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## **Small-World Brain Networks and General Intelligence: Investigating the Relationship across Diverse Analytical Decisions**

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## Abstract

**Background:** Barbey's Network Neuroscience theory posits a link between the general factor of intelligence ('g') and the dynamic reorganization of brain networks for system-wide flexibility and adaptation. The theory suggests that the brain's ability to reorganize its networks in a small-world manner forms the basis for the positive correlation observed across diverse cognitive abilities. However, there are conflicting findings regarding this relationship. Older studies like van den Heuvel et al. (2009) suggest a positive correlation, while more recent research, such as that of Kruschwitz et al. (2018), indicates a lack of association between them. This incongruity is yet another example of the pervasive reproducibility crisis within neuroimaging research, wherein methodological variability engenders disparate research outcomes (Carp, 2012). To address this challenge, multiverse analysis emerges as a crucial methodological approach to navigate the intricacies of analytical diversity and explore the nuanced relationship between general intelligence and small-world brain network topology.

**Objective:** To investigate the correlation between the general factor of intelligence ('g') and small-world brain network topology using 72 distinct analytical pipelines and to identify clusters of pipelines that exhibited comparable correlation patterns.

**Methods:** Whole-brain resting-state functional magnetic resonance imaging (fMRI) data of 827 participants was obtained from the Human Connectome Brain project. The data was processed using a carefully guided multiverse of analytical pipelines. Subsequently, small-worldness values were derived and examined for their correlation with the respective 'g' scores of the participants.

**Results:** Findings revealed little to no associations between the general factor of intelligence ('g') and small-world brain network topology across the 72 distinct analytical pipelines. The projection of relationships in lower-dimensional space exhibited minimal variability between pipelines, challenging previous positive findings.

**Conclusion:** Despite the absence of significant associations, this study highlights the significance of rigorous replication and methodological scrutiny in neuroimaging research to ensure the reliability and validity of findings. The utilization of multiverse analysis instilled confidence in our results, especially when consistency was observed across diverse analytical pipelines. Nevertheless, further investigation into refined metrics for calculating small-worldness is warranted.

# 1 Introduction

The advancement of neuroimaging technology has revolutionized our exploration of the neural underpinnings of cognitive functions. Particularly prominent in this domain is the analysis of brain network topology, which offers insights into the intricate architecture underlying various cognitive abilities. Among the myriad approaches, Barbey's Network Neuroscience theory stands out, linking brain network reconfiguration to intelligence and offering a novel framework for understanding the neural basis of general intelligence ('g').

Barbey's theory posits that 'g', or general intelligence, is intricately linked to the dynamic reorganization of brain networks. This dynamic process involves the continuous modification of network topology and community structure to enhance system-wide flexibility and adaptation (Barbey, 2018, p. 10).

As we delve deeper into examining this association, it becomes imperative to explore the broader landscape of intelligence research. Within this expansive domain, 'g' emerges as a pivotal construct, elucidating the hierarchical structure of cognitive abilities.

## 1.1 Theories of Intelligence

The concept of intelligence has been a subject of intense debate and inquiry in psychology for over a century. Spearheaded by the pioneering work of Charles Spearman in the early 20th century, the notion of a general factor of intelligence, often referred to as "g", emerged as a central construct in understanding human cognitive abilities. Spearman's two-factor model posited that individual differences in cognitive performance are influenced by both a general factor "g" representing overall cognitive ability, and specific factors, denoted as "s," unique to each task or domain (Spearman, 1904). Contemporary research has expanded the understanding of intelligence by introducing intermediate levels of broad abilities that capture shared variance across related cognitive domains.

At the lowest level of the hierarchy are specific abilities, reflecting individual differences in performance on distinct cognitive tasks. Examples of specific abilities include verbal comprehension (e.g., understanding written and spoken language), spatial reasoning (e.g., mental rotation tasks), mathematical abilities (e.g., arithmetic calculations), and social cognition (e.g., recognizing facial expressions). Moving up the hierarchy, broad abilities encompass clusters of related cognitive tasks, showing strong correlations within each domain. These broad abilities include crystallized intelligence (e.g., acquired knowledge and skills, such as vo-

cabulary and cultural knowledge) and fluid intelligence (e.g., problem-solving in novel situations, abstract reasoning). Furthermore, the Cattell-Horn-Carroll (CHC) theory of cognitive abilities expands upon Spearman's hierarchical model by proposing a broader array of specific and broad abilities. This theory identifies multiple broad abilities, such as visual-spatial processing, auditory processing, fluid reasoning, processing speed, and working memory, each consisting of various specific abilities. At the top of this hierarchy is the general factor, "g", which accounts for the overall performance across diverse cognitive domains and influences performance on both specific and broad abilities. Understanding the hierarchical organization of intelligence provides valuable insights into the nature and origins of individual differences in cognitive functioning, shaping ongoing research in the field of psychology and neuroscience.

Godfrey Thomson further advanced our understanding of intelligence as a global network phenomenon. Thomson's Sampling Theory of Mental Ability proposed that each item on an achievement test samples several neural bonds in the brain, leading to the emergence of 'g' as a result of intricate interactions among these neural elements. According to Thomson (1916, 1919, 1939), the degree of overlap among these neural bonds explains the positive manifold observed across diverse cognitive tasks, providing empirical support for Spearman's concept of 'g'. Moreover, contemporary psychological theories emphasize the mutual interactions among cognitive processes as the basis of 'g'. The Mutualism Model, proposed by Maas et al. (2006), posits that changes in one aspect of mental ability are partially autonomous, due to developmental maturation, and are based on growth in other areas, owing to mutual interactions between cognitive processes. This model provides a comprehensive framework for explaining individual differences in 'g' and elucidates the positive manifold observed across cognitive tasks.

## 1.2 Brain Network Topology and General Intelligence

In the realm of network neuroscience, these theoretical frameworks find resonance in the principles of brain organization that support the modularity of cognitive processes and dynamic reorganization of modular architecture to facilitate system-wide flexibility and adaptation. The interplay between modular and global network topology captures the essence of general intelligence, highlighting the optimal balance between autonomous and interactive cognitive processes. The interconnectedness of these ideas enhances our comprehension of the intricate relationship between brain organization and intelligence, underscoring the equi-

librium between self-contained and interactive elements in cognitive functioning (Barbey, 2018).

Global efficiency refers to the capacity of a network to efficiently integrate information across distant regions. A seminal work by Latora and Marchiori (2001) introduced the concept of efficiency in complex networks, laying the groundwork for understanding how brain networks balance information transfer over both short and long distances. Conversely, local efficiency focuses on the efficiency of information transfer within local neighborhoods of the network. This concept was further refined by Achard and Bullmore (2007), who proposed a measure of local efficiency to assess the fault tolerance of small subnetworks in the larger brain network context.

The human brain manages this delicate balance by incorporating aspects of both regular and random networks, resulting in a small-world topology (Watts and Strogatz, 1998; Bassett, 2006, 2017). According to Barbey et al. (2021), this small-world network architecture is characterized by short-distance connections that minimize wiring costs through high local clustering, as well as long-distance connections that facilitate global information processing by providing direct topological links or shortcuts with short path lengths. These features collectively enable the brain to achieve high levels of both local and global efficiency at a relatively low cost, thus representing a parsimonious organizational structure for human brain function (Sporns, 2000a, 2000b; Robinson et al., 2009). Moreover, this network topology encapsulates the modular (autonomous) and global (interactive) aspects crucial for general intelligence, as emphasized by Maas et al. (2006) and Barbey (2018).

Studies examining the relationship between brain network properties and cognitive abilities have provided valuable insights into the neural mechanisms underlying human general intelligence. Van den Heuvel et al. (2009) conducted one of the pioneering studies in this field, where they investigated the relationship between functional network efficiency and intellectual performance. Using functional magnetic resonance imaging (fMRI) data, they analyzed the characteristic path length of functionally connected brain regions during the resting state and found a negative correlation with full-scale IQ. This negative correlation suggested that individuals with greater topological proximity among brain regions tended to score higher on IQ tests, highlighting the role of network efficiency in supporting intelligence.

Building on this work, Santarnechchi et al. (2014) further explored the nature of connections underlying greater network efficiency in high-intelligence individu-

als. They distinguished between weakly connected and strongly connected nodes in the brain network and found that weak connections, representing long-range connections, accounted for more variance in intelligence scores than strongly connected nodes. This finding underscored the importance of long-range connections in supporting cognitive abilities and provided additional evidence for the relationship between brain network topology and intelligence. Langer et al. (2012) investigated functional brain networks derived from high-resolution resting-state EEG data and found a significant relationship between small-world network properties and intelligence. Their findings further support the notion that efficient brain network organization is associated with higher cognitive abilities. Additionally, Pamplona et al. (2015) explored the association between functional connectivity of the brain and intellectual performance in a longitudinal study. Analyzing resting-state fMRI data from a sample of healthy adults born and raised in Brazil over six years, they found that individuals with more efficient brain network organization at baseline exhibited better cognitive performance over time.

While these studies provide valuable insights into the relationship between brain network topology and general intelligence, the basis of this association remains broad and complex. Various conceptualizations of intelligence and inconsistent replication findings due to small and homogenous samples contribute to the complexity of the findings about this relationship. In 2018, Kruschwitz and colleagues set out to replicate the relationship found in the van den Heuvel et. al. (2009) paper using the Human Connectome dataset, which offered a significantly larger sample size compared to the original study involving only 20 participants, primarily with high IQ. However, despite the expanded sample size, they failed to observe any significant association between general intelligence and functional brain network organization. This outcome prompted discussions regarding the potential presence of false positives and low statistical power in previous studies, suggesting a need for further exploration of the relationship between brain network properties and cognitive performance (Button, 2013; Schnack and Kahn, 2016; Kruschwitz et. al., 2018).

Therefore, the present study examines both aspects of this proposed association by exploring the correlation between a specific measure of small-worldness, distinct from mere efficiency or path length, and a clear ‘g’ factor score instead of individual test performance. Despite the lack of significant findings regarding the relationship between general intelligence and functional brain network organization, the study underscores the importance of rigorous replication and methodological scrutiny in neuroimaging research to ensure the reliability and

validity of findings.

### 1.3 Navigating Challenges in Neuroimaging Research

Ensuring Flexibility and Reproducibility:

The landscape of neuroimaging research is marked by a paradoxical blend of excitement and uncertainty. While groundbreaking discoveries continuously unravel the mysteries of the brain's structure and function, methodological challenges, particularly from an analytical standpoint, cast a shadow over the work's credibility and reproducibility. At the heart of these challenges lies the inherent flexibility in analytical approaches used for processing neuroimaging data, which fosters innovation, but also introduces complexities that threaten the reliability of research outcomes.

Flexibility in neuroimaging data analysis allows researchers to explore a multitude of analytical approaches, from preprocessing techniques to statistical analyses, in their quest to decipher the brain's intricate workings. As demonstrated by Carp's seminal work in a systematic review of functional magnetic resonance imaging (fMRI) studies, the field is rife with diverse analytical pipelines, with almost as many unique approaches as there are studies (Carp, 2012). This variability not only complicates result interpretation but also raises concerns about the reproducibility of findings across studies.

Furthermore, the prevalence of variable analytical approaches among researchers studying similar phenomena in neuroimaging research exacerbates the challenge. Given the intricate nature of neuroimaging data and the multitude of analytical decisions involved, researchers may unwittingly diverge in their analytical choices, leading to disparities in research outcomes even when investigating the same phenomenon (Poldrack et. al., 2017). This divergence highlights the urgent need for standardized metrics and reporting formats to enhance comparability and reproducibility in neuroimaging research.

In this comprehensive exploration, the multifaceted challenges faced by neuroimaging researchers are highlighted, encompassing issues such as the lack of standardized metrics, reproducibility concerns, and the pitfalls of cherry-picking results and engaging in p-hacking practices. By examining these challenges and proposing potential solutions, the aim is to provide insights into improving the robustness and credibility of neuroimaging research.

### Challenges in Neuroimaging Research:

#### Methodological Complexity and Analytical Diversity

Neuroimaging data, derived from techniques such as functional magnetic resonance imaging (fMRI), positron emission tomography (PET), and diffusion tensor imaging (DTI), are inherently complex. The intricate interplay between neural activity, structural connectivity, and brain function necessitates sophisticated analytical methods. However, the diversity of analytical pipelines, each with its own set of parameters and assumptions, poses a significant challenge. Researchers often employ diverse methods for preprocessing, feature extraction, and statistical analysis, leading to variability in results and hindering cross-study comparisons (Botvinik-Nezer et. al., 2020).

#### Lack of Standardized Metrics and Reproducibility

A major impediment in neuroimaging research is the absence of standardized metrics for comparing results obtained from different analytical methods. While certain metrics demonstrate good reliability, variations in study designs and methodological factors hinder reproducibility. For instance, the choice of regions of interest and the type of metric employed (global or local) can significantly impact the reproducibility of graph-theoretic brain network metrics. This lack of standardization not only complicates result interpretation but also undermines the reproducibility of findings across studies (Deuker et. al., 2009).

#### Test-retest reliability

A crucial aspect of neuroimaging research presents a notable challenge to reproducibility within the field. The consistency of results across repeated measurements is often hindered by various factors such as participant motion, scanner variations, and preprocessing discrepancies. Additionally, the inherent complexity of brain activity and individual differences further complicates the reliability assessment process. The absence of standardized benchmarks for reliability exacerbates this challenge, making it difficult to establish consistent measures across different studies and modalities. Overcoming this hurdle necessitates the optimization of data acquisition protocols, mitigation of sources of variability, and the establishment of clear reliability standards across neuroimaging techniques (Andellini et. al., 2015).

#### Cherry-Picking Results and P-Hacking

The allure of statistically significant findings in neuroimaging research can lead to cherry-picking results and engaging in p-hacking practices. Cherry-picking involves selectively reporting significant findings while disregarding non-significant results, distorting the true representation of research outcomes. Similarly, p-

hacking entails engaging in multiple statistical tests or analytical approaches until a statistically significant result is obtained, increasing the risk of false positives. These practices not only compromise the integrity of research findings but also contribute to the replication crisis plaguing the field (Anderson and Liu, 2023).

## 1.4 Solutions to Enhance Flexibility and Reproducibility

### Multiverse Analysis Approach

The concept of Multiverse Analysis, as introduced by Steegen, Tuerlinckx, Gelman, and Vanpaemel (2016), involves analyzing data across various reasonable processing choices to reveal the sensitivity of statistical results to arbitrary decisions in data preparation. This method aims to provide a detailed picture of the impact of different processing steps on statistical outcomes, helping researchers move beyond a single data set analysis to a more comprehensive understanding of the data's implications. By exploring diverse analytical methods and parameters, Multiverse Analysis enhances transparency, showing the robustness or fragility of results, and identifying key choices affecting conclusions. This approach enables researchers to understand the impact of data processing choices on statistical results, ultimately enhancing the credibility and reliability of research findings in neuroimaging studies.

### Adherence to Reporting Standards and Guidelines

Standardized reporting formats and guidelines play a crucial role in enhancing the transparency and reproducibility of neuroimaging research. Initiatives like the Organization for Human Brain Mapping's Committee on Best Practices in Data Analysis and Sharing (COBIDAS) have formulated guidelines to improve reporting standards and promote transparency in neuroimaging research (Nichols et. al, 2016; 2017). By adhering to these guidelines, researchers can ensure that their studies are conducted and reported rigorously and transparently, facilitating comparisons with other studies and enhancing the reproducibility of findings.

### Pre-registration of Study Protocols

Pre-registration of study protocols and analysis plans can mitigate the risk of cherry-picking results and p-hacking by establishing a clear framework for data analysis before conducting the study. By registering their study protocols in publicly accessible repositories, researchers commit to transparency and integrity in their research practices, reducing the likelihood of bias (Hardwicke and Wagenmakers, 2021, Ottaviani and Decker, 2023).

Navigating the methodological challenges in neuroimaging research requires a multifaceted approach that addresses the complexities of data analysis while en-

suring transparency and reproducibility. By embracing innovative solutions such as the Multiverse Analysis approach, adhering to reporting standards and guidelines, and pre-registering study protocols, the neuroimaging community can overcome hurdles and advance our understanding of the brain with more credibility.

## 1.5 Understanding the Multiverse Approach

Multiverse Analysis introduces a novel paradigm for navigating the intricate analytical landscape of neuroimaging research. This approach transcends traditional singular analytical methodologies by creating an expansive “multiverse” of analysis. Within this multiverse, each universe represents a distinct analytical pathway shaped by varying parameters and methodology choices. Through systematic exploration of these diverse approaches, researchers gain insights into the complex interplay between analytical decisions and research outcomes. Rather than focusing solely on identifying the ”most robust” result, multiverse analysis seeks to understand the interactions and dependencies among diverse methodologies. Researchers scrutinize how variations in preprocessing steps, feature extraction methods, and statistical analyses influence outcomes. This exhaustive analysis reveals patterns, illuminating the strengths, weaknesses, and idiosyncrasies of each analytical pathway.

Furthermore, multiverse analysis enables comparative analyses across a myriad of pathways, facilitating the discernment of trends, discrepancies, and convergences in research outcomes. Through empirical validation and rigorous statistical inference, researchers gain deeper insights into the relative efficacy and reliability of various approaches. This empirical grounding not only fosters robust conclusions but also enhances the credibility of findings.

Central to this approach is the illumination of analytical trade-offs and the identification of optimal pathways within the analytical landscape. Through meticulous examination, researchers uncover trade-offs between computational efficiency, statistical power, and interpretability associated with diverse approaches. Additionally, Multiverse Analysis helps identify optimal pathways that strike a balance between analytical rigor and practical feasibility. These pathways serve as guiding beacons, offering insights into the most efficacious and reliable methodologies.

The multiverse approach represents a transformative paradigm that provides a comprehensive lens to navigate analytical diversity. By unraveling relationships between analytical approaches, conducting comparative analyses, and illuminating trade-offs, multiverse analysis empowers researchers to make informed choices and enhance the credibility of research outcomes.

## 2 Research Question

**Aim:** The present study aims to evaluate the relationship between ‘g’ and small-worldness as proposed by van den Heuvel et al. (2009) and investigate the lack of association reported by Kruschwitz et al. (2018).

**Hypothesis 1:** Employing diverse analytical pipelines on the same dataset will result in variability in outcomes, particularly in terms of the patterns of association between ‘g’ and small-worldness.

**Hypothesis 2:** Additionally, we anticipate that among the 72 pipelines included in the multiverse, there will be clusters of analytical pipelines sharing identifiable similarities in terms of correlation values.

## 3 Methods

### 3.1 Participants

The study included a total of 827 participants drawn from the Human Connectome Project (HCP) Young Adult 1200 subjects release (Glasser et al., 2016). Initially, 1096 participants with resting-state functional magnetic resonance imaging (rsfMRI) data were considered. However, exclusion criteria were applied due to missing values in neuroimaging data, depending on the specific measure and preprocessing scheme. For example, there were only 995 individuals with global signal regressed out. The exclusion criteria led to the final sample size ranging between 995 and 1014 participants.

In addition, demographic data and performance measures for cognitive tasks were available for a subset of participants ( $N = 838$ ) within the HCP-YA database. This subgroup comprised 449 females, 760 right-handed individuals, and three ambidextrous individuals, with an age range of 22 to 35 years. The final sample size with consideration for complete intelligence scores and processed neuroimaging data was 827.

### 3.2 fMRI Data

#### Acquisition

Resting-state fMRI data was obtained from subjects participating in the Human Connectome Project Young Adult dataset. Participants underwent four 15-minute runs of scanning using a 3T Siemens Connectome-Skyra scanner, acquiring 4800 volumes per subject. The scans were processed following the HCP minimal preprocessing pipeline.

Resting-state fMRI was chosen over task-based fMRI due to its ability to reveal the intrinsic functional architecture of the brain by examining spontaneous fluctuations in blood-oxygen-level-dependent (BOLD) signals (Fox and Greicius, 2010).

#### Preprocessing Steps

The preprocessing pipeline included B0-unwarping and normalization to the Montreal Neurological Institute (MNI)-152 template, as outlined in Glasser et al. (2016). B0-unwarping corrected distortions in images caused by susceptibility-induced field gradients, ensuring accurate registration and analysis. Normalization to the MNI-152 template served as a crucial step, providing a common reference space for comparing and combining data across different subjects and

studies. The data available for further processing had head motion artifacts regressed out of it.

### 3.3 Behavioral Data

#### Data source

The intelligence scores employed in this study were sourced from the Human Connectome Project (HCP) database, which provides demographic data and cognitive task performance measures. The final sample included N = 838 individuals, consisting of 449 females aged 22-35.

#### Calculation of ‘g’ factor scores

The ‘g’ factor scores utilized in this study were obtained from Kristanto et al. (2022) and were calculated following the methodology outlined by Dubois et al. (2018), who recommended employing a confirmatory factor analysis (CFA) framework for deriving ‘g’ factor scores from cognitive task data. Kristanto et al. (2022) utilized a battery of 15 carefully selected cognitive tasks (see Table 1), covering a broad spectrum of domain-specific abilities at stratum II, in line with the Cattell-Horn-Carroll (CHC) model. These tasks comprised in-scanner tests, assessments from the NIH Toolbox, and measures from the Penn Computerized Cognitive Battery.

The steps outlined by Dubois et al. (2018) for calculating ‘g’ factor scores involve utilizing a Confirmatory Factor Analysis (CFA) framework. CFA is preferred over Exploratory Factor Analysis (EFA) due to its stricter constraint on cross-loadings, ensuring a clearer definition of the general factor. In their methodology, Dubois et al. (2018) specified a bi-factor model with a general factor loading on all cognitive tasks and four group factors loading on subsets of tasks (see Figure 1). This design eliminates any cross-loadings of a task on multiple factors, maintaining the independence of group factors from each other and the general factor.

To ensure model identification, Dubois et al. (2018) imposed constraints such as fixing unstandardized loadings for specific tasks. The lavaan package (v. 0.5-23.1097) in R was used to execute the CFA model. Upon achieving model convergence, they evaluated fit indices, which indicated excellent fit with a Comparative Fit Index (CFI) of 0.974, Root Mean Square Error of Approximation (RMSEA) of 0.052, Standardized Root Mean Square Residual (SRMR) of 0.032, and Bayesian Information Criterion (BIC) of 27820.2.

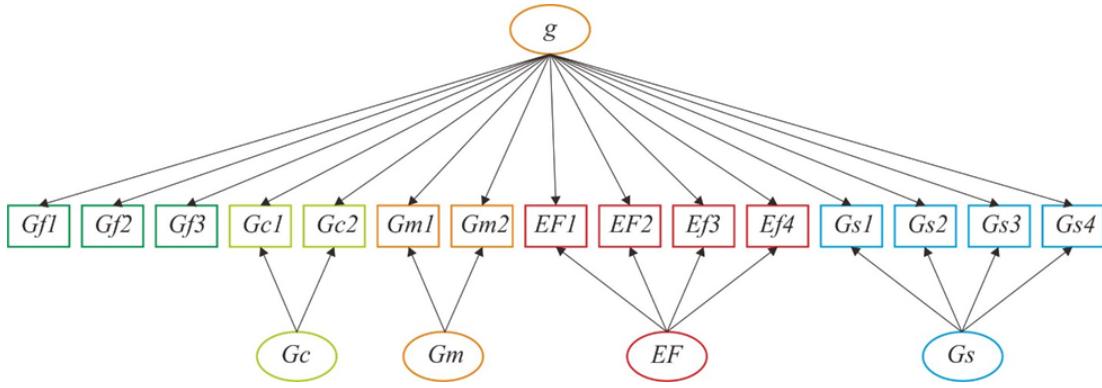
Furthermore, the variance explained by the general factor and group factors was

**Table 1:** Cognitive tasks and associated domain-specific abilities included in the Kristanto et.al. (2022) study

| Domain-specific abilities             | Tasks  |
|---------------------------------------|--|
| Reasoning ( <i>Gf</i> )               | Raven's Progressive Matrices ( <i>Gf1</i> )                                |
|                                       | Spatial Orientation Processing ( <i>Gf2</i> )                              |
|                                       | List-Sorting Working Memory ( <i>Gf3</i> )                                 |
| Comprehension Knowledge ( <i>Gc</i> ) | Oral Reading Recognition Test ( <i>Gc1</i> )                               |
|                                       | Vocabulary Comprehension ( <i>Gc2</i> )                                    |
| Memory ( <i>Gm</i> )                  | Verbal Episodic Memory ( <i>Gm1</i> )                                      |
|                                       | Picture Sequence Memory ( <i>Gm2</i> )                                     |
| Executive Function ( <i>EF</i> )      | Dimensional Change Card Sort – Color ( <i>EF1</i> )                        |
|                                       | Dimensional Change Card Sort – Shape ( <i>EF1</i> )                        |
|                                       | Flanker Inhibitory Control and Attention Task – Congruent ( <i>EF3</i> )   |
|                                       | Flanker Inhibitory Control and Attention Task – Incongruent ( <i>EF4</i> ) |
| Mental Speed ( <i>Gs</i> )            | Pattern Comparison Processing Speed ( <i>Gs1</i> )                         |
|                                       | Sustained Attention ( <i>Gs2</i> )   |
|                                       | Relational Processing 1 ( <i>Gs3</i> ) <sup>a</sup>                        |
|                                       | Relational Processing 2 ( <i>Gs4</i> ) <sup>a</sup>                        |

Source: Adapted from Kristanto, Daniel, Xinyang Liu, Werner Sommer, Andrea Hildebrandt, and Changsong Zhou. "What do neuroanatomical networks reveal about the ontology of human cognitive abilities?." *Iscience* 25, no. 8 (2022). Used with Permission from Daniel Kristanto.

examined from the standardized solution. They found that the general factor accounted for 64.0% of the variance, while the group factors collectively explained 17.2% of the variance. Factor scores for the general factor ('g') were derived using the regression method. To validate the findings, the scores derived from the CFA method were compared with those obtained from the EFA method, demonstrating a strong correlation between the two approaches ( $r=0.99$ ).



Source: Adapted from Kristanto, Daniel, Xinyang Liu, Werner Sommer, Andrea Hildebrandt, and Changsong Zhou. "What do neuroanatomical networks reveal about the ontology of human cognitive abilities?" *Iscience* 25, no. 8 (2022). Used with Permission from Daniel Kristanto. The original figure with the description can be found in their Supplementary Material (Supplementary Figure 1)

**Figure 1:** The bi-factor model used to quantify the ‘g’ factor scores

### 3.4 Guided Multiverse Approach

Neuroimaging studies present a rich tapestry of analytical pipelines, each holding the potential to unveil nuanced insights. However, the absence of standardized metrics for result comparison complicates interpretation. To address this challenge, we have embraced a multiverse approach, a method that navigates the vast landscape of potential analyses, fostering a more comprehensive understanding.

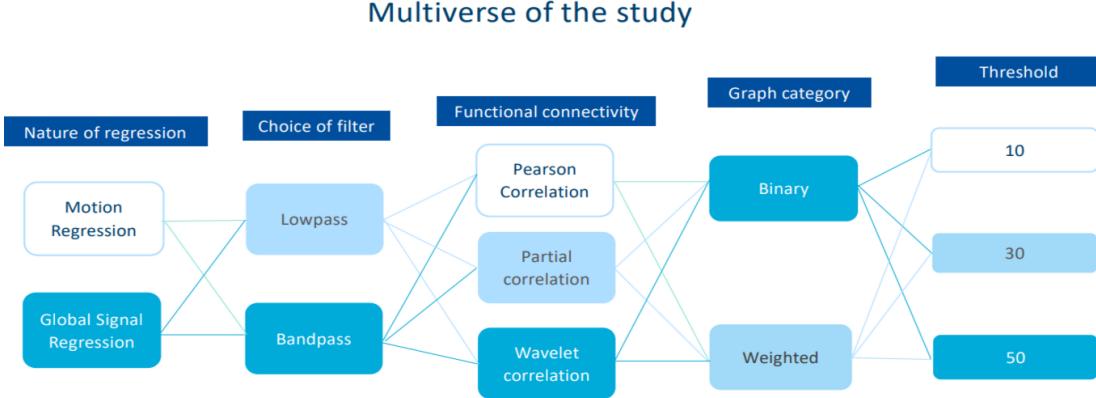
However, implementing a multiverse approach is inherently computationally demanding (Dafflon et. al., 2020). To tackle this challenge, a carefully guided multiverse of analytical choices was crafted with deliberate considerations made at each stage of the data processing and analysis, branching it into distinct pipelines.

#### Analytical Choices

The guided multiverse approach of the present study allows for the exploration of various analytical choices (see Figure 2), introducing variability and capturing the impact of seemingly arbitrary decisions on study outcomes.

All the key considerations were as follows:

1. Nature of Regression - Global Signal Regression (GSR) / Motion Regression  
The global signal (GS) is a time series of signal intensity averaged over all voxels in the brain, grey matter, or cortical gray matter. The decision to include or exclude this global signal following head motion regression can often have an impact on subsequent analyses and ultimately the results of the study. While global signal regression (GSR) is commonly utilized in resting-state fMRI studies to mitigate physiological noise, it may inadvertently eliminate neural activity



**Figure 2:** Multiverse of all the different forking paths at each step of the analysis

information embedded within the global signal. This decision bifurcates our multiverse analysis into two paths: one involving GSR and the other without it (i.e., motion regression only).

**Advantages:** GSR effectively reduces physiological noise, enhancing the quality of resting-state fMRI data by minimizing non-neuronal sources of variability such as respiratory and cardiac events. Hayasaka (2013) found that without global signal correction, correlation coefficients were positively biased, and certain brain regions became disconnected. This suggests that global signal correction may be necessary for more accurate results.

**Disadvantages:** GSR may inadvertently remove neural activity information present in the global signal, leading to the loss of valuable neurophysiological insights (Hahamy-Dubossarsky, 2014). Moreover, GSR on preprocessed data may unpredictably distort correlation matrices, raising concerns about potential errors (Murphy, 2009; 2017).

Chen et al. (2012) have suggested that the Signal-to-Global Noise Ratio (SGNR) can be used as a criterion to guide the decision on whether to perform GSR. This ratio quantifies the relationship between signal and global noise levels, providing insight into the potential effects of GSR on functional connectivity measures. Higher SGNR values, indicative of a stronger signal relative to global noise, are associated with more errors induced by GSR, suggesting that SGNR can be used as a criterion to inform the decision-making process. For instance, below a certain SGNR value (e.g., 7.03 as observed by Chen et al.), performing GSR may result in fewer errors, while above this threshold, it may induce more errors in functional connectivity measures.

## 2. Choice of Filter – Lowpass/Bandpass filtering

The choice of filtering—specifically between lowpass and bandpass filtering rep-

resents a critical decision point with distinct advantages and limitations.

Bandpass filtering serves multiple purposes in fMRI data analysis, effectively addressing technical noise and enhancing the signal-to-noise ratio (Blasi, 2020). By isolating low-frequency components essential for studying resting-state networks, bandpass filtering facilitates data comparison across subjects and sessions (Chen, 2008). However, it also introduces limitations, including the potential loss of high-frequency information, sensitivity to cutoff frequencies, and inflated functional connectivity estimates, especially in the presence of motion and cardiac artifacts (Birn, 2014; Kalthoff, 2011; Hallquist et al., 2013). The data was bandpass filtered in the range of 0.01-0.1 Hz for the pipeline with bandpass filtering.

Lowpass filtering is essential for enhancing signal quality in rsfMRI data, reducing high-frequency noise, and focusing on slow fluctuations fundamental for studying brain functional connectivity (Giove, 2009). While it improves the sensitivity and selectivity of fMRI data analysis, caution is needed to avoid attenuation of high-frequency components, smoothing spatial resolution, loss of sensitivity to rapid changes, and potential signal distortion (Kruggel, 1999; Lowe et al., 1997).

The choice between bandpass and lowpass filtering represents a trade-off between preserving high-frequency details and focusing on slow fluctuations. Researchers must carefully consider these advantages and limitations when selecting their filtering approach, ensuring that it aligns with the needs of the data and the goals of the study.

### 3. Functional Connectivity (FC) Measures - Pearson/Partial/Wavelet

Functional Connectivity (FC) measures provide insights into the interplay between brain regions, with various approaches available to quantify this interaction. In the current multiverse, three pathways were shaped by the choice of FC measures, namely Pearson correlation, Partial correlation, and Wavelet coherence analysis. Each selection creates a distinct analytical pipeline with specific assumptions, advantages, and disadvantages.

#### Pearson Correlation

**Assumptions:** Assumes linearity between brain regions and lacks full quantification of FC.

**Advantages:** Widely adopted due to simplicity and ease of interpretation.

**Disadvantages:** Limited by its assumption of linearity, which may not accurately capture complex neural interactions.

### Partial Correlation

Assumptions: Assumes a direct relationship between two regions after removing the influence of other regions.

Advantages: Useful for assessing the specific relationship between two regions while controlling for confounding factors.

Disadvantages: Limited by the need to specify which regions to control for, potentially introducing bias if relevant factors are omitted.

### Wavelet Coherence Analysis

Assumptions: Captures both temporal and spectral information, addressing non-stationarity in BOLD signals.

Advantages: Provides a comprehensive understanding of both time and frequency domains, allowing for the detection of dynamic changes in FC.

Disadvantages: Complexity in implementation and interpretation compared to simpler methods like Pearson correlation.

The choice of scales for the wavelet transform was critical for the resolution of the connectivity matrix. The selected scales ranged from 1 to 128, enabling the identification of patterns across a spectrum of low to moderate frequencies commonly observed in rsfMRI data. Researchers must consider the trade-offs between simplicity, interpretability, and comprehensiveness. Each approach offers unique insights into brain connectivity, and the choice depends on the specific research goals and the nature of the data being analyzed.

## 4. Category of Graph - Binary/Weighted

Brain functional connectivity can be displayed as a graph, either with binary edges (existence of a connection between two or more nodes) or with weighted edges (strength of the connection between two or more nodes).

### Binary Graphs

Advantages: Binarizing edges reduces computational expense, simplifying graph analysis. Binary edges are also straightforward to interpret, representing either the presence or absence of a connection between brain regions.

Disadvantages: Binary graphs oversimplify the underlying connectivity structure by disregarding the strength of connections between regions. It cannot capture nuanced variations in connectivity strength, potentially masking important information (He and Evans, 2010).

### Weighted Graphs

Advantages: Weighted graphs provide richer information for network analysis, facilitating the identification of subtle patterns and dynamics within the network

(Hallquist, 2018).

Disadvantages: Weighted graphs necessitate more complex computations due to the continuous nature of edge weights, leading to higher computational expense. This might introduce interpretational challenges, as the significance of specific weight values can vary across studies and contexts.

The choice between binary and weighted graphs in modeling brain functional connectivity entails trade-offs between computational efficiency and detailed representation. Binary graphs offer simplicity and computational ease but sacrifice information resolution, while weighted graphs provide richer connectivity insights at the expense of increased computational demands.

#### 5. Thresholding – 10/30/50 percentage of strongest connections

Thresholding in neuroimaging analysis refers to the process of determining which edges or connections in a graph network should be retained for further analysis based on their strength or significance. This step is crucial for striking a balance between computational cost and information retention.

##### Relative Thresholding

Advantages: Utilizing a relative threshold of the strongest connections tackles computational demands by limiting the number of connections included in the analysis.

Disadvantages: Relative thresholding does not account for absolute differences in correlation values between groups or conditions, potentially overlooking meaningful variations in connectivity strength. Setting a relative threshold involves an arbitrary decision without considering the underlying distribution of correlation values or the biological significance of specific connections (Langer, 2013).

Each analytical choice is a product of careful consideration, aiming to balance data interpretation and computational efficiency. The multiverse strategy acknowledges the diverse nature of neuroimaging analyses, providing a robust framework for future studies to explore refinements based on specific research questions and objectives.

## 3.5 Graph Metrics for Evaluating Small World Networks

The key metrics required for understanding small-world networks are the Local Clustering Coefficient (LCC) and the Characteristic path length (CPL) or average shortest path length. These metrics provide valuable insights into the organizational structure and communication efficiency of the brain's functional connectivity (Bassett and Bullmore, 2006; 2017).

**Local Clustering Coefficient (LCC):** A high LCC suggests the presence of a local community structure within the network. Nodes with a high LCC tend to form tightly interconnected clusters, fostering specialized information processing within localized regions. In contrast, a low LCC implies sparse or random connectivity between nodes. This may indicate a network with a less pronounced local organization, suggesting a more globally interconnected and distributed pattern.

**Characteristic path length (CPL):** The average shortest path length measures how efficiently information can traverse the network. A low CPL is indicative of efficient communication, suggesting that information can quickly and directly flow between different brain regions.

A combination of high LCC and low CPL is characteristic of a small world network (Watts and Strogatz, 1998). This balance reflects a network with both localized processing capabilities (high LCC) and efficient global communication (average shortest path length/CPL).

**Calculating Small Worldness:** Small worldness is a metric employed to assess whether a network exhibits small-world properties characterized by high local clustering and low characteristic path length. The traditional calculation often involves a ratio of observed network metrics to those of equivalent random and lattice graphs.

Formula: as calculated by Networkx sigma function<sup>[1]</sup>

$$\sigma(\text{sigma}) = \frac{C/C_{\text{rand}}}{L/L_{\text{rand}}} \quad (1)$$

In this formula:

$C$  is the average local clustering coefficient of the observed network.

$C_{\text{rand}}$  is the average local clustering coefficient of an equivalent random graph.

$L$  is the average shortest path length of the observed network.

$L_{\text{rand}}$  is the average shortest path length of an equivalent random graph.

Interpretation:

$C/C_{\text{rand}}$ : This represents how much the network's local clustering deviates from that of a random graph. A value greater than 1 suggests higher local clustering.

$L/L_{\text{rand}}$ : Reflects the efficiency of information transfer, comparing the actual network's average path length to that of a random graph. A value close to 1 indicates maintenance of short paths similar to randomness.

Overall  $\sigma$  (sigma): The ratio  $\sigma$  indicates the network's small-worldness. Sigma values greater than 1 suggest that the network possesses small-world characteristics.

Considerations: Networks exhibiting small-worldness balance local clustering with global efficiency, making them optimal for information transfer and communication. Sigma compares the network to equivalent random graphs, allowing for an assessment of its departure from random connectivity. The traditional small-worldness calculation may be influenced by the overall density of the network.

**Small World Propensity:** Small-world propensity is a relatively newer metric used to evaluate whether a network possesses small-world characteristics. Unlike Sigma, it aims to be less sensitive to the overall density of the network (Muldoon, Bridgeford, and Bassett, 2016).

Formula: as calculated by Networkx omega function<sup>[2]</sup>

$$\Phi(\phi) = \frac{L_{\text{rand}}}{L} - \frac{C_{\text{rand}}}{C} \quad (2)$$

Note. Phi ( $\phi$ ) is the symbol used in the literature to describe small-world propensity. Whereas, the equivalent function in Networkx to get the value of small world propensity is named omega.

In this formula:

$L_{\text{rand}}$  is the average shortest path length of an equivalent random graph.

$L$  is the average shortest path length of the observed network.

$C_{\text{rand}}$  is the average clustering coefficient of an equivalent random graph.

$C$  is the average local clustering coefficient of the observed network. Interpretation:

$L_{\text{rand}}/L$ : Represents the efficiency of information transfer. If close to 1, it suggests that the network maintains an average shortest path length similar to a random graph.

$C_{\text{rand}}/C$ : Evaluates the local clustering tendency. If less than 1, it indicates that the network exhibits higher local clustering compared to a random graph.

Overall  $\phi$  (phi): A positive  $\phi$  value suggests that the network possesses small-world properties.

Considerations: Omega function is considered less sensitive to the overall density of the network compared to some other small-worldness metrics. This metric provides a robust measure of small-worldness, offering a nuanced perspective on the network's architecture. It helps in comparing the small-world propensity of different networks with varying densities.

Both measures (Networkx sigma and Networkx omega) were used to calculate small worldness in the present study.

### Embedding algorithms

Embedding algorithms are techniques used in machine learning and data analysis to project high-dimensional data onto a lower-dimensional space while preserving certain properties or structures of the original data. The six algorithms used in the present study are described below.

- Locally Linear Embedding (LLE) is a nonlinear dimensionality reduction technique that preserves local relationships between data points. It seeks to find a low-dimensional representation of the data such that the local geometric structure is maintained (Roweis and Saul, 2000).
- Spectral Embedding (SE) is a method that utilizes spectral graph theory to embed data points into a lower-dimensional space. It aims to preserve pairwise similarities between data points by representing them as vectors in a lower-dimensional space (Belkin and Niyogi, 2003).
- t-Distributed Stochastic Neighbor Embedding (t-SNE) is a non-linear dimensionality reduction technique that emphasizes the preservation of local structure, making it particularly effective for visualizing high-dimensional data in two or three dimensions (Van der Maaten and Hinton, 2008).
- Uniform Manifold Approximation and Projection (UMAP) is a dimensionality reduction technique known for its ability to capture both local and global structures in high-dimensional data. It is an efficient and scalable algorithm that can be used for various applications, including visualization and clustering (McInnes, Healy and Melville, 2018).
- Potential of Heat-diffusion for Affinity-based Transition Embedding (PHATE) is a recently developed technique that leverages concepts from information theory and diffusion maps to capture complex non-linear relationships in high-dimensional data (Moon et. al., 2019).
- Principal Component Analysis (PCA) is a classical linear dimensionality reduction technique that identifies the axes of maximum variance in the data, enabling the representation of high-dimensional data in a lower-dimensional space while preserving as much variance as possible.

## 3.6 Code

All the code used to create the multiverse and to run on the HPC Cluster ROSA funded by the DFG under INST 184/225-1 FUGG is available on GitHub (<https://github.com/sumbul23/Multiverse-Project>). Along with a detailed explanation of the workflow.

## 4 Results

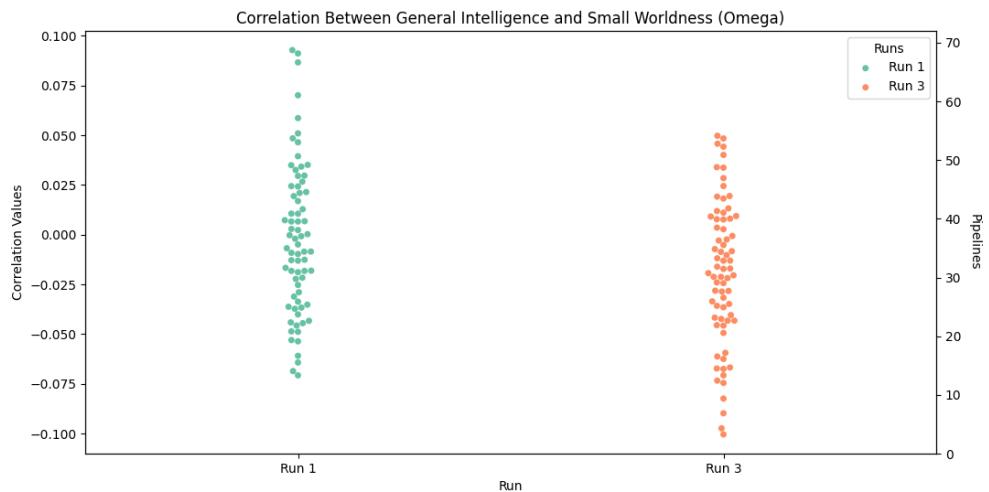
All  $72 \times 2$  analysis pipelines (for 2 sessions) were run on the HPC cluster ROSA to get the values for small-worldness ( $\sigma$ ) and small-world propensity ( $\omega$ ), as well as characteristic path length and average local clustering coefficient for each of the 827 participants.

### 1. Association between ‘g’ Factor Scores and Small World Network Metrics:

The correlation analysis revealed no significant associations between the ‘g’ factor scores and small-worldness, as calculated by Networkx  $\sigma$ , and small-world propensity, as calculated by Networkx  $\omega$  (see Figure 3).



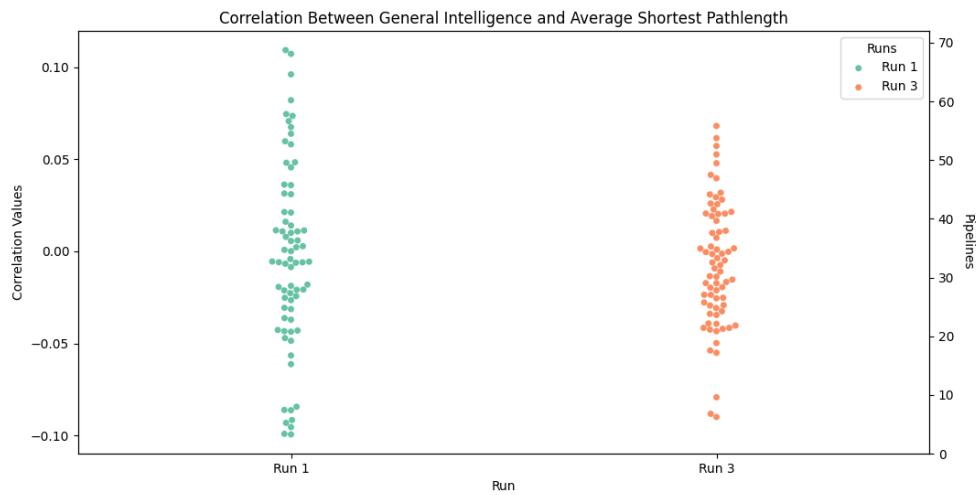
Note: Correlation values for both  $\sigma$  (top) and  $\omega$  (bottom) small-worldness measures are displayed on the Y axis (left) for all the 72 pipelines (sorted in ascending order for better visualization) displayed on the Z axis (right). The two runs (Session 1 and 3; data collected on different days) are represented in blue and red respectively.



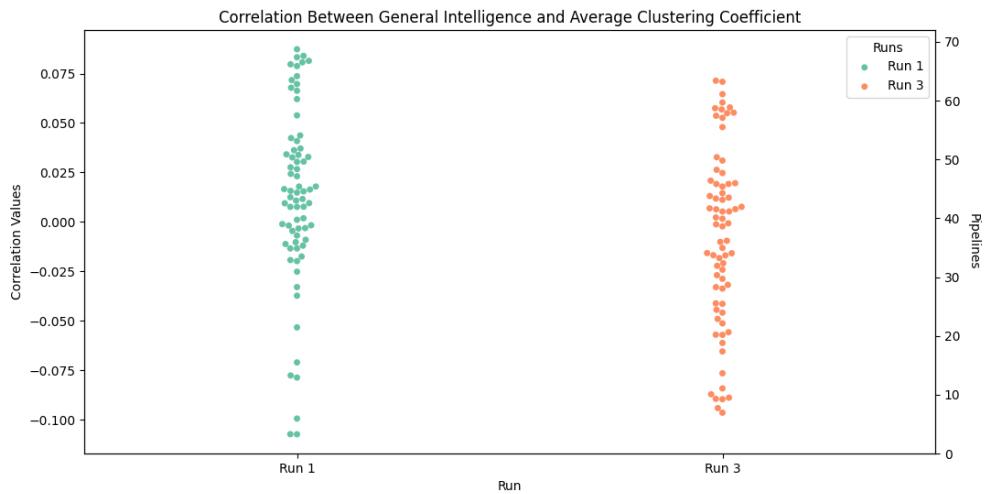
**Figure 3:** Results of correlation analysis-I

Similarly, no significant association was observed between general intelligence and characteristic path length and local average clustering coefficient (see Figure 4) of the small world graph network.

The correlations between ‘g’ factor scores and small-world network metrics fell within a very restricted range of  $[0.1 \text{ to } -0.1]$ . These correlations showed some variation between the different sessions (Run 1 and Run 3), however, this variability might be attributed to noise.



Note: Correlation values for both the average shortest path length (top) and average clustering coefficient (bottom) are displayed on the Y axis (left) for all the 72 pipelines (sorted in ascending order for better visualization) displayed on the Z axis (right). The two runs (Session 1 and 3; data collected on different days) are represented in blue and red respectively.

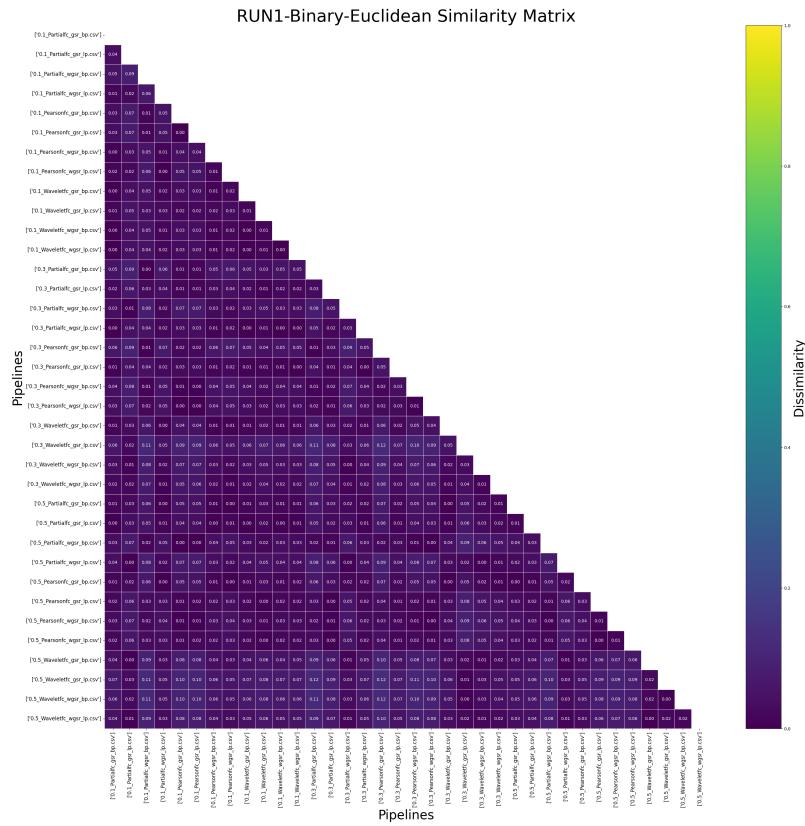


**Figure 4:** Results of correlation analysis-II

## 2. Similarity between pipelines:

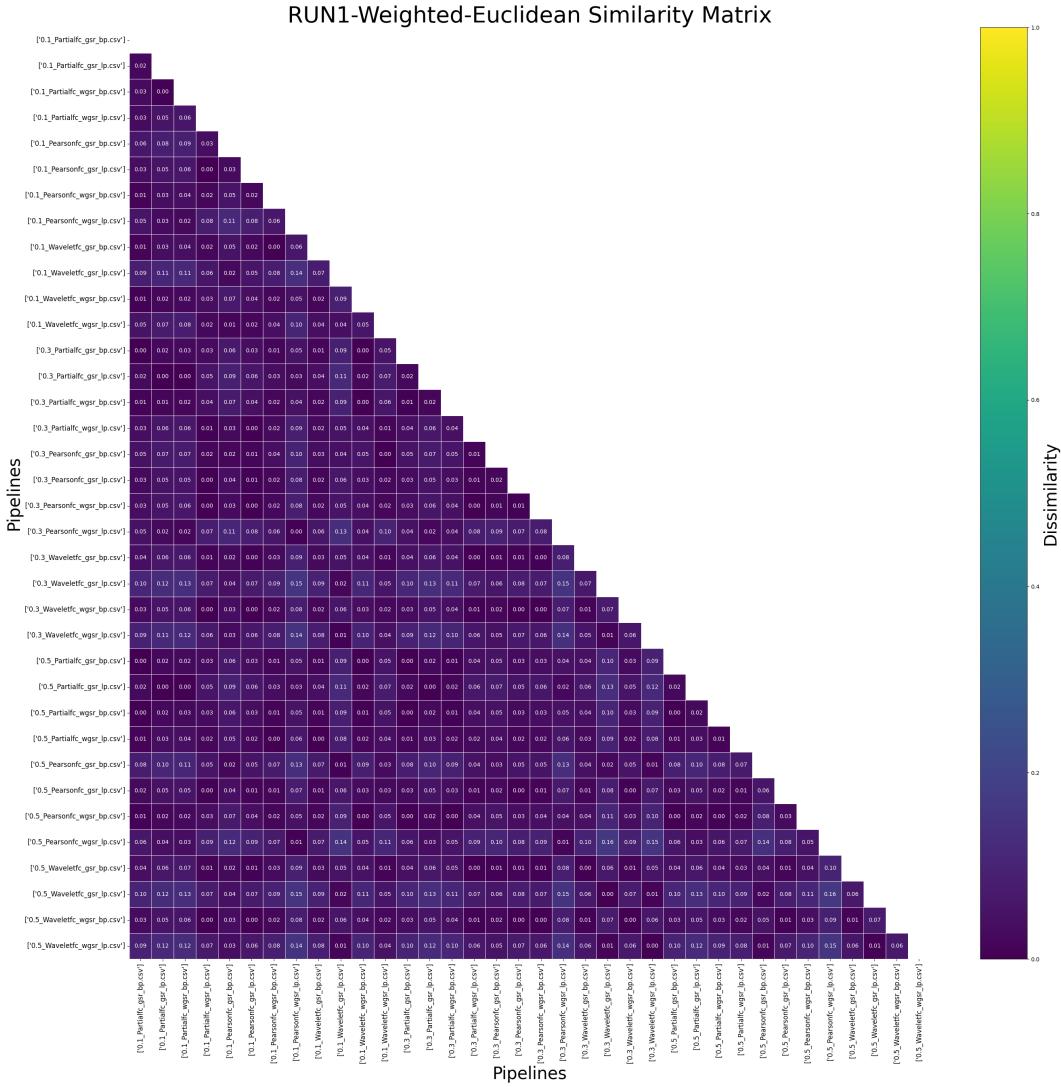
Similarity matrices were created using cosine similarity to evaluate the dissimilarity among all the pipelines for each run or session and between binary (see Figure 5 and Figure 7) and weighted graphs (see Figure 6 and Figure 8). All the pipelines showed high similarity across the different analytical methods and sessions. The level of agreement is particularly crucial because when different approaches produce roughly comparable results, it gives confidence that these findings are not dependent on a specific analytic approach.

## Figures: Similarity Matrices



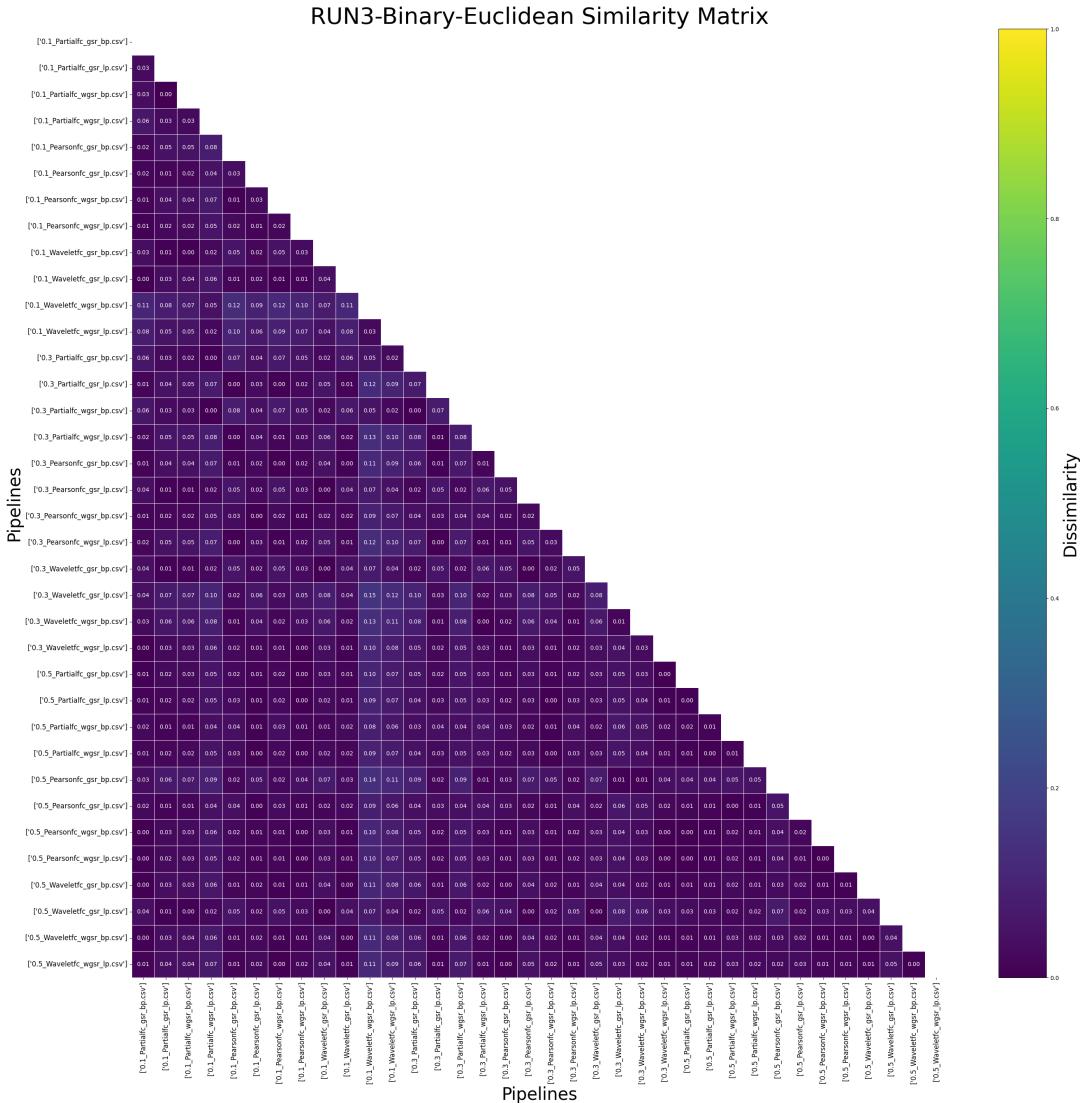
Note: Cosine similarity is a statistic that determines how similar two or more objects are, regardless of size. Mathematically, it computes the cosine of the angle between two vectors projected in a multidimensional space. Lower (darker color) values indicate higher similarity. Figure 5 displays the similarity matrix for all the pipelines created using binary graphs (36) with data from run 1.

**Figure 5:** Matrix for all the pipelines with binary graphs and data from run 1.



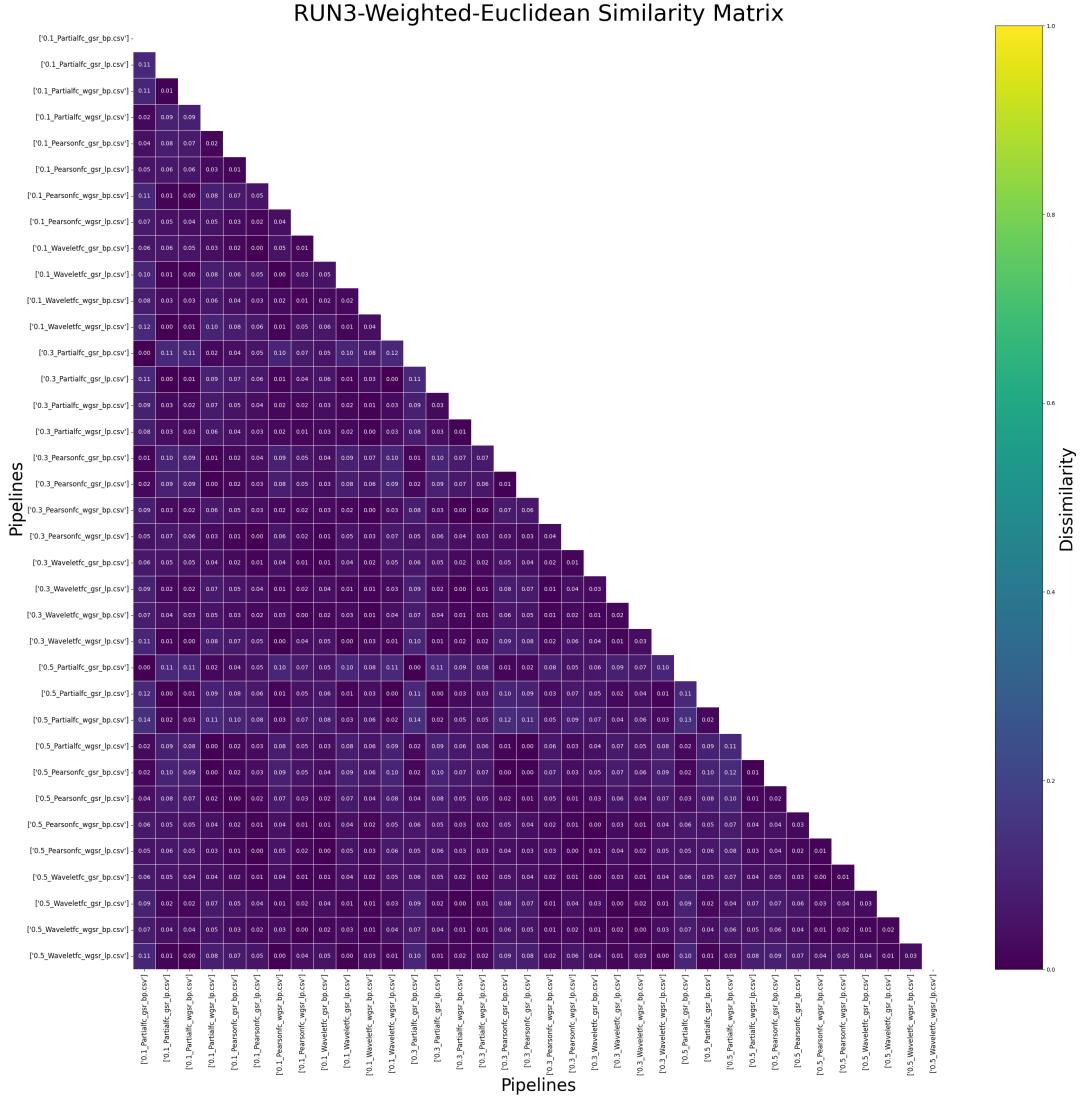
Note. Figure 6 displays the similarity matrix for all the pipelines created using weighted graphs (36) with data from run 1.

**Figure 6:** Matrix for all the pipelines with weighted graphs and data from run 1.



Note. Figure 7 displays the similarity matrix for all the pipelines created using binary graphs (36) with data from run 3 (data collected on a different day).

**Figure 7:** Matrix for all the pipelines with binary graphs and data from run 3.

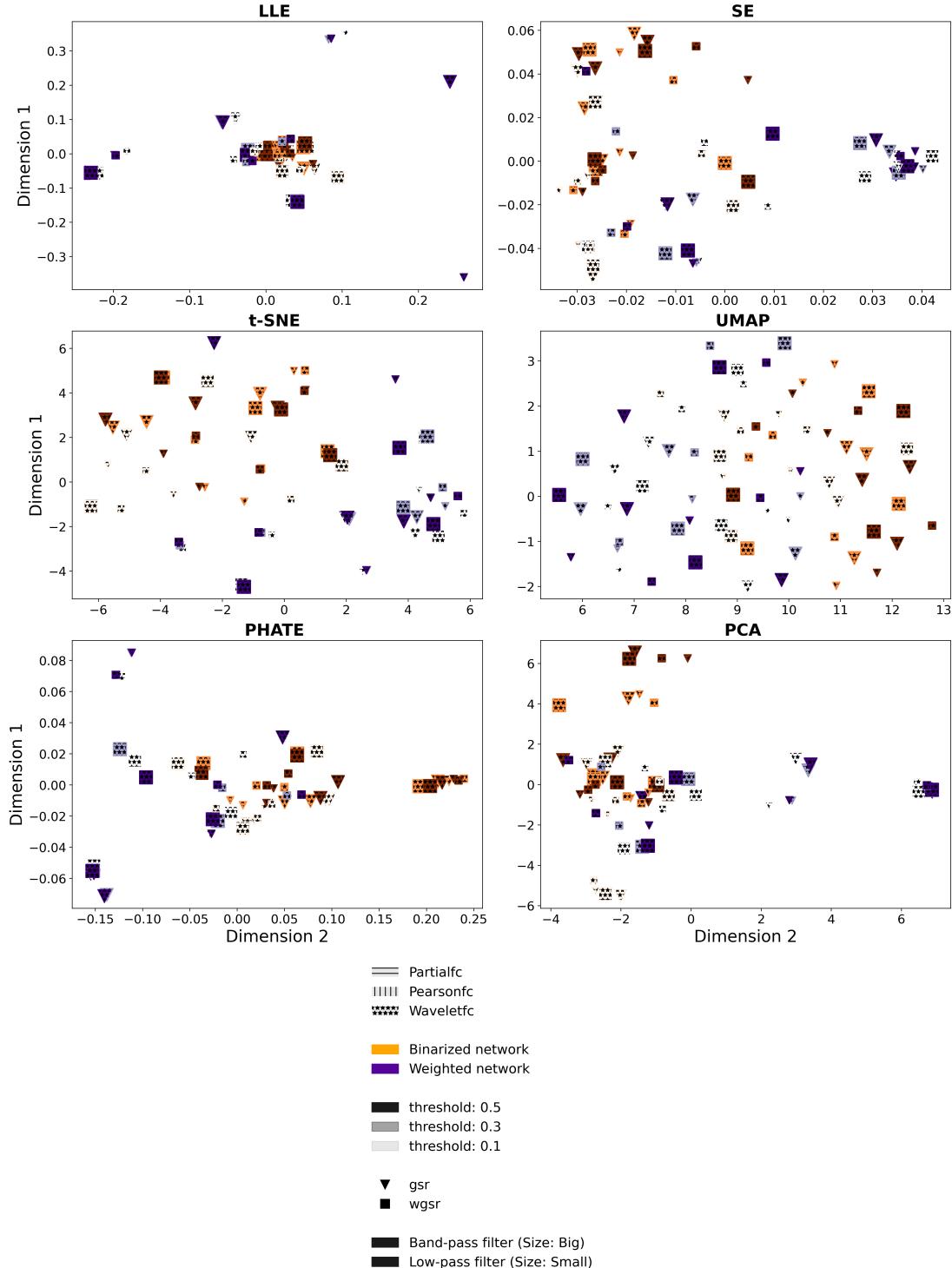


Note. Figure 8 displays the similarity matrix for all the pipelines created using weighted graphs (36) with data from run 3 (data collected on a different day).

**Figure 8:** Matrix for all the pipelines with weighted graphs and data from run 3.

### 3. Analyzing relationships in 2D:

To better understand the relationships between the analytical pipelines, we utilized six embedding algorithms to create a low-dimensional space capturing the full spectrum of these relationships (see Figure 9). Among the six algorithms utilized, including Locally Linear Embedding (LLE), Spectral Embedding (SE), t-distributed Stochastic Neighbor Embedding (t-SNE), Uniform Manifold Approximation and Projection (UMAP), Potential of Heat-diffusion for Affinity-based Transition Embedding (PHATE), and Principal Component Analysis (PCA), Uniform Manifold Approximation and Projection (UMAP) emerged as the most effective in preserving both the global and local structure of the data.

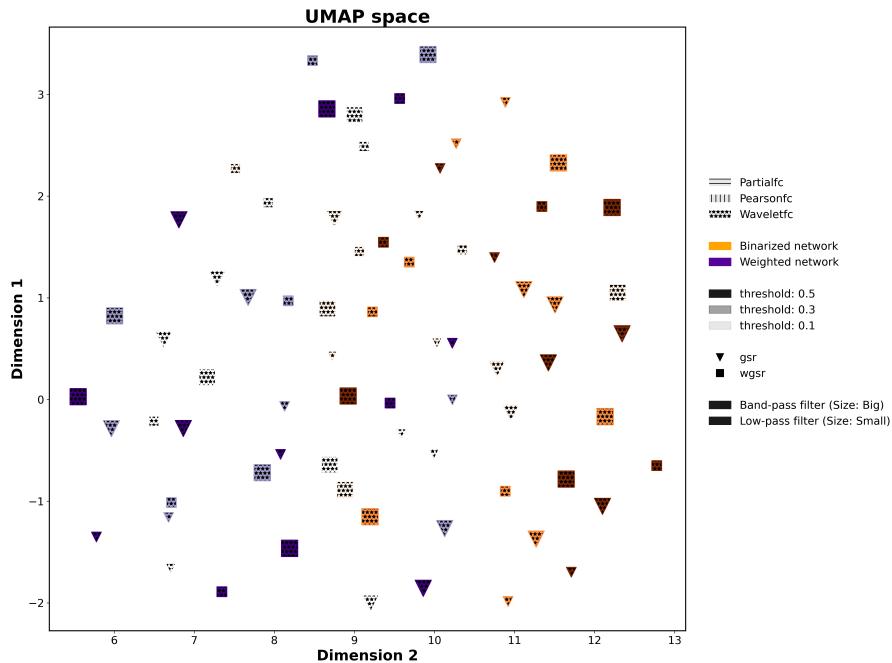


Note. Each point represents data with different kinds of processing and analysis steps in the multiverse across a two-dimensional space (Bigger symbols represent bandpass filtering and smaller ones represent low pass filtering; Nabla represents data without global signal, Square represents data with global signal; different kinds of hatching patterns are for the three types of functional connectivity, yellow color is for a binarized network and purple is for a weighted network; thresholding is represented by the transparency of the symbol). Figure 9 displays the results of dimensionality reduction for all six embedding algorithms. Pipelines that are closer in space exhibit similar performance than pipelines that are further away.

**Figure 9:** Dissimilarity in 2D

#### 4. Distinction between Binarized and Weighted Pipelines:

A clear distinction emerged between binarized and weighted pipelines in the UMAP representation (see Figure 10). This distinction may be linked to the higher number of small world graphs in pipelines with a weighted network, suggesting that the consideration of connection strength allows for a more nuanced representation of network connectivity patterns. However, it's important to note that binarizing a network doesn't necessarily compromise the relationship between small worldness and general intelligence, as the correlation values between pipelines with both weighted and binary networks did not exhibit significant differences in displaying higher correlation values.



Note. UMAP is a relatively newer dimensionality reduction technique that offers improved preservation of the data's intrinsic geometry compared to traditional methods like t-SNE. Pipelines with binary networks are clustered towards the right side of the 2D space as opposed to the overlapping representations in the other embedding algorithms.

**Figure 10:** Distinction between pipelines with binary and weighted graphs found in Uniform Manifold Approximation and Projection space

## 5 Discussion

This study aimed to investigate the purported relationship between the general factor of intelligence ('g') and small-world brain network topology, a relationship that has been explored in previous studies with varying results. Contrary to expectations and in alignment with the findings of the Kruschwitz study, conducted using the Human Connectome Dataset, no significant associations were observed between 'g' factor scores and various small-world network metrics. These metrics included Networkx sigma and omega small-worldness measures, and graph network measures such as the average local clustering coefficient and characteristic path length, across 72 combinations of analytical pipelines for rsfMRI data collected on two different days.

### Previous Findings and Discrepancies

Several previous studies (van den Heuvel et al., 2009; Langer et al., 2012; Pamplona et al., 2015; Hilger et al., 2017) have reported associations between lower characteristic path length in functional brain networks and higher general intelligence. However, the current study, along with the Kruschwitz study, did not replicate these findings. Notably, the correlations observed in our study fell within a very restricted range of [0.1 to -0.1], suggesting weak to negligible associations.

### Methodological Differences

Divergent results across studies were attributed primarily to methodological disparities, encompassing variations in both intelligence assessment tools and fMRI data collection and analysis techniques. Previous investigations relied on the Wechsler Adult Intelligence Scale (WAIS) for intelligence assessment, whereas our study, alongside the Kruschwitz study, utilized NIH Toolbox Cognition composite scores. These scores have exhibited substantial convergent validity ( $r = 0.89$ ) with WAIS measures, as demonstrated by Heaton et al. (2014). Methodological discrepancies in fMRI analysis were also implicated, particularly concerning connectivity measures and preprocessing steps. Prior studies, as detailed in Table 2, employed full correlation measures, which have faced critique for potentially incorporating indirect connections twice into graph analytical measures. In contrast, our study adopted full, partial, and wavelet correlation methods for functional connectivity calculation, yielding no discernible effects. Research conducted by Aurich and colleagues (2015) suggests that graph-theoretic metric measurements can vary depending on the preprocessing strategies employed. While our study operated on data preprocessed using the HCP minimal preprocessing pipeline, the Kruschwitz study introduced an additional preprocessing pipeline, ICA+FIX, yielding comparable results (Smith et al., 2015; Glasser et al., 2016).

Despite these precautionary measures, the possibility remains that discrepancies in data acquisition parameters and preprocessing pipelines may have contributed to disparate outcomes, as evidenced by the higher temporal resolution (TR: 0.5 s) of the data acquired by van den Heuvel et al. (2009) compared to the HCP data (TR: 0.72 s).

### **Demographic Characteristics and Power Analysis**

Furthermore, previous studies with positive findings had samples skewed towards more intelligent individuals (van den Heuvel et al., 2009; Pamplona et al., 2015), potentially limiting the generalizability of their results. Additionally, a post-hoc power analysis conducted by Kruschwitz et al. for van den Heuvel and the team's original study revealed insufficient power with only 19 participants to detect an effect of global network efficiency and intelligence. As displayed in Table 2, increasing sample size and preprocessing method complexity may be linked with the findings supporting a lack of association between general intelligence and graph network measures.

### **Arbitrary Choice of Thresholding**

The arbitrary choice of thresholding in our study could have influenced the results, as utilizing different thresholding approaches can lead to information loss, bias in network properties, and lack of reproducibility (van den Heuvel et. al., 2017; Theis 2023). To address these issues, researchers have explored various thresholding strategies, including statistical thresholding based on null models or network-specific criteria (Theis 2023). However, the choice of threshold can significantly impact the topological properties of the network (Langer 2013).

Thresholding strategies applied in previous studies reflected a spectrum of approaches in defining network connectivity. Kruschwitz et. al. (2018), employed a proportional thresholding approach, where networks were thresholded in the range of 0.1–0.5 in steps of 0.01. This method ensures that only a specific percentage of the strongest links are maintained in the resulting network. Langer and colleagues (2012) utilized a fixed set of thresholds ranging from 0.55 to 0.95 to threshold the mean correlation matrix, thereby retaining connections that exceed a predefined threshold across all subjects in the study. Hilger and team (2017) employed proportional thresholds for graph construction, defining them based on selecting a specific percentage of edges with the highest correlations. This resulted in five different binary adjacency matrices per person, representing varying proportions (10%, 15%, 20%, 25%, and 30%) of the strongest functional connections between nodes. Additionally, previous studies by Achard et al. (2007), and van den Heuvel et al. (2009) utilized a threshold (ranging from 0.05 to 0.5) to

investigate the impact of different thresholding levels on functional connectivity networks. In the present study, we employed a relative thresholding approach for three values (10%, 30%, and 50%) of the strongest connections in the resulting network.

Future studies might benefit from exploring the impact of different thresholding methods on small-world network characteristics.

**Table 2:** Comparison between previous studies and the current study

| Study   | Relationship<br>between<br>Intelligence<br>and Network<br>Metrics            | Intelligence<br>Assessment<br>Tool               | Connectivity<br>Measures  | Preprocessing Steps   | Sample<br>Size<br>Age (mean<br>+/- sd)<br>Gender(M/F) |
|---|--|--|---|---|---|
| van den Heuvel et al., 2009<br>(using resting state fMRI) | Lower characteristic path length associated with higher general intelligence | Wechsler Adult Intelligence Scale (WAIS)         | Full correlations   | Bandpass filtering (0.01–0.1 Hz)  | n = 19<br>29 +/- 7.8<br>M14 / F5                      |
| Langer et al., 2012<br>(using resting state EEG)          | Lower characteristic path length associated with higher intelligence         | Raven's Advanced Progressive Matrices (RAPM)     | Intracortical sources of brain oscillations using linear instantaneous dependence (coherence) | Partial regression analyses were conducted to examine EEG power and RAPM performance correlations after adjusting for age effects | n = 75<br>25.5 +/- 4.86<br>M75                        |
| Pamplona et al., 2015<br>(using rsfMRI)                   | Medium effect between characteristic path length and intelligence            | WAIS   | Full correlations   | Bandpass filtering (0.008–0.09 Hz), motion, white matter (WM) and cerebrospinal fluid (CSF) signal regression                     | n = 29<br>26.5 +/- 5.5<br>M13 / F17                   |
| Hilger et al., 2017<br>(using rsfMRI)                     | No significant correlation between global efficiency and WASI scores         | Wechsler Abbreviate Scale of Intelligence (WASI) | Full correlations   | Bandpass filtering (0.005–0.1H), motion, WM, CSF, and global signal regression  | n = 54<br>23.37 +/- 3.35<br>M31 / F23                 |

Continued on Page 32

| Study                                     | Relationship between Intelligence and Network Metrics | Intelligence Assessment Tool   | Connectivity Measures         | Preprocessing Steps  | Sample   |
|---|---|--|-------------------------------|--|--|
|   |   |  |                               |  | Size   |
|   |   |  |                               |  | Age (mean +/- sd)  |
| Kruschwitz et al., 2018<br>(using rsfMRI) | No correlation observed                               | NIH Toolbox Cognition composite scores:<br>Crystallized cognition; Fluid cognition; Total cognition; and Fluid intelligence as measured by Raven's Progressive Matrices test | Full and partial correlations | Minimal HCP preprocessing pipeline (no bandpass filtering);<br>Minimal HCP preprocessing pipeline and ICA+FIX (highpass filter with FWHM = 2355 s, regression of 24 motion parameters) | n = 1096<br>28.8 +/- 3.7<br>M500 / F596                    |
| Present Study<br>(using rsfMRI)           | No correlation observed                               | 15 cognitive tasks (see Table 1), spanning in-scanner tests, NIH Toolbox, and Penn Computerized Cognitive Battery  | Full, partial, correlations   | Minimal HCP preprocesing and Bandpass filtering;<br>Minimal HCP preprocesing, Bandpass filtering and GSR;<br>Minimal HCP preprocesing, Lowpass filtering;                              | n = 827<br>Smaller sample but similar to Kruschwitz et al. |

Note: In the study by Kruschwitz et al. (2018), ICA+FIX was employed as an additional preprocessing step. Independent Component Analysis (ICA) followed by FM-RIB's ICA-based X-noiseifier (FIX) constitutes a standard preprocessing approach in functional magnetic resonance imaging (fMRI) data analysis. ICA-FIX combines ICA for component separation with FIX for automated artifact removal, thereby enhancing fMRI data quality. A highpass filter with a full width at half maximum (FWHM) of 2355 seconds was applied to eliminate low-frequency drifts. Additionally, regression of 24 motion parameters, encompassing translations and rotations of the head during scanning, was performed to mitigate motion-related artifacts.

### **Challenges in Interpretation**

The graphs generated in our study exhibited minimal variation in their small-world characteristics, as evidenced by the similarity in values between graphs displaying small-world networks and those without. Despite employing measures like Networkx sigma and omega, this finding suggests potential limitations in accurately interpreting small-world properties using these functions. This limitation is particularly noteworthy given the intricate nature of real-world networks, which may not align precisely with theoretical models. Additionally, traditional methods of comparing network clustering to random networks, as noted by Telesford (2011), may produce misleading results. These traditional models assume random connectivity patterns and overlook the biological constraints and organizational principles governing brain networks. Moreover, the use of functional connectivity measures, as discussed by Hlinka (2012), can introduce bias into small-world estimates, further complicating the interpretation of network properties.

### **Low Correlation Values and Difficulty in Determining Clusters**

The correlation values observed in our study were very low and within a narrow range. Therefore, posing a challenge in interpreting the effects of employing various analytical techniques. This limitation hindered our ability to discern meaningful patterns or clusters among the diverse analytical pipelines used concerning the relationship between small-world network metrics and general intelligence. However, despite the complexities introduced by the low correlation values, our analysis benefited from exploring the data in lower-dimensional spaces, such as employing techniques like UMAP. Through this approach, we uncovered distinct patterns between binary and weighted graphs, where connection strength provided a nuanced representation of network connectivity patterns.

### **The Utility of Multiverse Analysis**

The findings of this study underscored the broader utility of multiverse analysis. While traditionally used to ensure the robustness of results, our study highlights its additional value in studies where correlation values do not reach statistical significance. By exploring how various decision points and methodological choices interacted within the multiverse, we gained deeper insights into the intricacies of our analytical process. This comprehensive exploration allowed us to understand why certain pipelines performed better than others, despite not achieving robust results. Therefore, while multiverse analysis serves a critical purpose in studies lacking statistical significance, it also plays a crucial role in studies with significant findings. By offering a more nuanced understanding of how different analytical pipelines perform and interact, the multiverse framework enables researchers to

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glean valuable insights into the underlying mechanisms driving the observed results. This comprehensive approach enhances the interpretability and reliability of findings, ultimately advancing our understanding of complex phenomena in fields such as network neuroscience.

## 6 Limitations and Conclusion

In this study, we aimed to investigate the relationship between general intelligence ('g') and small-world brain network topology using a multiverse of analytical pipelines. Contrary to previous findings, no significant associations were observed between 'g' factor scores and small-world network metrics, including Networkx sigma, Networkx omega, characteristic path length, and local average clustering coefficient.

Our analysis revealed several methodological challenges and limitations that may have influenced the results. These include the arbitrary choice of thresholding, challenges in interpreting small-world properties using existing measures like Networkx sigma and omega, and the difficulty in determining clear clusters of analytical pipelines due to low correlation values. Despite these limitations, our study contributes to the ongoing discussion surrounding the relationship between brain network topology and general intelligence. Future research in this area can address the methodological challenges and explore alternative approaches for calculating small-worldness in brain networks.

Overall, while our findings did not support the hypothesized relationship between general intelligence and small-world brain networks, they highlight the complexity of this relationship and underscore the need for further investigation using robust analytical methods and larger sample sizes. Our study underscores the complexities and challenges inherent in neuroimaging research, particularly concerning reproducibility. While the multiverse approach offers a systematic method for exploring methodological variations, its utility in our study was limited due to the low correlations observed. Regardless, rigorous methodological refinement and exploration approaches like the multiverse are essential to enhance the reliability and reproducibility of neuroimaging findings and advance our understanding of the human brain and cognition.

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I hereby confirm that this thesis is entirely my own work. I confirm that no part of the document has been copied from either a book or any other source – including the internet – except where such sections are clearly shown as quotations and the sources have been correctly identified within the text or in the list of references. Moreover, I confirm that I have taken notice of the ‘Leitlinien guter wissenschaftlicher Praxis’ of the University of Oldenburg.

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Date, Place

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Signature