Bayesian Extension of the Partial Correlation Likelihood Test: A Test for Distinguishing Latent Variable Models from Networks.

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Abstract

The Partial Correlation Likelihood Test is a test that can be used to distinguish latent variable models from network models. It does so by calculating each model's likelihood of underlying the data given the observed proportion of anomalous partial correlations. This paper aims to incorporate a Bayesian extension of this test, allowing a range of latent variable models to be compared to a range of network models in order to investigate which type of model is more likely to underlie the data. It was hypothesized that this extension would improve the performance of the test, as it can evaluate a range of models rather than just the two specific ones that are estimated in the original Partial Correlations Likelihood Test. In order to investigate this, a Monte Carlo study was conducted, with datasets that had a wide range of characteristics to investigate the behaviours of the tests under different circumstances. This study found very similar performances of the original test and the Bayesian extended test. The Bayesian test seems to perform better, or very similarly to the original test, when the number of variables is fewer than 10. Investigation into the relationship between the difference in likelihoods for each model revealed it to be a significant predictor of whether or not the test was correct, indicating that this could be a useful addition to the tests. Further research could focus on improving the Bayesian extension, for example by testing out the effect of changing the priors to fit the data better, or by including a statistic that represents the difference in likelihood to improve the interpretability of the tests.

Bayesian extension of the Partial Correlation Likelihood Test: A test for distinguishing latent variable models from networks.

Within psychometrics, there are two popular viewpoints regarding psychological constructs. The most common perspective is the latent variable theory, in which the psychological construct is a latent variable that acts as the common cause for the observable variables (Borsboom et al., 2003; Jauk et al., 2013). In this perspective, the common variance between the observable variables is due to the latent variable, and this common variance can be used to estimate a variable that measures this latent variable (Brown, 2015). One assumption of the latent variable theory is local independence (Mair, 2018b), which indicates that conditioning on the latent variables makes the correlations between the observable variables disappear. According to this theory, the latent variable explains the correlations between the observable variables.

Another view on psychological constructs that has gained popularity is the network perspective. In this perspective, the correlations between the observable variables aren't due to a latent variable. Rather, the observable variables can be mutually causal (Borsboom & Cramer, 2013; Cramer et al., 2010). The variables are connected to each other in a network, and the psychological construct could be some property of this network, such as its state or degree of connectivity (Van Bork et al., 2024). Taking depression as an example, a person's depressed state could result from a densely connected network of symptoms often associated with depression (Van Bork et al., 2024). From this perspective, depression does not cause the symptoms, but the combination of symptoms is what represents the depressed state.

In a statistical sense, these two models can be very similar, and can lead to almost identical predicted covariance matrices and fit indices (Williams, 2012). This means that both models can fit the data equally well, making it difficult to determine which model underlies the observed relationships. However, it does matter which model to adopt because they differ

in their practical implications. Take for example the notion of depression. When the viewpoint of latent variable theory is taken, then the common cause (the latent variable) should be addressed in order to relieve the depressed individual of their symptoms (Aswal et al., 2018). However, when a network perspective is adopted, then to relieve the depression, the focus needs to be on relieving the individual symptoms (Borsboom & Cramer, 2013; Van Bork et al., 2024). Because of the difference in these implications, van Bork et al. (2019) developed the Partial Correlation Likelihood Test, which can be used to differentiate whether the data more likely originate from a network or from a latent variable.

This Partial Correlation Likelihood Test (PCLT) rests on the assumption that partial correlations that originate from a unidimensional latent variable model are restricted in some ways that partial correlations originating from a network model are not. Specifically, the PCLT examines two key restrictions that are implied by a unidimensional latent variable model: partial correlations should not switch signs compared to their corresponding zero-order correlations (i.e., correlations without controlling for the other variables), and partial correlations should not exceed their respective zero-order correlations in magnitude.

In a unidimensional latent variable model, all observed variables are connected through a common latent variable, which constrains the possible correlation structures. As shown by Holland and Rosenbaum (1986), this structure ensures that partialling out other variables reduces the correlation's magnitude and cannot reverse its direction. The partial correlations that do reverse their sign or are stronger compared to their corresponding zero-order correlations, can be considered 'anomalous partial correlations' for the unidimensional latent variable model (M. N. Williams et al., 2022), as they are inconsistent with this model. The PCLT takes the proportion of anomalous partial correlations and uses this as a test statistic. This test statistic can then be compared to the probability distributions from the two models that shows the likelihood of these models given the test statistic.

The PCLT compares the best fitting unidimensional factor model and the best fitting network model that are estimated from the available data. This means that the uncertainty in the estimation of these models is not taken into account. Uncertainty in the context of Bayesian statistics aims to quantify the confidence that can be put in the point estimate of the parameters of the model (Vatsa, 2021). With Bayesian statistics, it is possible to estimate a posterior probability distribution for each parameter in the model. This posterior probability distribution expresses the certainty, or degree of belief, of each of the possible parameter values. It is still possible to derive a point estimate from this distribution, for example by selecting the parameter value with the highest probability. The posterior probability distribution gives additional information about this parameter value. When this distribution is wide, there is more uncertainty surrounding the estimate of the parameter's value. Whereas a narrower distribution indicates more certainty around these estimates (Lambert, 2018). This paper aims to incorporate this concept of uncertainty into the Partial Correlation Likelihood Test as developed by van Bork et al. (2019). Instead of the test being performed using the two best fitting models, a range of possible models are compared to determine which type of model is more likely given the observed proportion of anomalous partial correlations.

This study aims to investigate whether incorporating the concept of Bayesian uncertainty in the PCLT improves its ability to distinguish between unidimensional latent variable and network models. The performance of the PCLT will be compared to the performance of the Bayesian Partial Correlation Likelihood Test (BPCLT), in which the uncertainty of the models is taken into account. The expectation is that the performance of the PCLT will improve with this introduction of this uncertainty. As the original PCLT only uses the best-fitting models to simulate new datasets, it can only draw conclusions about these specific models. It is hypothesised that with the introduction of uncertainty regarding the model parameters, the issue of only being able to draw conclusions about this single model

will likely not be present, resulting in more accurate results from the test with the Bayesian addition.

Methods

In this paper, a Monte Carlo study was conducted using R (R Core Team, 2024) in a similar fashion to the article by van Bork et al. (2019) where the PCLT was first introduced. Multiple datasets were simulated with different underlying true models and characteristics. The true models underlying these simulated datasets were either unidimensional factor models or sparse gaussian graphical network models. Both the PCLT and the BPCLT were ran on these simulated datasets in order to compare the performance of both tests.

The Models

There are two models that are compared in this paper, namely Unidimensional Factor Models (UFMs) as shown in (1), and Sparse Gaussian Graphical Models (SGGMs), as shown in (2). The reasoning behind the choice for these two specific models will be explained later in this section. A UFM is a statistical model where the correlations between continuous observed variables can be explained by a single continuous latent factor. Each observed variable is a linear function of this latent factor plus some unique error (Mair, 2018a).

(1) $$\Sigma_{factor} = \lambda\psi\lambda' + \Phi$$

Here, Σ is the correlation matrix corresponding to the UFM. $\boldsymbol{\lambda}$ are the factor loadings, which represent the strength of the relationship between the latent variable and the observed variable. Φ a diagonal matrix with the variances of the error variables on the diagonal; $\phi_{ii} = 1 - \lambda_i^2$. The index i refers to each observed variable. The ψ is the variation of the latent variable. In a UFM, this term is one since there is only one latent variable present in this model.

A Gaussian Graphical Model (GGM) is a probabilistic model that represents the conditional dependencies between the variables (Mair, 2018c). Variables that are conditionally dependent are connected by an edge, whereas variables that are conditionally independent are not. A sparse GGM (SGGM) is a subset of the GGMs where some of the edge weights are 0, indicating that the nodes (the variables) are conditionally independent from each other.

(2) $$\Sigma_{network} = \Delta(\mathrm{I} - \Omega)^{-1}\Delta$$

Here $\Sigma_{network}$ is the correlation matrix corresponding to an SGGM. Ω is a weight matrix with zeros on the diagonal and the weights (representing the strength of the conditional dependencies) on the off diagonal. As mentioned before, in a sparse matrix, some of these weights can be zero, representing conditional independence for the corresponding variables. Δ is a diagonal matrix defined as $\delta_{jj} = \mathrm{p}_{jj}^{-\left(\frac{1}{2}\right)}$, with P being the precision matrix corresponding to the weight matrix, and I is the identity matrix. For both the UFM and the SGGM, the simulated data from Σ are multivariate normal.

Avoiding Model Equivalence

It is proven that the general class of GGMs (of which SGGMs are a subset) and the general class of factor models (of which UFMs are a subset) can be statistically equivalent (Epskamp, Maris, et al., 2018; Marsman et al., 2015). When two statistical models are equivalent, they produce the same means and variance-covariance matrices, making it impossible to statistically differentiate the two. A consequence of this is that if two equivalent models are compared in the PCLT, the test cannot distinguish between the models, as the data are (in)consistent with both models, thus neither choice would be (in)correct. But, as discussed in the introduction of this paper, the implications of the models are different,

therefore, as well as to fairly evaluate model performance, a constraint has to be put on (one of) the models in order to make sure that the two models are not statistically equivalent. A possible constraint would be to compare a UFM (i.e., of rank one), with a differently ranked network. However, the original PCLT (van Bork et al., 2019) has not been evaluated on models that are of a different rank yet. Therefore, this would not be the best option for this specific paper, since the aim is to compare how the original test compares to the Bayesian extension of the test. Another way to ensure that the models are not statistically equivalent, is to introduce sparsity in the GGM. This is because a network model that has an equivalent UFM has all edges present (van Bork et al., 2019). Introducing sparsity will ensure that the UFMs and SGGMs used to simulate the data for evaluating the tests, and those generated in the tests, are not equivalent.

Model Estimation

In Bayesian statistics, estimating a model starts with specifying prior distributions. A prior represents the initial belief about the range of possible parameter values before observing the data (Lambert, 2018). Once the data are incorporated, the prior is updated using Bayes' theorem (3) to obtain the posterior distribution, which reflects the updated beliefs given the observed data.

$$p(\theta|data) = \frac{p(data|\theta) \times p(\theta)}{p(data)} \tag{3}$$

In this formula, θ is the model parameter. $p(\theta|data)$ is the posterior probability distribution regarding the model parameter, $p(\theta)$ is the prior probability distribution regarding the model parameter, $p(data|\theta)$ is the likelihood, which shows the probability of the data given the parameter, and $p(data)$ is the probability of the data, when θ is integrated out (Lambert, 2018). The choice of priors plays a crucial role in Bayesian estimation, as it influences the resulting posterior distribution.

For the Bayesian estimation of the UFM, a prior is chosen for the factor loadings, the intercepts, and the residual variances of the observed variables. These prior beliefs are then updated using the data. Then, the posterior probability distribution is calculated. For the UFM, the bsem function from the Blavaan package (Merkle et al., 2021) was used. This function uses multiple weakly informative priors for the different parameters in the model, meaning that the variation in possible values according to the priors is wide, and can easily be overwritten by the data (Merkle & Rosseel, 2018). For the intercept of the observed variables, the default prior is a normal distribution with mean zero and a standard deviation of 32, allowing for a large range of possible values. For the intercept of the latent variable, the default prior is also a normal distribution with a mean of 0 and a standard deviation of 10 – a more informative prior for the latent variable, but still quite flexible. For the factor loadings, the default prior again consist of a normal distribution with a mean of 0 and a standard deviation of 10. Because the default prior for the factor loadings has a mean of 0, this means there is no initial preference about the direction of the loadings. For the residual variances of the observed variables, the default prior is a Gamma distribution with shape 1 and rate 0.5 and is used on the standard deviation scale, implying a mild preference for smaller standard deviations while still allowing for a wide range of values. All of the priors mentioned are the package's default and can be changed to fit different expectations for the parameter values. For this study, the defaults were not changed.

For the Bayesian estimation of the SGGM, there are two important prior distributions. The first one being the network structure, meaning which specific edges are present and which are not. The second important distribution are of the edge weights, meaning the strength of the conditional dependencies between the nodes (Huth et al., 2024). For the posterior density of the parameter values in the SGGM, the function easybgm from the package easybgm (Huth, 2024) was used, with the function specified to use 'BDgraph'

(Mohammadi & Wit, 2019). This package uses a Bernoulli distribution as a prior for the edges (Huth et al., 2024). The default is set to 0.5, indicating that each edge has a probability of 0.5 for being present or absent. In Bayesian statistics, you can acquire evidence for absence (Wagenmakers et al., 2015). This means that when enough evidence for absence is acquired for a specific edge, this edge can 'safely' be removed from the model. Another important prior distribution is regarding strengths of the conditional dependencies between the nodes. The 'BDgraph' uses a G-Wishart prior for this, with the default 2.5 (Huth et al., 2024). This means that the degrees of freedom for the G-Wishart prior are set to 2.5, allowing the posterior distributions of the values in the precision matrix to be influenced more by the data. If this value were higher, the prior would be more informative, and the data would thus have less influence on the posterior. For the BDgraph function, it is also possible to change the default priors. However, for this study, the defaults were used.

With the frequentist approaches used in the original PCLT, the UFMs are estimated using maximum likelihood estimation via the cfa function from the package "lavaan" (Rosseel, 2012), which fits confirmatory factor analysis models. The SGGMs are estimated using regularized partial correlations through the EBICglasso function from the package "qgraph" (Epskamp et al., 2012) which applies the graphical lasso with an Extended Bayesian Information Criterion (EBIC) for model selection. These methods rely on the data to estimate parameters without the use of prior or posterior distributions.

Observed Data Simulation

To evaluate the models, multiple datasets were simulated that would function as the data one would observe and apply the test to. To distinguish them from the datasets that will be simulated as part of the BPCLT and PCLT procedures, these datasets are referred to as the "observed datasets". For the simulation of the observed datasets the sample sizes ranged from

100 to 2000 in steps of 100. For each sample size, data were generated with five, 10, and 15 variables for both the UFM datasets and the SGGM datasets. For the SGGM datasets, edge density was set to 0.2, 0.5, and 0.8, meaning that 20%, 50%, and 80% of the possible edges are present, for each sample size and variable count. This resulted in 20 × 3 (for factor datasets) + 20 × 3 × 3 (for network datasets) = 240 conditions with unique characteristics. For each condition, 100 datasets were randomly generated. These conditions were chosen to closely mimic the original article by van Bork et al. (2019), and to ensure the tests were evaluated on a large range of possible conditions.

In order to generate data from an SGGM, a precision matrix (P) was randomly constructed, in which each off-diagonal element was specified to be either zero or sampled from a uniform distribution over the interval [-4, 4]. To ensure that the matrix was positive definite, the diagonal elements were set to the smallest eigenvalue plus an arbitrary small number (0.2). The precision matrix was forced to be symmetric by using the forceSymmetric function from the R package Matrix (Bates, Maechler & Jagan, 2024). The precision matrix was pre- and post-multiplied by a diagonal matrix (Δ) defined as $\delta_{jj} = p_{jj}^{-\left(\frac{1}{2}\right)}$. This resulted in a standardised precision matrix, which was then subtracted from the identity matrix (I) to obtain the weight matrix (Ω):

$$\Omega = I - \Delta P \Delta \tag{4}$$

This weight matrix (Ω) is a partial correlation matrix. Using the function pcor2cor from the package corpcor (Schafer et al., 2021), the corresponding correlation matrix is calculated. This correlation matrix is used in combination with the mvrnorm function from the MASS package (Venables & Ripley, 2003) to simulate observed data from the network.

In order to generate data that originate from a UFM, the factor loadings were randomly generated from a uniform distribution over the interval [0.1, 0.9] and [-0.1, -0.9].

The latent factors were generated from a standard normal distribution with a mean of 0 and a standard deviation of 1. Error variables were randomly generated by using the mvrnorm function from the MASS package (Venables & Ripley, 2003), with means of 0 and a diagonal covariance matrix with variances of 0.5 on the diagonal. To generate the observed variables, the latent variable was multiplied by the factor loadings, and the error variables were added:

(5) $$X_j = \lambda_j \times \Theta + \mathrm{E}_j$$

To investigate how the test behaved in situations where the data didn't strictly originate from only a UFM or only an SGGM, another type of dataset was generated using both the influence of a UFM and the influence of SGGM. This was done by generating a correlation matrix corresponding to a UFM using formula (1). Additionally, a correlation matrix that corresponds to an SGGM was generated. This was done in the same manner as described above. For the SGGM, edge density was set to be 0.5 for all combined datasets. The number of variables for the combined datasets was set to be 10. To get the covariance matrix $\Sigma_{combined}$, these two correlation matrices were added together. To investigate how the behaviours of the tests changed depending on whether the UFM or the SGGM had more impact on the data, the influence of the UFM compared to the SGGM on the covariance matrix of the observed variables varied between 0.2, 0.5, and 0.8. For example, if the influence of the UFM was 0.2, the covariance matrix of the observed variables was constructed as follows:

(6) $$\Sigma_{combined} = 0.2 \times \Sigma_{factor} + 0.8 \times \Sigma_{network}$$

The resulting $\Sigma_{combined}$ is a covariance matrix which was then used to generate data using the mvrnorm function from the MASS package (Venables & Ripley, 2003).

Bayesian Partial Correlation Likelihood Test

For each condition, 100 observed datasets were simulated for the Bayesian PCLT. The BPCLT works in six steps:

1. First, the proportion of anomalous correlations in the observed dataset is calculated and saved. This proportion will be referred to as the "observed proportion".

2. Then, using Bayesian statistical methods discussed previously, the posterior density distributions for the model parameters for the UFMs and SGGMs are calculated.

3. Then, from the density distributions of the UFM, one set of model parameters is sampled to select one fully parameterized UFM. The same is done for the posterior density distributions of the SGGM parameters. For this sampling procedure, an entire model was sampled rather than each model parameter individually. For the SGGM parameters, if the Bayesian test showed sufficient evidence for exclusion of an edge, the weight for that edge is put to zero instead of sampled from the posterior distribution of that edge. Sampling was repeated until a positive definite partial correlation matrix was obtained. If no positive definite matrix was found after 10 attempts, the nearPD function from the Matrix package (Bates, Maechler & Jagan, 2024) was applied. In this step, 1000 UFMS and 1000 SGGMs are sampled, resulting in 2000 models in total.

4. Each of these 2000 sampled models is used to simulate a new dataset. For each of these datasets, the proportion of anomalous correlations is calculated and saved.

5. These 2000 proportions are used to generate a density distribution for anomalous correlations for both the SGGMs and the UFMs.

6. Finally, the observed proportion of anomalous correlations is compared to the density distributions of both model types. The model type with the highest density at the observed proportion is selected to be the most likely model type given the observed proportion in the data.

These six steps were performed for all observed datasets.

Figure 1

The Six Steps of the Bayesian Partial Correlation Likelihood Test

1
Calculate covariance matrix of the data. Get proportion of anomalous correlations

$$\begin{pmatrix} s_1^2 & s_{12} & \cdots & s_{1k} \\ s_{21} & s_2^2 & \cdots & s_{2k} \\ \vdots & \vdots & \ddots & \vdots \\ s_{k1} & s_{k2} & \cdots & s_k^2 \end{pmatrix}$$

2
Calculate posterior density distributions of the model parameters.

M_f

Row	$\boldsymbol{\lambda_1}$	$\boldsymbol{\lambda_2}$	$\cdots$	$\boldsymbol{\lambda_k}$
1	$\hat{\lambda}_1$	$\hat{\lambda}_2$	$\cdots$	$\hat{\lambda}_k$
$\vdots$	$\vdots$	$\vdots$	$\ddots$	$\vdots$
n	$\hat{\lambda}_{1n}$	$\hat{\lambda}_{2n}$	$\cdots$	$\hat{\lambda}_{kn}$

M_n

Row	$\boldsymbol{\omega_{12}}$	$\boldsymbol{\omega_{13}}$	$\cdots$	$\boldsymbol{\omega_{k-1k}}$
1	$\widehat{\omega_{12}}_1$	$\widehat{\omega_{13}}_1$	$\cdots$	$\widehat{\omega_{k-1\,k}}_1$
$\vdots$	$\vdots$	$\vdots$	$\ddots$	$\vdots$
n	$\widehat{\omega_{12}}_n$	$\widehat{\omega_{13}}_n$	$\cdots$	$\widehat{\omega_{k-1\,k}}_n$

3
Randomly sample model parameters (1000 ×) from the n rows.

$$M_{f_1} = M_f[sample(1{:}n, 1),]$$
$$M_{f_2} = M_f[sample(1{:}n, 1),]$$
$$\vdots$$
$$M_{f_{1000}} = M_f[sample(1{:}n, 1),]$$

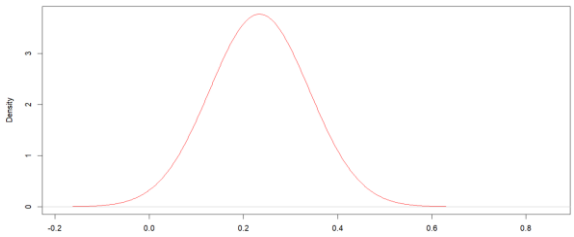
$$M_{n_1} = M_n[sample(1{:}n, 1),]$$
$$M_{n_2} = M_n[sample(1{:}n, 1),]$$
$$\vdots$$
$$M_{n_{1000}} = M_n[sample(1{:}n, 1),]$$

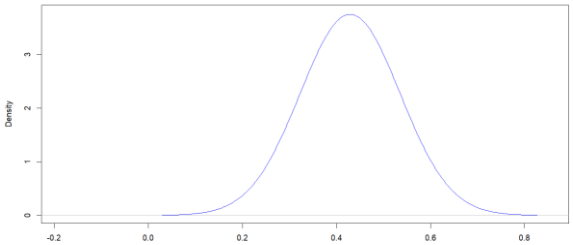
4
Calculate model implied covariance matrices for these parameters (1000 ×). Calculate anomalous correlations proportion from each dataset.

$$mvrnorm\left(\Sigma_{M_{f_1}}\right) \rightarrow Calculate\ Prop$$
$$mvrnorm\left(\Sigma_{M_{f_2}}\right) \rightarrow Calculate\ Prop$$
$$\vdots$$
$$mvrnorm\left(\Sigma_{M_{f_{1000}}}\right) \rightarrow Calculate\ Prop$$

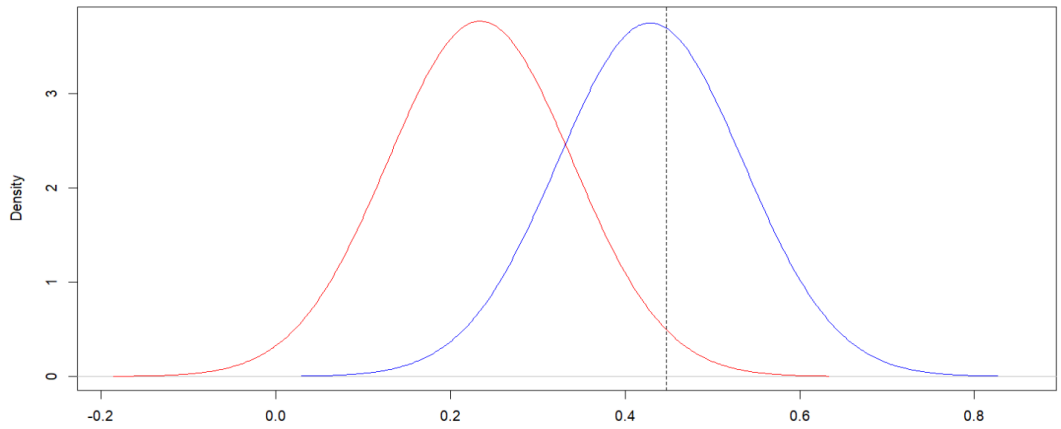
$$mvrnorm\left(\Sigma_{M_{n_1}}\right) \rightarrow Calculate\ Prop$$
$$mvrnorm\left(\Sigma_{M_{n_2}}\right) \rightarrow Calculate\ Prop$$
$$\vdots$$
$$mvrnorm\left(\Sigma_{M_{n_{1000}}}\right) \rightarrow Calculate\ Prop$$

5
Save anomalous correlation proportions to get the density distribution per model type.





6
Compare observed proportion to the density distributions. Select the model with highest density at the observed proportion.



Results

For the exact percentages of the results discussed below, see appendix A.

1. General

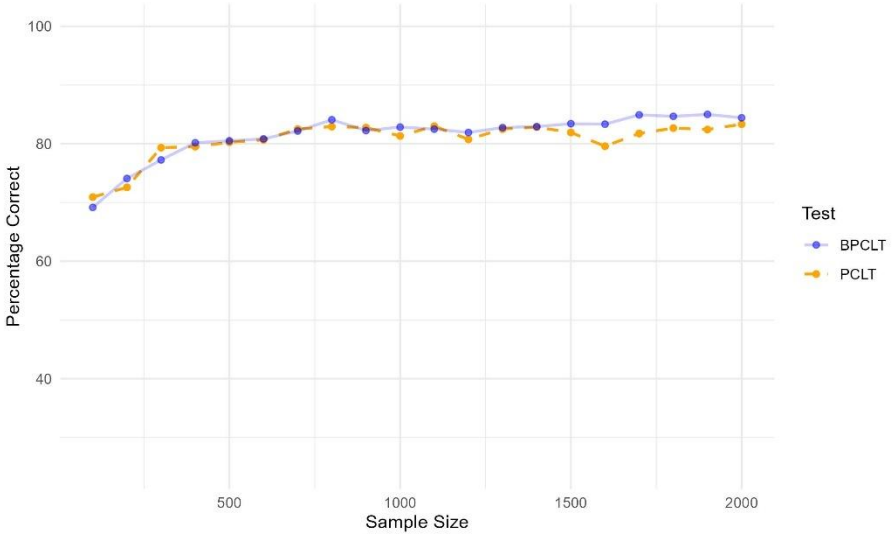
Taking all of the different observed datasets together, the BPCLT seems to perform very similar to the original PCLT, with an accuracy level of 81.5% and 80.7%, respectively. A t-test specified that there was no significant difference between the accuracies of these tests ($t(239) = -0.775, p = 0.439$). Both tests become more accurate as sample size increases, as can be seen in Figure 2. Zooming in on more specific types of datasets, different patterns seem to emerge depending on whether a BPCLT or PCLT was used.

1.1 Number of Variables

Focusing on the accuracy of the tests for different numbers of variables, the BPCLT has a higher accuracy at a lower number of variables compared to the PCLT. At five variables, the BPCLT has a higher accuracy compared to the PCLT. However, as the number of variables increases, so does the accuracy of the PCLT. For 10 and 15 variables, the accuracy of the PCLT is higher compared to the BPCLT (for specific percentages, see appendix A), this pattern can also be seen in Figure 3. An ANOVA showed that there is a significant interaction between test type (BPCLT or PCLT) and number of variables ($F(1, 476) = 35.6$, $p < .001$), indicating that the accuracy of the PCLT is influenced more by the number of variables.

Figure 2

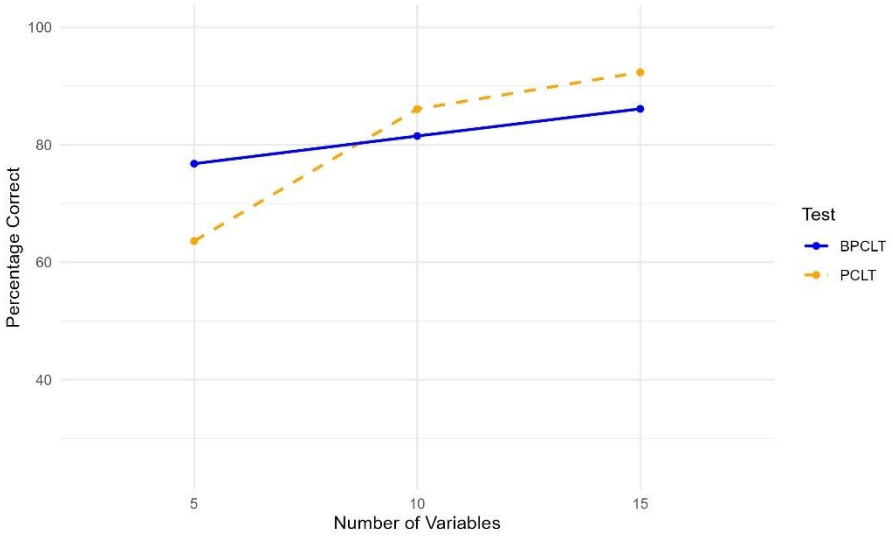
Comparison of PCLT and BPCLT accuracy – General Results



Note. This plot shows that the general performance for both tests is quite similar. They both become more accurate as sample size increases.

Figure 3

Average Accuracy per Number of Variables



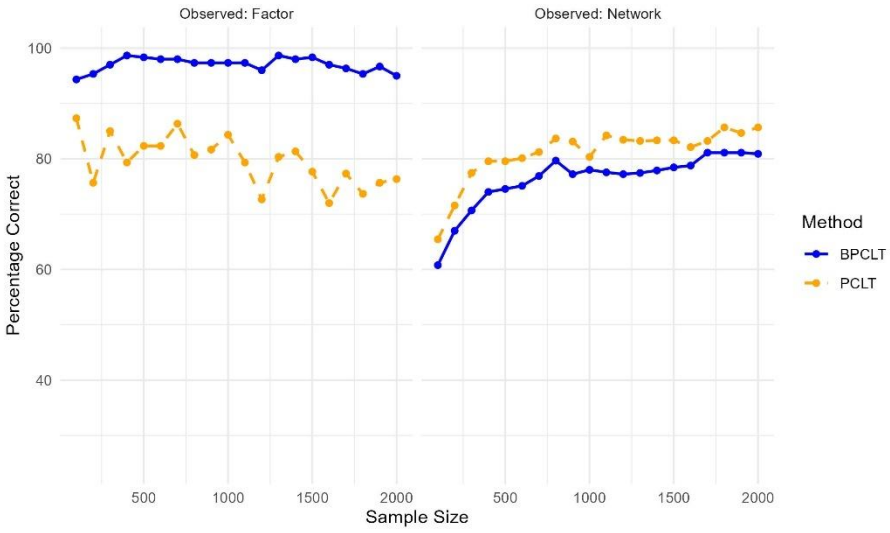
Note. This plot shows that number of variables has a bigger influence on the performance of the original PCLT compared to the BPCLT, for which the accuracy is more stable across different numbers of variables.

2. UFM and SGGM

looking at the overall performance, when the true model underlying the data is a UFM, the BPCLT is more accurate compared to the original PCLT. This switches when the true underlying model is an SGGM, in which case the original PCLT performs better compared to the BPCLT. The accuracies for the observed network datasets and the observed factor datasets per sample size are shown in Figure 4. In this figure, it shows that the original PCLT seems to be more stable across the different underlying models.

Figure 4

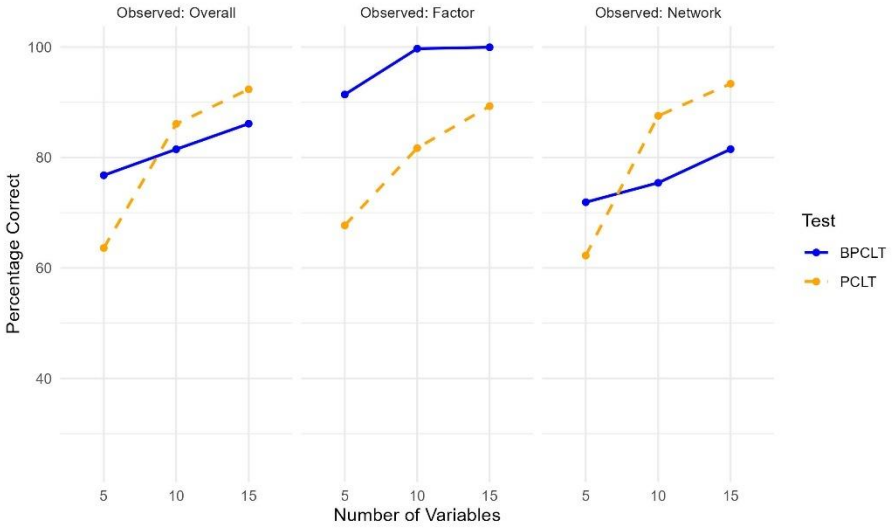
Accuracy for the Network and Factor Datasets per Sample Size



Note. This figure shows that the BPCLT performs better when the true underlying model is a UFM. The PCLT performs better when the true underlying model is an SGGM. Interestingly, performance for the PCLT tends to go down as sample size increases when the true underlying model is a UFM, which could indicate a bias towards selecting network for the PCLT.

Figure 5

Effect of Number of Variables on Accuracy per Model Type



Note: This figure shows that the accuracy of the BPCLT is less affected by the number of variables compared to the PCLT, which seems to be more affected by the number of variables. The BPCLT seems to be more affected by the underlying model type, in contrast to the PCLT, which behaves similar regardless of the true underlying model.

2.1 Number of Variables per Dataset Type

Figure 5 shows that for the BPCLT, the underlying model has more influence on its accuracy compared to the PCLT. The number of variables seems to affect the accuracy of both tests. An ANOVA confirmed that there was a significant interaction effect between test type and underlying model ($F(1, 472) = 65.2$, $p < .001$), but no significant interaction between underlying model and the number of variables ($F(1, 472) = 2.5$, $p = 0.12$). This means that the underlying model does not significantly influence the effect that the number of variables have on the accuracy of the tests.

2.2 Edge Densities

When the true underlying model is an SGGM, the accuracy for both tests increases as network density increases (see Figure 6). There was no significant interaction between edge density and test type ($F(1, 356) = 1.1$, $p = 0.30$). On average, the original PCLT seems to perform better at all edge densities compared to the BPCLT.

2.2.1 Number of Variables

Each of these network densities was also simulated with the number of variables ranging from five, to 10, to 15. The results are visualised in Figure 6. The BPCLT has a higher accuracy when the number of variables is 5 compared to the PCLT. This seems to persist in the lower network density range, as accuracy for a network density of 0.2 and five variables is higher for the BPCLT compared to the PCLT. However, as the number of variables increases, the accuracy of the PCLT surpasses that of the BPCLT (see Figure 6, Density: 0.2).

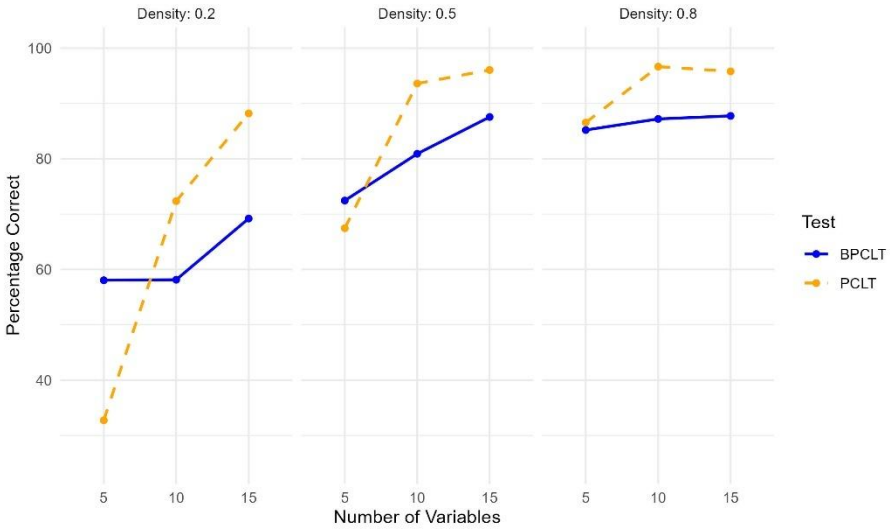
The same pattern can be found for the datasets where the true underlying model is a network with an edge density of 0.5. For these datasets, the BPCLT is slightly better at five variables, but the original PCLT surpasses the BPCLT in accuracy when 10 variables are introduced and stays more accurate at 15 variables. When the edge density is at 0.8, the original PCLT outperforms the BPCLT in all variations of numbers of variables. An ANOVA found a significant three-way interaction effect ($F(1, 352) = 52.4$, $p < .001$), corroborating these findings.

These results indicate that even though the original PCLT seems to be more stable across the different underlying models, the BPCLT appears to be more stable across different number of variables compared to the PCLT. Important to note that even though the BPCLT

appears to be more stable, the number of variables still has a significant effect when the edge densities are 0.2 and 0.5.

Figure 6

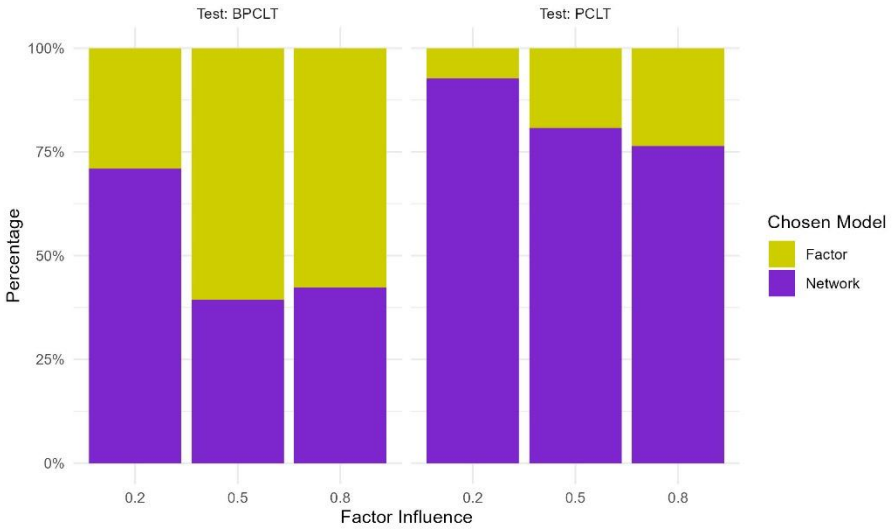
Accuracy for the Network Datasets – Different Edge Densities – Different Number of Variables



Note: This figure depicts that the PCLT is more affected by the number of variables compared to the BPCLT. This effect evens out as network density increases.

Figure 7

Model Choice for BPCLT and PCLT for Combined Datasets



Note: In this figure, it shows that the BPCLT seem to select UFMs more often when confronted with ambiguous data, while the PCLT seems to select the SGGMs more.

3. Combined Datasets

Remember that for the combined datasets, the datasets always had 10 variables, and the network density was 0.5. The factor influence was varied over 0.2, 0.5, and 0.8. Important to note is that for the combined datasets, neither model selection would be correct nor incorrect. These datasets were mainly used to increase the understanding of the behaviours of the two different tests.

For both tests, a pattern can be detected, which is visualised in Figure 7. If the factor influence increases from 0.2 to 0.5, the number of times that the UFM is selected as the most likely underlying model increases as well. When the factor influence increases from 0.5 to 0.8, this effect disappears for both tests. For all different levels of factor influence, the PCLT selects network more often compared to the BPCLT (for the exact percentages, see Appendix B). An ANOVA showed that there is a significant effect of factor influence on the proportion

of SGGMs selected *(*$F(1, 116) = 48.6$, $p < .001$), but no significant interaction between the tests and SGGMs selected *(*$F(1, 116) = 3.7$, $p = 0.06$). Zooming in on these results shows that there is a significant increase is the selection of UFMs when factor influence goes from 0.2 to 0.5 ($F(1, 76) = 12.6$, $p < .001$), but this effect disappears when going from a factor influence of 0.5 to 0.8 ($F(1, 76) = 1.3$, $p = 0.26$).

4. Exploratory Analysis – Absolute Density Distance as Bayes Factor

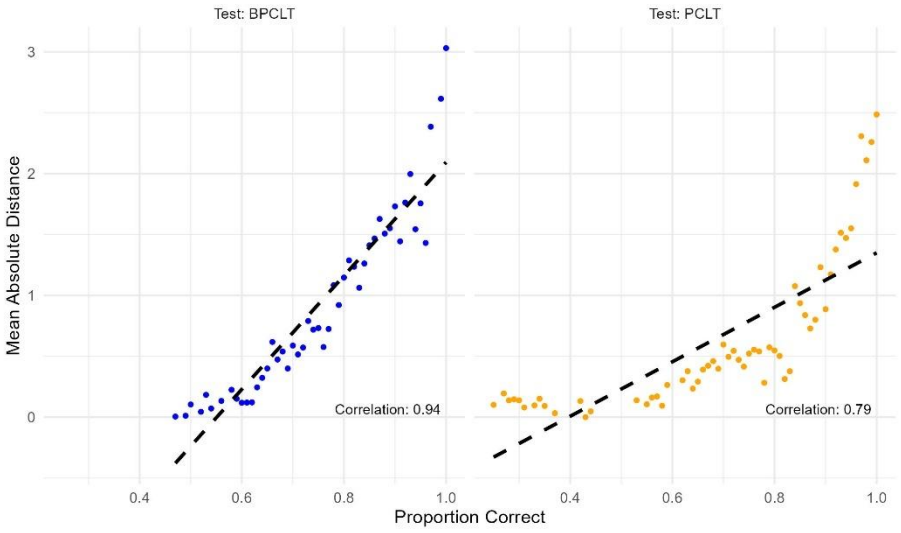
Recall that for both the PCLT and the BPCLT two distributions were compared in order to say which model was more likely given the observed proportion (see Figure 1, step 6). To investigate whether the distances between the model likelihoods at the point of the observed proportion had any relationship with the accuracy of the model, two explorative analyses were performed. The first being a simple correlation, to confirm whether or not there was a relationship between the proportion correct and the mean absolute distance between the density distributions. The second being a logistic regression, to evaluate whether the absolute density distance could predict whether the outcome of the test is correct.

To calculate the correlation, all of the observed datasets were used, and the proportions correct were ordered from low to high. Then, for each occurring value of proportion correct, the mean absolute distance between the model likelihoods was calculated. Both tests showed a positive correlation between the proportion correct and the mean absolute distance between the model likelihoods (see Figure 8). For the original PCLT, this correlation had a value of 0.79. For the BPCLT, this correlation was larger, at 0.94. Figure 8 shows this relationship. In this figure, it also becomes apparent that the relationship between mean absolute distance and proportion correct likely is not linear, indicating that a correlation is not the best way to measure the relationship as it assumes linearity.

To investigate this relationship further, a logistic regression was performed, which is visualised in Figure 9. For this, whether the test classified a dataset correctly or not was used as the binary outcome for the logistic regression, here 1 indicates correct and 0 indicates incorrect. The absolute distance between the model likelihoods was taken as the continuous predictor variable. For both tests, the absolute distance was a significant predictor for whether the outcome of the test was correct. The estimate coefficient for the PCLT regarding absolute distance was 2.03, with a standard error of 0.04 and a p-value of <2e-16. For the BPCLT, the estimated coefficient was 1.35, the standard error 0.03, and the p-value <2e-16. This means that for both tests, the absolute distance is a significant predictor of whether or not the outcome of the test is correct. Given the nature of this distance statistic (the likelihood of one model over the likelihood of another model), this statistic could be interpreted similarly to a Bayes Factor. An important difference between this distance statistic and the Bayes Factor is that the Bayes factor is the ratio of likelihoods given the data, and the distance statistic is the distance between the likelihoods given an observed proportion. However, it could be possible to report this distance statistic alongside the selected model of the test to indicate how certain the test is about the model it selected.

Figure 8

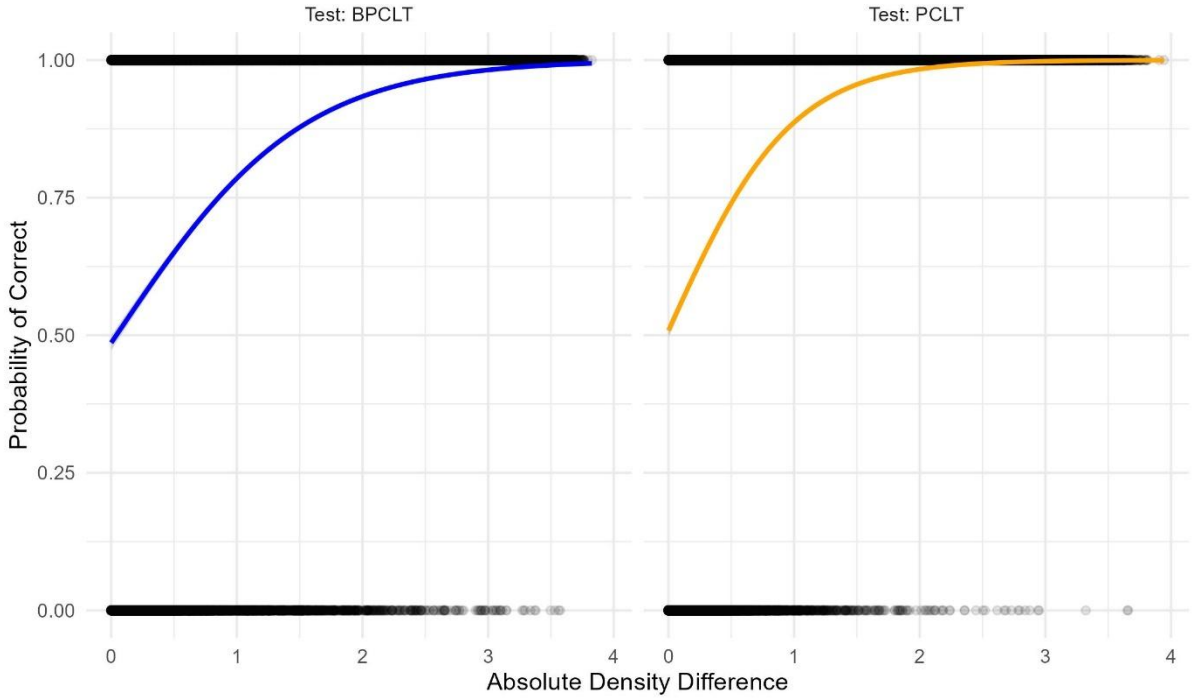
Correlation Between Mean Absolute Distance and Proportion Correct



Note: Looking at these results, it becomes apparent that the relationship between the mean absolute distance and the proportion correct might not be linear. Nevertheless, the figure shows that there is a clear positive relationship between the mean absolute distance and the proportion correct.

Figure 9

Logistic Regression of Mean Absolute Distance and Correct or Incorrect



Note: This figure shows the relationship between whether or not the test correctly classifies the underlying model. When the absolute density difference is zero (i.e., the likelihoods of the UFM and SGGM are equal), both tests perform around chance level. When the absolute density difference increases, so does the accuracy of both tests. For the PCLT, the probability of the test being correct is almost one when absolute density difference is higher than two. For the BPCLT, the probability of the test being correct is almost one when absolute density difference is higher than three.

Discussion

In this paper, the performance of the PCLT with a Bayesian extension was compared to the original PCLT. Results showed that the original PCLT appears to be more stable across different underlying models (i.e., whether the data originate from a UFM or an SGGM), while the BPCLT appears to be more stable when the number of variables changes from five, to 10, to 15 variables. But in general, the performance of the two tests are very similar. For these reasons, it is unclear which test is more accurate. Looking at the combined datasets shows that when confronted with ambiguous data, the BPCLT tends to select UFMs more often compared to the PCLT, which seems to select SGGMs more often. Indicating that the BPCLT seems to have a bias towards selecting UFMs or that the PCLT has a bias towards selecting SGGMs.

The fact that the BPCLT performs better at a lower number of variables is a positive takeaway from this study. The number of variables is one of the few parameters that the researchers will know when using this test. If the number of variables is less than 10, the BPLT will most often have a higher accuracy, or a very similar accuracy, compared to the PCLT. For both the PCLT and the BPCLT, accuracy increases as the number of variables increases, as well as when the edge density increases for the network datasets. An explanation for this would be that, as edge density and number of variables increases, so does the number of possible correlations. As there are more correlations to be found in general, more anomalous correlations can also be found, resulting in more accurate results for both tests.

An important limitation of this study is the use of the default priors in the packages used to estimate the UFMs and the SGGMs. This means that while ranges of models are compared, these ranges might not be the best possible ones for the specific dataset that the test is used on. Future research could look into the effect of using different priors, or different values for the priors, to see whether this increases the performance of the BPCLT.

Another interesting point for future research is the fact that this paper only compared UFM's and SGGMs, meaning that the behaviour of both tests when differently ranked models (i.e., non-unidimensional factor models, or differently ranked networks) are evaluated is still unknown. Further research could look into the performances of the tests when the underlying model is different from rank one, to see whether the tests can be expanded to include more types of models.

Aside from investigating the accuracy of the tests and comparing them, this paper also looked into the relationship between the accuracy of the tests and the Absolute Density Distance and found that the Absolute Density Distance was a significant predictor of whether or not the test was correct. This Absolute Density Distance can be implemented into the test, to be used alongside the model selected by the test as an index of certainty. Adding the Absolute Density Distance as a part of the test could be a great way to improve the usefulness of these tests. A possibility could be to change the distance into a ratio, resembling a Bayes factor. However, an important distinction between this ratio and a bayes factor is that this ratio is regarding an observed proportion, while the bayes factor is regarding an entire dataset. Nevertheless, this statistic could be used as a cut-off point, changing the output of the tests to be either selecting a UFM or an SGGM, to include a third option, namely inconclusive or not having enough evidence to select one model over the other. Another possibility for future research would be to look into the behaviour of this distance (or ratio) statistic when the dataset is the result of both a UFM and an SGGM, in order to investigate whether this statistic could also provide some additional information about the possibility of the dataset originating from both models.

This paper mainly showed that the BPCLT would be a good choice when the number of variables is low. The higher the number of variables, the less clear it becomes which tests works best. Adding a statistic of Absolute Density Distance in the output of the tests could be

a good addition to improve the usefulness and interpretability of these tests. Aside from these findings, future research could look into multiple additions or changes to the test in order to increase its usability and accuracy. Looking into the effect of different priors or different values of these priors would be a valuable next step, as well as adapting the use of the Absolute Density Distance the be as informative as possible. For example, by changing it to a ratio that would resemble a Bayes factor, or by using it as a cutoff point that would determine when the tests selects either of the models or doesn't select one as there is not enough information.

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Appendix A

PCLT Results Table

edge_dens	nvs	correct	100	200	300	400	500	600	700	800	900	1000	1100	1200	1300	1400	1500	1600	1700	1800	1900	2000	row_avg
	5	c	76	68	75	76	77	73	78	75	74	71	65	53	67	69	63	55	64	62	57	56	67.70
	5	i	24	32	25	24	23	27	21	24	25	28	28	42	25	29	32	29	28	33	27	25	27.55
	10	c	89	75	84	72	81	86	89	80	80	88	83	79	83	87	82	78	81	74	80	83	81.70
	10	i	11	25	16	28	19	14	11	20	20	12	17	21	17	13	18	22	19	26	20	17	18.30
	15	c	97	84	96	90	89	88	92	87	91	94	90	86	91	88	88	83	87	85	90	90	89.30
	15	i	3	16	4	10	11	12	8	13	9	6	10	14	9	12	12	17	13	15	10	10	10.70
0.2	5	c	29	29	29	35	28	33	33	35	35	25	30	37	27	34	28	31	28	42	43	44	32.75
0.2	5	i	71	71	71	65	72	67	67	65	65	75	70	63	73	66	72	69	72	58	57	56	67.25
0.2	10	c	58	57	69	59	67	74	76	74	77	75	79	73	74	77	77	73	68	79	77	84	72.35
0.2	10	i	42	43	31	41	33	26	24	26	23	25	21	27	26	23	23	27	32	21	23	16	27.65
0.2	15	c	75	74	86	90	81	80	88	92	93	89	91	91	94	88	93	89	92	90	95	93	88.20
0.2	15	i	25	26	14	10	19	20	12	8	7	11	9	9	6	12	7	11	8	10	5	7	11.80
0.5	5	c	62	66	59	64	69	62	70	69	68	63	76	71	71	71	67	66	74	72	67	62	67.45
0.5	5	i	38	34	41	36	31	38	30	31	32	37	24	29	29	29	33	34	26	28	33	38	32.55
0.5	10	c	73	84	92	93	96	95	91	93	92	93	96	98	96	96	99	99	97	97	96	96	93.60
0.5	10	i	27	16	8	7	4	5	9	7	8	7	4	2	4	4	1	1	3	3	4	4	6.40
0.5	15	c	72	85	91	94	99	99	94	99	99	98	98	96	99	99	100	99	100	100	100	100	96.05
0.5	15	i	28	15	9	6	1	1	6	1	1	2	2	4	1	1	0	1	0	0	0	0	3.95
0.8	5	c	65	72	87	91	85	84	88	92	89	84	90	89	91	89	86	85	92	93	87	92	86.55
0.8	5	i	35	28	13	9	15	16	12	8	11	16	10	11	9	11	14	15	8	7	13	8	13.45
0.8	10	c	81	90	98	95	100	98	94	99	97	97	99	97	98	97	100	99	99	98	97	100	96.65
0.8	10	i	19	10	2	5	0	2	6	1	3	3	1	3	2	3	0	1	1	2	3	0	3.35
0.8	15	c	74	87	86	95	91	96	97	100	98	99	99	99	99	99	100	98	99	100	100	100	95.80
0.8	15	i	26	13	14	5	9	4	3	0	2	1	1	1	1	1	0	2	1	0	0	0	4.20
		mean	70.92	72.58	79.33	79.50	80.25	80.67	82.50	82.92	82.75	81.33	83.00	80.75	82.50	82.83	81.92	79.58	81.75	82.67	82.42	83.33	80.67
		factor mean	87.33	75.67	85.00	79.33	82.33	82.33	86.33	80.67	81.67	84.33	79.33	72.67	80.33	81.33	77.67	72.00	77.33	73.67	75.67	76.33	79.57
		network mean	65.44	71.56	77.44	79.56	79.56	80.11	81.22	83.67	83.11	80.33	84.22	83.44	83.22	83.33	83.33	82.11	83.22	85.67	84.67	85.67	81.04
		nv5 mean	58.00	58.75	62.50	66.50	64.75	63.00	67.25	67.75	66.50	60.75	65.25	62.50	64.00	65.75	61.00	59.25	64.50	67.25	63.50	63.50	63.61
		nv10 mean	75.25	76.50	85.75	79.75	86.00	88.25	87.50	86.50	86.50	88.25	89.25	86.75	87.75	89.25	89.50	87.25	86.25	87.00	87.50	90.75	86.08
		nv15 mean	79.50	82.50	89.75	92.25	90.00	90.75	92.75	94.50	95.25	95.00	94.50	93.00	95.75	93.50	95.25	92.25	94.50	93.75	96.25	95.75	92.34
		ed02 mean	54.00	53.33	61.33	61.33	58.67	62.33	65.67	67.00	68.33	63.00	66.67	67.00	65.00	66.33	66.00	64.33	62.67	70.33	71.67	73.67	64.43
		ed05 mean	69.00	78.33	80.67	83.67	88.00	85.33	85.00	87.00	86.33	84.67	90.00	88.33	88.67	88.67	88.67	88.00	90.33	89.67	87.67	86.00	85.70
		ed08 mean	73.33	83.00	90.33	93.67	92.00	92.67	93.00	97.00	94.67	93.33	96.00	95.00	96.00	95.00	95.33	94.00	96.67	97.00	94.67	97.33	93.00

BPCLT Results Table

edge_dens	nvs	correct	100	200	300	400	500	600	700	800	900	1000	1100	1200	1300	1400	1500	1600	1700	1800	1900	2000	row_avg
	5	c	88	86	91	96	95	94	94	93	92	92	92	88	96	94	95	91	89	86	91	85	91.40
	5	i	12	14	9	4	5	6	6	7	8	8	7	12	4	6	5	7	9	12	5	7	7.65
	10	c	96	100	100	100	100	100	100	99	100	100	100	100	100	100	100	100	100	100	99	100	99.70
	10	i	4	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0.30
	15	c	99	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	99.95
	15	i	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.05
0.2	5	c	62	60	60	61	56	58	62	59	63	60	47	56	50	61	61	60	54	56	54	61	58.05
0.2	5	i	38	40	40	39	44	42	38	41	37	40	53	44	50	39	39	40	46	44	46	39	41.95
0.2	10	c	53	58	56	52	60	58	60	63	58	60	54	56	56	50	62	53	67	65	64	58	58.15
0.2	10	i	47	42	44	48	40	42	40	37	42	40	46	44	44	50	38	47	33	35	36	42	41.85
0.2	15	c	59	49	65	66	63	53	68	75	67	74	74	74	75	70	66	74	78	73	78	83	69.20
0.2	15	i	41	51	35	34	37	47	32	25	33	26	26	26	25	30	34	26	22	27	22	17	30.80
0.5	5	c	62	68	69	76	71	70	72	76	79	71	72	76	68	77	68	77	73	78	71	75	72.45
0.5	5	i	38	32	31	24	29	30	28	24	21	29	28	24	32	23	32	23	27	22	29	25	27.55
0.5	10	c	61	71	68	74	78	80	80	84	81	81	85	86	81	87	78	86	87	90	94	86	80.90
0.5	10	i	39	29	32	26	22	20	20	16	19	19	15	14	19	13	22	14	13	10	6	14	19.10
0.5	15	c	54	75	73	86	86	87	88	86	86	93	88	91	97	93	95	93	97	94	92	97	87.55
0.5	15	i	46	25	27	14	14	13	12	14	14	7	12	9	3	7	5	7	3	6	8	3	12.45
0.8	5	c	69	76	80	88	86	89	83	91	81	85	90	82	89	84	90	85	91	91	85	89	85.20
0.8	5	i	31	24	20	12	14	11	17	9	19	15	10	18	11	16	10	15	9	9	15	11	14.80
0.8	10	c	74	77	88	79	85	90	86	93	87	88	93	89	88	86	93	89	91	86	92	90	87.20
0.8	10	i	26	23	12	21	15	10	14	7	13	12	7	11	12	14	7	11	9	14	8	10	12.80
0.8	15	c	53	69	77	84	86	91	93	90	93	90	95	85	93	93	93	92	92	97	100	89	87.75
0.8	15	i	47	31	23	16	14	9	7	10	7	10	5	15	7	7	7	8	8	3	0	11	12.25
		mean	69.17	74.08	77.25	80.17	80.50	80.83	82.17	84.08	82.25	82.83	82.50	81.92	82.75	82.92	83.42	83.33	84.92	84.67	85.00	84.42	81.46
		factor mean	94.33	95.33	97.00	98.67	98.33	98.00	98.00	97.33	97.33	97.33	97.33	96.00	98.67	98.00	98.33	97.00	96.33	95.33	96.67	95.00	97.02
		network mean	60.78	67.00	70.67	74.00	74.56	75.11	76.89	79.67	77.22	78.00	77.56	77.22	77.44	77.89	78.44	78.78	81.11	81.11	81.11	80.89	76.27
		nv5 mean	70.25	72.50	75.00	80.25	77.00	77.75	77.75	79.75	78.75	77.00	75.25	75.50	75.75	79.00	78.50	78.25	76.75	77.75	75.25	77.50	76.78
		nv10 mean	71.00	76.50	78.00	76.25	80.75	82.00	81.50	84.75	81.50	82.25	83.00	82.75	81.25	80.75	83.25	82.00	86.25	85.25	87.25	83.50	81.49
		nv15 mean	66.25	73.25	78.75	84.00	83.75	82.75	87.25	87.75	86.50	89.25	89.25	87.50	91.25	89.00	88.50	89.75	91.75	91.00	92.50	92.25	86.11
		ed02 mean	58.00	55.67	60.33	59.67	59.67	56.33	63.33	65.67	62.67	64.67	58.33	62.00	60.33	60.33	63.00	62.33	66.33	64.67	65.33	67.33	61.80
		ed05 mean	59.00	71.33	70.00	78.67	78.33	79.00	80.00	82.00	82.00	81.67	81.67	84.33	82.00	85.67	80.33	85.33	85.67	87.33	85.67	86.00	80.30
		ed08 mean	65.33	74.00	81.67	83.67	85.67	90.00	87.33	91.33	87.00	87.67	92.67	85.33	90.00	87.67	92.00	88.67	91.33	91.33	92.33	89.33	86.72

Appendix B

PCLT Combined Table

f_infl	network/factor	100	200	300	400	500	600	700	800	900	1000	1100	1200	1300	1400	1500	1600	1700	1800	1900	2000	average
0.2	n	61	81	86	92	94	92	98	95	95	94	97	99	93	96	99	98	99	97	97	90	92.65
0.2	f	39	19	14	8	6	8	2	5	5	6	3	1	7	4	1	2	1	3	3	10	7.35
0.5	n	37	45	57	66	78	84	86	79	90	82	94	84	89	92	85	93	96	93	94	92	80.80
0.5	f	63	55	43	34	22	16	14	21	10	18	6	16	11	8	15	7	4	7	6	8	19.20
0.8	n	30	43	55	65	67	68	81	85	79	72	80	88	90	89	88	82	87	94	96	89	76.40
0.8	f	70	57	45	35	33	32	19	15	21	28	20	12	10	11	12	18	13	6	4	11	23.60

BPCLT Combined Table

f_infl	network/factor	100	200	300	400	500	600	700	800	900	1000	1100	1200	1300	1400	1500	1600	1700	1800	1900	2000	average
0.2	n	49	45	56	58	69	69	75	66	67	70	76	81	67	80	76	84	81	81	88	80	70.90
0.2	f	51	55	44	42	31	31	25	34	33	30	24	19	33	20	24	16	19	19	12	20	29.10
0.5	n	28	21	21	29	25	35	33	33	44	33	44	41	53	44	49	53	51	52	48	50	39.35
0.5	f	72	79	79	71	75	65	67	67	56	67	56	59	47	56	51	47	49	48	52	50	60.65
0.8	n	29	25	21	32	33	34	34	38	47	40	41	51	56	46	46	44	56	61	53	58	42.25
0.8	f	71	75	79	68	67	66	66	62	53	60	59	49	44	54	54	56	44	39	47	42	57.75