ESTIMATING FACTORS WITH PSYCHOMETRIC NETWORKS: A MONTE CARLO SIMULATION COMPARING COMMUNITY DETECTION ALGORITHMS

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ABSTRACT

Estimating the number of factors in multivariate data is at the crux of psychological measurement. Factor analysis has a long tradition in the field but it's been challenged recently by exploratory graph analysis (EGA), an approach based on network psychometrics. EGA first estimates a regularized partial correlation network using the graphical least absolute shrinkage and selection operator (GLASSO), and then applies the Walktrap community detection algorithm, which identifies *communities* (or factors) in the network. Simulation studies have demonstrated that EGA has comparable or better accuracy than contemporary state-of-the-art factor analytic methods (e.g., parallel analysis), while providing some additional advantages such as not requiring rotations and deterministic allocation of items into factors. Despite EGA's effectiveness, there has yet to be an investigation into whether other community detection algorithms could achieve equivalent or better perfomance. In the present study, we performed a Monte Carlo simulation using the GLASSO and two variants of a non-regularized partial correlation network estimation method and several community detection algorithms in the open-source *igraph* package in R. The purpose of the present study was to critically examine whether the network estimation and community detection components of EGA are optimal for estimating factors in psychological data as well as to provide a systematic investigation into how different community detection algorithms perform "out-of-the-box." The results indicate that the Fast-greedy, Louvain, and Walktrap algorithms paired with the GLASSO method were consistently among the most accurate and least biased across conditions.

Keywords community detection · latent factors · exploratory graph analysis · network psychometrics

1 Introduction

Many psychological phenomena are complex systems of related components. These components often form distinct clusters where there are many relations between some components relative to other components in the system. In psychology, these clusters are most often referred to as *factors* or latent attributes that underlie the relations between components. Identifying these factors are important for theory, scale construction and validation, and statistical analyses in psychology (Cattell, 1978). It's not surprising then that the accurate estimation of these factors has been one of the most active areas in psychological measurement.

Over the last half century, there have been several variants on methods that were developed to estimate the number of underlying factors in psychological data. The primary methods are principal component analysis (PCA) and factor analysis, which focus on extracting the common covariance between variables to derive factors. Within the PCA and factor analysis framework, there exist a plethora of variants that are aimed at improving the accuracy of these methods

such as parallel analysis (PA; Horn, 1965), K1 rule (eigenvalues greater than 1; Kaiser, 1960), and scree test (Cattell, 1966).

More recently, a new method called *exploratory graph analysis* (EGA; Golino & Epskamp, 2017) was introduced to the literature. EGA uses a network modeling framework, often referred to as *network psychometrics* (Epskamp et al., 2018), to first estimate the relationships between variables (i.e., estimate a network) and then the *communities* (or factors) that form from these relationships. The standard EGA algorithm first applies the graphical least absolute shrinkage and selector operator (GLASSO; Friedman, Hastie, & Tibshirani, 2008, 2014) to the inverse covariance matrix to estimate a Gaussian graphical model (GGM; Lauritzen, 1996) where edges (or lines) represent (regularized) partial correlations between nodes (or circles), which represent variables in the network. After, EGA applies the Walktrap community detection algorithm (Pons & Latapy, 2006), which uses random walks to determine the number and content of the communities in the network. The communities detected by the algorithm are shown to be mathematically equivalent to latent factors identified by factor models (Golino & Epskamp, 2017). Simulation studies have demonstrated that EGA estimates the correct number of factors as well as or better than most PCA and factor analysis methods (Golino & Epskamp, 2017). In addition to its accuracy, EGA also provides additional advantages such as avoiding the need for rotations (Guttman, 1953) and the deterministic allocation of items into factors (Golino, Shi, et al., 2020).

Despite the effectiveness of EGA in psychological data, there has been only one investigation, to our knowledge, into the effect of different network estimation methods (Golino, Shi, et al., 2020) and no investigations into the effect of different community detection algorithms. To date, the GLASSO has been the standard network estimation method applied across psychological network studies (Epskamp & Fried, 2018). Notably, there are other network estimation methods that are likely to estimate different network structures, which ultimately affects the estimation of the number and content of factors. Indeed, one simulation study compared the factor estimation accuracy of the GLASSO and triangulated maximally filtered graph (TMFG; Massara, Di Matteo, & Aste, 2016) methods using the Walktrap community detection algorithm (Golino, Shi, et al., 2020). This study found that the GLASSO network estimation method had better accuracy and less bias than the TMFG but both performed comparable to the best factor analytic techniques.

Other network estimation methods such as non-regularized GGMs have been put forward in the literature (Williams et al., 2019). These methods have been shown to have better performance when estimating the simulated network structure of dense (highly connected) networks, which are thought to be common in psychology (Williams & Rast, 2018). Despite their better performance when estimating the population network structure, there has yet to be an investigation in whether they perform better for estimating factors in networks. Similarly, the Walktrap community detection algorithm has yet to be evaluated against other algorithms, such as the Spinglass algorithm (Reichardt & Bornholdt, 2006), which have been used in the psychometric network literature (e.g., De Beurs et al., 2019). Despite their application, there has yet to be a systematic investigation that compares these algorithms in a psychological network context.

In general, most community detection algorithms were developed and validated on networks containing a large number of nodes (e.g., > 1,000; Lancichinetti & Fortunato, 2009; Yang, Algesheimer, & Tessone, 2016). Moreover, these algorithms may only work well for one type of problem or data structure (Gates, Henry, Steinley, & Fair, 2016). Because most psychological networks consist of fewer than 100 nodes, there is a need to verify which of these algorithms work best in conditions that are more commonly found in the psychological literature.

One recent simulation study systematically examined several freely available community detection algorithms in the context of brain networks (Gates et al., 2016). Brain networks are perhaps the closest comparison to psychological networks in that they are typically represented by correlational (rather than count) data and generally have fewer than 1,000 nodes. In their study, Gates and colleagues (2016) generated network models using structural equation modeling and manipulated several conditions that included the number of nodes and communities, size of edge weights (i.e., correlations), and correlations between communities. Of the six algorithms they examined, the Walktrap and Louvain (Blondel, Guillaume, Lambiotte, & Lefebvre, 2008) algorithms performed the best across conditions. Importantly, their study investigated conditions where there were a small number of nodes (i.e., 25 and 75).

2 Present Research

The goal of the present study was twofold: (1) compare the effects of different network estimation methods and (2) community detection algorithms on the accuracy of factor estimation in psychological data. For the network estimation methods, we used the standard network estimation method in EGA, the GLASSO, and compared its accuracy to two variants of a non-regularized partial correlation method that are based on neighborhood selection (Williams et al., 2019). These two variants differed solely on their criterion for model selection: Bayesian information criterion (BIC) and Akaike information criterion (AIC). For the community detection algorithms, we examined several freely available algorithms that were used in Gates et al.'s (2016) simulation study and included a few others that were freely available in the *igraph* package (Csardi & Nepusz, 2006) in R (R Core Team, 2020).

Our simulation study differed from previous studies that have compared these network estimation methods and community detection algorithms in a few ways. First, the data in this study were generated from a factor model rather than from an empirical dataset or network model (Gates et al., 2016; Williams et al., 2019). Although much of the psychometric network literature has focused on the substantive differences (i.e., hypotheses about the data generating model) between factor and network models (e.g., Borsboom, 2008; Schmittmann et al., 2013), our focus was on the accurate estimation of factors rather than the potentially different meaning of them. Second, this study specifically analyzed the accuracy of factor estimation rather than whether the true network structure was identified (i.e., correct number of edges; Williams et al., 2019). It's plausible that the true network structure may contain many edges that are not relevant for detecting factors, which may reduce the efficacy of contemporary community detection algorithms. Therefore, network estimation methods could differ on their utility (e.g., correct estimation of the true network structure vs. correct estimation of factors). Finally, the present simulation generates data that aligns with conditions more commonly found in psychological networks than previous studies; specifically, multivariate data with a relatively low number of factors (e.g., 1, 2, and 4) and variables per factor (e.g., 4, 8, and 12). With these conditions, the number of nodes in the network range from 4 to 48, which is considerably smaller than networks often observed in brain data (Gates et al., 2016). Importantly, we also generated data with cross-loading magnitudes that were across a larger range than previous simulations using EGA (Golino, Shi, et al., 2020).

3 Methods

3.1 Data Generation

We generated data from multivariate normal factor models following the same approach as Golino, Shi, et al. (2020). First, the reproduced population correlation matrix was computed:

$$\mathbf{R_R} = \mathbf{\Lambda \Phi \Lambda'},$$

where $\mathbf{R_R}$ is the reproduced population correlation matrix, lambda ($\mathbf{\Lambda}$) is the k (variables) $\times$ r (factors) factor loading matrix, and $\mathbf{\Phi}$ is the $r \times r$ correlation matrix. The population correlation matrix, $\mathbf{R_P}$, was then obtained by putting the unities on the diagonal of $\mathbf{R_R}$. Next, Cholesky decomposition was performed on the correlation matrix such that:

$$\mathbf{R_P} = \mathbf{U'U}.$$

If the population correlation matrix was not positive definite (i.e., at least one eigenvalue ≤ 0) or any single item's communality was greater than 0.90, then $\mathbf{\Lambda}$ was re-generated and the same procedure was followed until these criteria are met. Finally, the sample data matrix of continuous variables was computed:

$$\mathbf{X} = \mathbf{ZU},$$

where $\mathbf{Z}$ is a matrix of random multivariate normal data with rows equal to the sample size and columns equal to the number of variables.

To generate polytomous data, each continuous variable was categorized into five categories, resembling a 5-point Likert scale, with a random skew ranging from -2 to 2 on a 0.5 interval from a random uniform distribution following the approach of Garrido, Abad, and Ponsoda (2011, 2013).

3.2 Network Estimation Methods

3.2.1 GLASSO

The GLASSO uses the least absolute shrinkage and selection operator (LASSO; Tibshirani, 1996), which is a statistical regularization technique that reduces parameter estimates, with some estimates becoming exactly zero (for the mathematical notation, see Epskamp & Fried, 2018). The aim of this technique is to achieve a sparse network model—non-relevant edges are removed from the model, leaving only a subset of relevant (not necessarily significant) edges.

This sparsity is controlled by a parameter called *lambda* (λ). Lower values of lambda remove fewer edges, increasing the possibility of including spurious associations, while larger values of lambda remove more edges, increasing the possibility of removing relevant edges. When $\lambda = 0$, then the estimates are equal to the ordinary least squares solution (i.e., the partial correlation matrix). This parameter is thus an important part of model selection, striking a balance

between sensitivity (i.e., selecting relevant edges that are truly relevant) and specificity (i.e., removing edges that are truly not relevant).

The popular approach in the network psychometrics literature is to compute models across several values of λ (usually 100) and to select the model that minimizes the extended Bayesian information criterion (EBIC; Chen & Chen, 2008; Epskamp & Fried, 2018). The EBIC model selection uses a hyperparameter (γ) to control how much it prefers simpler models (i.e., models with fewer edges; Foygel & Drton, 2010). Larger γ values lead to simpler models, while smaller γ values lead to denser models. When $\gamma = 0$, the EBIC is equal to the Bayesian information criterion. In the psychometric network literature, this approach has been termed EBICglasso and is applied via the *qgraph* package (Epskamp, Cramer, Waldorp, Schmittmann, & Borsboom, 2012) in R. For continuous data, Pearson's correlations were computed; for polytomous data, polychoric correlations were computed.

Following the EGA approach (Golino, Shi, et al., 2020), the minimum λ value is set to .01, which is slightly larger than the default of .001. This is selected to reduce the prevalence of false positive edges in the network. Next, the γ value is set to .50, which is the default; however, it is iteratively decreased by .25, until reaching zero, based on whether any one node in the network is disconnected. If γ reaches zero, then the network is used regardless of whether any nodes are disconnected. Finally, a node that forms its own community is not included in as a part of the number of factors estimated (Golino, Shi, et al., 2020). This removes variables that are not identified to be a part of any factor in the network.

3.2.2 Non-regularized partial correlation networks

In addition, two variants of a non-regularized partial correlation estimation method were used. Both methods were based on a regression strategy called *neighborhood selection*, which uses node-wise multiple regression on each node in the network (Williams et al., 2019). Multiple regression coefficients have direct correspondence to the inverse covariance coefficients in that the negative regression coefficient ($-\beta_{ij}$) divided by the predictor variable's variance (σ_j^2) is equal to the inverse covariance between the regressed variable and the predictor variable given all other variables (θ_{ij}).

The multiple regression coefficients for each regressed variable are placed across the row of each target variable with the regressed variable's variance in its respective element's position (θ_{ii}^2; i.e., variance of each variable is on the diagonal). A common method for computing partial correlations is to take the square root of the product of the corresponding regression coefficients in the matrix and replacing their signs (i.e., $\rho_{ij} = sign(\beta_{ij})\sqrt{\beta_{ij}}, i \neq j$). Notably, this leads to an asymmetric covariance matrix where coefficients do not correspond to their respective transpose element (i.e., $\theta_{ij}^2 \neq \theta_{ji}^2$).

There are two approaches for determining whether an edge should be non-zero: the "and-rule" where both β_{ij} and β_{ji} must be non-zero and the "or-rule" where only one coefficient must be non-zero. Both approaches use a forward search strategy for determining non-zero coefficients, which removes predictor variables from each multiple regression that minimize some criterion until the minimum value of the criterion is achieved for the set of predictor variables. The coefficients that are not removed in the process of minimizing the criterion are retained in the network as non-zero edges, while the removed variables are set to zero.

This criterion is based on traditional model selection criteria AIC and BIC. The main difference between these criteria is that the BIC tends to penalize more complex models more severely than the AIC. In short, the AIC is better in conditions when a false negative is considered to be worse than a false positive, while BIC is better in conditions when a false positive is considered to be worse than a false negative.

For this study, we examined both the AIC and BIC approaches to edge selection with the "and-rule" because they were shown to have considerable differences (relative to the differences of the "and-rule" and "or-rule") in estimating the population network structure in previous simulations (Williams et al., 2019). Both non-regularized partial correlation network models were estimated using the *GGMnonreg* package (Williams, 2019) in R.

3.3 Community Detection Algorithms

This study focused on eight different community detection algorithms that are freely available via the R package igraph. These included the Walktrap (Pons & Latapy, 2006), Infomap (Rosvall & Bergstrom, 2008), Fast-greedy (Clauset, Newman, & Moore, 2004), Louvain (Blondel et al., 2008), Leading Eigenvalue (Newman, 2006), Label Propagation (Raghavan, Albert, & Kumara, 2007), Spinglass (Reichardt & Bornholdt, 2006), and Edge Betweenness (Girvan & Newman, 2002) community detection algorithms.

All community detection algorithms were implemented with their default arguments in order to evaluate their baseline, "out-of-the-box" performance without researcher direction (similar to Gates et al., 2016). Moreover, all network matrices were input with absolute values to avoid the bias of some methods performing better than others because of

their ability to handle negative associations. Below, we briefly describe *modularity*, a metric used to quantify the quality of community partitions, and then each algorithm (more detailed information can be found within their respective citations).

3.3.1 Modularity

A key definition for understanding many community detection algorithms is the concept of modularity (Newman, 2006). Modularity can be expressed as (Fan, Li, Zhang, Wu, & Di, 2007):

$$Q = \frac{1}{2w} \sum_{ij} (w_{ij} - \frac{w_i w_j}{2w}) \, \delta(c_i, c_j),$$

where w_{ij} is the edge strength (e.g., partial correlation) for a given node pair, and w_j are the node strength for node i and node j (respectively), w is the sum of all the edge weights in the network, c_i and c_j represents the community that node i and node j belong to, and δ is 1 if the nodes belong to the same community (i.e., $c_i = c_j$) and 0 if otherwise. Essentially, modularity reflects the extent to which communities have more connections within the community and fewer connections with other communities.

3.3.2 Walktrap

The Walktrap algorithm (Pons & Latapy, 2006) has been the most commonly applied algorithm in the psychometric network literature as the default of EGA (Golino & Epskamp, 2017; Golino, Shi, et al., 2020). The Walktrap algorithm begins by computing a transition matrix where each element represents the probability (based on node strength) of one node traversing to another. Random walks are then initiated for a certain number of steps (e.g., 4), using the transition matrix for probable destinations. Using Ward's agglomerative clustering approach (Ward, 1963), each node starts as its own cluster and merges with adjacent clusters (based on squared distances between each cluster) in a way that minimizes the sum of squared distances between other clusters. Modularity is then used to determine the optimal partition of clusters (i.e., communities).

3.3.3 Infomap

Similar to the Walktrap algorithm, the Infomap algorithm (Rosvall & Bergstrom, 2008) uses random walks. Different from the Walktrap algorithm, Infomap is derived from information theory with idea of "compressing" the conditional information of a random walk on the network into Huffman codes (a binary naming system; Rosvall & Bergstrom, 2008). The major difference between these two algorithms is that Infomap captures the conditional flow of information across the network in a way that maximizes the information (e.g., bits) of the random walk process. The partition function that optimizes this minimization is given by the entropy of movement between and within communities. The space of possible partitions is explored using a deterministic greedy search algorithm, which is refined using a simulated annealing approach.

3.3.4 Fast-greedy

The Fast-greedy algorithm (Clauset et al., 2004) uses modularity to identify optimal partitions in the network. Like the Walktrap algorithm, the Fast-greedy algorithm begins with each node considered as its own community and follows a hierarchical clustering algorithm. The algorithm then proceeds by iteratively combining neighboring communities in a greedy way: Each node is moved into a community that maximizes the modularity function. These aggregate communities are then merged until the modularity function can no longer be increased.

3.3.5 Louvain

The Louvain algorithm (also referred to as Multi-level; Blondel et al., 2008) is very similar to the Fast-greedy algorithm in that it iteratively uses modularity to optimize its partitions. It differs in that its motivation is to identify hierarchical structures in large networks, specifically it iteratively exchanges nodes between communities and evaluates the change in modularity until it no longer improves. Then, the algorithm collapses the communities into latent nodes and identifies edge weights with other observed and latent nodes, which provides the "multi-level" structure (Gates et al., 2016). In its use in this study, the algorithm was not used to identify hierarchical community structures in the network. Therefore, it's expected that this algorithm will closely align with the Fast-greedy algorithm. It's also important to note that the algorithm implemented in igraph is deterministic; however, other implementations are not (Gates et al., 2016; Rubinov & Sporns, 2010).

3.3.6 Leading Eigenvalue

The Leading Eigenvalue algorithm (Newman, 2006) is based on spectral properties of the network using eigenvector of the first eigenvalue to determine optimal community structures. Like Fast-greedy and Louvain algorithms, the Leading Eigenvalue algorithm uses modularity to optimize these structures. The algorithm begins by computing the first eigenvector of the modularity matrix and the network is split into two communities that improves the modularity. This process iteratively unfolds until there is no longer improvement in modularity.

3.3.7 Label Propagation

The Label Propagation algorithm (Raghavan et al., 2007) begins by assigning each node a unique label. Each node then adopts the same label that the majority of its neighbors have with ties being broken randomly. This continues iteratively until each node has the same label as the majority of its neighbors. The general notion of the algorithm is that a consensus will develop among the nodes in the network. Notably, this algorithm is not deterministic in that it produces different results with each run. In this study, only one run was implemented for each sample in order to evaluate its accuracy in its current form. Other strategies such as repeated sampling could be used to arrive at a relatively stable organization of communities (e.g., median network and community structures; Christensen & Golino, 2019; De Beurs et al., 2019; Lancichinetti & Fortunato, 2012).

3.3.8 Spinglass

The Spinglass algorithm comes from statistical physics and is based on the Potts model with the notion that "the problem of community detection can be mapped onto finding the ground state of an infinite ranged Potts spin glass" (Reichardt & Bornholdt, 2006, p. 1540). In essence, edges should connect nodes that are in the same spin state (i.e., community), while nodes in different states should be disconnected, which results in a "lower energy state" or ground state of the system. The model is simulated for some number of steps (e.g., 25) and the spin states in the end define the communities. Similar to the Label Propagation algorithm, this algorithm is not deterministic and only one run was implemented in this study.

3.3.9 Edge Betweenness

The Edge Betweenness algorithm (Girvan & Newman, 2002) was one of the first algorithms used to identify communities in networks. This algorithm finds edges that are frequently "between" other nodes in the network known as edge betweenness (based on the betweenness centrality; Freeman, 1977). Edge betweenness is calculated for the entire network and the edge with the highest betweenness value is removed. All edges that are affected by this removal have their edge betweenness value recalculated. This process repeats iteratively until no edges remain, making this algorithm substantially slower than the other algorithms. Modularity is used to determine the optimal cut-off.

3.4 Unidimensionality Adjustment

A well-known limitation of community detection algorithms is that they tend to favor multidimensional structures (Golino, Shi, et al., 2020). This is a consequence of what most of these algorithms were designed to do: identify modular components in large networks (i.e., > 1000 nodes). Because this issue resides in many of the community detection algorithms, all psychometric network models were adapted to the unidimensional approach found in Golino, Shi, et al. (2020).

Their approach works in the following way: generate a random multivariate normal dataset with a certain number of variables (e.g., four) with high factor loadings (e.g., .70) on a single factor and add these variables to the original dataset before computation of the (partial) correlation matrix. Then, compute the network and apply the community detection algorithm. If the algorithm estimates one or two factors, then the original data is unidimensional. If there are more than two factors are estimated, then the generated variables are removed, and the network and community detection algorithms are reapplied. The conceptual reasoning behind this is that the generated variables represent a cohesive single factor that is independent of the original data. Therefore, it is known that if there are two factors, then one will be the generated data and the other will be the original data. Based on recommendations by (Golino, Shi, et al., 2020), the number of variables generated in the simulated data was set equal to the variables per factor in the data generation conditions.

3.5 Parallel Analysis

As a comparison, two parallel analysis (PA) methods—principal axis factoring (PAF) and PCA—were used. These two methods (hereafter referred to as *algorithms* to correspond to the community detection algorithms) were chosen

because they have been extensively evaluated in the literature (e.g., Garrido et al., 2013) and have shown comparable performance with EGA in a previous simulation study (Golino, Shi, et al., 2020). In short, PA generates a larger number of random datasets, with an equivalent number of cases as the original dataset, by resampling (with replacement) from the original dataset (Horn, 1965). The number of factors (PAF) or components (PCA) whose eigenvalues in the original dataset are greater than the mean of the resampled datasets is suggested as the factor solution. The models were estimated using the minimum residual estimator.

3.6 Design

The population models were simulated from a multidimensional multivariate normal distribution with factor loadings for each item generated with $\pm.10$ deviance drawn from a uniform distribution. These factor loadings were manipulated to be small (.40), moderate (.55), and large (.70). Cross-loadings were also generated following a random normal distribution with a mean of zero and a standard deviation of .10. The correlations between factors (.00, .30, .50, and .70) and sample sizes (250, 500, 1000, 5000) were also manipulated. The number of factors—one, two, and four—were simulated to provide unidimensional and multidimensional structures that are commonly found in the psychological literature (Henson & Roberts, 2006). There were four, eight, and twelve variables per factor, which represented conditions common in scale development and validation.

The simulation design of the current study allowed for a mixed factorial design: $4 \times 4 \times 3 \times 3 \times 3 \times 2$ (factor correlations $\times$ sample size $\times$ number of factors $\times$ number of variables $\times$ factor loadings $\times$ number of responses) for a total of 864 simulated condition combinations. There were 500 samples generated for each condition.

3.7 Statistical Analyses

To evaluate the performance of the network and parallel analysis approaches, accuracy and bias were measured using the percentage of correct number of factors (PC), mean bias error (MBE; the average deviation away from the correct number of factors) and mean absolute error (MAE; the average absolute deviation away from the correct number of factors). These are defined below:

$$PC = \frac{\sum C}{N},\ for\ C = \begin{cases} 1 \text{ if } \hat{\theta} = \theta \\ 0 \text{ if } \hat{\theta} \neq \theta \end{cases},$$

$$MBE = \frac{\sum(\hat{\theta} - \theta)}{N},$$

$$MBE = \frac{\sum|\hat{\theta} - \theta|}{N},$$

where $\hat{\theta}$ is the estimated number of factors, θ is the population number of factors, and N is the number of sample data matrices simulated.

A second approach was used to quantify the accuracy of the item placement of the community detection algorithms, specifically, whether the items were being identified in the correct factor. The number of factors, for example, could be estimated correctly; however, some factors may have items that belong to a different factor than the population factor.

One common approach from the network science literature is to use normalized mutual information (NMI; Danon, Diaz-Guilera, Duch, & Arenas, 2005). NMI defines a confusion matrix, M, where the rows correspond to the population factors and the columns correspond to the estimated factors. The element, C_{ij}, refers to the number of items that are found in population factor i that are in the estimated factor j. Using the information-theoretic measure of mutual information, this defines NMI as:

$$NMI = \frac{-2\sum_{i=1}^{C_A}\sum_{j=1}^{C_B} M_{ij}\log(M_{ij}M/M_{i.}M_{.j})}{\sum_{i=1}^{C_A} M_{i.}\log(M_{i.}/M)\ +\ \sum_{j=1}^{C_B} M_{.j}\log(M_{.j}/M)},$$

where C_A is the number of population factors and C_B is the number of estimated factors. The NMI metric can be roughly interpreted as the proportion of items properly placed into the correct factor, but with a slightly larger penalty for items not placed in the correct factor.

4 Results

4.1 Accuracy and Bias

The overall performance of the network and PA methods and algorithms are presented in Figure 1. As shown in Figure 1, the number of responses did not have much effect on the accuracy of the GLASSO method but did have a considerable effect on the accuracy of the AIC, BIC, and PA methods. In fact, both parallel analysis algorithms dropped over 10% overall accuracy from continuous responses to polytomous responses ($\Delta_{PCA} = 10.1\%$ and $\Delta_{PFA} = 20.2\%$; Table 1). For the network methods, there was a general trend for the GLASSO method (79.9%) to perform better than the two variants of the non-regularized partial correlation method (AIC = 63.3% and BIC = 58.6%), which held across community detection algorithms and number of responses (i.e., continuous vs. polytomous data; Figure 1). As for the community detection algorithms, the Louvain (75.2%), Fast-greedy (74.9%), and Walktrap (73.8%) had the highest overall percent correct across the network methods (Table 1) and were the least affected by number of responses when used with the GLASSO method (Figure 1). When collapsed across number of responses, the Louvain, Fast-greedy, and Walktrap algorithm of the GLASSO method had the best accuracy (88.6%, 87.8%, and 87.1%) followed by the PCA algorithm of PA method (86.7%; Table 1).

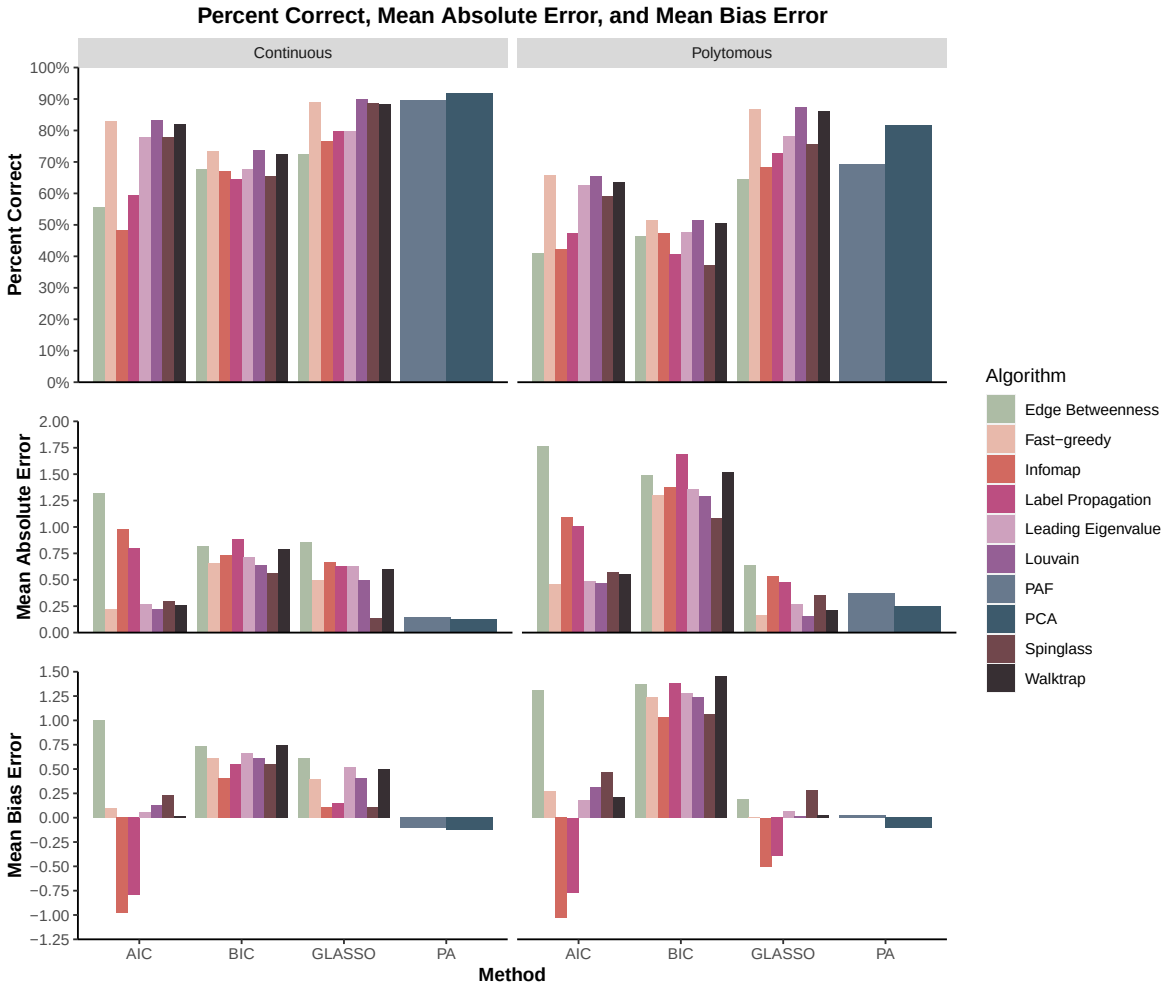

Figure 1: Accuracy and bias measures broken down by method, algorithm, and number of responses. PA = Parallel Analysis.

Notably, the Louvain and Fast-greedy algorithms had nearly equivalent performance within each network method (Table 1), which was expected as the Louvain algorithm is similar to the Fast-greedy algorithm with a modification for hierarchical structures (communities are not merged but rather nodes are switched between communities). The Spinglass algorithm, which has been one of the more commonly used algorithms in the literature (e.g., De Beurs et

al., 2019), was on the higher end of overall accuracy when used with the GLASSO method (80.8%) but was unable to estimate a large proportion of the conditions when used with the BIC (continuous = 0.81; polytomous = 0.84) and GLASSO (continuous = 0.58; polytomous = 0.34) methods. This inability of the Spinglass algorithm to estimate factors in the networks was likely due to the sparsity of the networks estimated by the BIC and GLASSO methods, which tended to estimate sparser networks than the AIC method. Therefore, the algorithm's performance must be evaluated with caution because its results were from a limited proportion of the samples examined.

Table 1: Percent Correct for Each Independent Condition

		Sample Size				# of Factors			# of Variables			Factor Correlations				Factor Loadings			Number of Responses		
Algorithm	**Method**	250	500	1000	5000	1	2	4	4	8	12	0.00	0.30	0.50	0.70	0.40	0.55	0.70	Continuous	Polytomous	**Overall**
Edge Betweenness (57.7%)	AIC	36.4	46.9	54.1	55.7	**83.7**	47.1	15.9	57.7	49.7	37.7	53.7	51.4	47.2	40.3	38.4	52.5	53.7	55.5	40.9	48.2
	BIC	31.7	53.7	68.8	73.1	77.8	53.2	41.5	65.4	58.0	48.4	65.7	61.8	55.3	45.2	37.4	64.2	68.4	67.6	46.2	57.0
	GLASSO	62.2	66.3	69.3	74.4	**98**	64.4	40.7	64.6	69.5	70.9	**80.5**	74.3	65.4	53.1	52.9	70.9	78.7	72.3	64.6	68.3
Fast-greedy (74.9%)	AIC	52.2	73.7	**84.4**	**87.9**	**89.7**	61.5	72.6	79.9	79.2	64.2	**80.9**	78.7	73.6	64.0	60.4	**81.4**	**81.4**	**83.0**	65.7	74.3
	BIC	30.9	55.1	73.7	**89.8**	76.3	54.0	58.2	75.4	63.1	50.0	69.6	66.8	61.6	51.9	42.6	69.7	74.2	73.3	51.5	62.5
	GLASSO	79.7	**86.8**	**89.8**	**93.7**	**98.7**	**80.0**	**84.4**	**85.3**	**89.2**	**89.0**	**94.7**	**92.2**	**87.3**	77.0	68.3	**93.0**	**99.3**	**89.1**	**86.7**	**87.8**
Infomap (58.1%)	AIC	38.2	43.6	49.7	49.6	**99.3**	18.2	21.4	41.7	48.8	44.9	52.0	48.6	43.0	37.2	34.2	41.9	59.9	48.1	42.3	45.2
	BIC	34.1	53.5	68.7	71.8	**81.7**	47.5	44.2	60.4	60.6	51.1	66.6	62.8	55.3	44.1	36.7	62.8	71.1	66.9	47.4	57.3
	GLASSO	67.1	71.7	74.3	75.4	**99.3**	51.5	65.1	60.9	75.3	**80.9**	**87.1**	**80.7**	68.3	53.1	50.3	72.8	**90.4**	76.6	68.4	72.3
Label Propagation (60.6%)	AIC	42.7	51.2	58.4	61.1	**95.9**	44.5	21.9	58.6	54.4	47.1	60.9	57.4	51.6	43.1	40.6	55.3	64.0	59.3	47.2	53.2
	BIC	27.4	48.5	65.1	68.9	73.1	50.4	36.0	63.2	52.5	43.3	59.8	56.8	51.2	42.9	34.6	58.6	63.9	64.5	40.7	52.7
	GLASSO	70.1	76.0	78.2	78.9	**98.4**	69.8	58.5	71.8	76.7	79.7	**89.6**	**83.5**	73.0	58.0	54.9	76.6	**93.4**	79.6	72.7	76.0
Leading Eigenvalue (69.0%)	AIC	58.3	71.1	76.1	75.8	**93.2**	68.6	50.3	71.7	73.7	65.4	75.8	73.8	69.8	61.4	61.5	76.4	73.0	78.0	62.5	70.2
	BIC	31.6	52.7	67.8	78.1	77.4	57.3	39.8	69.8	57.9	46.6	63.8	61.3	56.8	48.9	41.7	64.4	66.2	67.8	47.5	57.7
	GLASSO	74.6	78.4	79.6	**82.4**	**98.8**	**83.9**	52.6	77.2	79.2	**80.4**	**85.0**	**82.4**	78.4	69.8	65.5	**82.4**	**86.7**	79.6	78.3	78.9
Louvain (75.2%)	AIC	51.1	72.8	**84.3**	**90.1**	**89.2**	62.2	72.4	**80.9**	79.7	62.8	**80.5**	78.4	73.9	64.4	61.4	**81.3**	**80.5**	**83.1**	65.5	74.3
	BIC	31.0	55.0	73.4	**91.0**	76.0	54.4	58.8	76.1	63.5	49.9	69.6	66.9	61.9	52.6	43.7	70.0	73.7	73.8	51.5	62.8
	GLASSO	**80.2**	**87.2**	**90.4**	**95.3**	**98.7**	**81.4**	**85.3**	**85.9**	**90.0**	**89.9**	**94.8**	**92.7**	**88.4**	78.5	70.2	**93.4**	**99.4**	**89.9**	**87.4**	**88.6**
PFA (79.4%)	PA	59.1	78.8	**88.0**	**91.5**	75.1	**82.0**	**81.0**	69.2	**85.2**	**83.6**	**81.2**	**81.6**	79.9	74.9	64.0	**87.5**	**86.6**	**89.5**	69.3	79.4
PCA (86.7%)	PA	70.1	**87.9**	**92.3**	**96.4**	**98.4**	**87.1**	74.5	78.8	**90.5**	**90.7**	**94.5**	**93.1**	**88.2**	71.0	**81.1**	**88.3**	**90.6**	**91.7**	**81.6**	**86.7**
Spinglass (70.7%)	AIC	46.5	66.7	77.2	**83.2**	**80.9**	56.5	69.0	**80.6**	71.6	54.7	73.3	71.6	67.9	60.7	59.2	75.1	70.7	77.7	59.0	68.4
	BIC	30.1	48.9	62.0	**80.2**	56.7	38.8	60.5	**84.6**	56.9	42.4	56.2	54.0	51.4	46.6	53.2	56.9	48.1	65.4	37.2	52.4
	GLASSO	74.8	**82.0**	**84.8**	**86.9**	**91.8**	73.7	76.0	**84.7**	**80.5**	78.1	**84.7**	**83.7**	**80.9**	74.3	59.3	**85.3**	**89.5**	**88.7**	75.8	**80.8**
Walktrap (73.8%)	AIC	54.5	71.3	**80.3**	**85.8**	**92.0**	66.1	61.4	73.2	76.6	68.5	**80.3**	77.6	72.1	60.9	58.1	**80.4**	**80.0**	**82.0**	63.6	72.7
	BIC	31.1	54.5	72.1	**87.9**	76.8	56.2	52.8	72.6	62.6	50.4	69.2	66.1	60.5	50.4	41.5	68.8	73.3	72.6	50.4	61.6
	GLASSO	**80.4**	**85.9**	**88.0**	**93.0**	**98.6**	**83.7**	78.3	**82.2**	**88.8**	**90.4**	**94.8**	**91.7**	**86.3**	75.6	67.1	**91.9**	**99.3**	**88.3**	**86.0**	**87.1**

Note. Bolded values represent conditions where 80% or more of the replicated samples were estimated correctly. The algorithms are denoted with their percent correct across conditions in parentheses. PFA = Principal Factor Analysis and PCA = Principal Component Analysis.

When broken down by each simulated condition Table 1, the best performing methods and algorithms were similar across the overall results. The Louvain and Walktrap algorithms paired with the GLASSO method achieved 80% or better accuracy regardless of sample size followed by PCA and the Fast-greedy and Spinglass algorithms paired with the GLASSO method for sample sizes of 500, 1000, and 5000. For the number of factors, only the Fast-greedy and Louvain algorithms with the GLASSO method achieved 80% or better across all factors. The PA algorithms were split where PCA performed better with fewer factors (1 and 2) whereas PFA performed better with more factors (4). This finding is consistent with previous studies examining these algorithms (e.g., Golino, Shi, et al., 2020). The Walktrap algorithm with the GLASSO method achieved 80% or better for one and two factors and was nearly there with four factors (78.3%). A similar pattern was found for the number of variables: both the Fast-greedy and Louvain algorithms with GLASSO were above 85% accuracy across the number of variables, while the Walktrap algorithm with the GLASSO method achieved 80% accuracy or better. The PA algorithms and the Spinglass with the GLASSO method achieved 80% accuracy or better for two of three conditions.

Perhaps the two most influential conditions for accuracy were the correlations between factors and factor loadings. Most GLASSO and PA algorithms achieved at least 80% correct when there were orthogonal (.00) or small (.30) correlations between factors. When there were moderate (.50) correlations between factors, only the Fast-greedy, Louvain, Spinglass, and Walktrap algorithms of the GLASSO method as well as the PCA algorithm of the PA method achieved at least 80% or better accuracy. PA with the PFA algorithm was right on the edge (79.9%; Table 1). For large (.70) correlations between factors, no method and algorithm combination achieved at least 80% accuracy. The top performing combinations were the Louvain (78.5%), Fast-greedy (77.0%), and Walktrap (75.6%) algorithms with the GLASSO method as well as the PFA algorithm with the PA method (74.9%).

For the factor loadings, only the PCA algorithm of the PA method achieved at least 80% or better across the loadings conditions (Table 1). Notably, most of the network methods tended to struggle when there were low loadings (.40). The Louvain algorithm with the GLASSO method had the highest accuracy (70.2%) followed by the Fast-greedy and Walktrap algorithms with the GLASSO method (68.3% and 67.1%, respectively). When loadings were at least a moderate size ($\geq$ .55), the GLASSO method with several different community detection algorithms outperformed the PA algorithms. The top performing community detection algorithms—Fast-greedy, Louvain, and Walktrap—achieved at least 90% or greater accuracy, which was substantially larger than the best PA method's accuracies.

Digging into the bias measures, the three lowest MAE was for the PA method and PCA algorithm (0.19) followed by the PA method and PAF algorithm (0.26) and GLASSO method and Louvain algorithm (0.32; Figure 1). The other top PC community detection algorithms (Fast-greedy, Louvain, and Walktrap) were generally on the lower end across network methods in the order of GLASSO (0.32, 0.32, and 0.40, respectively), AIC (0.34, 0.35, and 0.41, respectively), and BIC (0.97, 0.96, and 1.15, respectively). In general, the MAE was much lower for the PA and GLASSO methods than the AIC and BIC methods. When split between number of responses, the AIC, BIC, and PA methods generally had greater values, while the GLASSO method had lower values in the polytomous data relative to the continuous data.

The MBE showed that the AIC method had many of the lowest (Walktrap = 0.11, Leading Eigenvalue = 0.12, and Fast-greedy = 0.18) and highest (Label Propagation = -0.78, Infomap = -1.01, and Edge Betweenness = 1.15) values, which largely corresponded with the each algorithm's PC (i.e., greater PC, lower MBE and lower PC, greater MBE; Figure 1). The PA methods were among the lowest MBE values with a slight tendency to underfactor (PAF = -0.03 and PCA = -0.12). Of the top accuracy community detection algorithms, there was a general tendency to overfactor ($\text{Fast-greedy}_{\text{GLASSO}}$ = 0.20, $\text{Louvain}_{\text{GLASSO}}$ = 0.20, and $\text{Walktrap}_{\text{GLASSO}}$ = 0.26). The MBE generally increased for the AIC and BIC methods in the polytomous data, while it generally decreased for the GLASSO and PA methods.

In sum, the GLASSO method and Fast-greedy, Louvain, and Walktrap algorithms were among the most accurate and least biased across all conditions. For the continuous data, the PA algorithms were among the most accurate and least biased with the top GLASSO algorithms being comparable. For the polytomous data, the top GLASSO algorithms outperformed all other methods and algorithms with the PA method and PCA algorithm following closely behind. In general, the methods could largely be split into two relative performance groups: high accuracy and low bias (GLASSO and PA), and low accuracy and high bias (AIC and BIC). Similarly, with respect to the methods, the algorithms could be split into three relative performance groups: high accuracy and low bias (Fast-greedy, Louvain, Walktrap, and PCA), moderate accuracy and moderate bias (Leading Eigenvalue, Spinglass, and PAF), and low accuracy and high bias (Edge Betweenness, Infomap, and Label Propagation).

4.2 Item Placement

Although accuracy and bias measures are important for determining the overall performance of the algorithms, community detection algorithms for the network methods allow for "deterministic" placement of items in factors, specifically the algorithms place items in factors without the researcher's direction. The meaning of deterministic is

used loosely because some algorithms (e.g., Label Propagation, Spinglass) are stochastic and therefore may perform better when item placements are aggregated and summarized across applications (e.g., consensus clustering approaches; Lancichinetti & Fortunato, 2012).

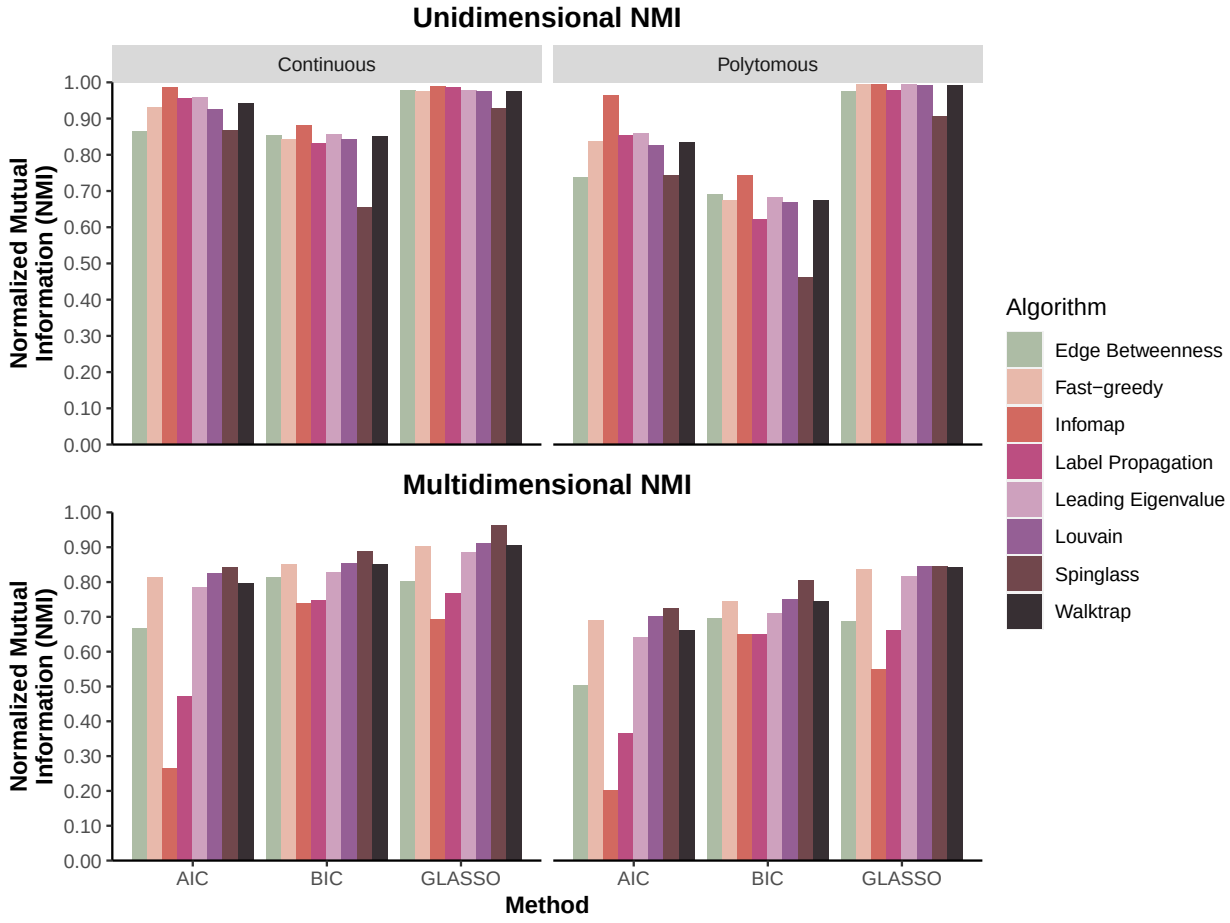

Figure 2: Normalized mutual information broken down by method, algorithm, and number of responses.

4.2.1 Unidimensional structures

In general, most of the algorithms had good performance (NMI > .80) regardless of number of responses (Figure 2). It's important to note that the NMI values largely correspond to the percent correct for unidimensional structures (see Table 1); however, NMI penalizes the number of variables that are not included in the largest factor (i.e., two variables not suggested to be in the largest factor will have a lower NMI than one variable not suggested to be in the largest factor). The BIC method tended to have the poorest performance and especially when the number of responses were polytomous. The AIC and GLASSO methods tended to have similar patterns of performance for each algorithm; however, the AIC method had lower values for the polytomous data relative to the continuous data, while the GLASSO method had comparable or higher values for the polytomous data relative to the continuous data. Overall, the GLASSO had the best NMI with several algorithms with values above .98 (in order from greatest to least): Infomap, Leading Eigenvalue, Louvain, Fast-greedy, Walktrap, and Label Propagation.

4.2.2 Multidimensional structures

Relative to the unidimensional structures, the NMI values were much lower across methods except for the BIC method. In contrast, the BIC method generally had better item placement with multidimensional structures (particularly for polytomous data). Consistent with the unidimensional results, most algorithms with the GLASSO method had higher NMI values than all other method and algorithm combinations regardless of the number of responses. Notably, the performance of the AIC method was much lower for multidimensional structures relative to unidimensional structures.

Indeed, the BIC method outperformed the AIC on each respective algorithm. Finally, the number of responses had a strong general effect, lowering NMI values about .10 or more across nearly all methods and algorithms. Across the number of responses, the best performing combinations were the Spinglass (0.89), Louvain (0.88), Fast-greedy (0.87), and Walktrap (0.87) algorithms with the GLASSO method. It's important to note, however, that the Spinglass algorithm could only achieve a solution in about half (56.5%) of the conditions relative to the algorithms.

4.2.3 Summary

Broadly, the GLASSO method had the best item placement performance and demonstrated the highest values of NMI for each respective algorithm. As a general trend across algorithms, the three most accurate and least biased algorithms—Fast-greedy, Louvain, and Walktrap—were also among the best performing on the NMI metric. Although this is not surprising, it was certainly not a given because algorithms could hypothetically provide imprecise estimates of the number of factors but have more accurate item placements. Overall, the item placement metric provides greater evidence that the GLASSO method, in combination with the Fast-greedy, Louvain, and Walktrap algorithms, is the best performing network method.

4.3 Best Algorithms

To provide more nuanced information on the interactions between conditions, we evaluated the accuracy of the top three network algorithms (Louvain, Fast-greedy, and Walktrap) with the GLASSO method and PA algorithms. Notably, all three network algorithms appear roughly comparable and were largely unaffected by the number of responses (Figure 1). Because of this, we present the results collapsed across number of responses.

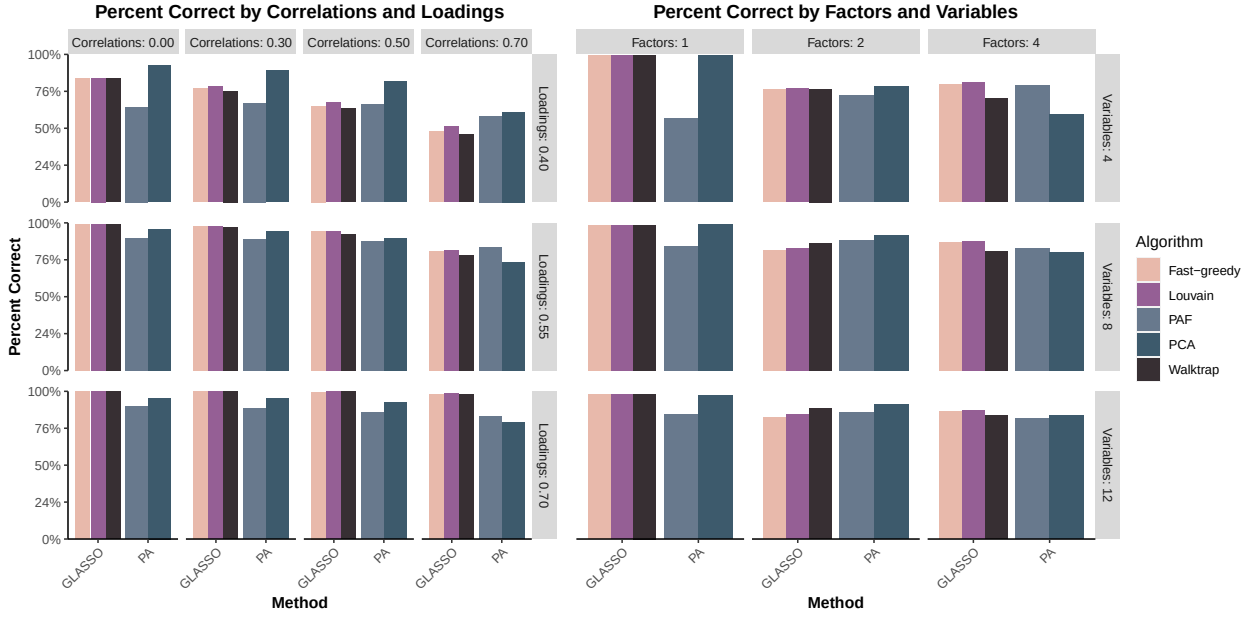

Figure 3: Percent correct broken down by correlations between factors and factor loadings (left) as well as number of factors and variables (right). PA = Parallel Analysis.

When the percent correct was broken down by correlations between factors and factor loadings (Figure 3, left), there was a general trend of increased accuracy as correlations between factors decreased and factor loadings increased. The size of factor loadings had a greater effect on accuracy (η_p^2 = .09) than the correlations between factors (η_p^2 = .03). The PA method and PCA algorithm had the best performance across correlations between factors when the factor loadings were small (0.40). The network algorithms, regardless of correlations between factors, performed as well as or better than both PA algorithms when the factor loadings were moderate (.55) and large (.70), replicating previous simulation findings (Golino, Shi, et al., 2020).

When the percent correct was broken down by number of factors and variables (Figure 3, right), there was a general trend of greater accuracy as the number of factors decreased (η_p^2 = .02). Conversely, there was a general trend of greater accuracy as the number of variables increased (η_p^2 = .01). There was a particularly interesting pattern for the PA method

when there were four variables and the number of factors increased: the PCA algorithm had much greater accuracy than the PAF algorithm when there was only one factor (99.0% and 56.6%, respectively), comparable accuracy when there were two factors (78.4% and 72.4%, respectively), and much lower accuracy when there were four factors (59.1% and 78.7%, respectively; Figure 3, right). Across the number of factors and variables conditions, the community detection algorithms with GLASSO were on par or better than the best performing PA method.

In general, the GLASSO method appears to be comparable to the PA method across all condition interactions except for when there were small loadings where the PA method and PCA algorithm were best. As for the network algorithms, the Walktrap algorithm appears to have decreased accuracy when there are few variables (4) and many factors (4), but otherwise all algorithms were relatively on par with one another.

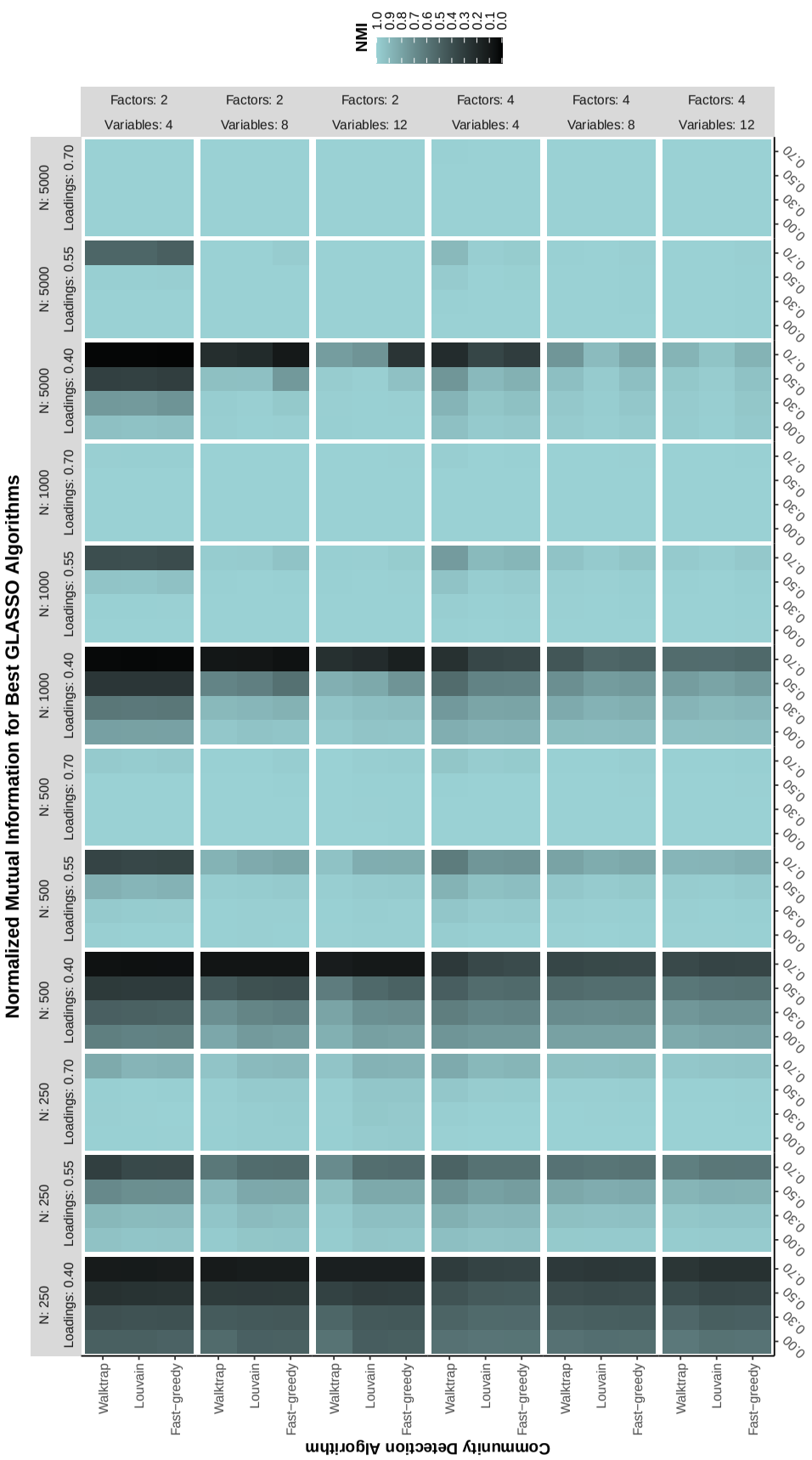

Figure 4: A heatmap of normalized mutual information broken down for best GLASSO community detection algorithms.

In Figure 4, we visualized the NMI broken down within each condition excluding the one factor condition. The one factor condition was excluded because there was little difference between algorithms (see Table 1 and Figure 2). In large part, the algorithms followed the same general patterns of performance across conditions. Algorithms had their worst NMI performance when factor loadings were small (.40), there were few factors (2), variables per factor (4), and when correlations between factors was large (.70). Increases in sample size tended to mitigate these effects except for when there were few variables per factor (4) and large correlations between factors (.70). When factor loadings were at least of moderate size (.55) and sample size was at least 500, then the algorithms performed exceptionally well.

As is evident in Figure 4, the largest effects on performance were for correlations between factors (η_p^2 = 0.14 or a moderate effect size; Cohen, 1992) and factor loadings (η_p^2 = 0.34 or a large effect size). Their interaction also had a moderate effect (η_p^2 = 0.12) on NMI performance. All other main effect and interaction effect sizes were relatively small in comparison ($\eta_p^2 \leq .04$); for example, factor loadings (η_p^2 = 0.03), number of variables (η_p^2 = 0.03), and the interaction between sample size and factor loadings (η_p^2 = 0.04).

5 Discussion

This study examined the performance (accuracy and bias) of different network methods and several community detection algorithms for estimating latent factors. To our knowledge, this is the most comprehensive evaluation of community detection algorithms for psychological data to date. As a comparison for these algorithms, we used state-of-the-art parallel analysis methods to benchmark these algorithms against traditional factor analytic approaches. In short, we found that some network algorithms were comparable to the PA algorithms and that this performance was dependent on the network estimation method and community detection algorithms being used. Specifically the Louvain, Fast-greedy, and Walktrap algorithms all performed as well as or better than the PA algorithms when the GLASSO network estimation method was used. Importantly, we also evaluated the community detection algorithms with two variants of a non-regularized network estimation method.

This study was the first, to our knowledge, to evaluate how different partial correlation network estimation methods performed when identifying factors in psychological factor models. Previous work had compared the GLASSO to a correlation-based method, the TMFG, with the GLASSO showing better performance in nearly all conditions (Golino, Shi, et al., 2020). Moreover, other work had evaluated the performance of the non-regularized partial correlation methods used in this study to estimate population network models (Williams & Rast, 2018; Williams et al., 2019). In these studies, the non-regularized partial correlation methods (i.e., AIC and BIC) outperformed the GLASSO on measures of specificity (avoidance of false positives) in the simulated network structure. In contrast, we found that although these methods may have performed better in estimating the true edges in the network, they did not perform better with respect to estimating the number or content of the factors in simulated unidimensional and multidimensional factor structures.

As for the community detection algorithms, there has been extensive evaluations of these algorithms across different literatures, but none were specific to psychological factor models. The closest comparison had been with brain network correlation structures (Gates et al., 2016). In Gates and colleagues' (Gates et al., 2016) study, they found that for correlation matrices the Walktrap algorithm outperformed the other algorithms on a measures of item placement. Notably, the Louvain algorithm performed the best when Euclidean Distance was used as a similarity measure. In general, our results largely jibe with their study, showing that the Walktrap and Louvain algorithms were among the best performing algorithms. It's important to note that the Louvain algorithm used in this study (from the igraph package in R) may have differed from the one implemented in their study (from the Brain Connectivity Toolbox in Matlab; Rubinov & Sporns, 2010) in regard to the stochasticity of the algorithm. In general, we demonstrated that these algorithms can also be considered the most optimal across many typical conditions of psychological networks, including better performance than state-of-the-art factor analytic approaches. Indeed, when data were categorical, which is often the case in psychology, these algorithms paired with the GLASSO network estimation method performed substantially better. This finding mirrors previous simulation studies and supports the notion that parallel analysis was designed for and works better with continuous data (Garrido et al., 2013; Golino, Shi, et al., 2020; Horn, 1965).

In consideration of the community detection algorithms that have often been used in the psychological literature, specifically the Walktrap and Spinglass algorithms, both performed relatively well compared to many of the other community detection algorithms. One critical finding was that while the Spinglass algorithm was among the best performing algorithms in this study it was not always able to estimate the number of factors in the network. This inability to estimate factors may have been to some networks having unconnected nodes. This was particularly noticeable for the BIC method, which produces the sparsest networks of the three network methods. Researchers should consider this when applying the Spinglass algorithm. Moreover, for stochastic algorithms, such as the Spinglass, researchers should

strongly consider using repeated sampling approaches to obtain better estimates (e.g., Christensen & Golino, 2019; Lancichinetti & Fortunato, 2012).

In regard to EGA, which has been one of the most common approaches for factor estimation from the network perspective, these results shed light on current practices and offer fruitful avenues forward. EGA uses the GLASSO network estimation method and Walktrap community detection algorithm, which performed favorably across simulated conditions in the current and previous simulation studies (Golino & Epskamp, 2017; Golino, Shi, et al., 2020). Our simulation was the first to evaluate the EGA approach in polytomous data, and the results mirror previous simulation studies that examined continuous and dichotomous data (Golino, Shi, et al., 2020). Notably, this simulation differed from our previous investigation by having a broader distribution of cross-loadings. The correspondence between the results suggests that EGA is not severely affected by number of responses or larger cross-loadings. We do, however, note that the item placement accuracy was lower when the correlations between factors (and therefore cross-loadings) were larger (.70) as well as when factor loadings were smaller (.40). This suggests that although the number of estimated dimensions may be accurate the placement of items might be less so.

Considering the other community detection algorithms, there is good evidence that the Louvain and Fast-greedy algorithm are worthwhile considerations for adoption into the EGA framework. Because the two algorithms are relatively similar and demonstrated similar performance, preference should be given to the Louvain algorithm because it also provides a hierarchical or "multi-level" structuring of factors. Such hierarchical structuring is important for determining different levels of taxonomies that often exist in psychological assessment instruments (e.g., personality, psychopathology; Christensen et al., 2020; Kotov et al., 2017). Moreover, an additional algorithm also provides another method to compare results from in EGA such that the best fitting or most theoretically consistent model can be chosen based on the results (e.g., Golino, Moulder, et al., 2020).

Our study has a couple limitations that are worth noting. First, the community detection algorithms evaluated in this study do not allow for the potential for overlapping community detection (e.g., Blanken et al., 2018), which may be more informative and substantively in line with some the data structures simulated in this study (e.g., variables that have strong cross-loadings on one or more factors) and real-world psychological data. Overlapping community detection algorithms would potentially also be advantageous for improving the accuracy of the predictions where variables may "flip" between communities in stochastic algorithms. Another limitation is that the data generated in this study were from factor models, which although are common in the psychological literature, may not conform to data that are generated by network models (e.g., Christensen & Golino, 2020). Generating data from a network model with a known community structure might involve first generating a cluster network model and then adding random edges between the clusters to achieve a specific topology such as a small-world network. In this way, the number of clusters (or communities) is known but the data are not specific to a factor model structure. Other approaches, such as those applied by Gates et al. (2016), should also be considered.

6 References

Blanken, T. F., Deserno, M. K., Dalege, J., Borsboom, D., Blanken, P., Kerkhof, G. A., & Cramer, A. O. J. (2018). The role of stabilizing and communicating symptoms given overlapping communities in psychopathology networks. *Scientific Reports*, *8*, 5854. https://doi.org/10.1038/s41598-018-24224-2

Blondel, V. D., Guillaume, J.-L., Lambiotte, R., & Lefebvre, E. (2008). Fast unfolding of communities in large networks. *Journal of Statistical Mechanics: Theory and Experiment*, *2008*, P10008. https://doi.org/10.1088/1742-5468/2008/10/P10008

Borsboom, D. (2008). Psychometric perspectives on diagnostic systems. *Journal of Clinical Psychology*, *64*, 1089–1108. https://doi.org/10.1002/jclp.20503

Cattell, R. B. (1966). The scree test for the number of factors. *Multivariate Behavioral Research*, *1*, 245–276. https://doi.org/10.1207/s15327906mbr0102_10

Cattell, R. B. (1978). *The scientific use of factor analysis in behavioral and life sciences*. Boston, MA: Springer. https://doi.org/10.1007/978-1-4684-2262-7

Chen, J., & Chen, Z. (2008). Extended bayesian information criteria for model selection with large model spaces. *Biometrika*, *95*, 759–771. https://doi.org/10.1093/biomet/asn034

Christensen, A. P., & Golino, H. (2019). Estimating the stability of the number of factors via Bootstrap Exploratory Graph Analysis: A tutorial. *PsyArXiv*. https://doi.org/10.31234/osf.io/9deay

Christensen, A. P., & Golino, H. (2020). Random, factor, or network model? Predictions from neural networks. *PsyArXiv*. https://doi.org/10.31234/osf.io/awkcb

Christensen, A. P., Golino, H., & Silvia, P. J. (2020). A psychometric network perspective on the validity and validation of personality trait questionnaires. *European Journal of Personality*. https://doi.org/10.1002/per.2265

Clauset, A., Newman, M. E. J., & Moore, C. (2004). Finding community structure in very large networks. *Physical Review E*, *70*, 066111. https://doi.org/10.1103/PhysRevE.70.066111

Cohen, J. (1992). A power primer. *Psychological Bulletin*, *112*, 155–159. https://doi.org/10.1037/0033-2909.112.1.155

Csardi, G., & Nepusz, T. (2006). The igraph software package for complex network research. *InterJournal, Complex Systems*, *1695*, 1–9. Retrieved from https://pdfs.semanticscholar.org/1d27/44b83519657f5f2610698a8ddd177ced4f5c.pdf

Danon, L., Diaz-Guilera, A., Duch, J., & Arenas, A. (2005). Comparing community structure identification. *Journal of Statistical Mechanics: Theory and Experiment*, *2005*, P09008. https://doi.org/10.1088/1742-5468/2005/09/P09008

De Beurs, D., Fried, E. I., Wetherall, K., Cleare, S., O'Connor, D. B., Ferguson, E., ... O'Connor, R. C. (2019). Exploring the psychology of suicidal ideation: A theory driven network analysis. *Behaviour Research and Therapy*, *120*, 103419. https://doi.org/10.1016/j.brat.2019.103419

Epskamp, S., Cramer, A. O. J., Waldorp, L. J., Schmittmann, V. D., & Borsboom, D. (2012). qgraph: Network visualizations of relationships in psychometric data. *Journal of Statistical Software*, *48*, 1–18. https://doi.org/10.18637/jss.v048.i04

Epskamp, S., & Fried, E. I. (2018). A tutorial on regularized partial correlation networks. *Psychological Methods*, *23*, 617–634. https://doi.org/10.1037/met0000167

Epskamp, S., Maris, G., Waldrop, L. J., & Borsboom, D. (2018). Network psychometrics. In P. Irwing, D. Hughes, & T. Booth (Eds.), *The Wiley handbook of psychometric testing, 2 volume set: A multidisciplinary reference on survey, scale and test development*. New York, NY: Wiley. https://doi.org/10.1002/9781118489772.ch30

Fan, Y., Li, M., Zhang, P., Wu, J., & Di, Z. (2007). Accuracy and precision of methods for community identification in weighted networks. *Physica A: Statistical Mechanics and Its Applications*, *377*, 363–372. https://doi.org/10.1016/j.physa.2006.11.036

Foygel, R., & Drton, M. (2010). Extended Bayesian information criteria for Gaussian graphical models. In J. D. Lafferty, C. K. I. Williams, J. Shawe-Taylor, R. S. Zemel, & A. Culotta (Eds.), *Advances in neural information processing systems* (pp. 604–612). Retrieved from http://papers.nips.cc/paper/4087-extended-bayesian-information-criteria-for-gaussian-graphical-models

Freeman, L. C. (1977). A set of measures of centrality based on betweenness. *Sociometry*, 35–41. Retrieved from https://www.jstor.org/stable/3033543

Friedman, J., Hastie, T., & Tibshirani, R. (2008). Sparse inverse covariance estimation with the graphical lasso. *Biostatistics*, *9*, 432–441. https://doi.org/10.1093/biostatistics/kxm045

Friedman, J., Hastie, T., & Tibshirani, R. (2014). *glasso: Graphical lasso – estimation of Gaussian graphical models*. Retrieved from https://CRAN.R-project.org/package=glasso

Garrido, L. E., Abad, F. J., & Ponsoda, V. (2011). Performance of Velicer's minimum average partial factor retention method with categorical variables. *Educational and Psychological Measurement*, *71*, 551–570. https://doi.org/10.1177/0013164410389489

Garrido, L. E., Abad, F. J., & Ponsoda, V. (2013). A new look at Horn's parallel analysis with ordinal variables. *Psychological Methods*, *18*, 454–474. https://doi.org/10.1037/a0030005

Gates, K. M., Henry, T., Steinley, D., & Fair, D. A. (2016). A monte carlo evaluation of weighted community detection algorithms. *Frontiers in Neuroinformatics*, *10*, 45. https://doi.org/10.3389/fninf.2016.00045

Girvan, M., & Newman, M. E. J. (2002). Community structure in social and biological networks. *Proceedings of the National Academy of Sciences*, *99*, 7821–7826. https://doi.org/10.1073/pnas.122653799

Golino, H., & Epskamp, S. (2017). Exploratory Graph Analysis: A new approach for estimating the number of dimensions in psychological research. *PloS ONE*, *12*, e0174035. https://doi.org/10.1371/journal.pone.0174035

Golino, H., Moulder, R., Shi, D., Christensen, A. P., Neito, M. D., Nesselroade, J. R., ... Boker, S. M. (2020). Entropy Fit Index: A new fit measure for assessing the structure and dimensionality of multiple latent variables. *Multivariate Behavioral Research*. https://doi.org/10.1080/00273171.2020.1779642

Golino, H., Shi, D., Christensen, A. P., Garrido, L. E., Nieto, M. D., Sadana, R., ... Martinez-Molina, A. (2020). Investigating the performance of Exploratory Graph Analysis and traditional techniques to identify the number of latent factors: A simulation and tutorial. *Psychological Methods*, *25*, 292–320. https://doi.org/10.1037/met0000255

Guttman, L. (1953). Image theory for the structure of quantitative variates. *Psychometrika*, *18*, 277–296.

Henson, R. K., & Roberts, J. K. (2006). Use of exploratory factor analysis in published research: Common errors and some comment on improved practice. *Educational and Psychological Measurement*, *66*, 393–416. https://doi.org/10.1177/0013164405282485

Horn, J. L. (1965). A rationale and test for the number of factors in factor analysis. *Psychometrika*, *30*, 179–185. https://doi.org/10.1007/BF02289447

Kaiser, H. F. (1960). The application of electronic computers to factor analysis. *Educational and Psychological Measurement*, *20*, 141–151. https://doi.org/10.1177/001316446002000116

Kotov, R., Krueger, R. F., Watson, D., Achenbach, T. M., Althoff, R. R., Bagby, R. M., ... Zimmerman, M. (2017). The hierarchical taxonomy of psychopathology (HiTOP): A dimensional alternative to traditional nosologies. *Journal of Abnormal Psychology*, *126*, 454–477. https://doi.org/10.1037/abn0000258

Lancichinetti, A., & Fortunato, S. (2009). Community detection algorithms: A comparative analysis. *Physical Review E*, *80*, 056117. https://doi.org/10.1103/PhysRevE.80.056117

Lancichinetti, A., & Fortunato, S. (2012). Consensus clustering in complex networks. *Scientific Reports*, *2*, 336. https://doi.org/10.1038/srep00336

Lauritzen, S. L. (1996). *Graphical models*. Oxford, UK: Clarendon Press.

Massara, G. P., Di Matteo, T., & Aste, T. (2016). Network filtering for big data: Triangulated Maximally Filtered Graph. *Journal of Complex Networks*, *5*, 161–178. https://doi.org/10.1093/comnet/cnw015

Newman, M. E. J. (2006). Modularity and community structure in networks. *Proceedings of the National Academy of Sciences*, *103*, 8577–8582. https://doi.org/10.1073/pnas.0601602103

Pons, P., & Latapy, M. (2006). Computing communities in large networks using random walks. *Journal of Graph Algorithms and Applications*, *10*, 191–218. https://doi.org/10.7155/jgaa.00185

Raghavan, U. N., Albert, R., & Kumara, S. (2007). Near linear time algorithm to detect community structures in large-scale networks. *Physical Review E*, *76*, 036106. https://doi.org/10.1103/PhysRevE.76.036106

R Core Team. (2020). *R: A language and environment for statistical computing*. Vienna, Austria: R Foundation for Statistical Computing. Retrieved from https://www.R-project.org/

Reichardt, J., & Bornholdt, S. (2006). Statistical mechanics of community detection. *Physical Review E*, *74*, 016110. https://doi.org/10.1103/PhysRevE.74.016110

Rosvall, M., & Bergstrom, C. T. (2008). Maps of random walks on complex networks reveal community structure. *Proceedings of the National Academy of Sciences*, *105*, 1118–1123. https://doi.org/10.1073/pnas.0706851105

Rubinov, M., & Sporns, O. (2010). Complex network measures of brain connectivity: Uses and interpretations. *NeuroImage*, *52*, 1059–1069. https://doi.org/10.1016/j.neuroimage.2009.10.003

Schmittmann, V. D., Cramer, A. O. J., Waldorp, L. J., Epskamp, S., Kievit, R. A., & Borsboom, D. (2013). Deconstructing the construct: A network perspective on psychological phenomena. *New Ideas in Psychology*, *31*, 43–53. https://doi.org/10.1016/j.newideapsych.2011.02.007

Tibshirani, R. (1996). Regression shrinkage and selection via the lasso. *Journal of the Royal Statistical Society. Series B (Methodological)*, 267–288. https://doi.org/10.1111/j.2517-6161.1996.tb02080.x

Ward, J. H. (1963). Hierarchical clustering to optimise an objective function. *Journal of the American Statistical Association*, *58*, 238–244.

Williams, D. R. (2019). *GGMnonreg: Estimate non-regularized Gaussian graphical models*. Retrieved from https://github.com/donaldRwilliams/GGMnonreg

Williams, D. R., & Rast, P. (2018). Back to the basics: Rethinking partial correlation network methodology. *Journal of Mathematical and Statistical Psychology*. https://doi.org/10.1111/bmsp.12173

Williams, D. R., Rhemtulla, M., Wysocki, A. C., & Rast, P. (2019). On nonregularized estimation of psychological networks. *Multivariate Behavioral Research*, *54*, 719–750. https://doi.org/10.1080/00273171.2019.1575716

Yang, Z., Algesheimer, R., & Tessone, C. J. (2016). A comparative analysis of community detection algorithms on artificial networks. *Scientific Reports*, *6*, 30750. https://doi.org/10.1038/srep30750