



# Mapping correlations of psychological and structural connectome properties of the dataset of the human connectome project with the maximum spanning tree method

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Published online: 7 August 2018  
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## Abstract

Genome-wide association studies (GWAS) opened new horizons in genomics and medicine by discovering novel genetic factors in numerous health conditions. The analogous analysis of the correlations of large quantities of psychological and brain imaging measures may yield similarly striking results in the brain science. Smith et al. (Nat Neurosci. 18(11): 1565–1567, 2015) presented a study of the associations between MRI-detected resting-state functional connectomes and behavioral data, based on the Human Connectome Project's (HCP) data release. Here we analyze the pairwise correlations between 717 psychological-, anatomical- and structural connectome-properties, based also on the Human Connectome Project's 500-subject dataset. For the connectome properties, we have focused on the structural (or anatomical) connectomes, instead of the functional connectomes. For the structural connectome analysis we have computed and publicly deposited structural braingraphs at the site <http://braingraph.org>. Numerous non-trivial and hard-to-compute graph-theoretical parameters (like minimum bisection width, minimum vertex cover, eigenvalue gap, maximum matching number, maximum fractional matching number) were computed for braingraphs of each subject, gained from the left- and right hemispheres and the whole brain. The correlations of these parameters, as well as other anatomical and behavioral measures were detected and analyzed. For discovering and visualizing the most interesting correlations in the 717 x 717 matrix, we have applied the maximum spanning tree method. Apart from numerous natural correlations, which describe parameters computable or approximable from one another, we have found several significant, novel correlations in the dataset, e.g., between the score of the NIH Toolbox 9-hole Pegboard Dexterity Test and the maximum weight graph theoretical matching in the left hemisphere. We also have found correlations described very recently and independently from the HCP-dataset: e.g., between gambling behavior and the number of the connections leaving the insula: these already known findings independently validate the power of our method.

**Keywords** Connectome · Braingraph · Maximum spanning tree

**Electronic supplementary material** The online version of this article (<https://doi.org/10.1007/s11682-018-9937-6>) contains supplementary material, which is available to authorized users.

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## Introduction

The technique of the genome-wide association studies (GWAS) has produced hundreds of discoveries connecting health conditions and individual genetic variations in the last decade (Manolio 2010). Since an enormous amount of human psychological, behavioral and brain imaging data were collected and deposited in the last several years, we are in the position of conducting similar studies in brain science, connecting imaging parameters with behavioral data. One of the most exciting possibilities is the comparison of magnetic resonance imaging findings with psychological data in large cohorts.

In the framework of the Human Connectome Project (McNab et al. 2013) structural and functional MR

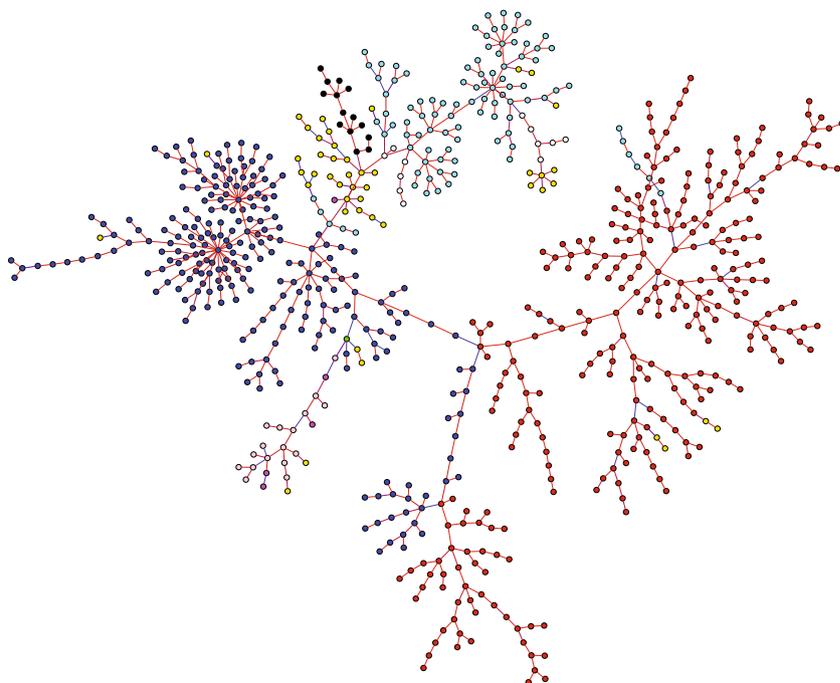
images were recorded, enriched by demographical and psychological measurements of hundreds of subjects. Smith et al. (2015) presented a study of the associations between MRI-detected resting state functional connectomes and behavioral data, based on the Human Connectome Project's (HCP) data of 461 subjects. The authors of Smith et al. (2015) computed 200-vertex resting-state functional connectomes, and they also selected a further 158 behavioral and demographical measures for each subject. For the 200 vertices there exist  $200 \cdot 199/2 = 19900$  vertex-pairs, consequently, a matrix of 461 rows (corresponding to subjects) and  $19900 + 158 = 20058$  columns (corresponding to vertex-pairs and the 158 measures) is considered. For dimension-reduction they applied principal component analysis with 100 principal vectors for each subject. After a very complex workflow that involved canonical correlation analysis for extensively filtered and processed matrix (involving, e.g., group independent component analysis, hierarchical clustering for group averages, rank-based inverse Gaussian transformation, and 314 “manually removed” demographical/anatomical and brain imaging parameters), they have found sets of connectome edges which have high co-variance with some weighted sums of demographic/anatomical measures (Figures 1 and 2 in Smith et al. 2015).

In the present contribution, we are following a very transparent and easy-to-follow data processing workflow in order to discover strong correlations between 717 psychological/anatomical and connectomical properties of

527 human subjects, originated from the data, published also in the Human Connectome Project (McNab et al. 2013). By our method one can identify a small, focused set of correlations between the items of a large set of inhomogeneous data. Apart from the less complex workflow, the main differences between our study and the work (Smith et al. 2015) are as follows:

- We study structural connectomes with 1015 vertices and thousands of edges, defined by neural tracts in the white matter (instead of resting-state functional connectomes with 200 vertices as in Smith et al. 2015);
- We compute several non-trivial graph-theoretical parameters for each structural connectome, and the correlation of the values of these parameters are evaluated with numerous other anatomical-, psychological-, and demographical properties. Therefore, in contrast with Smith et al. (2015), not the dimension-reduced set of 19,900 connectome-edges characterize each connectome, but rather several deep graph-theoretical parameters, like normalized minimum bipartition width or the size of the minimum vertex cover (Szalkai et al. 2015, 2016, 2017).
- The presentation of the results is also clear on the maximum weight spanning tree on Fig. 1 or its annotated-vertex versions at [http://pitgroup.org/static/graphmlviewer/index.html?src=correl\\_spanning\\_tree.graphml](http://pitgroup.org/static/graphmlviewer/index.html?src=correl_spanning_tree.graphml). Nodes, corresponding to data, measured by different methods are colored by different colors to help the easy evalua-

**Fig. 1** The maximum-weight spanning tree of the correlations of 717 quantities. The tabular data is given as supporting Table S1, and the interactive version of this figure can be viewed with node-labels at [http://pitgroup.org/static/graphmlviewer/index.html?src=correl\\_spanning\\_tree.graphml](http://pitgroup.org/static/graphmlviewer/index.html?src=correl_spanning_tree.graphml)



tion of the results. We have used the colors as follows: red nodes are corresponded to graph parameters, computed from the structural connectomes of the subjects; blue nodes correspond to the Brain area sizes; aquamarine nodes correspond to fMRI task scores, white vertices to the NIH Toolbox Cognition Domain (Gershon et al. 2013), pink nodes to NIH Toolbox Emotion Domain (Gershon et al. 2013), magenta vertices to NEO Five-Factor Inventory (Jr. and McCrae 1992; DeYoung et al. 2010; Riccelli et al. 2017), black nodes to Delayed Discounting Scores (Petry 2002; Swann et al. 2002) and green nodes to the gender of the subjects.

Finding correlations between the MRI-computed surface area or the thickness of the cortex with biological (Szalkai and Grolmusz 2018) or psychological (Riccelli et al. 2017; DeYoung et al. 2010) properties is also an active research area. Both works (Szalkai and Grolmusz 2018; Riccelli et al. 2017) apply the MRI data of the Human Connectome Project (McNab et al. 2013) for the area/thickness computations; the work (DeYoung et al. 2010) applied their own MR imaging and NEO Five-Factor Inventory testing resources. The work (Riccelli et al. 2017) describes correlations between the NEO Five-Factor Inventory (Jr. and McCrae 1992) and the anatomical features of the cortical lobes (i.e., area, relative area and thickness). The article (DeYoung et al. 2010) investigated the correlations between the MRI-identified volumes of distinct cortical areas and the parameters in the NEO Five-Factor Inventory. We, in the present contribution, consider additionally connectomical parameters and investigate the correlation between those values and several psychological properties, including the NEO Five-Factor Inventory.

In the present study, we are considering Pearson's product-moment correlation, which well describes the *linear connections* between attributes, and also Spearman's rank correlation, which well describes *non-linear connections* between attributes (Wonnacott and Wonnacott 1972).

Another difference of our work and Smith et al. (2015) is the demonstration of the results. It is very difficult to present, review and understand thousands of correlations given in very large matrices. Here we apply maximum weight spanning trees to the graph of correlations. The main advantage of the method is the easy visualization and the transparent presentation of the results: Suppose that we have  $n$  attributes (or, in other words, measures or data items), and we have computed the correlations between each pair of these  $n$  values. Then the results can be given in an  $n \times n$  matrix. For large values of  $n$ , the review of this large matrix is very difficult: in the present study we are using 717 attributes, therefore the  $717 \times 717$  matrix contains more than 500,000 entries. By applying the maximum weight spanning tree method described below, we will gain a graph

of just  $n = 717$  vertices and  $n - 1 = 716$  edges that can be visualized on Fig. 1 (or, with vertex-labels, on the interactive Figure [http://pitgroup.org/static/graphmlviewer/index.html?src=correl\\_spanning\\_tree.graphml](http://pitgroup.org/static/graphmlviewer/index.html?src=correl_spanning_tree.graphml)).

### Maximum weight spanning trees of correlations

Suppose we have a large number of attributes, describing the properties of a complex system. Frequently, a straightforward step in their analysis is the computation of the pairwise correlations of the attributes. If we have  $n$  attributes, then one can form  $n(n - 1)/2$  pairs from them, so we will need to compute that many pairwise correlations as well. Identifying the most “important” correlations from the set is, generally, not an easy task.

A possible natural requirement is generating a “non-redundant set” of correlations in the following sense: Suppose that random variable A strongly correlates with B, and random variable B strongly correlates with C, then, usually, A and C are also strongly correlated. Now, if we want to find a non-redundant set of correlations between A, B and C, it is an obvious idea to choose the two strongest correlation between them, say between A and B and between B and C, and to leave out the weakest, say the one between C and A. We can visualize those non-redundant “strong” or “important” correlations by a graph on vertices A, B and C, with two edges: AB and BC.

In the general case when  $n$  attributes are considered, we are interested in cycle-free connected graphs with the highest possible total weight of edges, where the weight of an edge is defined as the absolute value of the corresponding correlation. The cycle-free property ensures the non-redundancy, and the highest total weight of the absolute values of the correlations ensures that we have chosen the “most relevant” ones. Note that we need to consider the absolute values of the correlations since we are interested in both the largest negative and positive correlations.

The idea of constructing the maximum weight spanning tree from the pairwise correlation coefficients was applied before us in several settings.

Mantegna (Mantegna 1999) constructed a graph from financial equities, traded in stock markets, and weighted the edges of the graph by the correlations computed from the time series of the logarithms of the stock prices. It was found that – essentially – a maximum-weight spanning tree well-describes several known relations and suggests numerous new ones between the time series. In Bouchaud and Potters (2003) Section 9.3.5 and (Heimo et al. 2009) the maximum-weight spanning trees are computed explicitly in similar settings.

In Živković et al. (2009) correlations related to the co-expression of gene-pairs of the yeast (*S. cerevisiae*) were

computed, and a graph was constructed with the genes as the vertices and the co-expression correlation-weighted edges for each pair of genes. Next, a maximum weight spanning tree was computed and visualized for demonstrating a non-redundant system of strong correlations between the genes. Živković et al. (2009, Fig. 6).

More recently, in Ha et al. (2015), the maximum-weight spanning tree of the correlations is applied for feature selection in weakly-structured multimedia data. In Brida et al. (2015) a similar method is used for finding related attributes in a regional Italian hospitality industry.

## Methods

Our data source is the Human Connectome Project's (McNab et al. 2013) anonymized 500 Subjects Release. In the dataset diffusion- and functional MRI data, psychological test results, and some cognitive data are made public. Here we list the different types of data applied by us.

The subject data table from the Human Connectome Project, whose parameters are described in <https://wiki.humanconnectome.org/display/PublicData/HCP+Data+Dictionary+Public+Updated+for+the+1200+Subject+Release>, consists of 527 rows (corresponding to 527 subjects) and 451 attributes.

MRI images of the subjects were processed by the researchers of the Human Connectome Project with the Freesurfer software suite (Fischl 2012) to obtain the size of various regions of interests (ROIs), i.e., the area, thickness and volume of major cortical and sub-cortical areas of the brain. For cortical regions, only average thickness and surface area were available, so we multiplied these two quantities to obtain the approximate volume of the ROI. We divided the volume of an ROI by  $FS\_Mask\_Vol$  (Freesurfer Brain Mask Volume, i.e., roughly the brain volume) to obtain the *relative volume* of that region. We intended to compensate for brain size because it is already well known that males on the average have larger brains than females (Witelson et al. 2006). We added these new, relativized attributes to the data table.

Several psychological and cognitive tests were also performed with the subjects, and were recorded in the HCP Subject tables, described in <https://wiki.humanconnectome.org/display/PublicData/HCP+Data+Dictionary+Public+500+Subject+Release>. These included the MMSE (Mini Mental State Examination), various NIH Toolbox (Weintraub et al. 2013) cognitive tests (Picture Sequence Memory Test, Dimensional Change Card Sort Test, Flanker Inhibitory Control and Attention Test, Oral Reading Recognition Test, Picture Vocabulary Test, Pattern Comparison Processing Speed Test, List Sorting Working Memory Test), NIH

Toolbox Emotion Domain (Anger-Affect, Anger-Hostility, Anger-Physical Aggression, Fear-Affect, Fear-Somatic Arousal, Sadness, General Life Satisfaction, Meaning and Purpose, Positive Affect, Friendship, Loneliness, Perceived Hostility, Perceived Rejection, Emotional Support, Instrumental Support, Perceived Stress, Self-Efficacy), a test for self-regulation/impulsivity (Delay Discounting), Penn Line Orientation Test, Penn Continuous Performance Test, Penn Word Memory Test and Penn Emotion Recognition Test.

The subjects were also asked to perform some fMRI tasks, including identifying random and non-random shape movements, a working memory test (places, faces, body parts, and tools), language, math and gambling tasks.

We also added numerous attributes to the data table corresponding to various graph parameters of the connectomes of the subjects. These included the total number of the connectome edges, counted with weights, maximum matching and minimum vertex cover, Hoffman's bound (a bound for the chromatic number of the connectome), the eigen-gap of the transition matrix (which is a quantity connected with the properties of random walks on the graph), and the total number of edges exiting different lobes of the brain. These graph-theoretical quantities of the connectomes were defined in details and also computed in the articles (Szalkai et al. 2015, 2017).

We calculated the correlations between all possible pairs of the attributes (columns of the database). The goal was to obtain a non-redundant list of important correlations. Our observation was that correlation is transitive in most of the cases, so if A correlates with B and B correlates with C, then this usually implies that A correlates with C in some degree. Therefore, if we consider a complete graph whose vertices are the attributes, and whose edges represent correlations between two attributes, then our goal can be reformulated as follows: we want to find a subgraph without cycles (because cycles usually mean redundant correlations), and whose edges correspond to relatively large correlations (because larger correlations are more important than the others).

This optimization problem is essentially a maximum weight spanning tree problem, which can be solved by graph theoretical algorithms such as the Kruskal algorithm (Lawler 1976). The classical question is finding a *minimum* weight spanning tree, but by a straightforward transformation, the algorithm for the minimum weight spanning tree can be used for finding the maximum weight spanning tree. Indeed, let  $w_e$  be the weight (or in our specific application, the correlation) corresponding to edge  $e$ , and let  $W = \max w_e$ , taken for all edges  $e$ . Then the maximum-weight spanning tree with weights  $w_e$  is, at the same time, the minimum-weight spanning tree with weights  $W - w_e$ .

A similar correlation-based maximum spanning tree approach has already been used by other researchers (Mantegna 1999; Bouchaud and Potters 2003; Heimo et al. 2009; Živković et al. 2009; Ha et al. 2015; Brida et al. 2015). We applied this method to the HCP (Human Connectome Project) subject data table in its anonymized 500 Subjects Release (McNab et al. 2013): <http://www.humanconnectome.org/documentation/S500> in order to search for connections between psychological and cognitive scores, demographic data, and brain ROI sizes.

The possible age groups of the subjects were 22-25, 26-30, 31-35 and 36+. Only 3 of the subjects were 36 years or older. We translated the age groups to numbers the following way: 0 meant 22-25, 1 meant 26-30, 2 meant 31-35 and 3 meant 36+. We translated the “gender” attribute to 1 (male) and 2 (female). We had to convert these attributes to numbers so we can calculate correlations between them and other attributes.

We have computed both the Pearson’s product-moment correlation (this is “the correlation”, most frequently computed in science), which well describes the linear connections between attributes, and also Spearman’s rank correlation, which well describes non-linear connections between attributes (Wonnacott and Wonnacott 1972).

## Results

### Maximum spanning tree of Pearson’s correlations

The maximum spanning tree is visualized on Fig. 1 and in a more viewable form in an interactive figure at [http://pitgroup.org/static/graphmlviewer/index.html?src=correl\\_spanning\\_tree.graphml](http://pitgroup.org/static/graphmlviewer/index.html?src=correl_spanning_tree.graphml).

The spanning tree had 716 edges with non-zero correlation, and 717 attributes, so the graph contained 717 vertices. The weakest edge still had 15% correlation. The complete table describing the maximum-weight spanning tree, where the weights are the correlations, is given as Supporting Table S1.

The significance of the correlations was determined by multiplying their p-value with the total number of edges in the graph, which was  $717 * 716/2 = 256,686$ , because we wanted to correct for multiple observations: we made as many observations as the number of edges in the graph. Thus, we obtained an upper limit of the p-value of the correlations. This meant that eight correlations have been deemed insignificant, but all the other edges of the spanning tree belonged to significant correlations (this meant  $716 - 8 = 708$  edges). This indicated that almost all attributes of the database are more or less interdependent of each other.

The supplementary Table S1 contains a list of all the correlations in the spanning tree. The detailed descriptions of the parameters, referred in Table S1, are given in <https://wiki.humanconnectome.org/display/PublicData/HCP+Data+Dictionary+Public+Updated+for+the+1200+Subject+Release>.

## Discussion

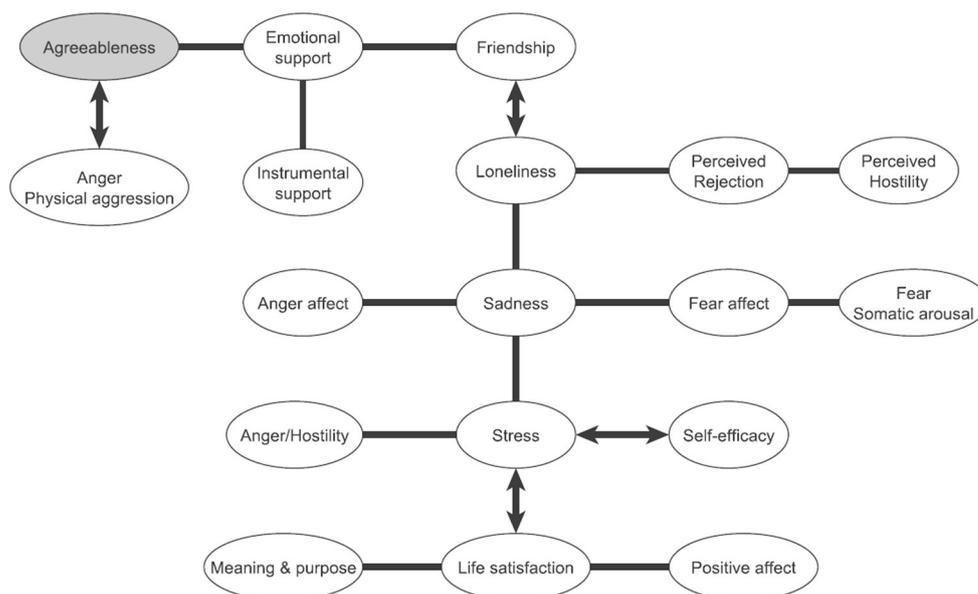
185 correlations referred to attributes which are either completely dependent on each other or are very close to a linear dependence (over 90% positive or negative correlation). Gray matter volume correlated with the volume of many cortical regions, which is not very surprising since these regions comprise the cortical gray matter. These included the superior frontal gyrus, the lateral orbitofrontal cortex, the precuneus, the middle temporal gyrus, the precentral gyrus, the fusiform gyrus and the rostral middle frontal gyrus (the list is incomplete).

Elements of the NIH Toolbox Emotion Domain showed a strong correlation with each other: sadness and fear affect, sadness and anger affect, sadness and perceived stress, sadness and loneliness, loneliness and perceived rejection, perceived hostility and perceived rejection, friendship and emotional support, friendship and loneliness (negative), life satisfaction and meaning and purpose, emotional and instrumental support, life satisfaction and positive affect, anger-hostility and perceived stress, life satisfaction and perceived stress (negative), perceived stress and self-efficacy (negative), fear affect and fear-somatic arousal. Even the weakest of these correlations was 49% strong, the strongest (sadness and fear affect) being 72% strong.

There were 17 attributes in the NIH Toolbox Emotion Domain, and they almost represented a connected subgraph in the spanning tree (see Fig. 2). This means that, by including the NEO-FFI Agreeableness attribute (which correlates positively with NIH Emotional Support and negatively with NIH Anger-Physical Aggression), we get an 18-vertex set which spans a 17-edge subtree of the spanning tree. This means that these attributes are strongly correlated with each other, comprising an important correlated subset of all the attributes.

The NEO-FFI personality scores appear to be correlated with certain NIH toolbox items, in a sense that they are leaves of those NIH toolbox items in the tree. NEO-FFI Neuroticism is a leaf of NIH Perceived Stress (correlation: 70%). NEO-FFI Conscientiousness is a leaf of NEO-FFI Neuroticism (correlation: -41%). NEO-FFI Extraversion is a leaf of NIH Friendship (correlation: 50%). An exception is NEO-FFI Agreeableness, which is not a leaf as it is connected to both NIH Anger-Physical

**Fig. 2** The attributes of the NIH Toolbox Emotion Domain. The connections are significant correlations in the constructed spanning tree. The double arrows denote negative correlations



Aggression (correlation: -45%) and NIH Emotional Support (correlation: 35%). An interesting finding is that NEO-FFI Openness to Experience is a leaf of the NIH Toolbox Oral Reading Recognition Test Unadjusted Scale Score (correlation: 32%). This indicates that good reading skills and openness to experience frequently come together. To sum up, we can observe a strong connection between the NEO-FFI personality scores and the NIH toolbox positive or negative affect scores. This can mean multiple things. Our interpretation is that our personality defines our emotions to a great extent, which can be measured by statistical means.

The NIH Toolbox Oral Reading Recognition Test is a very important hub in the spanning tree. Its unadjusted and age-adjusted versions are correlated with: Picture vocabulary task age-adjusted score (71%), Language task accuracy (49%), Penn Progressive Matrices Number of Correct Responses (47%), NIH Toolbox 2-minute Walk Endurance Test Age-Adjusted Score (43%), Delay Discounting Subjective Value for \$40K at 1 year (35%), Short Penn Continuous Performance Test Specificity (33%), NEO-FFI Openness to Experience (32%), MMSE score (31%) and Penn Word Memory Test Total Number of Correct Responses (31%). Most of these are cognitive tests. The walk endurance test score is very interesting since it draws a connection between physical and intellectual fitness. It also seems that people, scoring higher on the oral reading test, value a delayed payment higher than those with lower scores. There can be multiple reasons for this; the observed correlation could follow from their possible better financial status, financial skills or greater patience. We have covered the NEO-FFI connection above.

It seems that gender (male=1, female=2) correlates with the NIH Toolbox Grip Strength Test Age-Adjusted

Scale Score (-75%), the brain mask volume (-67%), the optic chiasm volume (-41%) and the NIH Toolbox Anger-Physical Aggression Survey Unadjusted Scale Score (-26%). All of these are significant. This means that men, on average, have greater grip strength, brain volume (especially optic chiasm volume) and are more aggressive physically.

The score of the walk endurance test correlates with the taste intensity score, although with one of the smallest significant observed correlations (-25%). Walk endurance seems to correlate with less perceived bitterness of quinine. The cause of this correlation is unknown to us.

Another interesting correlation is NIH Toolbox 9-hole Pegboard Dexterity Test: Age-Adjusted Scale Score, versus Maximum matching (left hemisphere, weight function: mean fractional anisotropy) (27%). The corrected p-value is rather high when compared to the other correlations ( $p=0.003$ ) but still significant. This is an important correlation because it shows a significant relationship between a parameter of the brain graph (connectome) and a brain performance score.

We expected the Age attribute to be a major hub of the spanning tree, but, interestingly, it was only a leaf of the attribute Right hemisphere cortical gray matter relative volume (correlation: -23%,  $p=0.037$ ). We think this is because all the subjects were rather young, so their cognitive and psychological scores did not depend heavily on their age. Still, it is interesting that cortical gray matter relative volume correlates with age even among relatively young subjects.

### Maximum spanning tree of Spearman's rank correlations

We also investigated how the spanning tree changes if we use Spearman's rank correlation coefficient instead of the

classical (Pearson's) correlation coefficient (Wonnacott and Wonnacott 1972). We computed the rank correlation of two attributes as follows: the values were ordered independently for the two attributes, and then each value was substituted with its rank in the ordering. If two or more attributes were equal, then their rank was defined as the same number, and the succeeding rank(s) were omitted. In other words, the rank of a value  $v$  was defined as the number of values strictly smaller than  $v$ , plus one. For example, the values 1, 1, 4, 13, 13, 45 were assigned the ranks 1, 1, 3, 4, 4, 6.

We calculated a maximum weight spanning tree for the rank correlations as well. The detailed data of the tree is given in Table S1 in the supporting material. The interactive figure with vertex labels is available at the address [http://pitgroup.org/static/graphmlviewer/index.html?src=correl\\_spanning\\_tree\\_rank.graphml](http://pitgroup.org/static/graphmlviewer/index.html?src=correl_spanning_tree_rank.graphml) (the interactive figure can be viewed by any contemporary browser, in case of difficulties, we suggest using Firefox or Chrome for viewing). The complete table describing the maximum-weight spanning tree, where the weights are the Spearman-correlations, is given as Supporting Table S2. The detailed descriptions of the parameters, referred in Table S2, are given in <https://wiki.humanconnectome.org/display/PublicData/HCP+Data+Dictionary+Public+Updated+for+the+1200+Subject+Release>.

This tree will be referred to as the *rank spanning tree* from now on, and the one using the traditional correlation coefficient will be referred to as the *original spanning tree*.

We examined those edges which are present in exactly one of the spanning trees. In the following analysis, we omitted the edges concerning two graph parameters or two brain area sizes. We also omitted those that connect two nodes (attributes) that can be exactly calculated from each other (e.g. the number of false positives and true negatives for some test). Edges which connect two attributes referring to subscores of the same task are also omitted.

There were 98 edges in each spanning tree that were not present in the other tree. As the trees contained 716 edges each, this means that approximately 13.7% of the edges were unique to the containing tree. In other words, the two trees were rather similar, having 86.3% of the edges in common. Among the unique edges, the vast majority were omitted from the analysis, or connected very similar nodes. For example, the unadjusted and age-adjusted version of an attribute, or the median reaction time and the number of correct responses for a task, or scores for two closely related tasks were considered similar attributes.

Some cognitive attributes were connected in a different way in the rank correlation tree when compared to the original correlation tree. For example, the IWRD and MMSE total scores were connected to the English reading score in the original tree, but connected to the Picture Vocabulary score in the rank tree. The computed score for

the NIH Toolbox Words-In-Noise test was connected to a sub-score of the Social fMRI task in the original tree, but connected to, again, the Picture Vocabulary score in the rank tree. This may suggest that the Picture Vocabulary score is strongly connected to these complex cognitive scores, but not necessarily in a linear fashion. The same goes for the Working Memory fMRI task, which was connected to the Picture Vocabulary score in the original tree, but connected to both a sub-score of the Relational task and the number of correct responses in the Penn Matrix Test in the rank tree.

An interesting connection between the volume of the right lateral ventricle and the number of correct happy identifications in the Penn Emotion Recognition Test was included in the rank correlation tree. However, we should note that the corrected p-value for this edge was very large, about 72. This means that there is a large likelihood that this connection was included by mere chance.

Regarding the graph parameters and the brain ROI sizes, the volume of the anterior corpus callosum and the relative volume of the mid-posterior corpus callosum were connected to two graph parameters (sum and minimum cut) in the original tree, but, surprisingly, these natural connections were no longer present in the rank tree. A graph parameter related to eigenvalues (Graph\_Left\_AdjLMaxDivD\_FiberNDivLength) was connected to the NIH Toolbox "Odor Identification Test" unadjusted score in the normal tree, but this connection was not included in the rank tree, which, on the other hand, contained an edge between Age and the age-adjusted score of the odor identification test (corrected p-value: 6%. That connection is somewhat surprising since the age-adjusted scores should not be correlated with age. This could mean that some tests are not well adjusted for age. Another possible explanation could be that, although the test score does not change significantly for the same person over the person's lifetime, but different generations may have different mean scores due to environmental factors.

## Conclusions

We have analyzed both the original Pearson's and Spearman's rank correlations with 717 psychological, anatomical and connectome-properties originated from the Human Connectome Project's subject 500-release. In this exploratory study, by applying maximum spanning trees for filtering the most important correlations, we have found several strong, novel correlations in the dataset by our new method. These results need also be verified by independent experts and methods before applying in the practice.

**Acknowledgments** Data were provided in part by the Human Connectome Project, WU-Minn Consortium (Principal Investigators: David Van Essen and Kamil Ugurbil; 1U54MH091657) funded by

the 16 NIH Institutes and Centers that support the NIH Blueprint for Neuroscience Research; and by the McDonnell Center for Systems Neuroscience at Washington University. VG was partially funded the NKFI-126472 grant of the National Research, Development and Innovation Office of Hungary.

**Data Availability** The MRI and the behavioral and demographic data the Human Connectome Project (HCP) can be accessed at <https://db.humanconnectome.org/>. The braingraphs, computed by us from the HCP data is available at the site <http://braingraph.org/download-pit-group-connectomes/>, without any registration. The interactive version of Fig. 1 can be viewed with node-labels at [http://pitgroup.org/static/graphmlviewer/index.html?src=correl\\_spanning\\_tree.graphml](http://pitgroup.org/static/graphmlviewer/index.html?src=correl_spanning_tree.graphml); the data of the spanning tree is given in Supplementary Table S1. The similar spanning tree with Spearman's rank correlations can be viewed at [http://pitgroup.org/static/graphmlviewer/index.html?src=correl\\_spanning\\_tree\\_rank.graphml](http://pitgroup.org/static/graphmlviewer/index.html?src=correl_spanning_tree_rank.graphml); the data of the spanning tree is given in Supplementary Table S2. The interactive figures can be viewed in any contemporary browser, in case of difficulties, we suggest using Firefox or Chrome for viewing.

**Compliance with Ethical Standards** This article does not contain any studies with human participants or animals performed by any of the authors.

**Conflict of interests Statement** The authors declare no conflicts of interests.

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