = \sum_{j \in s \neq r} E[A_{ij} | p_{i,out}, p_{j,out}]$$

$$= \sum_{j \in s \neq r} d_{i,out} \cdot d_{j,out} / (N - n_r) \cdot (N - n_s) \cdot p_{out}$$

$$= \frac{p_{i,out}}{p_{out}} \sum_{j \in s \neq r} p_{j,out}$$

$$\approx \frac{p_{i,out}}{p_{out}} (N - n_r) \cdot p_{out}$$

$$= p_{i,out} \cdot (N - n_r)$$

$$= d_{i,out}.$$