The usefulness of Bayesian graphical modelling with neuropsychological data

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Abstract

Neuropsychological functioning is assessed using a network approach, in which links are defined by the relation between the scores of different neuropsychology tests. Although neurobiology has shown that a balance between segregation and integration achieves respectively high specialisation and intercommunication in brain circuits, it is not known whether segregation and integration exist in neuropsychological networks. Indeed, the assessment of segregation require the elimination of conditional dependencies as scores between different tests that are highly correlated each other, i.e., those participants performing well, do the same in almost all tests. A novel method based on Bayesian graphical modelling valid for non-Gaussian data is applied to show that the neuropsychological functioning measured by 23 different tests scores in a population of $N = 1632$ children is organised into seven segregated domains: 1. Verbal memory and comprehension, 2. Visual constructional skills, 3. Verbal letter fluency, 4. Verbal category fluency, 5. Language, 6. Attention and processing speed, and 7. Executive function. These results are important for several reasons. First, the employed method is data-driven and does not assume any prior knowledge in neuropsychology, nor about the possible dependencies between tests. Second, the method results from rigorous Bayesian graphical modelling accounting for the strong non-Gaussianity present in the scores of neuropsychological tests. Third, the seven domains are obtained after evaluation of a very large population, overcoming sample-size effects. Fourth and last, the method provides a recommendation for clinical neuropsychologists, namely, the need of assessing at least one test in each of the seven domains for a more comprehensive and efficient evaluation.

Keywords: Clinical neuropsychology; Bayesian graphical model; non-Gaussian data; Cognitive domains; Neuropsychological networks

Introduction

Clinical neuropsychologists routinely perform several tests for assessing cognitive functioning in healthy individuals and clinical populations. This strategy implicitly assumes that each test measures a differentiated cognitive function such as attention, processing speed, learning and memory, executive function or language. In an indirect manner, it also assumes that segregated neural circuits are underlying the processing for each test. Although at the neuronal level it is generally accepted that a balance between segregation and integration ensures efficiency of brain circuits¹ [1, 2], yet whether such a balance exists in neuropsychological networks is not well understood.

A first limitation for addressing segregation in neuropsychological networks is that conditional dependencies across different tests are very high, as scores from different tests are highly correlated with each other. As a consequence, correlations between test pairs are usually confounded by the effect of a third test which in turn gives rise to spurious correlations. Here, using a network approach where links are defined by the score relation between the different tests, we assess conditional dependencies by the Bayesian Graphical modelling approach [3]. After network estimation, our approach allows for addressing segregation and integration by simply assessing the link strength, which is not possible by other alternative approaches used for clustering neuropsychological data such as Principal Component Analysis or Factor Analysis.

A second limitation to assess segregation is that the probability distribution of test scores is strongly non-Gaussian [4], although Gaussianity (or *normality*) is widely accepted in neuropsychology (eg., two examples are Student's t-test and ANOVA). At least two reasons are in favour of the Gaussianity assumption. First, if it holds, tests under this assumption have a greater power statistic. Second, Gaussianity is motivated by the central limit theorem, which states that the estimation of the population mean tend to be normally distributed when increasing the sample size. Here, in agreement with data, Gaussianity is not assumed, and this motivates the use of the approach based on Gaussian copula graphical models [5, 6].

The developing of accurate methods for detecting clusters between similar tests has special importance in neuropsychology. Thus, in agreement with the Classical Test Theory, conducted studies should involve a sequence of tests measuring different cognitive domains by simple procedures like transformation in percentile scales, T or D scores [7, 8], in a manner that clinical neuropsychologists can estimate the global cognitive status of an evaluated participant. The specific sequence of tests should be defined with regard to the function they measure, and therefore, accurate methods for detecting relation between tests are extremely relevant for designing optimal sequences of tests in an efficient evaluation.

Bayesian graphical model in which non-Gaussianity can be adopted in agreement with data will be a useful procedure to accurately assess conditional probabilities and therefore build neuropsychological networks. From these networks, the aim of this study is to obtain cognitive domains defined as clusters of tests such that their scores are highly related within a cluster and lowly related between them.

¹Segregation refers to functionally specialised circuits performing distinct tasks separately, whereas integration requires coordinated activation between the different segregated circuits.

Material and Methods

Participants

$N = 1632$ (female 845, male 787) healthy children were recruited in nine Colombian cities (Barranquilla, Bogota, Bucaramanga, Cali, Cucuta, Ibague, Medellin, Neiva, and Tunja) with age = 11.51 ± 3.36 .

Inclusion criteria: 1. Age between 6 and 17 years, 2. Born and living in the same country where the protocol was administered, 3. Spanish as primary language, 4. Intelligence Quotient (IQ) bigger than 80 according to the Test of Non-Verbal Intelligence [9], 5. Score smaller than 19 on the Children’s Depression Inventory [10], and 6. being enrolled in a regular private or public school.

Exclusion criteria: 1. History of a central nervous system disease associated with neuropsychological problems (e.g., epilepsy, brain injury, movement disorders, multiple sclerosis, brain tumor, stroke), 2. History of alcohol abuse and/or consumption of psychotropic substances, 3. Active or uncontrolled systemic disease associated with cognitive impairment (e.g., diabetes mellitus, hypothyroidism, vitamin B12 deficiency), 4. History of psychiatric illness (e.g., major depression, bipolar mood disorder, psychosis), 5. Severe sensory deficits (e.g., loss of vision and/or hearing) that affect any test performance, 6. Medications that could alter cognitive performance, 7. Intellectual or learning disability or other developmental disorder, 8. History of pre-, peri-, or post-natal problems (e.g., hypoxia, jaundice, seizures, hydrocephalus, spina bifida, neuromuscular disorders), 9. Score bigger than 5 in the Alcohol Use Disorders Identification Test [11] for participants 12 years and older, and 10. Psychoactive substances such as heroin, barbiturates, amphetamines, methamphetamines, or cocaine in the last 6 months for participants 12 years of age and older.

Ethical considerations

Each recruiting Institution got the approval from its Local Ethical Committee. In all of them, and prior to initiating the assessment, parents received and reviewed the study information. Informed consent was requested to 12 years children and older, and for younger children, always to their parents or guardians. Informed consent included information related to the aim of the study, rights of participants, duration/place of the assessment and contact information for the local researcher responsible for the study. The neuropsychological battery, which lasted approximately 90 minutes was administered individually in a single day to all participants at schools and/or universities. All the neuropsychological tests were administered according to the specific guidelines of each test. All participants were volunteers who did not receive financial compensation for participation. Data collection began in January 2016 and finished in May 2017. Full details are described in studies reviewing the methodology [12, 13].

Data

Data was acquired as part of a larger study to generate statistical normative data for a series of neuropsychological measures [12]. For all the $N = 1632$ children a neuropsychological battery was administered consisting of $m = 23$ different scores

(see Table 1), which had a total duration of about 90 minutes. Except for TMT-A, REY_Copy, REY_Memory and Token-test, all the scores were non-continuous. Missing scores were excluded, so that our data had no missing values across all the different tests.

Weighed Kolmogorov- Smirnov (WKS) statistic for testing non-Gaussianity

Deviations from Gaussianity were quantified using Weighted Kolmogorov-Smirnov (WKS) statistic, which is a variation of the KS test correcting for the effects of the tails [14]. As in the standard KS scenario, WKS provides an estimation of the distance between the two compared distributions, here, data were confronted with a theoretical normal distribution. In particular, for a given test we calculated its mean and standard deviation over the entire population and generated 10000 random samples following a normal distribution with such parameters. Subsequently, the average across all the samples were taken, providing an accurate measure of normality divergence.

Neuropsychological networks

The interactions between the different tests are assessed using a graphical model $G = (V, E)$, in which the tests constitute the graph nodes V (vertices) and E (edges) the links, defined as pairwise interactions.

The graph structure and link strengths are inferred adopting a Bayesian formalism. Herein, $P(\theta|data)$ is known as the *posterior* probability and represents the encoding probability of hyperparameter θ within a model given the observed data. Bayes theorem ensures the relation $P(\theta|data) = P(data|\theta)P(\theta)/P(data)$, where $P(data|\theta)$ is the usual *likelihood*, $P(\theta)$ is the *prior* distribution and $P(data)$ is the *evidence*, which is the marginal probability obtained by summing across all possible models. There are several strategies for obtaining posterior estimates of θ . A common one may involve finding the value of θ which maximises the posterior distribution. A different approach involves sampling directly from the posterior resorting to Markov Chain Monte Carlo (MCMC) methods, which is the methodology adopted in this study.

Given the observed data, the posterior distribution for the graph G and the precision matrix $K \equiv \Sigma^{-1}$ (defined as the inverse of the data covariance matrix) can be written through the Bayes Rule as follows

$$P(G, K|data) \propto P(data|G, K)P(K|G)P(G), \quad (1)$$

where data is encoded in a matrix of $m = 23$ scores and $N = 1632$ observations.

The prior distribution for the form of the graph $P(G)$ is assumed to follow a discrete uniform distribution over the graph space, such that each different graph among all the ensemble in the graph space is equally probable.

Regarding the prior distribution of the precision matrix $P(K|G)$, we used the G-Wishart distribution [15] with the form

$$P(K|G) \propto |K|^{\frac{(d-2)}{2}} \exp \left\{ -\frac{1}{2}tr(DK) \right\} \quad (2)$$

where $|\dots|$ is the determinant operator, d the degrees of freedom and D a positive definite matrix.

Since the G-Wishart distribution is a conjugate prior of the multivariate normal distribution (which is the assumed likelihood in this modelization [6]), the posterior distribution of K conditionally on graph G finally reads

$$P(K|\text{data}, G) \propto |K|^{\frac{(d^*-2)}{2}} \exp \left\{ -\frac{1}{2} \text{tr}(D^* K) \right\} \quad (3)$$

where $d^* = d + N$ and $D^* = D + \mathbf{z}^T \mathbf{z}$, where $\mathbf{z}$ is a centred single point of the observed data.

We adopt two different sampling strategies depending whether we assume or not that the data follow a Gaussian distribution. For the Gaussian assumption, we follow an efficient birth-death Markov Chain Monte Carlo (MCMC) sampling algorithm [3]. For the non-Gaussian scenario, the birth-death MCMC sampling strategy is adapted incorporating the copula graphical model approach according to [16]. Moreover, when Gaussianity is not assumed, the Gaussian copula approach as developed in [5] and [16] is directly applied to non-continuous variables, whereas continuous variables are transformed to the nonparanormal family following [17], which is equivalent to the Gaussian Copula family.

During the sampling procedure, each iteration adds or removes a network link $e \equiv \overline{ij}$ connecting any two nodes i and j , which after convergence provides a robust estimation of the interactions strength in the posterior distribution. Following [3], the inclusion link probability is calculated as

$$P_{\overline{ij}} = \frac{\sum_{t=1}^T I(\overline{ij} \in G^{(t)}) W(K^{(t)})}{\sum_{t=1}^T W(K^{(t)})} \quad (4)$$

where $t = 1, \dots, T$ represent iteration number and $W(K^{(t)})$ is the waiting time for the graph $G^{(t)}$ with the precision matrix $K^{(t)}$ (for further details see [6]). $I(\overline{ij} \in G^{(t)})$ denotes the inclusion operator, equal to one or zero if $\overline{ij}$ was respectively present or absent in $G^{(t)}$.

To build neuropsychological networks, each link was calculated for each pair of tests using the equation (4).

The sampling computation and network estimation was obtained using *BDgraph* 2.56 R package [16], considering 10^6 iterations for the posterior calculation, in which the first 60% of them were used for transient iterations which ensured convergence.

Topological metrics in neuropsychological networks

For comparison between Non-Gaussian and Gaussian networks, we calculated three different standard metrics: global strength (total connectivity per node), average path length (the average length of all the shortest paths from or to the vertices in the network) and transitivity, aka clustering coefficient (the ratio of the triangles connected to the vertex and the triples centered on the vertex). The three metrics were calculated using *igraph* 1.1.2 R package.

Identification of major neuropsychological domains

After all graph links were estimated using equation (4), the major neuropsychological domains were identified by performing unsupervised clustering. In particular, we built a first distance matrix as $1 - \hat{P}$ with $\hat{P}$ given by (4) for the non-diagonal

elements and, in addition, we fixed the diagonal terms to 1 (the distance from each element to itself must be equal to zero). Next, we computed a second matrix $\mathcal{D} \equiv (d_{ij}) = 1 - r_{ij}$, where r_{ij} is the pairwise Pearson correlation between rows i and j in the matrix $1 - \hat{P}$. Therefore, two elements are closer in matrix $\mathcal{D}$ if they have a similar pattern of global integration within the network. The hierarchical clustering was performed on matrix $\mathcal{D}$ with the McQuitty’s linkage that provided a dendrogram, cut at depth such that the average Silhouette coefficient is maximum. At that level, we obtained the resulting major neuropsychological domains. We repeated the same strategy in the two scenarios of Gaussian and non-Gaussian. All steps in the algorithm were implemented in R (Version 3.4.4) and dendrograms were represented with circular visualisation [18].

Results

To obtain segregation of neuropsychological networks one has to overcome the conditional dependencies between different tests. This is illustrated in Figure 1, where the network connectivity values (measured by pairwise Spearman correlation) between all pairs are extremely high.

In addition, neuropsychological scores are strongly non-Gaussian. This is illustrated in figure 2, where Q–Q (quantile-quantile) plots show strong deviations from Gaussianity. Deviations were also quantified by the WKS statistic. In general, all the variables exhibited non-Gaussian characteristics, with Recognition, Token test and the three M-WCST having the larger deviations.

After convergence (figure S1), we obtained two different neuropsychological networks, one assuming data were Gaussian distributed and the other non-Gaussianity (figure 3). In general, the non-Gaussian assumption leads to more dense graphs, yielding a greater global strength (185.94) as compared to the Gaussian case (159.84). In addition, a decrease in the average path length occurs in the non-Gaussian with respect to the Gaussian scenario (1.0 vs 1.09), as well as an increase in the clustering coefficient (1.0 vs 0.92), both indicating a different topology in the two networks.

When comparing the two networks in figure 3, both underestimated or overestimated links appear. Thus for instance, the link between REY_Copy and SDMT together is by far the most underestimated one, as the link probability varies from almost zero in the Gaussian case to almost one for the non-Gaussian scenario. This difference is closely followed by the links from SDMT to Total-Recall, Stroop_W_C to Stroop_word, R to Peabody and M_WCST_error to Delayed_Recall. Therefore, underestimated links are existing interactions not captured when assuming Gaussianity.

In contrast, links from Token Test to M-WCST_Cate, M-WCST_error, F and REY_memory, and from TMT-A to M-WCST_Cate and M-WCST_error exhibit high strength assuming Gaussianity, which abruptly disappear for the non-Gaussian case. Therefore, overestimated links correspond to spurious interactions, only observed under the Gaussianity assumption but not in the real situation of non-Gaussianity.

An advantage of a network approach is that we can easily obtain which test plays a major integrating role by ranking all tests with regard to their strength. Figure 4 shows that the *Token Test* is a hub (highest strength) in the Gaussian scenario but only due to a link over-estimation. The same occurs to a lesser extent with

M-WCST_Cate and M-WCST_error. On the other hand, the integrating role of SDMT and Stroop_W_C are highly increased when non-Gaussianity is assumed. Importantly, we also observed that nodes with smaller strength were the more non-Gaussian (figure S2, $r=-0.568$, $p=0.005$), indicating that non-Gaussianity was associated to topological aspects.

Subsequently, from the obtained neuropsychological networks we identified the major neuropsychological domains (figure 5). Three domains were identified in the Gaussian scenario and seven in the non-Gaussian case, thus the latter overcoming the former to categorise the tests into more specific and specialised cognitive areas.

Moreover, not only the number of domains differed between Gaussian and non-Gaussian scenarios, but the clusters were also different in both scenarios. For example, in the non-Gaussian case, STROOP constructors (assessing attention and information processing) were clustered together with SDMT, which involves speed processing, whereas in the Gaussian scenario, this cluster also incorporated Peabody, which concentrates on vocabulary, and Fruits and Animals, which account for verbal category fluency. In contrast, these last two tests clustered in a separate domain for non-Gaussianity together with the Total-Recall test, possibly resembling word retrieval in categories during the application of this test, and TMT-A, maybe as an attempt to maximise the processing speed to achieve the greatest number of words. Another clear difference occurred for Peabody and Token test, which participated as an unique cluster in the non-Gaussian scenario in contrast to separated clusters for the Gaussian case. On the other hand, executive function as measured by M-WCST_perse, M-WCST_Cate and M-WCST_error were organised into a differentiated cluster for the non-Gaussian case, but not for Gaussianity. Finally, both Gaussian and non-Gaussian assumptions clustered together P/A/M/S/R/F letter tests, indicating that the Gaussian assumption is sufficient to capture all interactions into the letter verbal fluency domain.

Discussion

Examining the quantitative similarities of different neuropsychological tests is of crucial importance for designing efficient strategies in clinical neuropsychology. While a multitude of specialised tests exist in the field, a full evaluation has limitation due to the total duration used for the evaluation. In this study, 23 different scores were administered within approximately 90 minutes of duration - which demands notable human and clinical resources. Thus, determining how different test performances cluster together might reduce evaluation time by avoiding unnecessary tests during a full assessment. This aim poses a number of challenges. First, conditional dependencies between different tests are very high leading to spurious correlations. Specifically, methods are necessary to remove correlations between pairs caused by the effect of third variables. Second, most of the methods assume test scores are Gaussian distributed, but this assumption is inaccurate. Here, we have introduced a novel method based on Bayesian graphical modelling valid for non-Gaussian data. The method determines conditional probabilities in the posterior distribution, which are the links of the neuropsychological networks. This approach allows the determination of the major domains, the ones that neuropsychologists should take into account for an efficient evaluation.

The results have identified seven major cognitive domains that yield a similar

behaviour as measured by the interacting role of the nodes of the network. As a consequence, selecting just a representative test is sufficient to assess the cognitive performance of the participants in that domain, thus reducing the evaluation time. For instance, one criterion could include selection of the test nearest to the cluster centroid (mean of all tests). Alternatively, a different criterion could determine the test with the shortest evaluation time. Thus, for instance, following the second criterion, neuropsychologists should administer a battery of the seven following tests: S, Token Test, Stroop_color, Fruits, REY_memory, Delayed_Recall and M-WCST_error, which reduces the evaluation time to approximately 20 minutes, thus saving more than two thirds (70 min) of assessment time for each participant.

Furthermore, once the inherent structure of the data have been clustered into major domains and a representative score for each cluster has been chosen, one could attempt to evaluate the association between representative tests and other external variables, such that age, years of education or the level of parents' study. Alternatively, one could incorporate those external variables such as age or years of education as additional nodes in the network. This would allow for the determination of which domains those external variables cluster with, which indicate the need of stratifying the population when studying that specific domain.

This approach is aligned with the increasing criticism of the assumption that neuropsychological data fits a Gaussian distribution [19], when most of the distributions are non-normal [20]. In the line of this research, methods appropriate for non-Gaussian data are needed in neuropsychology [21]. With regard to univariate analyses (*i.e.*, comparing scores from a given test in two different populations), non-parametric statistics can indeed overcome the Gaussian limitation, and are valid in general for any class of probability distribution. Here, this method goes beyond univariate group comparisons to assess pairwise relations needed to build the neuropsychological networks.

The Bayesian graphical formalism used here allows the elimination of third variable interactions when studying how two variables interact each other. However, other existing methods such as the inverse of the covariance matrix, *i.e.*, the so-called partial correlation (PC) analysis, can also eliminate third node interactions [22]. If data are Gaussian distributed, indeed PC can eliminate full dependencies in third variables [23]. The striking difference is that, for non-Gaussian data, PC does not guarantee the total elimination of third variable effects [23], and for this reason, our method overcomes the partial correlation approach, as it accounts for non-Gaussian conditional dependencies. Thus, to show differences between PC and our approach, we obtained a more sparse graph for the former as compared to the latter (the global strength was 28.64 for PC and 185.94 in our case). An additional advantage of our method as compared to PC is that the sampling strategy followed here is based on an exhaustive exploration of all possible links in the graph space, and as a consequence, our method easily converges to the underlying graph, a feature more difficult to obtain by a single-point estimate as provided by the PC analysis.

We have also shown that when comparing the Gaussian vs the non-Gaussian assumption, major discrepancies in the network topology occur on those tests where deviations from Gaussianity are stronger. For example, Gaussianity assumption assigns Token test, M-WCST_Cate and M-WCST_error and a more important integration role than necessary. In contrast, Gaussianity does not capture the most important role that SDMT has in the neuropsychological network.

The results of this study have implication in diagnosing cognitive disorders. For instance, when comparing a pathological population with a healthy one, since these results suggest that SDMT exhibits the maximum strength (and therefore it has the biggest dependency with all other tests), this might therefore indicate the value of this test as a better neuropsychological biomarker in some diseases. But this research needs a further clarification. In conclusion, the seven domains identified in this paediatric population include verbal memory and comprehension, viso-constructional skills, phonological and semantic verbal fluency, language, attention and processing speed, and executive function. It is important to emphasise the existence of these seven domains to be widely accepted in modern neuropsychology, but our approach is purely data-driven and did not assume any prior organisational structure between tests. Therefore, our results are validating current knowledge in clinical neuropsychology. Whether the same domains are obtained in adults with a similar data-driven approach should be investigated.

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Test	Test Scores	Cognitive Function
Rey Osterrieth Complex Figure Test	Total REY_Copy Total REY_Memory	Viso Constructional skills
STROOP Test	Total Stroop_word Total Stroop_color Total Stroop_W_C	Attention Processing speed
Modified Wisconsin Card Sorting Test	Total M-WCST_Cate Total M-WCST_perse Total M-WCST_error	Executive functions
Symbol Digit Modalities Test	SDMT	Attention-Processing Speed
Trail Making Test	Total TMT-A time	Attention
Token Test	Total Token.Test	Comprehension
Phonologic and Semantic-Verbal Fluency	F/A/S/M/R/P Total Animals Total Fruits	Verbal Fluency
Peabody Vocabulary Test PVT-III	Total Peabody	Vocabulary
Learning and Verbal Memory Test (TAMVI)	Total_Recall Total Delayed_Recall Total Recognition	Verbal Memory

Table 1: Neuropsychological evaluation consisted in 9 different tests.

Figure 1: **High conditional dependencies in neuropsychological networks.** Pairwise Spearman correlations reveal a dense map in the connectivity of neuropsychological networks, indicating high conditional correlations in the given data. Neuropsychological networks are built with $m=23$ different tests (working as nodes in the graph) and $(N \times N)/2 - N$ links (symmetric connectivity matrix without terms in the principal diagonal) defined as the relation between tests.

Figure 2: **Strong deviation from Normality in neuropsychological tests.** A Quantile-quantile (QQ) plot shows data quantiles as a functional of Theoretical Normal quantiles. Therefore, deviation from the straight line indicate non-Gaussianity. Deviations were also measured by the weighted Kolmogorov-Smirnov (KS) statistic, which is a variation of the KS test correcting for the effects of the tails. *Recognition*, *Token test* and the three *M-WCST* tests shown the larger deviations.

Figure 3: Inferred Neuropsychological networks are different for the Gaussian (left, red) or non-Gaussian (right, blue) assumption. For the two cases, we only plot the upper triangular connectivity matrix as both matrices are symmetrical. Notice that two classes of mistaken links might exist: 1. Underestimated or missing links, when Gaussian do not detect interactions but they exist for the non-Gaussian case. 2. Overestimated or spurious links, where they exist only as a result of the Gaussian assumption.

Figure 4: **Integration role in neuropsychological networks.** The total strength (a.k.a. degree) measured as the total sum of weights from each test to the rest in each neuropsychological network reveals that some nodes might have a low integration role in the Gaussian case but in fact they are high in the non-Gaussian scenario (for instance, SDMT and Stroop_W_C). In contrast, other tests seem to be highly integrating but this is just a wrong consequence obtained from Gaussianity (for instance, Token.Test, Recognition, M-WCST_Cate and M-WCST_error).

Figure 5: **Major neuropsychological domains.** After cutting the hierarchical tree at the level in which the average Silhouette coefficient is maximum, three domains were identified for the Gaussian case (depicted in three different branch colors) and seven domains for the non-Gaussian case (depicted in seven different branch colors).

Figure S1: **Convergence of link posterior probabilities.** For each link, we plot the time evolution of its posterior probability in the two sampling strategies corresponding to assume either Gaussian or non-Gaussian data. For both cases, the convergence is guaranteed after a transient period, exhibiting the robustness of employed method for estimating the neuropsychological network. Notice that the graph topology drastically changes depending on whether or not normality is assumed.

Figure S2: **Weighted Kolmogorov-Smirnov statistic as a function of the node strength in the Non-Gaussian scenario.** Therefore, the more non-Gaussian is the test as quantified by WKS, the smaller strength is that test in the neuropsychological network. Black points correspond to different tests, blue line the fitted curve and the grey shadow area the confidence intervals at 0.05 significance level.