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Exploring Estimation Procedures for Reducing Dimensionality in Psychological Network Modeling

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ABSTRACT

To understand psychological data, it is crucial to examine the structure and dimensions of variables. In this study, we examined alternative estimation algorithms to the conventional GLASSO-based exploratory graph analysis (EGA) in network psychometric models to assess the dimensionality structure of the data. The study applied Bayesian conjugate or Jeffreys' priors to estimate the graphical structure and then used the Louvain community detection algorithm to partition and identify groups of nodes, which allowed the detection of the multi- and unidimensional factor structures. Monte Carlo simulations suggested that the two alternative Bayesian estimation algorithms had comparable or better performance when compared with the GLASSO-based EGA and conventional parallel analysis (PA). When estimating the multidimensional factor structure, the analytically based method (i.e., EGA.analytical) showed the best balance between accuracy and mean biased/absolute errors, with the highest accuracy tied with EGA but with the smallest errors. The sampling-based approach (EGA.sampling) yielded higher accuracy and smaller errors than PA; lower accuracy but also lower errors than EGA. Techniques from the two algorithms had more stable performance than EGA and PA across different data conditions. When estimating the unidimensional structure, the PA technique performed the best, followed closely by EGA, and then EGA.analytical and EGA.sampling. Furthermore, the study explored four full Bayesian techniques to assess dimensionality in network psychometrics. The results demonstrated superior performance when using Bayesian hypothesis testing or deriving posterior samples of graph structures under small sample sizes. The study recommends using the EGA.analytical technique as an alternative tool for assessing dimensionality and advocates for the usefulness of the EGA.sampling method as a valuable alternate technique. The findings also indicated encouraging results for extending the regularization-based network modeling EGA method to the Bayesian framework and discussed future directions in this line of work. The study illustrated the practical application of the techniques to two empirical examples in R.

KEYWORDS
Network psychometrics; dimensionality assessment; estimation procedures; community detection algorithm; Bayesian estimation

Introduction

Examining the structure and dimensions of variables is essential to understand many psychological data. Psychology typically uses measurement instruments to define a domain of functioning. Identifying the underlying dimensions of the multivariate psychological data is an important endeavor to determine how the data can be summarized into a smaller set of meaningful variables (i.e., dimensions), which are often used as inferences for psychological phenotypes. Analyzing data with overfactored dimensions often runs the risk of misspecifying the model, harming predictions, and losing knowledge translation. Furthermore, psychological theories often rely on detecting latent structures to understand human traits, in the fields such as intelligence (Garcia-Garzon et al., 2019), personality (Geiser et al., 2021), and creativity (Silvia, 2008). Recovering the number of latent factors plays a critical role in constructing psychological theories.

Multivariate psychological data are often perceived as proxies for latent variables that interact with each other

(Bollen, 2014). Existing rules for assessing dimensions in psychology are under the latent variable modeling framework and can be classified into three categories (Garrido et al., 2016). The first category applies statistical tests such as maximum-likelihood, generalized least squares, and asymptotically distribution-free methods to assess dimensions. The second category relates to the mathematical and psychometric criteria including Kaiser-Guttman criterion (Kaiser, 1960), parallel analysis (Horn, 1965), and the minimum average partial method (Velicer, 1976). The third category relies on rules of thumb, such as the scree test (Cattell, 1966) and variables with significant loadings (Floyd & Widaman, 1995) to determine the number of factors. All the above-mentioned estimation methods are based on the latent variable modeling framework, in which observed variables are believed to co-occur due to an underlying unobserved (latent) attribute that has caused the covariation between the observed variables.

The development of network models offers a new perspective to understanding psychological data. By demonstrating that a general factor model can be estimated using a fully connected network model, van der Maas et al. (2006) proposed using a network model to examine the dynamic relationships between variables, which rest on reciprocal mutualism or the idea that variables directly and mutually reinforce one another. Methodological advances (Borsboom et al., 2011; Borsboom & Cramer, 2013) and substantive applications (e.g., Fried et al., 2015; Ron et al., 2021) have since increased to study psychological behaviors in this area. Epskamp (2016) introduced a network model as a formal psychometric model, which proposes that symptoms, as measured by psychometric items or scale scores, directly and reciprocally cause each other (Borsboom & Cramer, 2013; Cramer et al., 2010; van Bork et al., 2017; van der Maas et al., 2006). Network models conceptualize observed variables (e.g., symptoms) as nodes, and links between nodes as edges that represent statistical relationships between symptoms or behaviors (e.g., Epskamp, 2016). Although psychological network models and latent variable models possess contrasting perspectives regarding why variables are related, studies have demonstrated that both models are statistically equivalent under certain conditions in the binary (Epskamp et al., 2018b; Holland, 1990; Kac, 1969; Marsman et al., 2015, 2018; McCullagh, 1994), polytomous (Christensen et al., 2023b), and continuous (Waldorp & Marsman, 2022) data. The network structures of nodes and edges are commonly estimated in network psychometrics using Gaussian graphical model (GGM; Lauritzen, 1996) for normally distributed data.

Built upon GGM, which described the conditional dependence structures of psychological constructs (Lauritzen, 1996; Wainwright et al., 2008), Golino & Epskamp (2017) developed a new assessment technique using a network modeling perspective. The technique, exploratory graph analysis (EGA; Golino & Epskamp, 2017), estimates a network and then applies a clustering algorithm to assess the factor dimensionality. Liu (2021) developed a similar regularized Gaussian graphical clustering that was based on regularized partial correlations and the Louvain community detection algorithm to determine the number of cell clusters. Golino & Epskamp (2017); Golino et al. (2020) found an equal or superior performance of EGA to conventional latent variable based techniques in assessing factor structures. The researchers showed through a decomposition using the Woodbury matrix identity (Woodbury, 1950) that oblique factors are statistically equivalent with clusters of nodes (i.e., sets of connected nodes) and orthogonal factors are statistically equivalent with unconnected clusters in GGM, when the data generation mechanism is a factor model. Further, Christensen & Golino (2021) showed that factor loadings are statistically equivalent with a modified version of node strengths (i.e., sum of all connections to a node) that takes into consideration of the dimensionality structure, represented as network loadings.

The current mainstream approach for assessing dimensionality in network psychometrics uses frequentist inference (i.e., EGA; Golino & Epskamp, 2017; Golino et al., 2020). Exploring alternative estimation approaches to the GLASSO-based EGA offers advantages. First, on the one hand, the GLASSO-based EGA method as a regularization based approach studies point estimates but does not yield sampling distributions (Epskamp et al., 2018a), thus posing limitations for further statistical inference (Hastie et al., 2009). On the other hand, when using Bayesian estimation methods, one can obtain the full posterior probability distributions for the edges that capture connections between nodes and use the estimated posterior distributions to extract different types of information about the edges. This includes obtaining point estimates such as posterior mean or posterior median as well as creating interval estimates to establish a plausible range for significance. Bayesian inferences can further be drawn based on the information (Gelman et al., 2015). Despite a nonregularized bootstrapping strategy was introduced to estimate $\boldsymbol{\Theta}$ (Williams et al., 2019), Williams (2021) advised against bootstrapping LASSO penalized estimates to conduct significance tests, as the point mass at zero in sparse network likely results in the distorted sampling distribution. In addition, before evaluating factor structures, researchers may have some level of understanding regarding those structures. Under such a situation, Bayesian estimation has the capacity to incorporate the prior belief or knowledge based on substantive theory to the parameter estimation. For example, consider assigning a prior distribution (e.g., a conjugate Wishart distribution) to the precision matrix in graphical models, which represent dependencies between variables in a network. Based on the degree of uncertainty of connections among nodes, one could assign informative or noninformative priors to express the relationships between variables. While noninformative priors reflect the lack of specific information about the parameters being estimated and are typically flat and vague, informative priors incorporate specific prior knowledge or information and can strongly influence the posterior distribution. By expressing the knowledge and beliefs through specifying values and incorporating priors in Bayesian methods, the posterior distribution can represent the range of potential characteristics researchers may have based on prior data or beliefs (e.g., Serang et al., 2014). For example, in a personality test, if one is certain about the likely shape and spread of a personality trait, one may assign an informative scale matrix as the hyperprior to the precision matrix, which will have a greater weight on posterior estimates. One may also increase the value of the hyperprior for the degrees of freedom to reflect a more informative prior in the personality traits. On the contrary, if one is uncertain or has limited prior information, one may assign a noninformative scale matrix along with degrees of freedom hyperprior to capture the uncertainty using the noninformative prior. Thus, prior theory can play a role in determining the network structure using the Bayesian estimation.

This study examined alternative algorithms in EGA framework to assess dimensionality in multivariate psychological data. The study also explored four additional full Bayesian techniques that showed promising results to develop dimensionality assessment to Bayesian graphical models. The remainder of the study is organized as follows. We first review the EGA framework for assessing dimensionality in network psychometric models. Next, we discuss two Bayesian estimation methods to estimate the model parameters for GGM. Then, we discuss decision rules to reach the level of sparsity and introduce a community detection algorithm to detect patterns in the network structures. Furthermore, we explore four full Bayesian techniques for evaluating the feasibility of dimensionality assessment in full Bayesian framework within psychological networks. We investigate the performance of the proposed Bayesian techniques using three Monte Carlo simulation studies and end with discussion and future directions.

Exploratory graph analysis framework for assessing dimensionality

Exploratory graph analysis (EGA) refers to a network psychometric modeling framework to assess dimensionality in multivariate data. The EGA's core idea (Golino & Epskamp, 2017) combines undirected network models (Lauritzen, 1996) with community detection algorithms (Newman, 2006), specifically estimating a network structure first and then applying a clustering algorithm to detect the undirected weighted network clusters and estimate the underlying number of latent factors. EGA has found to perform equally well or better than parallel analysis using principle component analysis (PApca; Horn, 1965). The current study achieves two goals. Up to now, the EGA framework primarily uses the *graphical least absolute shrinkage and selection operation* (GLASSO; Friedman et al., 2008) to point estimate the undirected network structure. This study investigates two Bayesian algorithms to estimate the network structure by obtaining the structure's posterior distributions. The study shows that the new algorithms produce smaller mean squared errors and are more stable than the GLASSO-based EGA. Second, the study explores four full Bayesian techniques and finds promising outcomes to extending dimensionality assessment in network psychometrics within Bayesian framework.

Part I. Existing GLASSO-based EGA algorithm

The GGM can be used to model the conditional dependence or independence of pairs of continuous variables in the network (Højsgaard & Lauritzen, 2008; Sekulovski et al., 2023; Waldorp & Marsman, 2022). Let $\boldsymbol{y}$ be a random vector of k responses and is assumed to be normally distributed, $\boldsymbol{y} \sim N_k(\boldsymbol{\mu}, \boldsymbol{\Sigma})$, with the mean vector $\boldsymbol{\mu} = (0_1, \ldots, 0_k)'$ and a $k \times k$ positive definite covariance matrix $\boldsymbol{\Sigma}$. By determining which off-diagonal elements in the precision matrix, $\boldsymbol{\Theta} = \boldsymbol{\Sigma}^{-1}$, are nonzeros, the undirected weighted network graph is obtained and used to construct an adjacency matrix. The adjacency matrix follows that

$$A_{ij} = \begin{cases} 1, & if \;\; \theta_{ij} \neq 0, \;\; 1 \leq i \leq j < k \\ 0, & otherwise \end{cases}.$$

The precision matrix has a selected edge if the corresponding adjacency matrix has an element 1, and zero otherwise. The selected edges, after being standardized and reversed the sign, are partial correlations between two variables y_i and y_j, given all other variables in $\boldsymbol{y}, \boldsymbol{y}_{-(i,j)}$ on their off-diagonal elements (Epskamp et al., 2018c). The partial correlations show conditional dependency and are represented as

$$Cor(Y_i, Y_j | \boldsymbol{y}_{-(i,j)}) = -\frac{\theta_{ij}}{\sqrt{\theta_{ij}}\sqrt{\theta_{ij}}}. \tag{1}$$

A weighted network is formed using partial correlations as shown in Equation 1, in which each variable $\boldsymbol{y}_k$ represents a node, and the partial correlations between variables are represented as edges between the nodes. A nonzero partial correlation represents the conditional dependence between nodes, whereas the zero partial correlation represents that the two nodes are independent conditional on all other nodes. Because the number of free parameters in the precision matrix can grow quadratically with the number of variables, a sparse network is typically assumed (Epskamp et al., 2017; Epskamp & Fried, 2018).

The GLASSO-based EGA (Golino & Epskamp, 2017) estimates the GGM using the penalized maximum likelihood estimation. It uses a variant of the *least absolute shrinkage and selection operation* (LASSO; Tibshirani, 1996) regularization technique known as GLASSO (Friedman et al., 2008) to estimate the sparse inverse covariance matrix and compute an associated Extended Bayesian Information Criterion (EBIC; Foygel & Drton, 2010). The graph with the best EBIC is selected as the final graph. Once the graphical structure is obtained, the GLASSO-based EGA applies the walktrap community detection algorithm (Pons et al., 2006) to iteratively find the optimal clustering solution. By penalizing the model complexity while estimating the statistical model, regularization converges to the true network structure under sparse networks (Ravikumar et al., 2011). Later, a few methodological improvement was made over the GLASSO-based EGA (Golino et al., 2020). The researchers adjusted the default value of the hyperparameter γ for EBIC, which determines whether a parsimonious model with fewer connections is favored, to make the result of EGA more stable. Furthermore, the researchers developed a unidimensionality expand rule to accommodate assessing unidimensionality within the EGA method.

Part II. Two new EGA algorithms based on posterior distributions

While the GLASSO-based EGA method (Golino et al., 2020; Golino & Epskamp, 2017) has received popularity in applications in various disciplines (e.g., Rosenthal et al., 2021; Rotundo, 2002), it is not without limitation. Statistical inference could be limited by using only the point estimates of the precision matrix obtained from the regularized partial correlation network using GLASSO (Friedman et al., 2008). In addition, conducting significance tests by bootstrapping LASSO penalized estimates could pose challenges in sparse networks (Williams, 2021), where many edges are estimated as exactly zero, leading to a distortion in distribution of sampling statistics.

Bayesian estimation

This section discusses estimating network structures by generating their posterior distributions using Bayesian priors that are conjugate or have invariant property for the posterior reparameterization. The GGM can be estimated either analytically or using posterior sampling in Bayesian methods (Williams, 2021; Williams & Mulder, 2020). In the analytical approach, a Wishart prior distribution, which is conjugate for the precision matrix $\boldsymbol{\Theta}$ (Kubokawa & Srivastava, 2008) is used. The normal density function of the multivariate normal data $\boldsymbol{Y}$ can be written as

$$p(\boldsymbol{Y}|\boldsymbol{\Theta}) = (2\pi)^{-k/2}|\boldsymbol{\Theta}|^{1/2}\exp\left(-\frac{1}{2}\boldsymbol{Y}\boldsymbol{\Theta}\boldsymbol{Y}'\right).$$

Following a conjugate Wishart prior $W(\nu, c\boldsymbol{I}_k)$ to $\boldsymbol{\Theta}$, with degrees of freedom ν ($\nu = k+1$), identity matrix $\boldsymbol{I}_k$, and a constant c with a small value, the density function of the prior is

$$p(\boldsymbol{\Theta}) = \frac{|\boldsymbol{\Theta}|^{(\nu-k-1)/2}\exp\left[-tr(c\boldsymbol{I}_k^{-1}\boldsymbol{\Theta})/2\right]}{2^{\nu\times k/2}\Gamma\left(\frac{\nu}{2}\right)|c\boldsymbol{I}_k|^{\nu/2}}.$$

Thus, the joint posterior density for the precision matrix $\boldsymbol{\Theta}$ follows

$$p(\boldsymbol{\Theta}|\boldsymbol{Y}) \propto p(\boldsymbol{Y}|\boldsymbol{\Theta})p(\boldsymbol{\Theta}),$$

where $\boldsymbol{Y}$ is a $n \times k$ matrix drawn from a multivariate normal distribution. Due to conjugacy, the posterior distribution also has a Wishart distribution,

$$\boldsymbol{\Theta}|\boldsymbol{Y} \sim W(\nu + n, (S + c\boldsymbol{I}_k)^{-1}),$$

where n is the sample size and $\boldsymbol{S}$ is the sums of squares matrix $\boldsymbol{Y}'\boldsymbol{Y}$. The posterior distribution of $\boldsymbol{\Theta}$ is

$$p(\boldsymbol{\Theta}|\boldsymbol{Y}) = |\boldsymbol{\Theta}|^{\frac{(n+\nu-k-1)}{2}}\exp\left(-\frac{1}{2}tr\left[(\boldsymbol{S} + c\boldsymbol{I}_k^{-1}) \times \boldsymbol{\Theta}\right]\right).$$

As the number of variables in the network increases, the degrees of freedom in the prior specification for the precision matrix also increases, so does the prior mean have a greater weight on the posterior mean. The posterior mean of the precision matrix $\boldsymbol{\Theta}$ can be expressed as

$$E(\boldsymbol{\Theta}|\boldsymbol{Y}) = (\nu + n)(n\boldsymbol{S} + c\boldsymbol{I}_k^{-1})^{-1}.$$

Accordingly, the analytical approach derives the graphical structure and constructs the posterior probabilities for the edges. Using this conjugate Wishart distribution as a prior could produce a posterior distribution, which could then be used to generate posterior samples and construct credible intervals (Zhang, 2021).

The second approach uses a different prior setup that allows to compute the posterior distribution for the partial correlation matrix. This sampling-based approach applies a Jeffreys' prior $|\boldsymbol{\Theta}|^{(p+1)/2}$ and derives a posterior distribution that follows a Wishart distribution $\boldsymbol{\Theta}|\boldsymbol{Y} \sim W(n-1, S^{-1})$ (Williams, 2021). By specifying Jeffreys' prior, one does not favor any particular values of the precision matrix $\boldsymbol{\Theta}$, but rather relies solely on the dimension and the degrees of freedom of the distribution. One can draw posterior samples, $s = 1, \ldots, S$, to construct a posterior distribution for the $k \times k$ precision matrix (Barnard et al., 2000), which can be denoted as

$$\boldsymbol{\Sigma} = -\left(\left[diag(\boldsymbol{\theta})^{(s)}\right]^{-1}\boldsymbol{\Theta}^{(s)}\left[diag(\boldsymbol{\theta})^{(s)}\right]^{-1}\right),$$

where $\boldsymbol{\theta}$ are the square roots of $diag(\boldsymbol{\Theta})$. Based on the posterior samples of the precision matrix, one can define the region of practical significance for the null area that provides support for determining the conditional dependency and independency between edges as well as practical equivalency around zero (Kruschke, 2011).

Level of sparsity

Generating Bayesian posterior distributions does not result in absolute zero but rather in probability. Thus, one could define an area around the null value in posterior distribution that is practically equivalent to no effect. This range is the region of practical equivalence (ROPE; Kruschke, 2014). ROPE, the region of which can be used as a "null" hypothesis, can be used to test whether a parameter is significant or not (Kruschke & Liddell, 2018; Shi et al., 2019).

Bayesian estimation using ROPE does not directly lead to a sparse network. The nonzero small estimates typically represent weak edges, which are spurious or false positive connections in the network, even among conditionally independent nodes (Costantini et al., 2015). In the current study, we propose penalizing model complexity by controlling for the level of sparsity. By defining a null region using ROPE, one can check the percentage of credible intervals that is the region and determine the level of sparsity. A null hypothesis will be rejected if there is a low percentage of credible intervals within ROPE, and it will be retained when a high percentage of credible intervals fall within the ROPE (J. Kruschke, 2014).

The study uses the ROPE idea to estimate the network structure. Specifically, we use Bayesian credible intervals to limit spurious edges and yield a sparse estimate for $\boldsymbol{\Theta}$. The Bayesian credible intervals, built upon the posterior probability distribution for $\boldsymbol{\Theta}$, summarize the posterior probability that the true edge effect is within an interval. A 90% credible interval summarizes the posterior mass and demonstrates that there is a 90% probability that the true network structure (i.e., edges) falls within the specified interval range, assuming that the alternative hypothesis one specifies is true (Morey et al., 2016; van Doorn et al., 2021; Wagenmakers et al., 2018). While larger credible intervals indicate a higher level of sparsity in $\boldsymbol{\Theta}$, low credible intervals lead to non-zero elements in the network. In an extreme case when the credible intervals fall into zero, all the off-diagonal elements in the precision matrix are non-zeros and $\boldsymbol{\Theta}$ becomes the original Wishart posterior distribution. It is advisable to select a credible interval range that is consistent with the underlying substantive theory. In other words, one establishes credible intervals based on how likely an unknown network structure lies within a particular range. Through a simulation study, Williams (2021) discovered that the analytic-based approach better controlled the Type I error rates in small-sampled conditions (i.e., sample size less than 1000) than the sampling-based approach, although both techniques converge to a similar performance asymptotically

The current study will use both the analytic-based and sampling-based Bayesian approaches to estimate the GGM and compare their performances. In this study, we will adopt a 90% credible interval for both the analytic-based and sampling-based Bayesian techniques to demonstrate the confidence level of the true network structures and limit spurious edges. Researchers may designate other credible intervals to fit into their underlying theoretical framework.

Clustering algorithm

We assess the underlying factor structure of the multivariate data by applying a community detection algorithm to the estimated graphical networks. After estimating the GGM through Bayesian methods and applying the designated level of specificity to the sampling-based technique, one obtains graphical networks representing relationships between nodes. In a psychological context, the nodes having a similar psychological construct are densely connected, whereas the nodes with orthogonal constructs are expected to be further away. In previous studies that used GLASSO to estimate the GGM, the links between nodes belonging to the same construct are expected to be stronger than the connections between nodes from distinct constructs (Golino et al., 2020; Golino & Epskamp, 2017). In this study, we use the Louvain community detection algorithm (Blondel et al., 2008) to the graphical structures to detect the optimal partitions in a network and define the dimensions in the data.

The community detection algorithms can be understood through the concept of modularity (Newman, 2006). Modularity measures the degree of connectivity between nodes in a community. The Louvain algorithm initiates a separate individual community for each node and records the modularity in this state; the algorithm then moves each node into a neighboring community and notes down a new modularity. The change in modularity between both states is compared. The node remains in the original community if the modularity has no gain and belongs to the adjacent community if there is a gain in modularity. This is an iterative process until the modularity does not improve and a local maxima is achieved. Hierarchical network structures can be further detected through aggregating networks in Louvain. Specifically, the algorithm moves individuals to an aggregated network, records the modularity at each state, and compares the connectivity (i.e., modularity) between states to optimize the partitions. The process is repeated until a global maxima between the expected and actual number of edges is achieved in a community (Christensen et al., 2023a; Gates et al., 2016).

We suggest utilizing the Louvain algorithm for the proposed method for three primary reasons. First, Christensen et al., (2023a) discovered through a well-planned simulation that when coupled with GLASSO, the Louvain algorithm was one of the most effective approaches to identify network community structures. Gates et al. (2016) had a similar finding when exploring brain network correlation structures. Second, the Louvain has the advantage of detecting hierarchical structures (Blondel et al., 2008; Gates et al., 2016; Jiménez et al., 2023). Bayesian methods have advantage in handling hierarchical structures in data in terms of model specification, quantifying parameter uncertainties, and, model estimation with the incorporation of prior beliefs (e.g., Gelman et al., 2015; Gelman & Hill, 2002). For example, Bayesian methods use a single principle, Bayes' Theorem, for parameter estimation. The technique not only uses the prior distribution and the likelihood function but also has the capacity to include information about hyperpriors. This enables the capture of random effects in variables, which offers additional information for more precise parameter estimation (Jongerling et al., 2023; Shi et al., 2023b). Furthermore, the MCMC methods in Bayesian approach enable the simultaneous estimation of multiple hierarchical structures, which have been found to better model uncertainties at each level within the Bayesian framework (e.g., Lee & Newell, 2011). Proposing Louvain to the alternative Bayesian algorithms allows the potential to detect hierarchical network structures in future studies. Third, compared to the Louvain community detection technique, the walktrap algorithm (Pons et al., 2006), as the default algorithm for the GLASSO-based EGA (Golino & Epskamp, 2017) method, may encounter scalability challenges as it could become computationally expensive for the walktrap technique in large or hierarchical networks (Lancichinetti et al., 2008).

The EGA.analytical and EGA.sampling methods

This study proposes the application of two Bayesian priors to EGA framework in network psychometric modeling for assessing factor structures. Specifically, we discuss two prior setups in the models, which vary based on the way the Bayesian methods are used to determine the structure of the conditional (in)dependence. The first model estimates the conditional dependence structure using the analytical-based Bayesian approach with a conjugate Wishart prior, and is termed the EGA.analytical method. The second model, the EGA.sampling method, adopts a sampling-based Bayesian approach to estimate a sparse network structure. In this study, we establish the interval of values in which there is a 90% probability of containing the true values, known as 90% credible intervals, in the posterior samples of the EGA.analytical and EGA.sampling methods to regulate the degree of sparseness. Researchers may opt for a value range different from 90% to account for their prior knowledge and beliefs about the network structure in practice. Both the EGA.analytical and EGA.sampling methods use the Louvain community detection algorithm to assess the undirected weighted network clusters. To address the issue of unidimensionality, we use the above-mentioned expand adjustment rule (Golino et al., 2020) by creating an auxiliary dimension and adjusting unidimensionality through the auxiliary factor structure in the EGA.analytical and EGA.sampling techniques.

Because the true factor structure is unknown in practical settings, the discussed techniques assess the factor structures by verifying the unidimensional structure first and then proceeding to assess the multidimensionality. Specifically, after obtaining an empirical dataset with a sample size of *N*, the techniques would simulate a dataset with the same sample size of *N* as the empirical dataset with a hypothetical factor structure consisting of four items and factor loadings of 0.7. This ensured that a non-unidimensional solution would be obtained when estimating the network structures. The process involves combining the simulated data with the actual data and using either an analytical-based or sampling-based Bayesian estimation approach to estimate the network structure. The sampling-based Bayesian estimation incorporates a designated specificity level and controls for sparseness. The output is a network graphical structure based on the partial correlation matrix estimated using the Bayesian approaches. The Louvain community algorithm is then applied to identify community partitions. If the returned number of factors is 2 or less, the algorithm stops and records unidimensionality. If not, the process is repeated to determine multidimensionality. The final estimated multidimensional structure is calculated as the estimated dimension, which excludes the simulated hypothetical dimension. See Figure 1 for a detailed description of the EGA.analytical algorithm; EGA.sampling algorithm followed a similar procedure.

Part III. Exploring four full Bayesian procedures for small samples

While the study has identified certain advantages of the studied Bayesian algorithms when compared to conventional regularization-based EGA technique (Golino et al., 2020), it is important to note that these advantages are somewhat limited in scope in that the focus primarily centers around alternative estimation methods for network structure. The benefits of Bayesian methods for addressing issues related to small sample sizes are not clearly evident in the current findings, despite Bayesian methods offering the advantage of addressing this through the incorporation of priors (e.g., McNeish, 2016; Shi & Tong, 2017).

In this section, we provide a conceptual exploration of four alternative Bayesian techniques to assess dimensionality in small sampled conditions through network models. The four techniques are discussed in terms of how they supplement certain aspects where the above discussed EGA.analytical and EGA.sampling approaches have limitations and weaknesses.

First, we discuss two Bayesian alternatives to classical NHST about the inclusion and exclusion of network edges. The approaches use findings from Bayesian hypothesis testing regarding the presence or absence of edges together with clustering algorithms to assess dimensionality. One problem with the ROPE idea discussed above in Bayesian methods is that the fundamental question of null hypothesis testing (e.g., E.-J. Wagenmakers et al., 2020; Wagenmakers et al., 2016) remains. This means that we reject the null when the null or the null regions are tested to be different from being zero. The associated problem of simply rejecting the null does not lead us to the conclusion that the alternative is true. Bayesian hypothesis testing, on the other hand, allows researchers to distinguish between not having evidence of network connections and having evidence that network connections are absent (e.g., Borsboom et al., 2021; Wagenmakers et al., 2018), and thus, may facilitate the decision about whether to include or exclude certain network connections (i.e., edges) among nodes in a network.

The central idea of using the Bayesian hypothesis testing to assess dimensionality is to use the Bayes factor, a direct measure of the relative evidence for two models to quantify the uncertainty of including edges and then assess dimensionality of those included edges. We discuss two approaches to determining the conditional dependency, depending on how we measure or quantify the evidence for the edge inclusion and exclusion. The first method computes the posterior inclusion probability (PIP) to determine the graph structure (Huth et al., 2023; Williams & Mulder, 2020) and uses the community detection algorithm to partition dimensions. Specifically, we compare the likelihood of the data through a single-model Bayes factor (Kass & Raftery, 1995; Morey & Rouder, 2011) under the structure in which the edge is present against the structure where the edge is absent. We term this single Bayes factor method as *EGA.pip*. The *EGA.pip* method is based on one model-averaged estimate (Huth et al., 2023; Williams et al., 2019) that is sensitive and fluctuates depending on the conditional dependency of the current edge on other edges (Sekulovski et al., 2023) when quantifying the edge inclusion uncertainty. To mitigate this potential issue from the single Bayes factor approach, the second method computes the inclusion Bayes factor using

```
Algorithm 1 EGAanalytical for Assessing Dimensionality
Require: An empirical dataset with $n$ observations and $p$ variables.
function CheckUnidimensionality
    Generate a unidimensional structure simdata with four items and factor loadings of 0.70.
    Column bind simdata with the empirical data empdata into a new data frame expanddata.
    Specify a conjugate Wishart prior and apply the analytical-based Bayesian method to estimate the posterior distribution of the precision matrix for expanddata.
    Obtain the estimated partial correlation matrix (i.e., BGGM) from the posterior mean.
    Create a network graphical structure of the estimated partial correlation matrix.
    Identify the clusters of the graphical structures using the Louvain community detection algorithm.
    Return the number of factors as the number of communities estimated by the Louvain algorithm.
    if the returned number of factors $\leq 2$ then
        Return the number of factors $= 1$.
        Unidimensionality is detected and recorded.
    end if
end function
function CheckMultidimensionality
    if the returned number of factors $> 2$ then
        Specify a conjugate Wishart prior and apply the analytical-based Bayesian method to estimate the posterior distribution of the precision matrix for the original empirical data empdata.
        Obtain the estimated partial correlation matrix (i.e., BGGM) for empdata from the posterior mean.
        Create a network graphical structure of the estimated partial correlation matrix.
        Identify the clusters of the graphical structures using the Louvain community detection algorithm.
        Return the number of factors as the estimated number of factors in the algorithm.
        Multidimensionality is detected and recorded.
    end if
end function
```

Figure 1. Algorithm for the analytical-based (EGA.analytical) method.

Bayesian modeling averaging to determine the presence of network connections (Sekulovski et al., 2023). Through using Bayesian model averaging (Hinne et al., 2020; Hoeting et al., 1999), one obtains a single inclusive Bayes factor that accounts for all possible structures simultaneously (Huth et al., 2023; Sekulovski et al., 2023). By quantifying the uncertainty of edge inclusion or exclusion through the inclusive Bayes factor, one can subsequently determine the conditional dependence structure. Studies have shown this approach to be more robust (Sekulovski et al., 2023). We then use the Louvain clustering algorithm to assess dimensionality in a network and term this approach *EGA.incBF*. Based on a comparable approach to estimating the effect size measure in experimental analysis-of-variance designs using Bayesian methods to estimate the posterior distribution (Marsman et al., 2019), these methods could potentially offer a broader Bayesian perspective and enhance the study's robustness.

Second, assigning Bayesian priors is not limited to assigning priors to only model parameters. In this study, we consider alternative priors that explicitly take into account the graph structure. Introduced by Rotundo (2002), the *G*-Wishart distribution was a probabilistic model for dealing with graphical structures and accommodating graph-related information. As a conjugate prior for the likelihood, the *G*-Wishart distribution has gained a growing popularity as a prior for the precision matrix for the multivariate data, especially in GGM (Dobra et al., 2011; van den Boom et al., 2022). Being a generalization of the traditional Wishart distribution, the *G*-Wishart distribution contains hyperparameters that govern the shape and spread of the distribution. Unlike traditional Wishart distribution which typically assumes a fixed scale matrix, the *G*-Wishart distribution has an additional parameter, degrees of freedom, that allows the scale matrix to vary (Mohammadi et al., 2023; Mohammadi & Wit, 2015a). By specifying the prior probability for including edges on the graph structure, one can better accommodate the varying degrees of sparsity and structure in the precision matrix. This will in turn allow a more flexible representation of dependency structures within a network. The *G*-Wishart distribution can be used for analyzing covariance structures in models with expanding dimensions and rising complexity (Wang, 2012). It is advantageous in incorporating prior knowledge or beliefs about the precision matrix structure in Bayesian inference in graphical models. We first apply a *G*-Wishart distribution to the precision matrix to obtain the graphical structure, and then use the Louvain algorithm to determine its dimensions. We term this method as *EGA.gwishart*.

Third, up to now, all discussions about dimensionality reduction involves estimating and clustering the model parameters for GGM to identify the optimal structure. That said, an alternative Bayesian method may involve directly sampling the underlying structure to model the uncertainty associated with selecting the optimal structure. Indeed, the graph structure in GGM is another type of unknown mechanism (Mohammadi & Wit, 2015a), where direct structure selection could be conducted and then complemented by clustering. Specifically, one may directly develop Bayesian structure learning in GGM that jointly estimates graph structure and precision matrix, with various search algorithms (e.g., Hinne et al., 2014; Lenkoski, 2013; Mohammadi et al., 2023; Mohammadi & Wit, 2015a). In this study, we directly sample the underlying structure and covariance matrix from the posterior distributions of all visited graph structures (Love et al., 2019; Mohammadi & Wit, 2015b). This sampled posterior structure contains the posterior probabilities associated with all explored structures, with higher values indicating higher posterior probabilities of structure selection. By assessing the graphical weights of a specific structure that reflects the number of iterated structures being visited (Huth et al., 2023; Mohammadi & Wit, 2015b), we determine the uncertainty associated with the optimal structure and then apply the community detection algorithm to assess the dimensionality of the graph structures. We term this structure selection and clustering algorithm as *EGA.structure*.

Monte Carlo simulation studies

We evaluated the performance of the discussed techniques in assessing the multidimensional and unidimensional factor structures *via* three Monte Carlo simulation studies. In the first two simulation studies, we compared the proposed methods with two existing dimensionality assessment techniques, the GLASSO-based network psychometric tool (EGA; Golino & Epskamp, 2017; Golino et al., 2020) and parallel analysis using principal component analysis eigenvalues (PApca; Horn, 1965). In the third simulation, we compared performance of multiple Bayesian-based techniques.

Simulation study 1 - assessing multidimensionality

Simulation design

In the simulation, we studied five potentially influential variables (see Table 1 and Table 5), including number of factors, number of items, factor loadings, interfactor correlations, and sample size. These manipulated conditions represented factor analytic scenarios commonly seen in psychological studies (e.g., Comrey & Lee, 2013; Garrido et al., 2016; Kane et al., 2005). Specifically, the data generating factor model had two, three, or five factors, representing multidimensionality factor designs. where each factor had four, six, or eight items. All the models had three levels of factor loadings that represented large (0.7), medium (0.55), and low (0.4) magnitude. Because correlated factors likely affect the performance of dimensionality techniques (e.g., Garcia-Garzon et al., 2019; Garrido et al., 2016), we manipulated the interfactor correlations to range from orthogonal (0), mild (0.3), moderate (0.5), to high (0.7). Sample sizes had three levels, representing small (250), medium (500), and large (1000) sampled conditions.

Table 1. Simulation design for studies 1 and 2.

Influential Factors	# of Factor Levels	Levels
Number of factors *F*	4[1]	1, 2, 3,5[1]
Number of Items per Factor *I*	3	4, 6, 8
Factor Loadings λ	3	0.4, 0.55, 0.7
Interfactor Correlations *r*	4	0, 0.3, 0.5, 0.7
Sample Size *N*	3	250, 500, 1000

Note:[1]Includes the multidimensional and unidimensional designs

The sample data matrices were generated according to the following common factor model procedure. First, we computed the population correlation matrix $\boldsymbol{R_R}$ as

$$\boldsymbol{R_R} = \boldsymbol{\Lambda\Phi\Lambda}' + \boldsymbol{\Psi},$$

where $\boldsymbol{R_R}$ is the population correlation matrix, $\boldsymbol{\Lambda}$ represents the population factor loading matrix, $\boldsymbol{\Phi}$ denotes the population factor correlation matrix, and $\boldsymbol{\Psi} = 1 - diag(\ \boldsymbol{\Lambda\Phi\Lambda}')$. The next step was performing a Cholesky decomposition of $\boldsymbol{R_R}$, such that

$$\boldsymbol{R_R} = \boldsymbol{U}'\boldsymbol{U},$$

where $\boldsymbol{U}$ is an upper triangular matrix. Finally, we computed the sample data matrix of continuous variables $\boldsymbol{X}$ as

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

where $\boldsymbol{Z}$ denotes the multivariate normal distribution for the continuous variables, with rows equal to the sample size and columns equal to the number of items.

We applied four analytic methods to evaluate and compare the performance of the dimensionality assessment techniques in the common factor model. The first two methods were what we proposed in the study. The first method, called the EGA.analytical method, used a Bayesian analytic approach with a conjugate Wishart prior to estimate the graphical structure. The method then used the Louvain community detection algorithm to extract communities. The second method, called the EGA.sampling method, used a sampling-based Bayesian approach to obtain posterior samples. The technique set a 90% credible interval to control sparsity and used the same Louvain procedure as the EGA.analytical method to partition clusters. The remaining two methods were established dimensionality reduction techniques for comparison purposes. Specifically, we applied the GLASSO-based EGA technique (Golino et al., 2020) as the third method. In the previous literature, Golino et al. (2020) compared EGA with other traditional dimensionality assessment techniques including Kaiser's eigenvalue-greater-than-one rule (K1; Kaiser, 1960), parallel analysis using principal component analysis eigenvalues (PApca; Horn, 1965), and parallel analysis using principal axis factoring (PApaf; Humphreys & Ilgen, 2016). Their studies found that PApca had the overall best comparable performance to EGA over K1 and PApaf. Thus, we selected PApca as the fourth method and examined its performance in the current study to align with prior work.

All data were generated and analyses were conducted in R (R Core Team, 2013). We used the *EGAnet* package (Golino et al., 2023) and *BGGM* package (Williams & Mulder, 2021) to conduct the two Bayesian estimation techniques, the *EGAnet* package (H. Golino et al., 2023) and the *qgraph* package (Epskamp et al., 2012) to conduct the EGA analyses, the *nFactors* package (Raiche et al., 2020) to conduct the PApca analyses, and the *igraph* package (Csardi, 2006) to conduct the Louvain community detection. We ran a total of 5,000 iterations for the MCMC chains in the two Bayesian estimation methods. A total of $3 \times 3 \times 3 \times 4 \times 3 = 324$ conditions were studied for the multidimensional design. Each simulated condition was replicated 500 times.

Evaluation criteria

We evaluated the performance of the proposed Bayesian methods to assess the number of factors and compared them with existing dimensionality assessment techniques. We investigated the hit rate (HR), mean bias error (MBE), and mean absolute error (MAE) of the estimated number of factors across simulation replications. Let F denote the true number of factors in the population. Let $\hat{F}$ denote the estimated number of factors from the kth simulation replication. For $\widehat{F_k} = F$, we counted it as hit in the kth replication; conversely, for $\hat{F}_{k+1} \neq F$, we counted it as miss in the $(k+1)th$ replication. The hit rate is defined as

$$HR = \frac{number\ \ of\ \ hit}{number\ \ of\ \ hit + number\ \ of\ \ miss}$$

which indicates the percentage of replications correctly recovering the true number of factors from the data generation process. The hit rate ranges from 0 and 1 and can be seen as a metric for assessing accuracy.

MBE measures the average of the differences between the estimated number of factors and the true population factor. It is defined as

$$MBE = \frac{\Sigma_{k=1}^{K}(\widehat{F_k} - F)}{K}.$$

MBE measures the bias of the predicted performance of the dimensionality assessment technique. A positive MBE indicates that the model is biased toward overestimating the true number of factors, while a negative MBE shows that the model underestimates the true factors. An MBE of 0 indicates no bias in the estimation.

MAE captures the average of the absolute difference between the estimated and the true number of factors. It is represented as

$$MAE = \frac{\Sigma_{k=1}^{K}|\widehat{F_k} - F|}{K}.$$

MAE is a measure of the average magnitude of the errors in estimating the factor structure. While an

MAE of 0 indicates no errors, higher values of MAE show greater magnitude differences in estimation errors.

To further determine the impact of the manipulated factors and their interactions on the performance of the proposed Bayesian methods, we conducted ANOVAs for each method, where the hit rate was the dependent variable and the five manipulated data conditions were the independent variables. We employed the partial eta squared statistic (η_p^2) as a metric to gauge the magnitude of the effect, with effect sizes of 0.01, 0.06, and 0.14 being categorized as small, medium, and large, respectively (Cohen, 1992).

Simulation results

Table 2 summarized the HR, MBE, and MAE for the four models. Table 3 presented the main and interaction effects from the ANOVAs. The interaction effect with large or close to large effect sizes (i.e., $\eta_p^2 \geqslant 0.13$) was further illustrated in Figure 2.

The two psychometric models that used Bayesian priors (i.e., EGA.analytical and EGA.sampling approaches) had comparable performance to EGA and PApca in terms of high hit rate (HR), low mean biased error (MBE), and low mean absolute error (MAE) across conditions examined in the study. As shown in Table 2, the EGA and EGA.analytical methods had the best HRs (0.84) overall. Furthermore, the EGA.analytical method had the smallest MBEs and MAEs out of all four methods. At the same time, the EGA.sampling method had the third-best HR (0.80), which was higher than the PApca method (0.78). The EGA.sampling method also had smaller and better MBEs and MAEs than both the EGA and PApca methods. The results additionally examined ANOVA interactions and effect size stabilities across manipulated conditions (see Table 3). The sub-section below broke down the performance by manipulated factors.

Factor loadings

The two Bayesian techniques performed better than EGA and PApca with higher HRs and better MBE and MAE when the factor loadings were medium to high. When the factor loading was low (0.40), EGA had the highest HR while the EGA.analytical method had the smallest MBE and MAE. Specifically, when the factor loading was high ($\lambda = 0.7$), the two Bayesian estimation methods had the highest HRs (0.97 and 0.96, respectively), as compared to EGA (0.91) and PApca (0.88). The two Bayesian estimation methods also had

Table 2. HR, MBE, and MAE for EGA.analytical, EGA.sampling, EGA, and PApca in multidimensionality assessment.

	Factor loading			Variables per factor			Factor correlations				Number of factors			Sample size			
Method	0.4	0.55	0.7	4	6	8	0	0.3	0.5	0.7	2	3	5	250	500	1000	Total
									Hit Rate (HR)								
PApca	0.65	0.81	0.88	0.65	0.8	0.88	0.99	0.96	0.82	0.35	0.87	0.78	0.68	0.69	0.79	0.86	0.78
EGA	0.69	0.9	0.91	0.74	0.87	0.91	0.96	0.94	0.89	0.57	0.89	0.87	0.76	0.77	0.85	0.88	0.84
EGA.analytical	0.62	0.88	0.97	0.83	0.86	0.82	0.90	0.88	0.83	0.73	0.89	0.92	0.70	0.69	0.87	0.95	0.84
EGA.sampling	0.58	0.86	0.96	0.83	0.83	0.74	0.87	0.84	0.79	0.69	0.79	0.82	0.79	0.59	0.85	0.95	0.80
									Mean Biased Error (MBE)								
PAPApca	−0.7	−0.39	−0.24	−0.71	−0.39	−0.23	0	−0.05	−0.3	−1.42	−0.13	−0.34	−0.86	−0.62	−0.42	−0.28	−0.44
EGA	−0.31	−0.2	−0.23	−0.49	−0.18	−0.06	−0.03	−0.04	−0.07	−0.84	−0.06	−0.15	−0.54	−0.29	−0.21	−0.24	−0.25
EGA.analytical	−0.15	−0.07	−0.02	−0.20	−0.07	0.02	−0.04	−0.06	−0.08	−0.14	0.07	0.04	−0.35	−0.10	−0.09	−0.06	−0.08
EGA.sampling	0.32	0.07	0.01	−0.06	0.13	0.33	0.1	0.12	0.14	0.18	0.24	0.23	−0.07	0.4	0.04	−0.04	0.13
									Mean Absolute Error (MAE)								
PAPApca	0.71	0.39	0.24	0.71	0.39	0.23	0.01	0.06	0.3	1.42	0.13	0.34	0.87	0.63	0.42	0.28	0.45
EGA	0.52	0.22	0.23	0.52	0.26	0.16	0.07	0.1	0.16	0.93	0.11	0.21	0.62	0.42	0.28	0.26	0.31
EGA.analytical	0.41	0.13	0.03	0.21	0.16	0.20	0.11	0.14	0.19	0.32	0.12	0.09	0.36	0.36	0.15	0.06	0.19
EGA.sampling	0.58	0.17	0.04	0.19	0.22	0.37	0.17	0.2	0.27	0.42	0.29	0.25	0.24	0.56	0.17	0.06	0.26

Note: PApca = parallel analysis with principal component analysis eigenvalues; EGA = exploratory graph analysis; EGA.analytical = analytically-based Bayesian exploratory graph analysis; EGA.sampling = sampling-based Bayesian exploratory graph analysis

Table 3. ANOVA effect size for the hit rate dependent variable.

Main Effect	PApca	EGA	EGA.analytical	EGA.sampling	Interaction Effect	PApca	EGA	EGA.analytical	EGA.sampling
FL	0.18	0.17	0.24	0.25	FL:VF:FC	0.08	0.02	0.01	0
VF	0.16	0.07	0.01	0.02	FL:VF:F	0	0	0.01	0.01
FC	0.6	0.28	0.07	0.06	FL:VF:N	0	0.01	0.01	0.02
F	0.12	0.06	0.1	0	FL:FC:F	0.03	0.01	0.01	0
N	0.1	0.06	0.15	0.22	FL:FC:N	0.04	0.01	0.03	0.03
Interaction Effect	PApca	EGA	EGA.analytical	EGA.sampling	FL:F:N	0	0	0.02	0.02
FL:VF	0	0	0.02	0	VF:FC:F	0.03	0	0	0
FL:FC	0.1	0.02	0.04	0.02	VF:FC:N	0.03	0	0	0
FL:F	0.01	0.03	0.03	0	VF:F:N	0	0	0.01	0.01
FL:N	0.01	0.09	0.04	0.08	FC:F:N	0.01	0	0	0
VF:FC	0.13	0.14	0.01	0	FL:VF:FC:F	0.02	0	0.01	0
VF:F	0	0	0.01	0.03	FL:VF:FC:N	0.03	0	0	0.01
VF:N	0	0	0.02	0.05	FL:VF:F:N	0.01	0	0.01	0.01
FC:F	0.08	0.03	0	0	FL:FC:F:N	0.02	0.01	0.02	0.01
FC:N	0.05	0.01	0	0	VF:FC:F:N	0.01	0	0	0
F:N	0.01	0	0.03	0	FL:VF:FC:F:N	0.05	0	0	0

Note: FL = factor loading; VF = variables per factor; FC = factor correlation; F = number of factors: N = sample size; PApca = parallel analysis with principal component analysis eigenvalues; EGA = exploratory graph analysis; EGA.analytical = analytically-based Bayesian exploratory graph analysis; EGA.sampling = sample-based Bayesian exploratory graph analysis. Cell values are partial eta squared effect size estimates. The unidimensional condition was excluded from the analyses due to not crossing with the factor correlation variable.

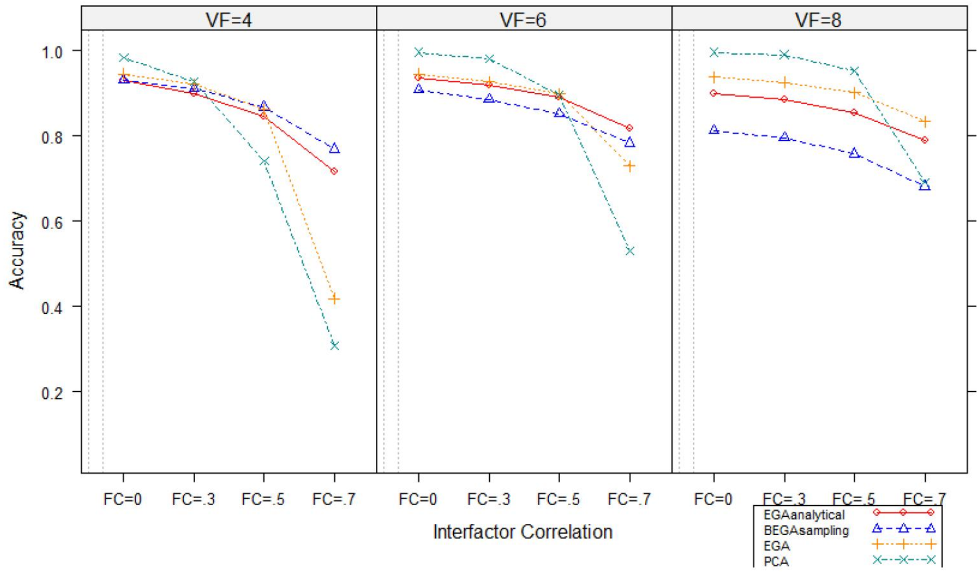

Figure 2. ANOVA interactions for EGA.analytical, EGA.sampling, EGA, and PApca ($\eta^2_{p.EGA} = 0.14$, $\eta^2_{p.PCA} = 0.13$).

the lowest MAEs (0.03 and 0.04, respectively), as compared to EGA (0.23) and PApca (0.24), as well as the lowest MBEs (−0.02 and 0.01, respectively), as compared to EGA (−0.23) and PApca (−0.24). As the factor loading decreased to 0.55, EGA and the EGA.analytical method had the highest HRs (0.90 and 0.88, respectively), followed by the EGA.sampling method (0.86) and PApca (0.81). At the same time, the EGA.analytical approach produced the smallest MAE (0.13), followed by the EGA.sampling method (0.17), EGA (0.22), and PApca (0.39); following a similar pattern, the EGA.analytical method and the EGA.sampling method had the smallest MBEs (−0.07 and 0.07, respectively), as compared to EGA (−0.20) and PApca (−0.39). When the factor loading decreased to 0.4, the four methods performed differently in terms of HRs, MBEs, and MAEs. EGA had the highest HR, followed by PApca, the EGA.analytical method, and the EGA.sampling method. the EGA.analytical method had the lowest and best MBE and MAE, followed by EGA, the EGA.sampling method, and PApca.

Interfactor correlations

The two Bayesian techniques had apparently outstanding performance in terms of high HRs and low MBEs and MAEs under high interfactor correlation (0.7). EGA had the best performance when the interfactor correlations were 0.5, while PApca performed the best as the interfactor correlation decreased to 0.3 and lower. Specifically, when the interfactor correlations were 0.7, the EGA.analytical method and the EGA.sampling method demonstrated clear higher HRs (0.73 and 0.69, respectively) than EGA (0.57) and PApca (0.35), respectively. The EGA.analytical method and the EGA.sampling method also had better MBEs and MAEs than EGA and PApca. When the interfactor correlations were 0.50, EGA had the best HR, MBE and MAE, followed by the EGA.analytical method with the second highest HR the second lowest MBE and MAE. As the interfactor correlations decreased (0.3 or less), PApca had the best HR, MBE and MAE, followed by EGA, EGA.analytical, and the EGA.sampling method.

Number of factors

In the presence of five factors, the EGA.sampling method performed the best with high HRs and low MBEs and MAEs. The EGA.analytical method performed the best when there were 3 factors in the data, and EGA performed the best when having 2 factors in the data. Specifically, with five factors, the EGA.sampling method had a pronounced performance with the highest HR and the lowest MBE and MAE among the four techniques. EGA had the second best HR, while the EGA.analytical method had the second best MBE and MAE. The PApca technique performed the least well in these three evaluation criteria under the condition. Having 3 factors in the study, the EGA.analytical method performed the best with high HRs and low MBEs and MAE, followed by EGA, the EGA.sampling method, and PApca, As the number of factors decreased to 2, EGA had the best performance. When compared with PApca, the EGA.analytical method had lower HR while MBE and MAE. The EGA.sampling method performed the least well under these conditions.

Variables per factor

With eight items per factor, while EGA had the highest HR and smallest MAE, the EGA.analytical method had the smallest MBE among the four methods. With six items per factor, EGA had the highest HR while the EGA.analytical method had the smallest MBE and MAE. In the presence of four items per factor, the EGA.analytical method and the EGA.sampling method performed the best with the highest HR and the EGA.sampling method had the smallest MBE and MAE. Specifically, when each factor had eight items, EGA had the highest HR, followed by PApca, the EGA.analytical method, and the EGA.sampling method. The EGA.analytical method had the smallest MBE, followed by EGA, PApca, and the EGA.sampling method. With regards to MAE, EGA performed the best, followed by the EGA.analytical method, PApca, and the EGA.sampling method. When each factor had six items, EGA had better HR (0.87) than the EGA.analytical method (0.86), while worse MBE (−0.18) than the EGA.analytical method (−0.07) and higher MAE (0.26) than the EGA.analytical method (0.16). As the items decreased to four per factor, the two Bayesian techniques performed the best in terms of HR, MBE, and MAE. The EGA.analytical method and the EGA.sampling method had the best HRs (0.83), followed by EGA (0.74) and PApca (0.65); the EGA.sampling method also had the smallest MAE (0.19), closely followed by The EGA.analytical method (0.21), EGA (0.52), PApca (0.65), as well as the best MBE (−0.06), followed by the EGA.analytical method (−0.20), EGA (−0.49), and PApca (−0.71).

Sample size

When the sample sizes were medium to large (i.e., $N \geq 500$), the two Bayesian methods outperformed in terms of the best HRs, MBEs and MAEs. Specifically, when $N = 1000$, the HRs for the EGA.analytical method., EGA.sampling, EGA, and PApca were 0.95, 0.95, 0.88, and 0.86, respectively; the MBEs for the four methods were −0.06, −0.04, −0.24, and −0.28, respectively; and the MAEs for the EGA.analytical method., the EGA.sampling method, EGA, and PApca were monotone increasing, as 0.06, 0.06, 0.26, and 0.28, respectively. A similar pattern appeared under the medium sample sized condition (i.e., $N = 500$). The EGA.analytical method and the EGA.sampling method produced better or identical HRs than EGA and PApca, and smaller MBEs and MAEs than the other two techniques. As the sample size decreased to 250, EGA and PApca had higher HRs than the EGA.analytical method, while the EGA.analytical method had the best MBE and MAE. The EGA.sampling method did not perform well under these conditions.

ANOVAs

We further conducted ANOVAs to assess the impact of the manipulated variables and their interactions. In the ANOVAs, the HR was the dependent variable and the five manipulated data conditions were the independent variables. The ANOVAs estimated up to four-way interactions. The effect sizes for the ANOVAs were presented in Table 3. Of note, the EGA.analytical method was the only method that did not have an interaction with a medium or up effect size ($\eta_p^2 \geqslant 0.06$), and the EGA.analytical method and the EGA.sampling method were the only techniques that did not have interactions with a large effect size ($\eta_p^2 \geqslant 0.14$). In terms of the main effects, PApca had the highest effect sizes, showing that the accuracy of PApca was largely affected by the variability of factor loadings, interfactor correlations, sample size, number of factors, and number of variables per factor.

The two-way interaction VF (variables per factor) * FC (interfactor correlations) yielded close to large effect sizes for EGA ($\eta_{p.EGA}^2 = 0.14$) and PApca ($\eta_{p.PApca}^2 = 0.13$), respectively, which demonstrated the variabilities of the EGA and PApca methods in producing accuracies. We plotted this two-way interaction which demonstrated large effect sizes (see Figure 2) to further investigate and compare the performances of the four methods. Under the four variable per factor condition, the two Bayesian techniques had relatively stable HRs across interfactor correlation conditions, whereas the performance of EGA and particularly PApca varied largely across varying interfactor correlations. Specifically, when the factors were uncorrelated, PApca had the highest HR (≈ 0.98), with the EGA.analytical method, the EGA.sampling method and EGA having slightly lower and similar HRs (≈ 0.92). The four methods had similar HRs ($\approx$ 0.90) when the interfactor correlation was 0.3. As the interfactor correlations increased to 0.5, PApca had a large drop in HR to around 0.7. When the interfactor correlations climbed to 0.7, PApca had a huge plummet in HR (≈ 0.30), and so did EGA (≈ 0.40), while the two Bayesian approaches remained relatively high in accuracy ($\approx$ between 0.71 and 0.76). Similar patterns were seen when each factor had 6 items. When there were 8 items per factor, the EGA.analytical method, the EGA.sampling method, and EGA had stable performances across varying interfactor correlations, while PApca had sharp drop in HR when the interfactor correlation increased.

In sum, the results showed that across the studied conditions, EGA and EGA.analytical had the highest HRs (0.84), followed by EGA.sampling (0.80) and PApca (0.78); EGA.analytical had the lowest and best MBE (−0.08), followed by EGA.sampling (0.13), EGA (−0.25), and PApca (−0.44); and EGA.analytical had the lowest and best MAE (0.19), followed by EGA.sampling (0.26), EGA (0.31), and PApca (0.45). Furthermore, across manipulated data conditions and their interactions, the EGA.analytical method was the least affected by varying levels of data conditions both in the main and interaction effects, followed by EGA.sampling and EGA. The performance of PApca was largely affected by varying levels of manipulated data conditions.

Simulation study 2 - assessing unidimensionality

Unidimensionality remains a challenge in network psychometric models. The EGA.analytical and EGA.sampling models developed in the study applied the expand unidimensionality adjustment rule (Golino et al., 2020). We carried out a second simulation study to assess the effectiveness of the expand adjustment rule proposed to the current two Bayesian models.

Data were generated using a similar design as in the multdimensional setting (see Table 1), except that the true data generating process was from a one-factor (i.e., unidimensional) model. A total of $3 \times 3 \times 4 \times 3 = 108$ conditions were studied for the unidimensional design and each condition was replicated 500 times. The EGA.analytical and EGA.sampling methods started with the expand adjustment rule to verify whether there was a unidimensional factor structure. After verifying the unidimesionality, the techniques proceeded to check for multidimensionality in the absence of the unidimensionality (See Figure 1).

Table 4 presented a summary of the HR, MBE, and MAE values for the four techniques, which were defined in a similar way as in the multidimensional setting. The findings showed that the EGA.analytical and EGA.sampling methods demonstrated satisfactory performance when assessing unidimensionality. In comparison to the other two existing techniques, PApca demonstrated outstanding performance, achieving almost perfect HR (99.92%), followed closely by EGA (99.38%), the EGA.analytical method (93.61%) and the EGA.sampling method (92.67%). PApca also exhibited near-zero values for MBE and MAE, with EGA closely following behind. The EGA.analytical and EGA.sampling methods exhibited lower HRs (93.61% and 92.67%, respectively) and higher MBEs and MAEs (0.11), although these results were still considered quite favorable.

Simulation study 3 - comparing Bayesian techniques in small sample size

Small-sampled conditions are not uncommon in behavioral and social sciences. Yet existing techniques discussed above do not offer a flawless solution to addressing this challenge. In this simulation study, we

Table 4. HR, MBE, and MAE for EGA.analytical, EGA.sampling, EGA, and PApca in unidimensionality assessment.

Method	Factor loading			Variables per factor			Sample size			Total
	0.40	0.55	0.70	4	6	8	250	500	1000	
					Hit Rate (HR)					
PApca	99.76%	100%	100%	99.80%	99.96%	100%	99.78%	99.98%	100%	99.92%
EGA	98.12%	100%	100%	99.84%	99.40%	98.89%	98.46%	99.67%	100%	99.38%
EGA.analytical	87.43%	95.47%	97.91%	99.56%	96.39%	84.84%	81.99%	98.81%	100%	93.61%
EGA.sampling	85.22%	95.04%	97.76%	98.24%	96.11%	8367%	79.59%	98.42%	100%	92.67%
					Mean biased error (MBE)					
PApca	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
EGA	0.02	0.00	0.00	0.00	0.01	0.01	0.02	0.00	0.00	0.01
EGA.analytical	0.14	0.05	0.02	0.00	0.04	0.18	0.20	0.01	0.00	0.07
EGA.sampling	0.25	0.07	0.03	0.02	0.06	0.26	0.32	0.02	0.00	0.11
					Mean absolute error (MAE)					
PApca	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
EGA	0.02	0.00	0.00	0.00	0.01	0.01	0.02	0.00	0.00	0.01
EGA.analytical	0.14	0.05	0.02	0.00	0.04	0.18	0.20	0.01	0.00	0.07
EGA.sampling	0.25	0.07	0.03	0.02	0.06	0.26	0.32	0.02	0.00	0.11

Note: PApca = parallel analysis with principal component analysis eigenvalues; EGA = exploratory graph analysis; EGA.analytical = analytically-based Bayesian exploratory graph analysis; EGA.sampling = sampling-based Bayesian exploratory graph analysis

compared the analytical-based EGA approach (i.e., *EGA.analytical* using the Bayesian conjugate Wishart prior) with the other four above-discussed Bayesian techniques (i.e., *EGA.pip*, *EGA.incBF*, *EGA.gwishart*, *EGA.structure*) under the small sample size condition. This served as an exploration of the feasibility of expanding EGA into full Bayesian framework.

Data were generated using a design similar to the multidimensional and unidimensional settings, but with specific attention given to conditions having small sample sizes (see Table 5). A total of $2 \times 2 \times 2 \times 3 = 24$ conditions were studied on each of the five Bayesian techniques and each condition was replicated 100 times. Each technique started with the expand adjustment rule (Golino et al., 2020) to assess the unidimensional factor structure and then proceeded to assess the multidimensional factor structure only if the unidimensionality was not identified. For the *EGA.pip* method, a PIP value of 0.5 or higher indicated support for including the edge, and thus the edge was selected; otherwise, it was excluded. For the *EGA.incBF* method, an inclusion Bayes factor value $BF_{10} \geq 1$ indicated that there was evidence supporting the inclusion of the edge. Conversely, $BF_{10}<1$ indicated that the edge was excluded. For the *EGA.gwishart* method, we assigned the value of 3 to the degrees of freedom hyperprior to indicate a non-informative prior for the *G*-Wishart distribution. For the *EGA.structure* method, the structure was directly sampled from the posterior distributions of the visited structures, and the structure visited most frequently was selected as the final structure. We used the adjacency matrix of the selected graph to determine the level of sparsity for the *EGA.structure* method. All the above-mentioned techniques used the Louvain community detection algorithm to assess dimensionality after the graphical structure was determined.

The HRs for the five techniques were presented in Figures 3 and 4. Tables 6 and 7 presented the MAE and MBE values for the five Bayesian techniques. The findings showed that the Bayesian techniques illustrated great promise in small sampled conditions. The two Bayes factor based approaches (i.e., *EGA.pip* and *EGA.incBF*) and the direct structure selection technique (i.e., *EGA.structure*) exhibited outperformance

Table 5. Simulation design for study 3.

Influential Factors	# of Factor Levels	Levels
Number of factors *F*	3[1]	1, 2,5[1]
Number of Items per Factor *I*	2	4, 8
Factor Loadings *λ*	2	0.4, 0.7
Interfactor Correlations *r*	2	0, 0.7
Sample Size *N*	1	250

Note: [1]Includes the multidimensional and unidimensional designs

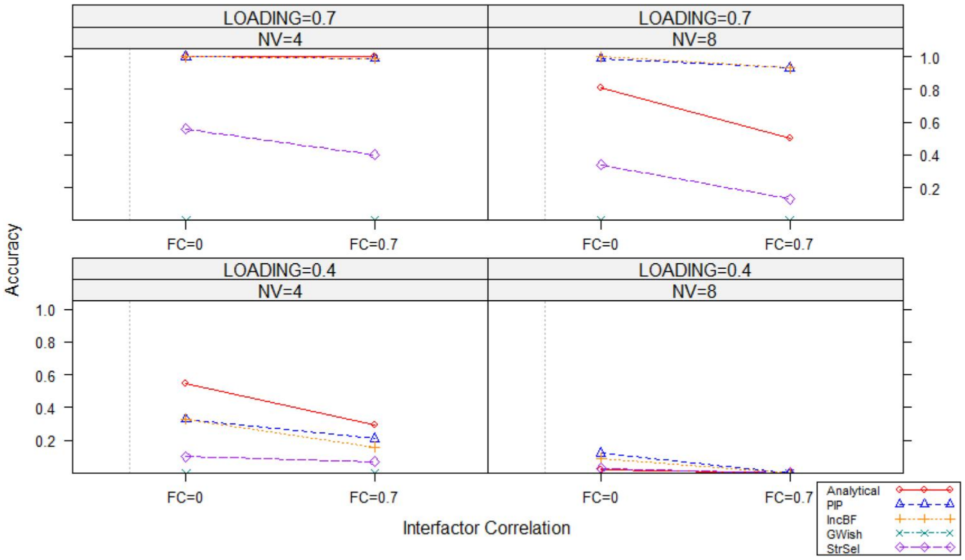

Figure 3. Hit rates for five Bayesian techniques with two factors when $N = 250$.

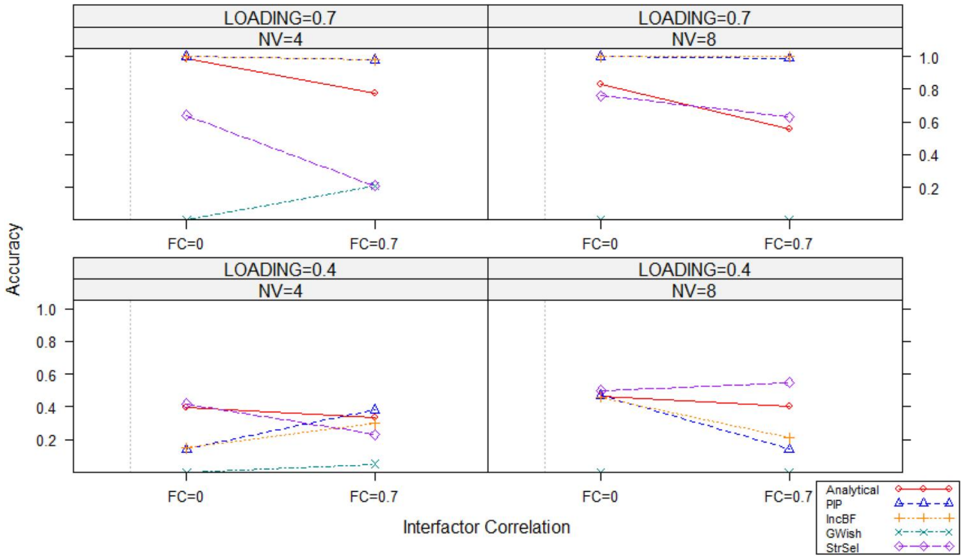

Figure 4. Hit rates for five Bayesian techniques with five factors when $N = 250$.

Table 6. Mean absolute errors for five Bayesian techniques when $N = 250$.

True F	Loadings	Nitems	FCorrelations	EGA.analytical	EGApip	EGAincBF	EGAgwishart	EGAstructure
2	0.4	4	0	0.414	1.220	1.180	3.420	1.700
			0.7	0.343	0.900	0.870	2.540	1.140
		8	0	1.798	1.800	1.920	4.110	1.840
			0.7	2.101	2.520	2.480	4.010	1.960
	0.7	4	0	0.000	0.000	0.000	1.000	0.440
			0.7	0.000	0.010	0.010	1.000	0.420
		8	0	0.192	0.010	0.000	1.000	0.860
			0.7	0.586	0.070	0.070	1.000	1.260
5	0.4	4	0	0.545	1.800	1.930	6.540	0.280
			0.7	0.293	0.630	0.550	2.960	0.910
		8	0	0.424	0.790	0.740	7.760	0.190
			0.7	0.747	1.430	1.330	6.650	0.170
	0.7	4	0	0.010	0.000	0.000	1.000	0.400
			0.7	0.222	0.020	0.020	0.770	0.870
		8	0	0.051	0.000	0.000	1.000	0.210
			0.7	0.020	0.010	0.000	1.010	0.230

Table 7. Mean biased errors for five Bayesian techniques when $N = 250$.

True F	Loadings	Nitems	FCorrelations	EGA.analytical	EGApip	EGAincBF	EGAgwishart	EGAstructure
2	0.4	4	0	0.414	1.220	1.180	3.420	1.700
			0.7	0.343	0.900	0.870	2.540	1.140
		8	0	1.798	1.800	1.920	4.110	1.840
			0.7	2.101	2.520	2.480	4.010	1.960
	0.7	4	0	0.000	0.000	0.000	1.000	0.440
			0.7	0.000	0.010	0.010	1.000	0.420
		8	0	0.192	0.010	0.000	1.000	0.860
			0.7	0.586	0.070	0.070	1.000	1.260
5	0.4	4	0	−0.545	1.800	1.930	6.540	−0.280
			0.7	−0.293	0.630	0.550	2.960	−0.910
		8	0	0.424	0.790	0.740	7.760	0.190
			0.7	0.747	1.430	1.330	6.650	0.170
	0.7	4	0	−0.010	0.000	0.000	1.000	−0.400
			0.7	−0.222	−0.020	−0.020	0.770	−0.870
		8	0	−0.051	0.000	0.000	1.000	−0.210
			0.7	0.020	−0.010	0.000	1.010	−0.230

under the conditions with an increasing true number of latent factors and question items, which had challenged the EGA.analytical and EGA.sampling methods, especially in small sample size conditions. Specifically, with a high factor loading (i.e., $\lambda = 0.7$), the two Bayes factor based techniques, *EGA.pip* and *EGA.incBF*, demonstrated consistently better hit rates, MBEs and MAEs than the *EGA.analytical* and other Bayesian techniques. The advantage is more apparent when the true number of factors is 5 and the number of items increased from 4 to 8. The structure selection technique *EGA.structure* had a pronounced performance with the low factor loading (i.e., $\lambda = 0.4$) condition with the true number of items being large. Under these conditions, the *EGA.structure* yielded the highest hit rates and better MAE and the advantage is more apparent when the number of true factor increases to 5.

In sum, the four Bayesian techniques demonstrate encouraging outcomes in conditions that have otherwise been challenging for the EGA.analytical and EGA.sampling approaches. The two Bayes factor based techniques, *EGA.pip* and *EGA.incBF*, that used Bayesian hypothesis testing to assess dimensionality were particularly promising, as evidence by the outperformance of the two techniques in conditions discussed above. The reason the two techniques performed similarly across the studied conditions was because we did not impose sparsity in the data generating structure. The Bayesian model average technique is expected to be more robust with sparse structure (Sekulovski et al., 2023). We expect the *EGA.incBF* will perform better than the single model *EGA.pip* method when the underlying structure of the data is sparse with fewer connections. The direct structure sampling technique *EGA.structure* also demonstrates considerable promise, excelling in conditions where the GLASSO-based EGA and the Bayesian *EGA.analytical* method have struggled. Moreover, it offers an alternative venue beyond estimating GGM model parameters to assess dimensionality through graphical models. In this simulation setup, we did not observe improvement in performance from the *EGA.gwishart* method that used the *G*-Wishart prior. We expect its performance may improve with the specification of a more informative hyperprior in future studies.

Two empirical examples using R

This section illustrates the applications of the two alternative estimation methods to the EGA technique based on Bayesian methods using two empirical examples *via* the *EGAnet* package (version 2.0.6, H. Golino et al., 2023) in R. In the first example, we assess the factor structures of a Big Five personality test using the EGA.analytical technique. The BIG Five personality test, traditionally assessed through factor analysis, is widely recognized for having five personality domains, including openness to experience (O), conscientiousness (C), extraversion (E), agreeableness (A), and emotional stability or neuroticism (N), known as the OCEAN model. In this example, a total of 1,015,341 participants each answered 50 personality items, adopted from the Big-Five Factor Markers from the International Personality Item Pool (IPIP; Goldberg et al., 2006) as part of a nonprofit initative to inform public about psychology and personality research. The IPIP items were administered with a 5-point Likert-type scale ranging from 1 (strongly disagree) to 5 (strongly agree). The dataset is publicly available at OpenPsychometrics.org.

The *EGA.analytical* and EGA.sampling methods are executed as a branch of the *EGAnet* package (version 2.0.6; H. Golino et al., 2023) in the current version. End-users first install the *EGAnet* branch from the *Gihub* repository, using the code illustrated below. After calling the *EGAnet* package, we use *EGA*() function to call the EGA.analytical technique and analyze the data. The data to be analyzed need to be in a raw data format, with rows showing the number of sample size and columns showing the number of observed variables. We will call the EGA.analytical technique by specifying an estimation model that calls *model* = *BGGM* and *analytic* = *TRUE*, a community detection algorithm by specifying the *algorithm* = *louvain* argument, and a desired level of credible interval by specifying the *cred* argument in the function. The EGA.analytical technique is currently available to handle only continuous or mixed-type response format. Thus, one needs to specify the response format in the *type* argument. The argument of *plot* = *TRUE* will display the estimated network plot with the package's default plot color. Alternatively, in this example, we produced an identical network plot with a colorblind friendly version using the following code below. Furthermore, while the *EGAnet* package has the walktrap community detection algorithm (Pons et al., 2006) as its default, end-users have the flexibility to specify other community detection algorithms. In the *EGA.analytical* method, we used the *Louvain* community detection algorithm and specified the credible interval level of 90%. Altogether, we assess the dimensionality of the personality data using the following R code.

```
devtools :: install_github("hfgolino/EGAnet", ref = "bega")
library (EGAnet)
EGAanalytical <- EGA(big5, model="BGGM", analytic = TRUE, algorithm="louvain", cred = 0.9, type="continuous", plot = FALSE)
plot(EGAanalytical, color.palette = "blue.ridge2", edge.color = c("blue", "red"), node.alpha = 1)
```

Using the above R code produces the five-dimensional layout of the Big Five Personality Test as well as the item assignments from the EGA.analytical technique, shown in Figure 5. This network plot of dimensionality assessment helps visualize the grouping of the 50 question items. The colors of the nodes represent latent factors; question items having the same colors are grouped in the same factor. The result showed a clean five dimensional result in the personality questionnaires. The first dimension (red nodes) represents extraversion and comprises 10 related items such as E1: *"I am the life of the party"*. The second dimension (blue nodes) signifies emotional stability or neuroticism and contains 10 items, such as N1: *"I get stressed out easily"*. The third dimension (green nodes) show agreeableness and consists of 10 items, such as

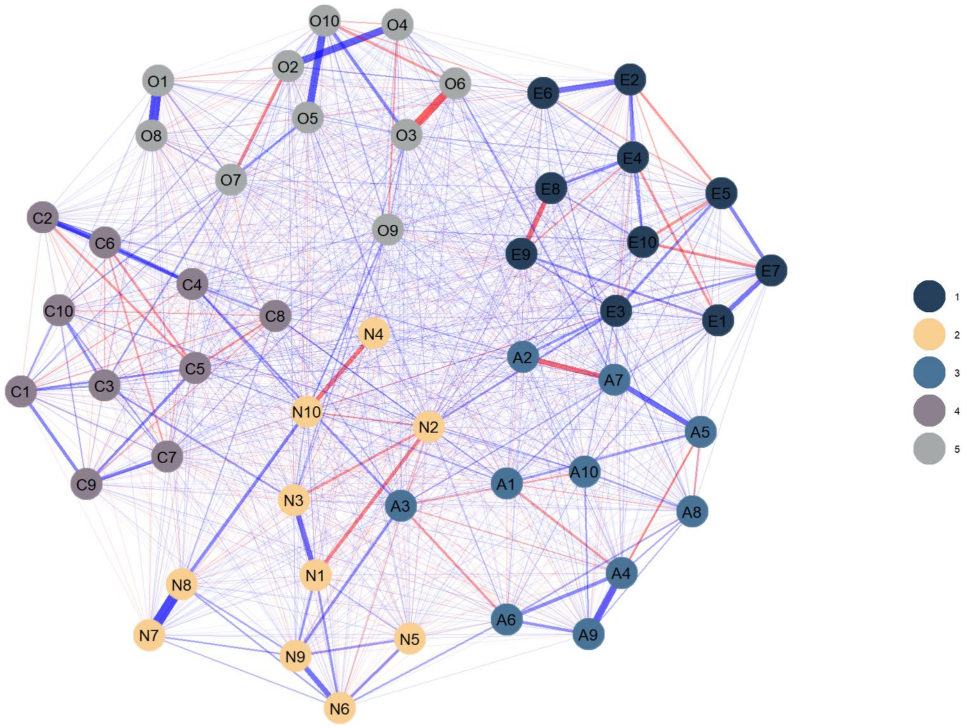

Figure 5. Network plot of using the EGA.analytical method for the big five personality test.

A8: *"I take time out for others"*. The fourth dimensionality (orange nodes) exhibits conscientiousness and includes 10 items such as C1: *"I am always prepared"*. Lastly, the fifth dimension (yellow nodes) reflects openness to experience and contains 10 related items such as O3:*"I have a vivid imagination"*. In addition, this network plot can help immediately confirm that the 50 personality question items have been accurately assigned to their respective underlying latent factor structure.

The second example assesses the dimensionality of the Athens Insomnia Scale (AIS), a widely-used screening tool for insomnia. The dataset is available from the *depression* data from the *EGAnet* package. A sample of 573 participants (69.3% female) completed an AIS involving eight question items, which were listed in Table 8. We use the EGA.sampling technique to assess the AIS' dimensionality and call the *EGA*() function to implement the EGA.sampling technique with the following code.

```
AISdata = depression ([,70:77])
EGA(AISdata, model = "BGGM", analytic = FALSE,
algorithm="louvain",
cred = 0.9, type="continuous", uni.method="expand",
plot = TRUE)
```

Table 8. Athens insomnia scale questions.

Item Number	Questions
Item 1	Sleep induction
Item 2	Awakenings during the night
Item 3	Final awakening earlier than desired
Item 4	Total sleep duration
Item 5	Overall Quality of sleep
Item 6	Sense of well-being during the day
Item 7	Functioning during the day
Item 8	Sleepiness during the day

To compare the result from the EGA.sampling method with that from EGA, we apply the EGA technique to the same dataset with the following R code. The *uni.method* arguments in both codes shows the application of the *expand* method to address potential unidimensionality.

```
EGA(AISdata, plot = TRUE, uni.method="expand")
```

Figure 6 compares the network plots from the EGA.sampling and the GLASSO-based EGA techniques for assessing AIS' dimensionality. Both techniques yield identical number of three dimensions and assign items to these dimensions in a similar way, with the exception of one item that differs. Specifically, the EGA.sampling method grouped item 8 (sleepiness during the day) more closely with one's daytime well-being (item 6) and daytime functioning (item 7), whereas using EGA, daytime sleepiness (item 8) is thought to be more closely related to sleep duration (item 4) and sleep quality (item 5). In terms of the actual content, the outcome of the EGA.sampling method appears to be more sensible, with the second cluster being related to the daytime impact.

We further compare the fit measures from both results using the Total Entropy Fit Index (TEFI; H. Golino et al., 2021). TEFI is an entropy-based measure developed from information theory to check the dimensionality structure of the data and has been found to provide equally or more accurate results than traditional fit measures. Lower TEFI indicates better fit of the model to the data. Results showed that the TEFIs for the EGA.sampling and EGA techniques were −1.66 and −1.63, respectively. The finding indicates that the EGA.sampling method leads to a 3-factor structure that fits slightly better than the 3-factor structure suggested by EGA.

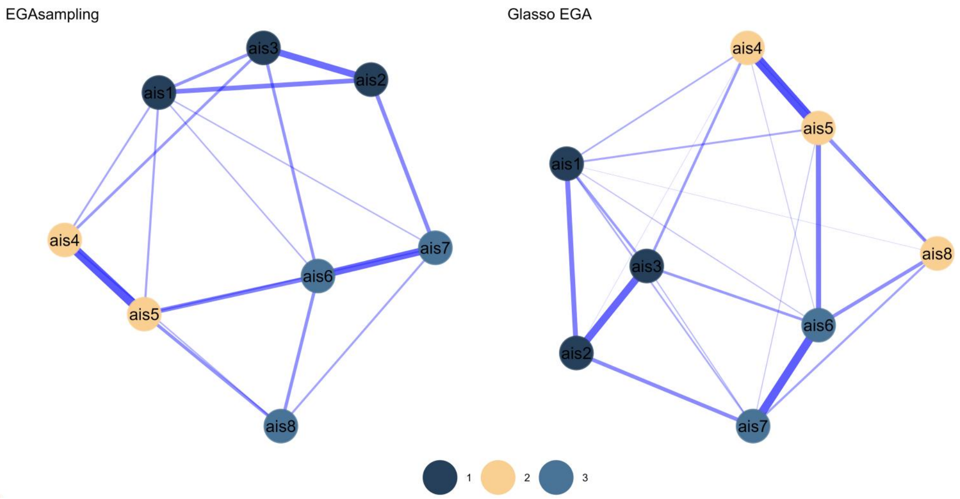

Figure 6. Network plot comparisons of using the EGA.sampling and the glasso-based EGA for the Athens insomnia scale.

Discussion

This study examined alternative estimation algorithms, particularly using Bayesian methods to the conventional GLASSO-based EGA (Golino et al., 2020; Golino & Epskamp, 2017) in network psychometric models to assess the dimensional structures of the multivariate data. In particular, the EGA.analytical method computed the Gaussian graphical structures analytically from a conjugate Wishart prior distribution (Kubokawa & Srivastava, 2008) and used the Louvain community detection algorithm (Blondel et al., 2008) to partition the nodes and assess dimensions. The EGA.sampling technique adopted a sampling-based Bayesian approach using Jeffreys' prior (Williams, 2021) and then applied the Louvain community detection algorithm (Blondel et al., 2008) to detect dimensionality. Both approaches applied the expand adjustment rule (Golino et al., 2020) to evaluate the potential unidimensional factor structure in the model. In addition, the study explored four full Bayesian network techniques to assess dimensionality in the context of small sample conditions. We compared the performance of the proposed two Bayesian estimation methods (i.e., EGA.analytical and EGA.sampling) *via* two Monte Carlo simulation studies with the GLASSO-based EGA and the eigenvalue-based parallel analysis (i.e., PApca). We also compared the performance of the four full Bayesian techniques with the EGA.analytical method in a third simulation study.

The study found that when estimating the multidimensional structures, EGA had the highest HR, followed by EGA.analytical, EGA.sampling, and PApca. The EGA.analytical method had the smallest and most accurate MBE and MAE, followed by the EGA.sampling method, EGA, and PApca. Although the EGA.analytical approach had a slightly lower overall HR than EGA by 2.38%, it had a significantly better MBE by 32.26% and a better MAE by 60%. Given that the small difference in HR did not outweigh the large difference in MBE and MAE, the EGA.analytical method had the best tradeoff between accuracy and mean biased/absolute errors. The EGA.sampling method had a lower overall accuracy but also lower mean biased and mean absolute errors than EGA. Further, the EGA.sampling method had better accuracy and smaller errors than PApca. Both Bayesian techniques had more stable performance across the main and interaction effects of the data conditions than EGA and PApca. When considering the different factors studied, the EGA.analytical method demonstrated the best balance among the four techniques. This was observed when studying 3 or 5 factors, 4 or 6 items per factor, medium to high factor loadings (0.55 or higher), high factor correlations (0.70), and medium to large sample size (500 or more). On the other hand, EGA performed the best when dealing with 2 factors, 8 items per factor, small factor loadings (0.40), or medium factor correlations (0.50), and PApca performed the best when the factor correlations were small (0.30 or less). When the sample size was 250, EGA had the highest HR, while the EGA.analytical method had the best MBE and MAE. In terms of estimating the unidimensional structure, the PApca technique yielded the highest HR, as well as the best MBE, and MAE. The tied EGA and EGA.analytical approaches followed closely, and then the EGA.sampling method. Among the four full Bayesian techniques, the two Bayesian hypothesis testing based methods (i.e., *EGA.pip* and *EGA.incBF*) and the Bayesian direct structure selection technique demonstrated superior performance as the true number of latent factors and observed items increased when the sample size is small. These are conditions where the EGA.analytical and EGA.sampling methods struggle most. In sum, the study recommends using EGA.analytical as an alternative tool for assessing dimensionalities and advocates the usefulness of EGA.sampling as a valuable alternate technique. The findings also indicated encouraging results for extending the regularization-based EGA network modeling to the full Bayesian framework. The alternative estimation approaches were not intended to replace existing dimensionality detection techniques such as the GLASSO-based EGA or parallel analysis but provided another view and opportunity to examine the multivariate data.

Using Bayesian estimation to assess dimensionality offers certain advantages and there is potential to extend the dimensionality assessment in network models to full Bayesian framework. First, we can incorporate prior knowledge into the graph structures and derive a posterior distribution of the parameters in the Bayesian estimation. By obtaining a complete posterior distribution, we can examine the parameter estimates of interest within a specified range for further analysis. This advantage is reflected in the EGA.analytical and EGA.sampling methods with reduced mean biased/absolute errors and greater consistency across various conditions compared to those from the ROPE-based EGA.analytical, the GLASSO-based EGA and the *PApca* methods. Second, the Bayesian estimation obtains the posterior probabilities of graphical structures rather than a fixed point estimate to evaluate the conditional dependence relationships between variables. The estimated distributional details of the structures provides additional computational insights, such as distributions, centrality, and empirical standard errors. This information pieces allow flexibility in adjusting the sparsity level of the graphical structure, which contrast with the sparsity regularization used in the GLASSO-based EGA's regularization process. The Bayesian methods do not produce a sparse matrix for the graphical structures directly, but need decision rules to control sparsity. Establishing rules that correspond to an appropriate level of sparsity will benefit the estimation of the graphical structures. We conducted preliminary studies and found an improved accuracy in the techniques when tailoring the sparsity level to data specific conditions. We think this also explained why the EGA.sampling technique outperformed EGA.analytical in certain conditions as the former allows the potential to control sparsity of the graphical structure. Consequently, with an appropriate decision rule, the EGA.sampling method is more likely to detect the true dimensions. Additionally, engaging the dimensionality assessment to full Bayesian framework demonstrate both theoretical potential and empirical evidence of promise. Bayesian hypothesis testing overcomes the issues associated with the classical NHST. By focusing on the posterior density of edge weights, the Bayes factor based Bayesian hypothesis testing quantifies the sampling uncertainty *via* probabilities to determine whether edges should be included or excluded. Using this information on the quantified uncertainty of edge inclusion, the hypothesis that the accuracy of the dimensionality assessment will improve is supported by evidence from the simulation study conducted under conditions of small sample sizes in this research. Furthermore, by conducting direct structure sampling from the posterior distributions, the Bayesian method numerically calculates the relational uncertainties between nodes through edges and applies the decision rules to generate network sparsity that are consistent with substantive interpretability.

Substantively, we see the EGA.analytical and EGA.sampling methods useful for both theoretical and applied purposes. With respect to theory, the psychological literature is replete with debates regarding the factor structure of scores where replicable good fit for a multidimensional structure is difficult to find through traditional confirmatory techniques. For example, different models have been proposed for the structure of affect scores beyond a two-dimensional positive-negative structure. Although the addition of an arousal dimension (i.e., high versus low activation potential) has garnered the most empirical attention (e.g., Shi et al., 2023a), other dimensions (e.g., responsibility/control, certainty, situational-control, depth of experience, and regulatory focus) have been offered (Baas et al., 2008; Smith & Ellsworth, 1985). Assessing dimensionality holds considerable promise here and in similar cases where strong factor correlations are likely in attempts that go beyond a simple, two-dimensional structure (e.g., Jorgensen et al., 2021). In general, in literature where there is a proliferation of theory, constructs, and measures, such as leadership (Antonakis & House, 2014), career proactivity (Jiang et al., 2023), personality (Hough et al., 2015), we see potential in the studied methods to contribute to theoretical debates surrounding the multidimensional nature of phenomena.

We also see considerable promise for the methods to be leveraged for the practical purpose of mapping a complex outcome space onto potential test batteries to optimize prediction. A good case in point is the development and validation of test batteries for predicting work performance and hiring employees. Working from a clear conceptualization and operationalization of work performance is critical to the development and weighting of component predictor test scores. It is not uncommon for a job analysis to point to 20 or more, if not dozens of, work performance components. The EGA.analytical and EGA.sampling methods could be leveraged to reduce the components to a theoretically meaningful and optimally weighted set of criterion dimensions that guide the selection and weighting of predictor tests. In this way, the methods could support traditional criterion-related validation studies as well as synthetic validation efforts (Johnson & Carter, 2010). In the same vein as the preceding paragraph, we see potential in the methods for addressing debates in the scholarly literature regarding the dimensionality of work performance (Carpenter et al., 2021; Murphy & Shiarella, 1997; Rotundo, 2002).

The current study demonstrates the detection of latent factors through detecting the clustering of the network graphical structures estimated using Bayesian methods. This study presents an initial exploration of the potential benefits of incorporating Bayesian methods into the realm of psychological networks to assess dimensionality. It incorporates a novel Bayesian estimation method to evaluate the dimensionality within the psychological network framework. While the study has identified certain advantages of Bayesian methods when compared to conventional regularization-based EGA technique (Golino et al., 2020), it is important to note that these advantages are somewhat limited in scope in that the focus primarily centers around alternative estimation methods for network structure. Future studies could expand the scope of the work in this line of research, especially in terms of considering the development of structure selection models to assess dimensionality and assign membership using various alternative Bayesian techniques.

The study had a few additional future directions to explore. First, the current study for EGA.sampling predetermined a value range of 90% as the credible interval, which reflected the probability of the true value falling into the range. However, this value range was not based on prior knowledge and could potentially be updated by researchers to improve the performance of the EGA.sampling method. By adjusting the probability range, researchers can change the sparseness or density of the network, which could lead to better performance of EGA.sampling. Second, in the current study, the conjugate or the Jeffreys' priors were used in the Bayesian estimation, which may explain why the Bayesian approach did not show much improvement in small sample size conditions. The use of informative priors in future studies could potentially help to improve the performance in such conditions by incorporating previous information as additional data (e.g., Serang et al., 2014; Shi & Tong, 2017; Zhang et al., 2007). The performance of the proposed Bayesian network psychometric framework could be enhanced by developing and incorporating informative priors.

Note that the Louvain and fast-greedy community detection algorithms reached a similar accuracy when detecting the communities from the BGGM. We proposed the Louvain algorithm for the developed EGA.analytical and EGA.sampling approaches in the current study mainly due to Louvain's ability to accommodate hierarchical structures. It may not be obvious in the current simulation setup where all the data are from a single level factor structure, however, the EGA.analytical and EGA.sampling approaches with the Louvain algorithm allow potential to address the hierarchical structures such as in the bifactor model or the hierarchical factor models. We showed evidence that the expand adjustment rule performed very well in detecting the unidimensional structures in this study. The Louvain algorithm with an adjusted hyperparameter (resolution = 0.95) performs optimally and should be considered in future studies (Christensen et al., 2023b). Adjusting for unidimensionality remains open for future directions.

In conclusion, this study developed and systematically evaluated two approaches based on Bayesian network psychometric models, EGA.analytical and EGA.sampling, for the dimensionality assessment of psychological data. The results indicate that both approaches show promise as valuable alternative techniques to existing methods such as EGA and parallel analysis. Specifically, EGA.analytical demonstrated the best tradeoff between accuracy and estimation errors, while EGA.sampling exhibited improved performance when controlling for sparsity of the graphical structure. The use of Bayesian techniques offers several advantages, such as capturing uncertainty, facilitating statistical inference, and providing opportunities to control for sparsity levels. Moreover, the Louvain algorithm employed in the EGA.analytical and EGA.sampling approaches offers potential for addressing hierarchical structures. Future research should focus on refining aspects of the EGA.sampling method, such as adjusting the credible interval value range, incorporating informative priors, and further exploring unidimensionality adjustments. By doing so, the proposed Bayesian network psychometric framework can be further enhanced, offering researchers additional tools to analyze and understand complex data structures.

Article information

Conflict of Interest Disclosures: Each author signed a form for disclosure of potential conflicts of interest. No authors reported any financial or other conflicts of interest in relation to the work described.

Ethical Principles: The authors affirm having followed professional ethical guidelines in preparing this work. These guidelines include obtaining informed consent from human participants, maintaining ethical treatment and respect for the rights of human or animal participants, and ensuring the privacy of participants and their data, such as ensuring that individual participants cannot be identified in reported results or from publicly available original or archival data.

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