





# Statistical Evidence in Psychological Networks

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## Abstract

Psychometric network models have become increasingly popular in psychology and the social sciences as tools to explore multivariate data. In these models, constructs are represented as networks of observed variables, and researchers often interpret the presence or absence of edges as evidence for or against conditional associations between variables. However, the statistical evidence supporting these edges is rarely evaluated. Here we show that a large proportion of reported network findings are based on weak or inconclusive evidence. We reanalyzed 293 networks from 126 published papers using a Bayesian approach that quantifies the evidence for each edge. Across studies, one-third of edges showed inconclusive evidence ( $1/3 < BF_{10} < 3$ ), about half showed weak evidence ( $BF_{10} > 3$  or  $BF_{10} < 1/3$ ), and fewer than twenty percent were strongly supported ( $BF_{10} > 10$  or  $BF_{10} < 1/10$ ). Networks based on relatively large sample sizes yielded more robust results. Our study shows that networks are often supported by too little evidence from the data for results to be reported with confidence, not meaning that results are flawed but rather suggest caution in interpreting individual edges.

**Keywords:** *network psychometrics, Bayesian inference, reanalysis, statistical evidence, database*

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# 1 Introduction

Throughout the social sciences, network analysis has become an established psychometric method for multivariate data analysis over the past two decades<sup>1,2</sup> and particularly in clinical psychology.<sup>3–6</sup> Many applications of psychometric networks are motivated by a conceptual framework in which existing constructs are reconceptualized as emergent properties of multivariate systems, including mental health<sup>4</sup>, intelligence<sup>7</sup>, and personality.<sup>8</sup> A psychological network consists of *nodes*—the variables making up the construct of interest—and *edges* between the nodes—conditional associations between two variables.<sup>9</sup> Importantly, psychological networks are crucially distinct from social networks, where nodes represent individuals, urban hubs, or businesses. Entire research projects and special issues have been devoted to evaluating and promoting the network approach in the social sciences<sup>10–13</sup>, resulting in several thousand empirical, methodological, and theoretical network papers in a short period of time.<sup>3,6</sup>

To ensure that networks contribute to a cumulative science, the results must be robust—the estimated models must have sufficient statistical support from the data. Results that are not sufficiently supported by the data can lead to overconfident or even flawed inferences and thereby impede scientific progress.<sup>14–16</sup>

Many of the most popular network methods cannot adequately express the statistical support for their results from the data, which has led to concerns about the robustness of network results in the literature.<sup>17,18</sup> A prominent concern is that psychological networks are highly parameterized models that require increasingly large datasets to allow for robust inference.<sup>1,17,19</sup> However, it is difficult to determine whether a dataset is large enough to support the highly parameterized model. Bootstrap-based methods have been proposed to assess the uncertainty underlying network results<sup>20</sup> but because networks are commonly estimated using regularization (i.e.,  $l_1$ -regularization) the estimator has a limiting distribution that is non-Gaussian with a point mass at zero and therefore bootstrap is ineffective for constructing valid confidence regions or p-values, especially in combination with the information criteria used for penalty selection.<sup>21,22</sup> Therefore, alternative methods are needed to assess uncertainty. A Bayesian approach to network analysis avoids these issues and provides a principled way to estimate the uncertainty underlying network analysis<sup>23–26</sup>, estimating both the uncertainty regarding the edge presence or absence as well as the uncertainty of the strength of present edges.

Despite the advantages that Bayesian methods offer in estimating the statistical evidence underlying networks and the increasing availability of these methods in statistical software<sup>27</sup>, there have been few network studies that have used Bayesian methods. As a result, the robustness of psychological network results remains elusive. To date, only one paper has reanalyzed a single dataset in a Bayesian framework to investigate the uncertainty in the estimated network edges<sup>28</sup>, and two others have used the Bayesian approach to estimate the uncertainty associated with their network results.<sup>29,30</sup> Despite large sample sizes, most edges from these studies’ networks were found to lack statistical support, further highlighting the need to examine the statistical evidence supporting published network structures. These results, and general concerns about the robustness of estimated networks, raise the question of whether published network results are sufficiently supported by data such that one can be confident in the estimated network.

In this paper we provide a first answer to this question, using a large-scale Bayesian reanalysis of psychometric networks. Analyzing 293 networks from 126 published papers, we estimate whether there is evidence for the presence or absence of each edge for each

of the cross-sectional networks. To do this, we first systematically searched psychological network papers published between January 2010 and March 2023. We requested the raw data for papers that met our criteria and analyzed their networks using the Bayesian approach. In these analyses, we focus on the statistical evidence for edge presence or absence using the Bayes factor<sup>31</sup> and how the strength of the evidence is related to sample size (i.e., the number of observations per possible edge). We also examine the relationship between the strength of statistical evidence for edge presence and the edge weights—the partial correlation. Our study highlights areas for improvement in psychometric networks and provides researchers with an open-access website **ReBayesed** (<https://uvasobe.shinyapps.io/ReBayesed/>) to evaluate the statistical support in previously published networks.

## 2 Results

### 2.1 Systematic Review

The selection of datasets followed predefined criteria and the PRISMA guidelines (see Figure 1).<sup>32</sup> We searched for papers published between January 2010 and March 2023 using a combination of two methods: (1) a systematic search for papers that reference psychometric networks in the title, keywords, or abstract, and (2) citation tracking of eighteen key network papers, including tutorials, R packages, and seminal theoretical papers. The list of papers, as well as any other material associated with the project, can be found in the OSF repository <https://osf.io/n8r9g/>.

Our search identified 4,720 unique papers that underwent a title and abstract screening. Based on this screening, 1,423 papers were deemed eligible, meaning the paper published a cross-sectional network analysis of psychometric variables. Authors of these eligible papers were invited to complete a short questionnaire to assess final inclusion. We received 443 unique responses (31.13%) to the questionnaire, of which we included 126 papers that met the final inclusion criteria: willingness and ability of authors to share their raw data, use of psychometric measures as nodes, estimation of a Gaussian graphical model, and the ability to reproduce the descriptive statistics from the data noted in the original publication (see Figure 1 for the distribution of excluded papers and networks). All included papers were published between 2015 and 2023. Papers contained an average of 2.3 estimated networks, with up to 15 networks per paper using a different sample, measurement point, or set of variables, resulting in a total of 293 extracted networks. Networks were not uniformly distributed across psychology sub-fields. Most networks were published in clinical psychology ( $k = 147$ ), followed by personality psychology ( $k = 49$ ), and social psychology ( $k = 31$ ). Some further papers focused on public health ( $k = 5$ ), education ( $k = 5$ ), diagnostics ( $k = 5$ ), and organizational psychology ( $k = 2$ ) with some not falling into any of these subfields ( $k = 50$ ).

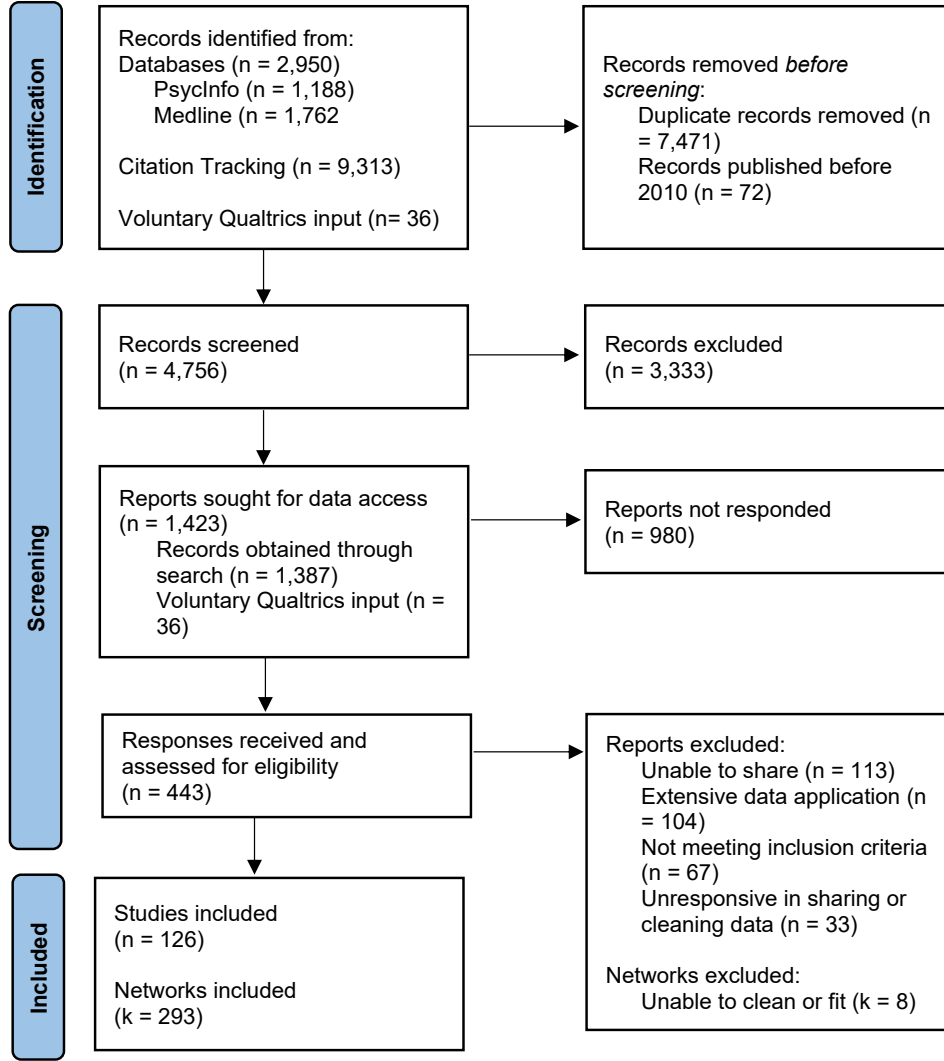


Figure 1: **PRISMA 2020 protocol**. Flow diagram outlining the selection of papers and networks.<sup>32</sup>

## 2.2 Quantifying the Statistical Evidence for Published Network Models

We estimated the networks in using the Bayesian approach and computed the uncertainty underlying the presence and absence of network edges (i.e., for details see the Analysis subsection in Methods). For all network edges, we obtained the Bayes factor for edge presence  $BF_{10}$ <sup>31</sup>, which provides the strength of the statistical evidence in favor of edge presence in the network as opposed to the edge absence. We grouped the Bayes factor values into five categories according to the amount of evidence following scientific conventions.<sup>33–35</sup>  $BF_{10} < 1/10$  indicates strong evidence for edge absence,  $BF_{10} < 1/3$  indicates weak evidence for edge absence,  $BF_{10}$  between  $1/3$  and  $3$  indicates inconclusive evidence for either presence or absence,  $BF_{10} > 3$  indicates weak evidence for edge presence and  $BF_{10} > 10$  indicates strong evidence for edge presence. Note that although these thresholds are commonly used in Bayesian inference, they reflect subjective decisions and are not grounded in the inherent behavior of the Bayes factor. We used open intervals, as such the endpoints were not included.

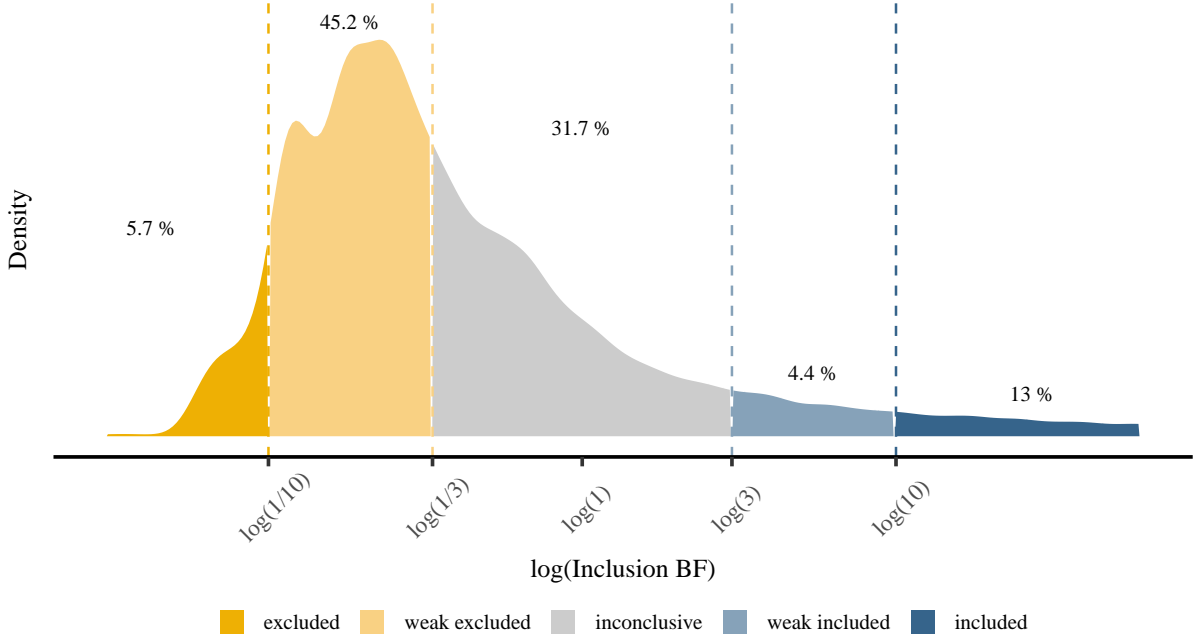


Figure 2: **Statistical evidence for edge presence or absence across all networks.** Density plot showing the distribution of the log Bayes factor for all edges from the 293 networks. Percentages indicate the relative amount of edges falling into the respective evidence category. We colored the area under the curve according to the evidence categories of the Bayes factor  $BF_{10}$  range: (1) Dark yellow indicates strong evidence for absence ( $BF_{10} < 1/10$ ). (2) Light yellow indicates weak evidence for absence ( $BF_{10} < 1/3$ ). (3) Grey indicates inconclusive evidence for either presence or absence ( $1/3 < BF_{10} < 3$ ). (4) Light blue indicates weak evidence for presence ( $BF_{10} > 3$ ). (5) Dark blue indicates strong evidence for presence ( $BF_{10} > 10$ ).

Considering all edges across all networks, we found no or weak statistical evidence for the presence or absence of most edges (see Figure 2). Specifically, we found inconclusive evidence for the presence or absence of one-third of all edges across all published networks (31.7%), and for an additional 49.7% of the edges, we found only weak evidence (weak presence: 4.4%, weak absence: 45.2%). Thus, more than 80% of all edges had insufficient evidence to support robust inference. There was compelling evidence for the presence of 13% of the edges and 5.7% of the edges showed compelling evidence for edge absence. As illustrated in Figure 2, the percentages are based on the chosen Bayes factor categorization conventions<sup>33–35</sup> and shifting the categorization cutoffs may lead to different percentages, highlighting the sensitivity of the percentages to the chosen standard of evidence.

### 2.3 The Relationship Between the Strength of Statistical Evidence and Relative Sample Size

We found inconclusive or weak evidence for the presence or absence of most of the edges in our analyses, meaning that oftentimes there is too little data to be confident about the estimated edges. However, the strength of the statistical evidence for edge presence or absence is strongly determined by the sample size relative to the number of possible edges (i.e., the relative sample size) of the network. When there are relatively few observations, the strength of the evidence for those network edges should be inconclusive or weak. In

datasets with larger sample sizes relative to the number of parameters, the evidence for its edges should be mostly conclusive.

In our datasets, the sample size ranged from 23 to 388,286 cases, with a median of 467. The number of variables ranged from three to 86, with a median of 14 variables. Since a network with  $p$  variables contains  $p(p-1)/2$  edges, the number of cases per edge in the collected datasets ranged from less than one to 7,060, with a median of five cases. The range in relative sample size affected the amount of statistical evidence for edge presence or absence. With higher relative sample sizes, the statistical evidence for networks increased, making them more suitable to derive robust inference (see Figure 3).

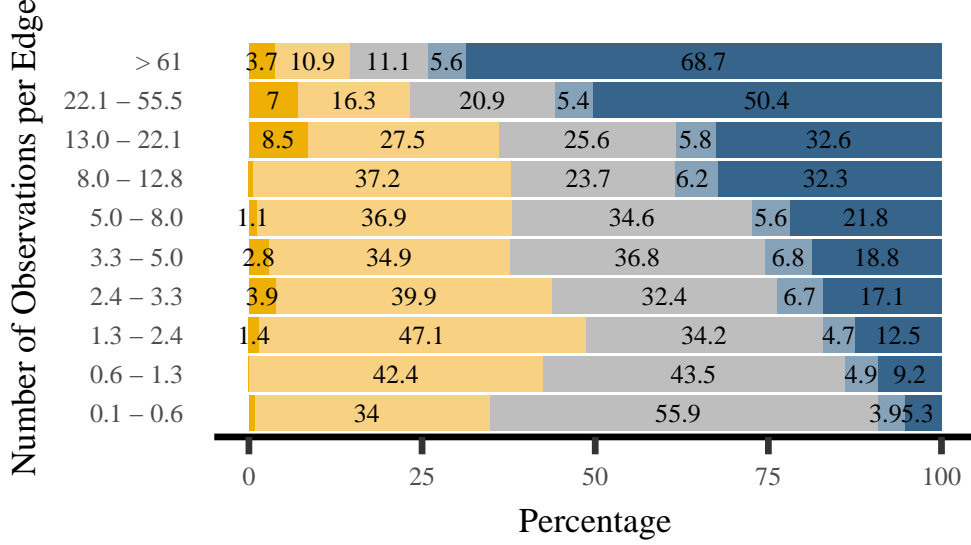


Figure 3: **Statistical evidence depending on relative sample size.** Bar plot illustrating the percentage of uncertainty across relative sample size groups. Each bar represents networks of a particular relative sample size group, which we split into ten groups made up of an equal number of networks. Edge evidence was categorized according to the inclusion Bayes factor  $BF_{10}$ : (1) Dark yellow indicates the percentage of edges with strong evidence for absence ( $BF_{10} < 1/10$ ). (2) Light yellow indicates weak evidence for absence ( $BF_{10} < 1/3$ ). (3) Grey indicates insufficient evidence ( $1/3 < BF_{10} < 3$ ). (4) Light blue indicates weak evidence for presence ( $BF_{10} > 3$ ). (5) Dark blue indicates strong evidence for presence ( $BF_{10} > 10$ ).

As expected, we found mostly inconclusive evidence in the datasets with the smallest relative sample sizes, while we found mostly strong evidence for edge presence in the datasets with the largest relative sample sizes. In the group with the fewest observations per edge (i.e., 0.1 – 0.6 observations per edge), we found inconclusive evidence for the presence or absence of 55.9% of the edges, evidence for the presence of 5.3% of edges, weak evidence for the presence of 3.9% of the edges, and 34% of the edges showed weak evidence for absence. In contrast, in the group with the highest relative sample size (i.e., more than 61 observations per edge), we found inconclusive evidence of edge presence or absence for only 11.1% of the edges, weak evidence for the presence of 5.6% of the edges and absence for 10.9% of the edges, and conclusive evidence of presence for 68.7% of the edges and absence for 3.7% of the edges. While the amount of statistical evidence

is strongly related to the relative sample size, a high relative sample size does not ensure conclusive evidence (see supplementary Figure A1). There is an increasing amount of evidence for the presence or absence of edges with increasing relative sample size, but there is no direct relationship; for similar relative sample sizes, there is a huge variability in the amount of evidence that could be related to, for example, the strength of the effect.

Furthermore, there might be some moderation effects on statistical evidence, if relative sample size varies systematically across a third variable. In the analyzed networks, the relative sample size of estimated networks differed between psychological subfields. Networks in organizational psychology had the most observations per edge (median of 15.2), followed by diagnostics (median of 11.3), public health (median of 8.4), and personality (median of 6.5). As such, the percentage of statistical evidence also differed with certain subfield networks supported by more statistical evidence than others (see supplementary Figure A2). In addition, the relative sample size also differed across sample populations. In clinical psychology, samples obtained from the general public had a higher relative sample size than clinical samples (i.e., individuals with a diagnosed mental disorder). As such, networks obtained from the general public are supported by more statistical evidence than those estimated from clinical or mixed samples (see supplementary Figure A3).

## 2.4 Do Large Edge Weights Imply Compelling Evidence for Edge Presence?

The above results show that for a large proportion of edges in the networks we analyzed, there is insufficient evidence to determine their presence or absence. But which edges are the ones with little statistical evidence? It might seem intuitive that stronger edges are supported by more evidence and weaker edges would be supported by less evidence. Researchers often focus on interpreting the strongest edges in the network and largely ignore the weaker ones. Consequently, if the stronger edges are indeed supported by more evidence, the risk of not robust or erroneous inferences from the interpreted edges may be minimal.

The estimated edges had a partial correlation ranging from  $-0.68$  to  $0.92$ , with the majority of the estimated partial correlations falling between  $-0.10$  and  $0.20$ . If the size of the estimated effect were the only factor determining the evidence, we would expect a sharp pitchfork-shaped relationship between the size of the estimated effect and the logarithm of the Bayes factor.<sup>31</sup> However, this was not the case for our analyses, as Figure 4 shows that larger edge weights do not correspond to greater strength of evidence. Looking at the evidence categories, we see that there is a large overlap between the corresponding range of estimates across categories. Partial correlations for edges with inconclusive evidence ranged from  $-0.38$  to  $0.38$ , which are edge weights that were also found to correspond to edges categorized as weak or strong evidence of presence in other cases. This was most pronounced for a large proportion of edges with edge weights between  $0.1$  and  $0.2$  and between  $-0.2$  and  $-0.1$ , for which we found many cases of inconclusive, weak, and strong evidence. These results also apply to the case of evidence of edge absence. The partial correlations for the edges with evidence of absence ranged from  $-0.02$  to  $0.02$ . However, for some edges with estimates in this range, we also found weak evidence of absence or even inconclusive evidence. There were edges for which we found evidence of presence that only had an estimated partial correlation of  $0.01$ . In sum, there is no sharp relationship between the size of the effect and the strength of the

evidence.

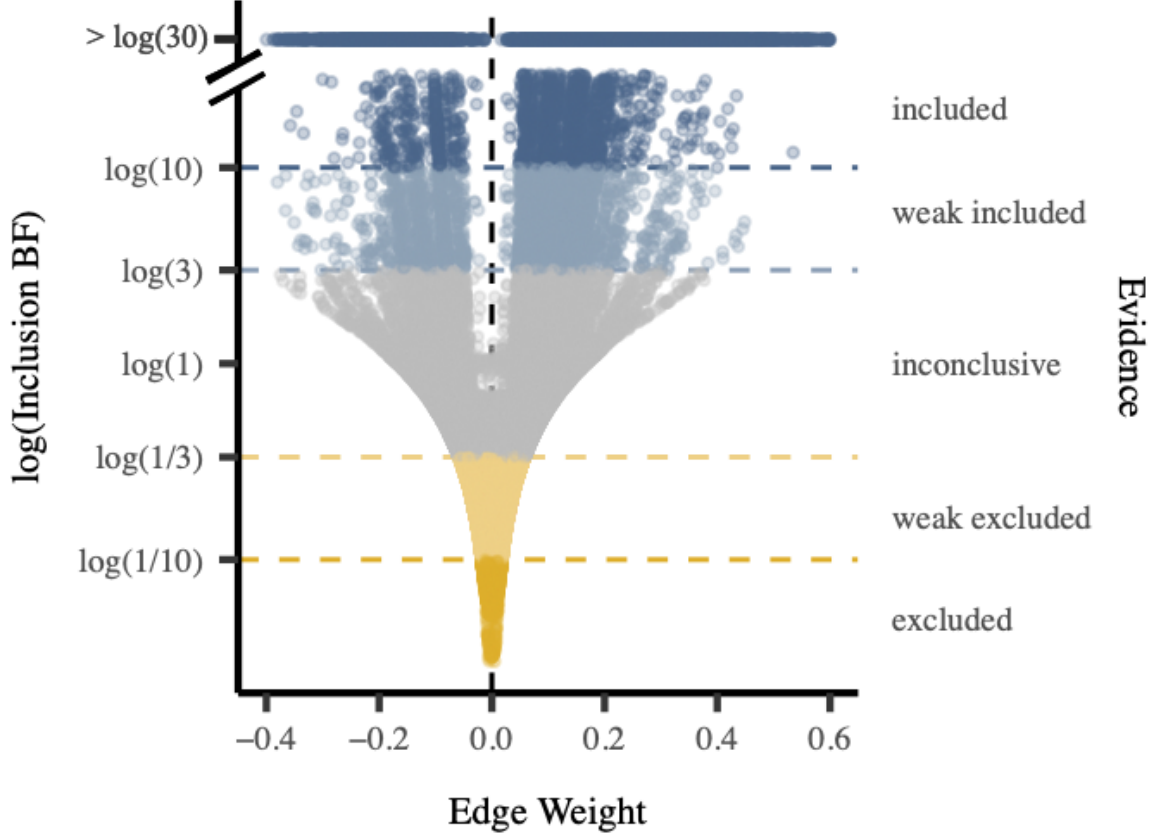


Figure 4: **Edge weight estimates (i.e., partial correlations) and their evidence.** The x-axis represents the edge weights—the partial correlations. The y-axis represents the log of the Bayes Factor. Each dot represents one edge in the 293 networks, which are colored according to the evidence category. (1) Dark yellow indicates strong evidence for absence ( $BF_{10} < 1/10$ ). (2) Light yellow indicates weak evidence for absence ( $BF_{10} < 1/3$ ). (3) Grey indicates inconclusive evidence ( $1/3 < BF_{10} < 3$ ). (4) Light blue indicates weak evidence for presence ( $BF_{10} > 3$ ). (5) Dark blue indicates strong evidence for presence ( $BF_{10} > 10$ ).

In networks with a higher relative sample size, there was a clearer correspondence between edge weight and edge evidence (see supplementary Figure A4). In particular, networks with many observations per parameter showed edge weights corresponding more closely to a particular edge evidence category. As edge weights increased, so did the evidence for edge presence, while edge weights around zero showed weak to strong absence evidence. Contrarily, networks with the fewest observations per parameter showed limited edge weight and evidence correspondence with similar partial correlations being categorized into any of the evidence categories. To quantify the visual alignment between edge estimates and inclusion Bayes factors across the categories, we computed the correlation between squared partial correlations and Bayes factors. The correlations were highest in the “many” (0.66) and “moderate” (0.61) evidence categories, lower in the “fewest” (0.57), and lowest in the “most” (0.52) category—reflecting the varying degrees



of correspondence visible in the figure.

## 2.5 Robustness and Numerical Checks

In our analyses, we had to make several choices that may influence our findings. To assess how sensitive our results are to these choices, we performed several robustness and numerical checks.

First, results may depend on the certain prior distribution we specified for our model. To assess that, we performed a prior sensitivity analysis, examining what the results would have been if we had used a different standard deviation in the prior distribution (i.e., Matrix-F distribution) of edge weights (see the Analysis subsection in Methods). Changing the standard deviation in the prior distribution of the edge weights altered the results, particularly the percentage of edges with weak or strong evidence for absence (see supplementary Figure A5). Using a smaller prior standard deviation for the edge weights increases the percentage of edges for which we find inconclusive evidence from 23% to 37.6%. Conversely, using a larger prior standard deviation dramatically decreases the percentage of edges for which we find evidence for absence dramatically from 18.5% to 3.4%. However, the percentage of edges for which we find evidence for presence barely changes, increasing only slightly from 12.3% to 13.3% with a smaller standard deviation, similar to edges with weak evidence for presence, which fluctuates between 3.7% and 4.8%.

Second, many papers discussed more than one network, though some of those may solely be supplemental analyses. For example, researchers may assess the network of depression across all individuals (i.e., main network) and then conduct a robustness check for age differences (i.e., supplemental networks). It may be that the main networks are systematically different from the other networks because they are based on a larger sample size or fewer nodes both of which could lead to a higher relative sample size. Therefore, we assessed the differences between the main (i.e., the first network discussed in a paper) and supplemental networks. The main networks had a similar distribution over the categories of edge evidence as the full set of networks, suggesting that they are not inherently more suitable for robust inference (see supplementary Figure A6).

Lastly, as expected, the Bayesian estimates of edge weights—partial correlations—mostly aligned with the frequentist estimates (see supplementary Figure A7). Edges estimated as negative using the Bayesian approach were also estimated to be negative with the frequentist approach, and the same holds for positive edge weights. Although the estimates corresponded, there was not a direct match; most edge weights differed in absolute value by at most 0.1. For correlational effects such as the edges estimated here, this would amount to a difference considered a small effect size. Thus, the frequentist and Bayesian edge weights largely aligned, with the Bayesian approach offering the additional advantage of quantifying the statistical evidence for the presence or absence of edges.

## 3 Discussion

We investigated the strength of evidence supporting the presence or absence of individual network edges. Reanalyzing 293 networks from 126 papers led to three key findings: First, we found strong evidence for the presence or absence of one in five edges in published psychological networks ( $BF_{10} > 10$  or  $BF_{10} < 1/10$ ) and weak evidence for their presence in another half of the edges ( $BF_{10} > 3$  or  $BF_{10} < 1/3$ ). A Bayes factor greater than ten

in favor of edge presence indicates that the observed data are at least ten times more likely under a model that includes the edge than under a model that excludes it. For the remaining one third of the edges, we found inconclusive evidence for their presence or absence ( $1/3 < BF_{10} < 3$ ). Second, we found that the sample size relative to the number of edges is a key determinant of evidential strength. As this relative sample size increases, the proportion of edges supported by inconclusive evidence decreases. In networks with high relative sample sizes, most edges were supported by strong evidence. Third, effect size can be an informative source for relative evidence when uncertainty and sample size are taken into account. However, if these are not taken into account, estimated effect size is not necessarily a good substitute for statistical evidence.

Our results suggest that conclusions about the presence or absence of specific network relations should be interpreted with caution, as many such relations are supported by limited evidence. While concerns about the evidential strength of network edges have been raised previously,<sup>17,18</sup> our study adds to this discussion by quantifying the extent of the concern. About half of the decisions to include or exclude edges from the networks were weakly supported by the data. Another third showed no clear evidence either way. These results suggest that the presence or absence of a reported edge is often uncertain. However, this does not mean that network analysis as a whole is flawed. Rather, it means that the data does not strongly support conclusions about many of the individual edges. If researchers report on most edges in their networks, many of their conclusions may be overstated, some may also be incorrect. The severity of this concern depends in part on the Bayes factor thresholds applied. Although the thresholds we employed are widely accepted in Bayesian inference,<sup>33–35</sup> they reflect subjective choices rather than being grounded in the inherent properties of the Bayes factor. Changing these cutoffs results in different percentage of edges that are insufficiently supported by data.

The Bayes factor approach we employ offers a distinctive advantage: it quantifies the strength of evidence for both the inclusion and exclusion of network relations, and crucially, it can also indicate when the data provide limited support for either hypothesis. The capacity to distinguish between evidence of absence (i.e., a relation is likely not present) and absence of evidence (i.e., the data are insufficient to decide) is particularly powerful. Without this distinction, interpreting the absence of an edge in a network becomes ambiguous—did the analysis provide compelling evidence that the edge is not present, or was there simply not enough data to detect it? This ambiguity has contributed to debates over the replicability of network structures, with some interpreting inconsistencies across samples as evidence of poor replication.<sup>36–39</sup> However, others have correctly noted that such inconsistencies often stem from sampling variability.<sup>28</sup> Our own analyses support this view: we found that sample size was a key determinant of the strength of the evidence for or against specific network relations. Based on our results, we recommend that researchers rigorously assess the strength of evidence underlying their network models, ideally using Bayesian approaches that explicitly quantify support for or against specific relations.

In addition, our findings offer ideas for how to make use of the extensive body of existing empirical networks in the future. First, our results suggest that many individual network studies provide inconclusive evidence for specific network relations, limiting their standalone contribution to cumulative psychological science. One of the key strengths of the Bayesian approach, however, is that it offers several principled avenues for evidence accumulation.<sup>40,41</sup> For example, results from individual studies can be integrated by sequentially updating priors and Bayes factors as new data become available.<sup>42</sup> Replication

Bayes factors allow researchers to formally evaluate whether new data corroborate previous findings, and Bayesian evidence synthesis enables the combination of results across studies while accounting for uncertainty.<sup>43</sup> In addition, Bayesian models can incorporate prior theoretical expectations directly, offering a route to theory-driven cumulative modeling.<sup>44</sup> Alongside solutions grounded in the Bayesian graphical modeling approach we use in this paper; meta-analytic network methods have also been proposed as part of a broader methodological toolkit.<sup>45–47</sup> That said, many of these approaches remain underdeveloped in the context of network models. Advancing methodologies for Bayesian evidence accumulation, whether through updated posteriors, replication metrics, or synthesis techniques, should be a key priority for future work. Doing so will strengthen the foundation for cumulative, evidence-based theory building in psychological network research.

Second, our findings have important implications for the interpretation and application of network models in psychological research. In recent years, such models have increasingly been used to inform clinical decisions and theory development—for example, by selecting intervention targets based on the presence or strength of specific edges.<sup>48–50</sup> However, our results suggest that many individual network relationships are supported by limited statistical evidence, raising concerns about the extent to which these models can reliably guide data-informed decisions. This issue may be even more pronounced in longitudinal designs with few time points per individual, where limited data further reduce the evidential support for estimated networks.<sup>51</sup> Without explicitly evaluating the strength of evidence behind network results, there is a risk of overconfidence and unwarranted conclusions, both in applied and theoretical contexts. We therefore advocate for more cautious interpretation of network findings, particularly when they are used for purposes beyond description. We note that the concern of limited statistical evidence can be one of several other challenges of the network application, as models often do not distinguish within- and between-person effects, have inadequate sampling frequency, large amounts of missing data, functional misspecification, and the omission of relevant variables.

To ensure that others can build on our work, all analyzed networks from this study are included in our open-access website **ReBayesed**. Applied researchers can use the database to identify robust findings across networks by highlighting which edges can be interpreted with confidence, facilitating robust meta-analytic studies. Additionally, the database serves as a comprehensive resource for locating previous publications on specific topics, narrowing literature reviews, and pinpointing research gaps. For quantitative researchers, the database provides crucial information to enhance analysis methods and adapt them to the data sets actually analyzed in the field. For example, this information can be employed for informed prior elicitation in the Bayesian estimation of network density or partial correlations following detailed guidelines.<sup>44</sup> Due to the similarity between network methods and other statistical approaches, the database’s utility extends beyond network research to other related fields, such as latent variable or regression analysis.<sup>52</sup>

We advocate for a Bayesian approach to network analysis because it enables researchers to quantify the strength of evidence supporting the inclusion or exclusion of individual relations in a network model. Our results show that most network relations are supported by, at best, weak evidence, which highlights the importance of making uncertainty explicit. Ignoring this uncertainty can lead to overconfident or even misleading conclusions.<sup>53</sup> That said, uncertainty itself is not inherently problematic. Even weak or ambiguous evidence can be informative, provided it is communicated transparently.

The real issue arises when uncertainty is overlooked and strong conclusions are drawn without adequate evidential support. Unfortunately, the current tools for quantifying uncertainty in network models are limited. The most commonly used method in network psychometrics is bootstrapping.<sup>20</sup> However, when combined with regularization and model selection, bootstrap intervals become difficult to interpret and cannot reliably inform decisions about whether a relation should be included in the model. In contrast, the Bayesian framework offers a principled way to quantify uncertainty and compare competing hypotheses. It provides interpretable measures of evidential strength and supports transparent reporting, even in the face of inconclusive results. Bayesian methods enable researchers to more accurately communicate what their data do and do not support.

Our conclusions are subject to a number of limitations. First, we analyzed only a subset of available published papers, likely introducing bias in the type of reanalyzed networks. Large cohort studies might not be included because they require extensive data application procedures, which we deliberately did not investigate. Due to the commonly large sample size, we would expect these network findings to be supported by more evidence. Additionally, individual researchers may not share data due to privacy concerns or loss of access, which are likely studies with smaller sample sizes and thus showing less evidence for edge presence and absence. Second, we used a Bayesian single-model approach to quantify the evidence, focusing on the most plausible model to estimate the edge weights.<sup>31</sup> This approach overlooks the uncertainty about the most plausible model, whereas Bayesian model-averaging accounts for this uncertainty, considering other nearly likely models.<sup>53–55</sup> The single-model approach may provide less extreme evidence of edge presence and absence compared to model-averaging, which is more sensitive to misspecifications and less sensitive to null results. Third, the networks reanalyzed here were all cross-sectional or from a single time point of a panel network, limiting conclusions about the statistical evidence underlying longitudinal network estimation. We expect longitudinal networks to pose even greater concerns due to the difficulty of obtaining sufficient data and models requiring even more parameters to be estimated.<sup>51</sup> Bayesian approaches are particularly useful in longitudinal networks to accurately quantify the evidence for findings.<sup>56</sup> Research should assess the extent to which longitudinal network research is supported by data.

Lastly, multiplicity may pose an additional concern. Psychological network analysis requires estimating the presence or absence of many edges simultaneously, which involves a large number of statistical comparisons. Although Bayes factors are computed for each edge individually, interpreting the network structure as a whole raises concerns about multiplicity: when many Bayes factor tests are performed simultaneously, some edges may appear to be supported—or unsupported—due to chance alone. To account for multiplicity in Bayesian network estimation, it is important to consider the prior on the model structure. A fixed prior probability on edge inclusion does not correct for multiplicity unless the inclusion probability is treated hierarchically and changes with the number of possible edges.<sup>57</sup> A hierarchical prior, such as a beta-binomial, adjusts for network sparsity and provides automatic multiplicity correction. The multiplicity concern is most pronounced in sparse networks with small sample sizes, while in denser networks with more data, the effect of multiplicity correction is minimal.<sup>57</sup> At this moment, hierarchical priors are only implemented for ordinal variables.<sup>24</sup> Such implementations would be fruitful for Gaussian graphical models alike.

## 4 Conclusion

Our study shows that networks are often supported by too little evidence from the data for results to be reported with confidence. We view our results as a cautionary tale about the confidence with which previously published network results can be interpreted. We argue that future work should use a Bayesian approach to express the statistical evidence for the presence or absence of edges from the estimated network. The ability to distinguish between evidence of presence or absence and the absence of evidence allows network researchers to report their results with confidence.

## 5 Methods

We have made available our systematic review plan, all data exclusions, and all study measures. Search criteria, selection guidelines, aggregated data, and analysis code are available in the project repository on the open science framework (OSF) at <https://osf.io/n8r9g/>. We analysed third-party data in our project, which we are not allowed to further share as raw data. When available, we added a link to the respective public repository with the raw data in the OSF folder and provide all R scripts used for data cleaning. We do share the aggregated statistics such as covariance and correlation matrix for all analysed datasets. The data were analyzed using R Version 4.4.1<sup>58</sup> on a MacOS server with Darwin 20 operating system. Specifically, we used the R packages **easybgm** (Version 0.1.2), **BGGM** (Version 2.1.3), and **tidyverse** (Version 2.0.0) for network estimation, visualization, and analysis.<sup>59–61</sup> The code for the open-access website is available at [github.com/KarolineHuth/ReBayesed](https://github.com/KarolineHuth/ReBayesed). The design and analysis of this study were not preregistered.

### 5.1 Systematic Search and Citation Tracking

We searched for datasets that have been used to publish cross-sectional, empirical networks of psychometric variables in human participants. We searched for relevant papers through (1) a systematic search and (2) citation tracking of relevant papers. First, we conducted a systematic search for all papers related to psychopathology and network analysis. Search terms were derived in collaboration with a librarian based on papers considered relevant to the project. We only derived search terms for psychopathology because this is the main area of application and the use of these methods in other sub-fields was too broad to derive specific keywords. The search was conducted in PsycInfo and Medline in March 2023. Second, to search for all papers published outside the field of psychopathology, we used Web of Science citation tracking of influential papers in the field, such as reviews, methodological contributions, and tutorial papers. We performed citation tracking based on 18 papers that were identified after consultation with experts in the field.<sup>1,4,20,62–76</sup> We restricted the search to papers published after 2010 when the network approach in psychology began to be implemented in empirical studies.

### 5.2 Title and Abstract Screening

After de-duplication, papers were screened based on their title and abstract to determine whether they met the inclusion criteria. Specifically, papers had to have estimated an empirical network whose variables were obtained with psychometric scales, and ethical approval and written consent were required unless the study was exempt. In addition, the network model had to be a Gaussian graphical model (GGM) for multivariate normally distributed data. Although we also collected data from Ising models (i.e., multivariate binary variables) and mixed graphical models (i.e., a mix of binary, ordinal, and continuous data) there were too few studies to conduct a specific reanalysis for these model types (i.e., 28 Ising models and eight mixed graphical models).

Articles were excluded if they did not meet the inclusion criteria. If it was unclear whether the criteria were met, the study was classified as undecided and reviewed later. To reduce selection bias, we provided detailed guidelines on inclusion criteria to all individuals who screened articles and documented screening decisions on Rayyan.<sup>77</sup> Although

it is standard practice to have two independent reviewers, due to the large number of search results and the scope of the project, only one reviewer reviewed each article.

### 5.3 Data Acquisition

For papers that met the inclusion criteria based on title, keywords, and abstract, we obtained the corresponding author’s email from the databases. If no email was available, we checked the full text of the paper and manually searched the web for the first author’s email. Authors were emailed and asked to complete a three-minute Qualtrics questionnaire about the dataset, including questions about the papers subfield, network model (i.e., GGM, Ising, MGM), variable types, and data sharing ability. Non-responders or publications for which we could not find a valid email were excluded. Researchers could also submit Qualtrics responses for articles that were not included in our search but that they felt were relevant.

Submitted Qualtrics responses underwent a final review to ensure compliance with inclusion criteria. Data available in public repositories (e.g., OSF and Mendeley Data) were directly downloaded and processed. Authors willing to share non-public datasets were invited to upload their data to a secure, ISO/IEC27001-certified server. Data were stored in encrypted form and accessed using two-factor authentication. Authors were instructed to submit a fully anonymized dataset, including transformed variables if they were used (e.g., reverse coded variables, summed scores, etc.). Two reminders were sent before non-responding publications were excluded.

Publications requiring additional information or extensive application procedures (e.g., a detailed analysis plan or legal agreement) were excluded due to time constraints.

### 5.4 Data Extraction

Publications often included multiple networks, and we extracted information for each. For example, if a publication analyzed an overall network and then divided the sample into younger and older participants, we extracted three networks: one for the overall group, one for the younger participants, and one for the older participants. Networks differed in terms of the analyzed time point, the sample, and the variables included. Each extracted network and corresponding dataset was assigned a unique publication- and network-specific ID. Metadata and raw data were extracted for each network.

Metadata was stored in an online spreadsheet. We recorded the network model, number of nodes, sample size, topic (e.g., clinical, educational, social), subtopic (e.g., specific constructs assessed), variable types (i.e., binary, continuous, mixed), questionnaires, node names, sample type (e.g., clinical, general population, mixed), and data repository link.

Raw data were processed according to detailed guidelines. Each dataset was manually cleaned to match the dataset used in the original publication. We ensured that data were fully anonymized, each column represented a network node, variables were recoded or preprocessed as needed (e.g., summed scores), rows represented participants, and the number of rows matched the sample size in the paper. Missing data were imputed using the R package **missForest**.<sup>78</sup> When data cleaning required additional information or when there were discrepancies in sample size, we contacted the original authors. Data from authors who did not respond were excluded. In total we obtained data from 126 papers that we used in this manuscript.<sup>79–203</sup>

## 5.5 Analysis

We reanalyzed all of the data sets using a Bayesian approach to psychometric network analysis. A psychometric network consists of a set of nodes (i.e., the variables) and a set of edges, which describe the unique association between two nodes after controlling for all other nodes in the network. An edge between two nodes indicates that the variables are conditionally dependent, while an absent edge indicates conditional independence. The set of present or absent edges between nodes encodes the network structure and is denoted by  $\mathcal{S}$ . The weight of the present edges is contained in the matrix  $\Theta$ , which can be transformed into partial correlations  $\rho$ —the edge weights in GGMs. Positive values indicate positive partial correlations and negative values indicate negative partial correlations. In the cross-sectional data analyzed here, the edges weights are symmetric such that  $\rho_{ij} = \rho_{ji}$ . All data were modeled as a Gaussian graphical model (GGM).<sup>69,204</sup> Some variables were ordinal rather than continuous, so there may have been more appropriate modeling choices, such as the copula GGM<sup>205</sup> or the ordinal MRF.<sup>24</sup> These models are conceptually better suited to handle the ordinal nature of the data. However, we chose to use the same estimation across all datasets and to adopt the model commonly applied in empirical research of ordinal data, which is still predominantly the GGM.

We used a Bayesian approach to estimate the (matrix of) edge weights  $\Theta$  of the GGM. The Bayesian approach uses the data to update prior beliefs about the edge weights to posterior beliefs using Bayes’ rule. These prior beliefs are specified in terms of probability distributions that express, for each possible value of the edge weight, how plausible that value is, a priori. With the specified prior beliefs and the collected data, one can use Bayes’ rule to determine the posterior distribution of beliefs about the edge weight values. The posterior distribution contains everything we know about the edge weights after having seen the data.

The Bayesian approach can be used to test for the presence and absence of particular edges in the network. We will consider the hypotheses  $\mathcal{H}_1^{(ij)}$ :  $\rho_{ij} \in (-1, 1)$  that an edge between variables  $i$  and  $j$  is present in the network, which we want to test against the competing hypothesis  $\mathcal{H}_0^{(ij)}$ :  $\rho_{ij} = 0$  that the edge is absent in the network.<sup>25,26,205</sup> We compare these two hypotheses using the Bayes factor.<sup>34,40</sup> The Bayes Factor (BF) for comparing the two hypotheses  $\mathcal{H}_0^{(ij)}$  and  $\mathcal{H}_1^{(ij)}$  for the presence or absence for the edge between  $i$  and  $j$  is given by the ratio of their marginal likelihoods:

$$BF_{10} = \frac{p(\text{data} \mid \mathcal{H}_1^{(ij)})}{p(\text{data} \mid \mathcal{H}_0^{(ij)})}.$$

The approach adopted in our analysis targets the partial correlations in isolation instead of modeling the whole edge matrix in one.<sup>26</sup> The Bayes factor can be computed as

$$BF_{10} = \frac{p(\text{data} \mid \mathcal{H}_1^{(ij)})}{p(\text{data} \mid \mathcal{H}_0^{(ij)})} = \frac{p(\rho_{ij} = 0 \mid \mathcal{H}_1^{(ij)})}{p(\rho_{ij} = 0 \mid \text{data}, \mathcal{H}_1^{(ij)})},$$

which is the ratio of the prior (i.e.,  $p(\rho_{ij} = 0 \mid \mathcal{H}_1^{(ij)})$ ) to the posterior density (i.e.,  $p(\rho_{ij} = 0 \mid \text{data}, \mathcal{H}_1^{(ij)})$ ) of the focal parameter  $\rho_{ij}$ , evaluated at the test point  $\rho_{ij} = 0$ .<sup>206,207</sup> This is termed the Savage-Dickey ratio and is one of many approaches to obtain the Bayes factor.<sup>31</sup>

The Bayes factor can be interpreted as the weight of evidence from the data.<sup>208</sup> For example,  $BF_{10} = 5$  means that the data are five times more likely under a structure where



the edge was present than under a structure where it was absent. The Bayes factor is a continuous measure of support, where values greater than one indicate evidence for the presence of the edge and values less than one indicate evidence for its absence. Bayes factors between  $\frac{1}{3}$  and 3 are generally interpreted as inconclusive evidence, indicating that one does not have enough evidence to conclude that the edge is present or absent. Values less than  $\frac{1}{3}$  and greater than 3 is interpreted as weak evidence, and values less than  $\frac{1}{10}$  and greater than 10 are interpreted as strong evidence for absence or presence, respectively.<sup>33,34</sup> These interpretive thresholds are conventional and widely used, however, should be viewed as guidelines as their cutoffs are not strictly given by statistical rules.

We used the Bayesian methodology for network analysis implemented in the R package **BGGM**.<sup>26,60</sup> The approach uses a matrix-F prior on the edge weights with the prior standard deviation set to the default value of 0.25.<sup>209</sup> The Matrix-F prior was proposed as a more flexible prior choice for covariance matrices.<sup>209</sup> The Matrix-F prior is defined as:

$$\Theta \sim \text{Matrix-F}(\nu, \delta, B),$$

where  $\nu > p - 1$  controls the behavior near the origin and  $\delta > 0$  controls the behavior in the tails,  $B$  is a positive definite scale matrix. The Matrix-F prior can also be written as a scale mixture of Wishart distributions with an inverse Wishart mixture distribution:

$$\Theta \mid \Psi \sim \text{Wishart}(\nu, \Psi)$$

$$\Psi \sim \text{Inverse-Wishart}(\delta + p - 1, B)$$

which means it can be thought of as a ratio of two Wishart-distributed matrices. The Matrix-F prior is a conditionally conjugate extension of the Wishart prior, offering an extra hyperparameter that enhances flexibility and control over prior beliefs. Its stronger shrinkage toward the identity matrix helps stabilize estimates in high-dimensional, dense psychological networks, which are often based on small samples. Unlike the inverse-Wishart, it avoids overconfident estimates and induces a scaled beta distribution on partial correlations, making it easier to incorporate prior knowledge. Given these advantages, the Matrix-F prior is particularly well-suited for the challenges commonly faced in psychological research.<sup>26</sup>

The Bayesian methodology of **BGGM** can be used to obtain the posterior distribution of the network parameters, assuming all edges are in the model. The posterior inclusion probability can be obtained from the single-model Bayes factor by assuming that edge presence or absence is equally plausible a priori. The adopted approach has been shown to produce consistent Bayes Factors such that there is increasing evidence for edge inclusion for present edges and increasing evidence for edge exclusion for absent edges.<sup>26</sup> For each network, we extracted the Bayesian parameter estimates, Bayesian posterior edge inclusion probabilities, and single-model Bayes factors, as well as the metadata.

For a detailed description of the Bayesian statistics in psychological research, we refer the reader to Wagenmakers et al. (2018)<sup>41</sup>, and for networks in particular, we refer the reader to Huth et al. (2023).<sup>27</sup> For a detailed, mathematical description of the approach employed in this paper, we refer the reader to Williams (2020).<sup>26</sup>

## 5.6 Robustness and Numerical Checks

We conducted several robustness and numerical checks. First, we examined the robustness of our conclusions to our choice of the standard deviation in the prior distribution of edge

weights, which was the matrix-F prior with a standard deviation equal to the default value of .25, as discussed in the previous section. To assess the impact of this prior choice on the results, we ran our analyses with different values for the standard deviation in the prior distributions. Specifically, we varied the prior standard deviation over  $\sqrt{1/8}$ ,  $\sqrt{1/16}$ , and  $\sqrt{1/24}$ .

Second, we assessed whether the additionally extracted networks were differentially supported by evidence, as opposed to the main networks. Multiple networks are derived from the same paper, with up to 15 networks per paper. Often, the main network is split by a categorical subgroup, and then differences between groups are assessed as a supplementary, but not main, analysis. Because these additional networks may only be supplementary analyses, they may not necessarily be the focus of the main inference. Therefore, a lack of evidence underlying these networks may not be as critical. To assess potential differences, we repeated our report by only including the main networks.

Lastly, we reanalyzed each dataset also with the frequentist approach as implemented in the *ggmModSelect* algorithm.<sup>210</sup> The algorithm uses glasso estimation in combination with BIC model selection. In the first step, the algorithm generates a range of networks varying the lasso tuning parameter, using the EBIC criterion to choose the optimal lasso tuning value. Consequently, the network is re-estimated without regularization for non-zero edges. Lastly, a stepwise model search is adopted which adds and removes edges until the EBIC is optimized. We compared the edge weights obtained with this approach to the Bayesian edge weights to illustrate their correspondence.

## 6 Data Availability:

Search criteria, selection guidelines, and aggregated data are available in the project repository on the open science framework (OSF) at <https://osf.io/n8r9g/> with the identifier DOI 10.17605/OSF.IO/N8R9G. We analysed third-party data in our project, which we are not allowed to further share as raw data. When available, we added a link to the respective public repository with the raw data in the OSF folder and provide all R scripts used for data cleaning. We do share the aggregated statistics such as covariance and correlation matrix for all analysed datasets.

## 7 Code Availability:

Readers can find all materials, including the analysis code and figures from this manuscript in the OSF repository: <https://osf.io/n8r9g/>.

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## 9 Author Contribution Statement:

**Conceptualization:** K. Huth, S. Keetelaar, J. Haslbeck, and M. Marsman; **Formal Analysis:** K. Huth; **Writing – Original Draft Preparation:** K. Huth; **Writing – Review & Editing:** K. Huth, S. Keetelaar, J. Haslbeck, R. van Holst, and M. Marsman.

## 10 Competing Interest Statement:

The authors declare that there were no conflicts of interest with respect to the authorship or the publication of this article.

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