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Genome-Wide Association Study of Brain Connectivity Changes for Alzheimer's Disease

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ABSTRACT

Variations in the human genome have been found in the literature to be an essential factor that affects susceptibility to Alzheimer's disease. Genome-wide association studies (GWAS) have identified genetic loci that significantly contribute to the risk of Alzheimers. The availability of genetic data, coupled with brain imaging technologies have left room for further discovery. Using data integration methodologies and new study designs. Although methods have been proposed for integrating image characteristics and genetic information towards studying Alzheimers, the measurement of disease is often taken at a single time point, therefore, not allowing the disease progression to be taken into consideration. In longitudinal settings, we analyzed neuroimaging and single nucleotide polymorphisms dataset obtained from the Alzheimer's Disease Neuroimaging Initiative for three clinical stages of the disease, including controls, early mild cognitive impairment and Alzheimer's Disease patients. We conducted a GWAS regressing the absolute change of specific global connectivity metrics on the genetic variants, and used the GWAS summary statistics to compute the gene and pathway scores. We observed significant associations between the change in structural brain connectivity and genes previously reported to biologically manipulate the risk and progression of certain neurodegenerative disorders, including Alzheimer's disease.

Introduction

Alzheimer's disease (AD) is a neurodegenerative disease with believed onset in the hippocampus and subsequently spreads to the temporal, parietal, and prefrontal cortex[1]. Symptoms of the disease worsen over time, and as the patient's condition declines, AD ultimately leads to death. Causes of the disease are yet unclear, and it has even been hypothetised to be related to external bacteria[2]. However, 70% of AD risk is believed to be contributed by complex genetic risk factors[3]. The apolipoprotein E (APOE) gene, for example, is located on chromosome 19, and the protein carries cholesterol in the brain, affecting diverse cellular processes. Carriers of the APOE allele $\varepsilon 4$ have three times the risk of developing AD as compared to non-carriers[4]. Although APOE $\varepsilon 4$ is the primary genetic risk factor that contributes to the development of late-onset AD; its effect accounts for only 27.3% of the overall disease heritability - which is estimated to be 80%[5].

In order to estimate the remaining heritability of AD, many attempts and efforts have been made to uncover more genetic risk factors. Genome-wide studies have successfully identified sngle nucleotide polymorphisms (SNPs) which affect the development of AD[6–8]. Understanding the underlying biological process of the disease, and identifying more potential genetic risk variants, will contribute to the development of disease-modifying therapies.

On the other hand, the recent advancements in imaging technologies have provided more opportunities for understanding the complexity of how the brain connects, and at the same time, enhancing and forming a more reliable basis for neuroimaging and human brain research[9]. By means of merging brain imaging with genetics, previous studies proposed different ways of analyzing this integrated data, in order to discover genetic factors that affect the structure and function of the human brain. Significant efforts in this area have been made worldwide by the Enhancing Neuroimaging Genetics through Meta-Analysis (ENIGMA)[10] project. The methods offered several diverse ways to link together two heterogeneous collections of data - brain imaging and genetic information - depending on the hypothesis under study, and hence, the type of images and genetic information.

Stein et al.[11] used the T1 weighted Magnetic Resonance Imaging (MRI) scans from the Alzheimer's Disease Neuroimaging Initiative (ADNI)[12] and developed a voxel-based GWAS method (vGWAS) that tests the association of each location in the

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brain (each voxel), with each SNP. To quantify the phenotype, they used the relative volume difference to a mean template at each voxel, and their method, vGWAS, can be applied to other brain maps with coordinate systems. Although vGWAS did not identify SNPs using a false discovery rate of 0.05, they highlighted some genes for further investigation. More recently, other studies on the genetics of brain structure implemented a genome-wide association of the volume in some sub-cortical regions, and successfully identified significant genetic variants[13,14]. Additional efforts in the literature include the development of multivariate methods that aim at identifying the imaging-genetics associations through applying sparse canonical correlations, to adjust for similarity patterns between and within different clinical stages of the disease - an assumption which is hardly met[15].

Connectomics[16], or the study of the brain connectome, is a novel advancement in the field of neuroimaging. A structural or functional brain connectome is a representation of the brain, and its connections, as one network. The connectome comprises of nodes representing different and distinct regions in the brain, and edges representing the functional or structural connection between brain regions. More specifically, the edges of a structural connectivity network are defined by the anatomical tracts connecting the brain regions[17]. Those are extracted from diffusion tensor imaging (DTI), a type of images which detects the diffusion of the water molecules in the brain. Furthermore, the connectome can be summarised by several global and local network metrics[17] which allow the study of the brain as one entity, the comparison of different groups of participants, as well as the study of variation between and within different brain regions.

In an attempt to understand the healthy brain aging, Wu et al.[18] carried out a longitudinal study of the structural connectome in healthy participants. Their analysis evaluated the association of the annual change in both the local and global network characteristics with age, but no genetic investigation was carried out in relation to those longitudinal features. In another study Jahanshad et al.[19] conducted a GWAS on dementia subjects using connectivity patterns as a phenotype, and identified the genetic variant rs2618516 located in the SPON1 gene, however, this study considered cross sectional phenotype, collected at one specific time point.

In this paper, we used a dataset from ADNI (`http://adni.loni.usc.edu/`) to perform four quantitative GWAS, with the longitudinal change in the brain connectome used as a phenotype. we used the absolute difference in the longitudinal integration and segregation global network metrics to represent the change in structural brain connectivity. After obtaining the GWAS summary statistics for all the SNPs typed in the original data, we aggregated their p-values using the PAthway SCoring ALgorithm (PASCAL) software[20] and computed genome-wide gene and pathway-scores. Our result identified a number of genes significantly associated with the change in structural brain connectivity, including ANTXR2, OR5L1, IGF1. ZDHHC12, ENDOG and JAK1. Most of those genes were previously reported to biologically manipulate the risk and progression of certain neurodegenerative disorders, including Alzheimer's disease.

Results

Analysis Pipelines

In this work, we used a longitudinal imaging dataset, combined with the genetic variation information at the SNP-level. Our sample consists of three groups which represent three distinct clinical stages of Alzheimer's disease. Specifically, we are using; healthy individuals (controls), Early mild cognitive impairment (MCI), and Alzheimer's patients. Aiming at studying the genetic effect on the longitudinal change in the brain structure for those groups, we conducted genome-wide tests of the associations between the single imaging features with different levels of genetic variations. Those imaging features were derived from an intensive map of the brain's neural connections. The overall pipeline of our experiment is summarized in Fig. 1.

Descriptive Statistics of Brain Imaging Features

Using the DTI images at both baseline and a follow-up visit after 12 months, the brain connectome was constructed. We obtained four global network metrics, as explained in the Methods section. We chose network transitivity and Louvain modularity to represents network segregation, along with characteristic path length and weighted global efficiency to represent the brain integration[17].

Each of those four metrics represents, quantitatively, the whole brain network as a single value. Supplementary Fig. S2 illustrates both the distribution of the network metrics in the data, in the baseline and follow-up, for the three participants categories. The figure also shows the association patterns of the metrics. A similar figure that illustrates the distribution of the absolute difference between the baseline and follow-up metrics is shown in Supplementary Fig. S3, it compares the three groups in each sub-figure. To have a general idea of how the differences between these connectivity metrics are distributed, we plotted four boxplots, as shown in Supplementary Fig. S1, for the three groups combined.

To verify that the longitudinal change are consistent and not the result of artifacts, we initially compared the imaging features between the two-time points. More precisely, Table 1 shows the results of the non-parametric Wilcoxon test between baseline and follow-up features. The test ranks the values of the paired measurements and compares their central values. In this

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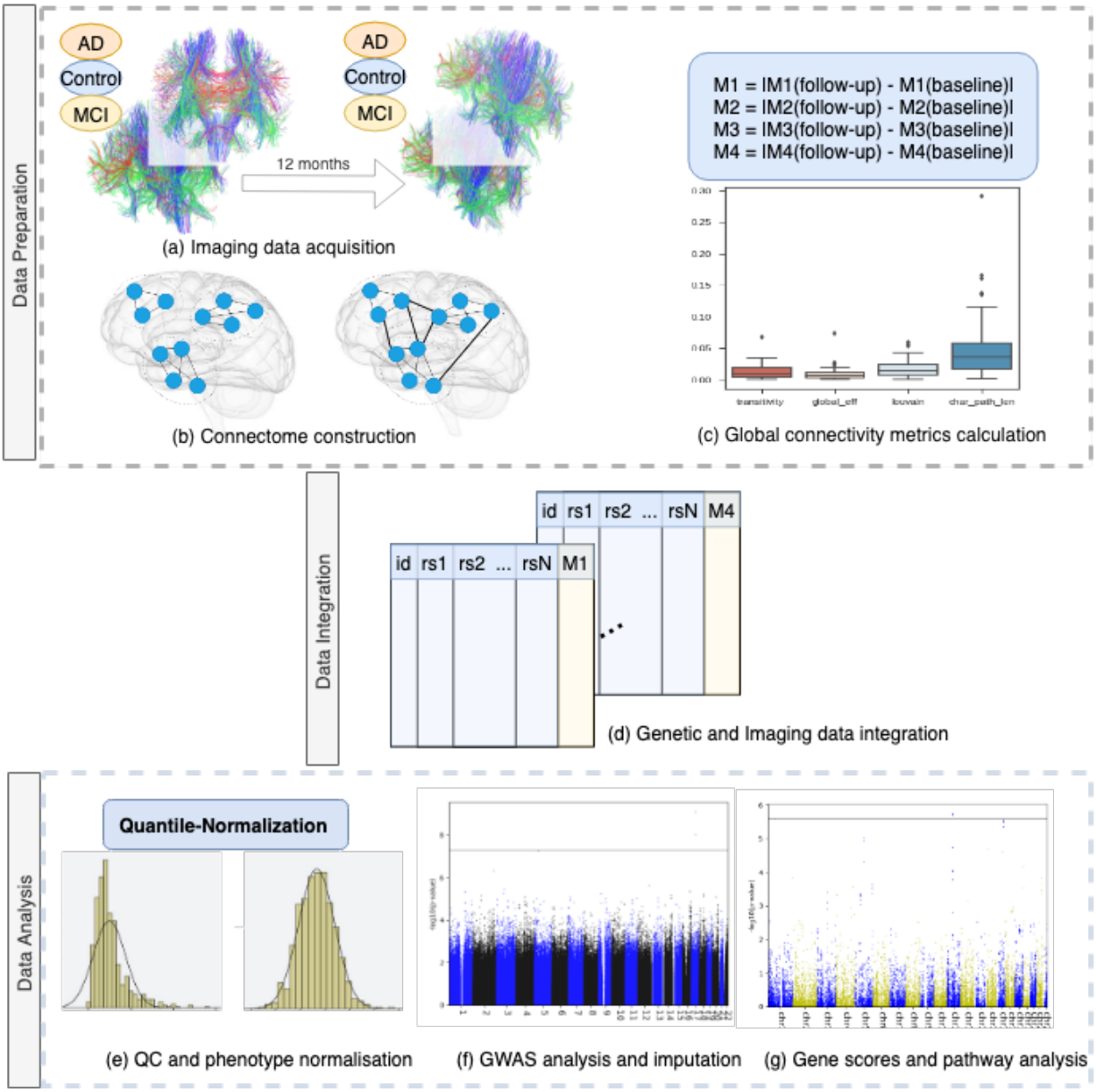

Figure 1. The analysis pipeline: (a) The DTI images were collected at two time points, for three clinical stages of AD. (b) The images were processed using distinct brain regions from the Automated Anatomical Labeling (AAL) atlas, and two structural connectomes were constructed for each participant at each time point. (c) Global connectivity metrics were computed, along with the absolute difference between the baseline and follow-up measures. (d) The latter were merged (as phenotypes) with the PLINK FAM files for all subjects present in both datasets. (e) All essential quality control procedures were performed before GWAS analysis, besides the quantile normalization of phenotypes. (f) GWAS was conducted using PLINK, and, (g) the resulting summary statistics were used by PASCAL software to calculate the gene- and pathway-scores accounting for LD patterns using a reference dataset.

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test, we used the AD patients and controls, most of the metrics turned out to have significant longitudinal differences in the AD brain, but not in a healthy brain. Figure 2 compares the four metrics at the two time points, for each group individually, utilizing their boxplots.

Table 1. Non-parametric Wilcoxon test of the difference between brain connectivity features at baseline and follow-up

Group	**P-values with * are significant**		
	Network Metric	Statistic	P-value
AD	Characteristic path length	107.0	0.0057*
	global efficiency	98.0	0.0033*
	Transitivity	226.0	0.6664
	Louvain	114.0	0.0086*
MCI	Characteristic path length	612.5	0.0891
	global efficiency	672.0	0.2196
	Transitivity	760.0	0.5972
	Louvain	712.0	0.3630
Control	Characteristic path length	496.0	0.2465
	global efficiency	55.0	0.1172
	Transitivity	517.0	0.3421
	Louvain	529.0	0.4062

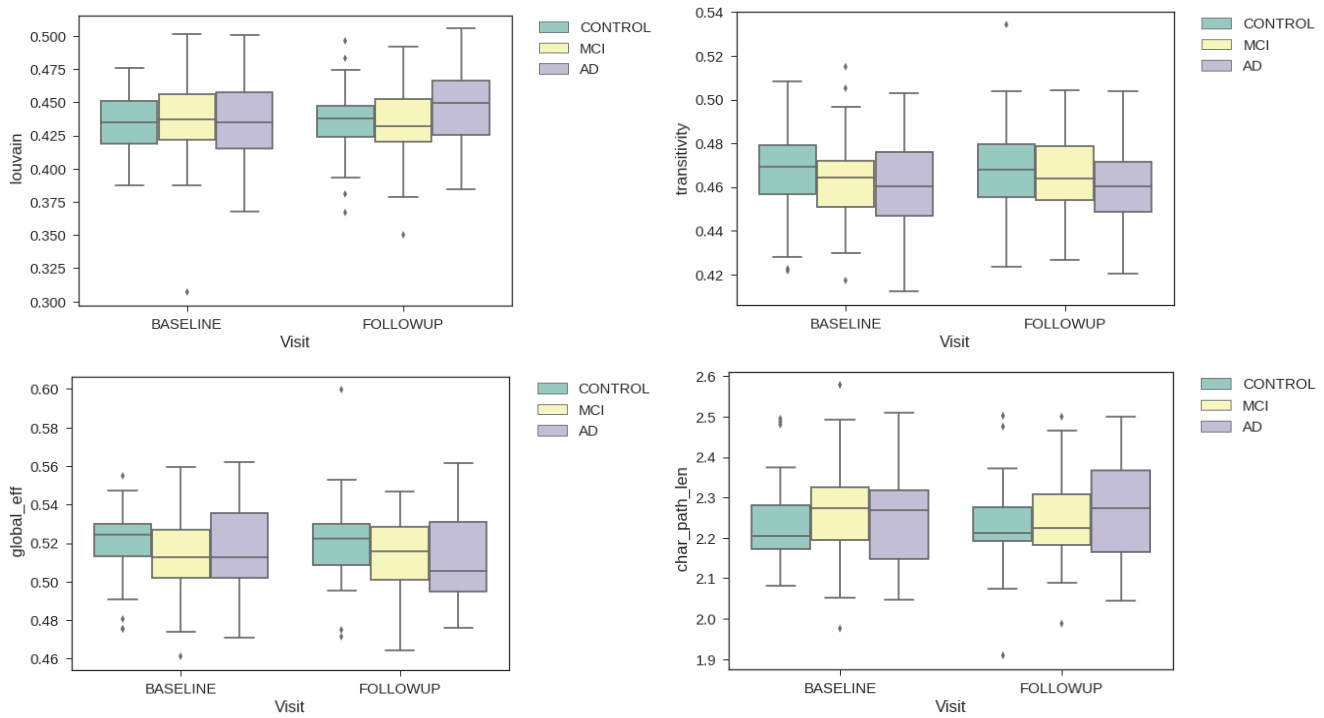

Figure 2. Boxplots for global network metrics to compare AD and controls in the baseline (green) and follow-up (yellow). The metrics are, Louvain modularity (top left), transitivity (top right), global efficiency (bottom left) and characteristic path length (bottom right). It is evident that at least the means for the AD population are different while for the others they are generally unvaried.

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Integrated Analysis

After we obtained our phenotypes of interest, given by the longitudinal changes of the features between the two time points, we started to prepare our data for genome-wide association analysis (see Fig. 1) by first integrating the phenotypes and genotypes.

Quality Control and Data Prepration

There are necessary quality control procedures that precede GWAS analysis, their application on our sample is explained in detail in the Methods section. Briefly, they include cleaning the data such as removing all SNPs with small sample sizes, and individuals with relatedness, as well as population stratification correction — Fig. 3 shows the plots after correcting for the population stratification. We quantile-normalised our phenotypes to allow the use of the linear model in GWAS.

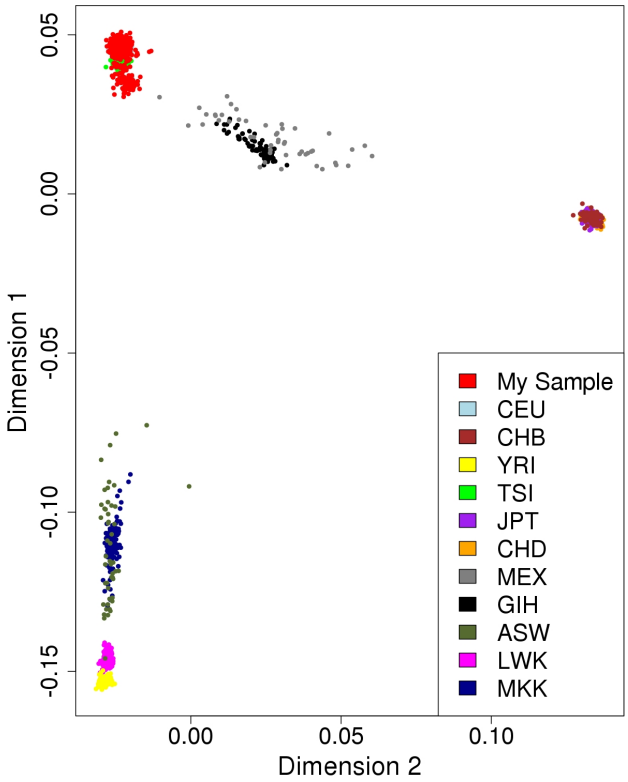

Figure 3. Quality control procedures: The plot shows the estimated ancestry of the genotypes of each study sample (in red) after applying the Multi-Dimensional Scaling (MDS). It also compares the genotype of the samples with a multiple ancestry reference.

Genome-Wide Association Analysis

GWAS was conducted by regressing the normalised longitudinal changes of global connectivity metrics (response variable) on the SNPs' minor allele frequencies (independent variable), one SNP at a time. Using PLINK[21] we conducted four quantitative GWAS - one for each network metric, after which we performed a Gaussian imputation of GWAS summary results. Figure 4 shows the imputed GWAS results for the change in brain segregation metrics. The Manhattan sub-plots appear on the left, while the corresponding quantile-quantile (qq)-plots are on the right. Figure 5 shows the imputed GWAS results for brain integration metrics. The x-axis of the Manhattan plot represents the physical location along the genome, while the y-axis is the $(-\log 10(p-value))$, and each dot represents a single SNP. In the qq-plots, the diagonal line represents the expected (under the null hypothesis) distribution of p-values, and similar to the Manhattan plot, each dot in the qq-plot represents a single SNP.

The top 15 SNP - including the significantly associated SNPs - obtained after imputation of GWAS p-values for the absolute difference in Louvain modularity, transitivity, global efficiency and characteristic path length, are shown in Supplementary Table S1, Supplementary Table S2, Supplementary Table S3 and Supplementary Table S4, respectively. The actual GWAS Manhattan plot for the absolute difference in segregation and integration metrics before imputation are illustrated in Supplementary Fig. S4 and Fig. S5, respectively.

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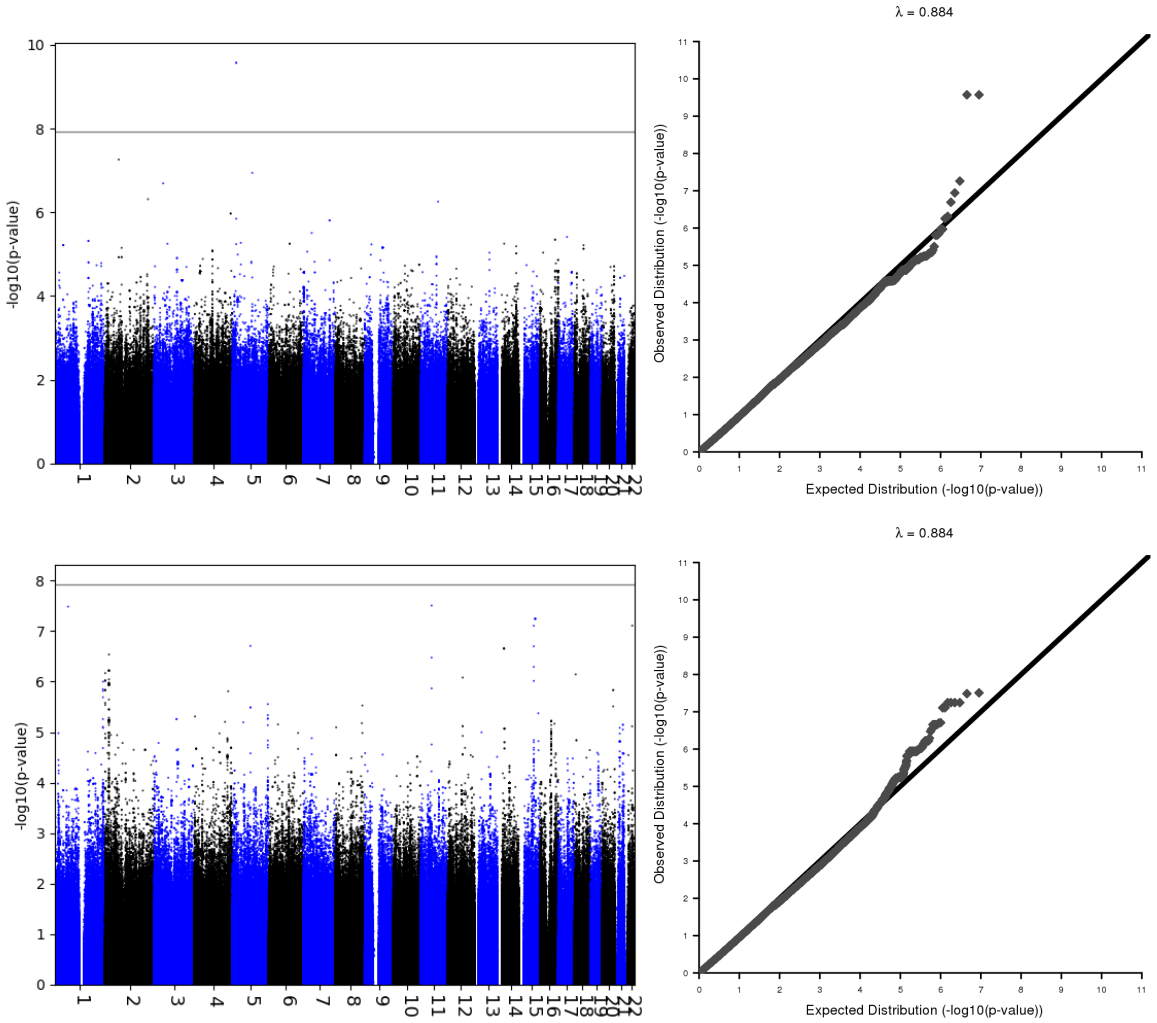

Figure 4. Imputation results of GWAS summary statistics for the change in segregation metrics. Top plots represent the change in Louvain modularity phenotype Manhattan plot (left) and quantile-quantile (qq)-plot (right). Bottom plots represents the change in transitivity phenotype. Louvain modularity imputation results show small evidence of deviation of measures before the tail of the distribution.

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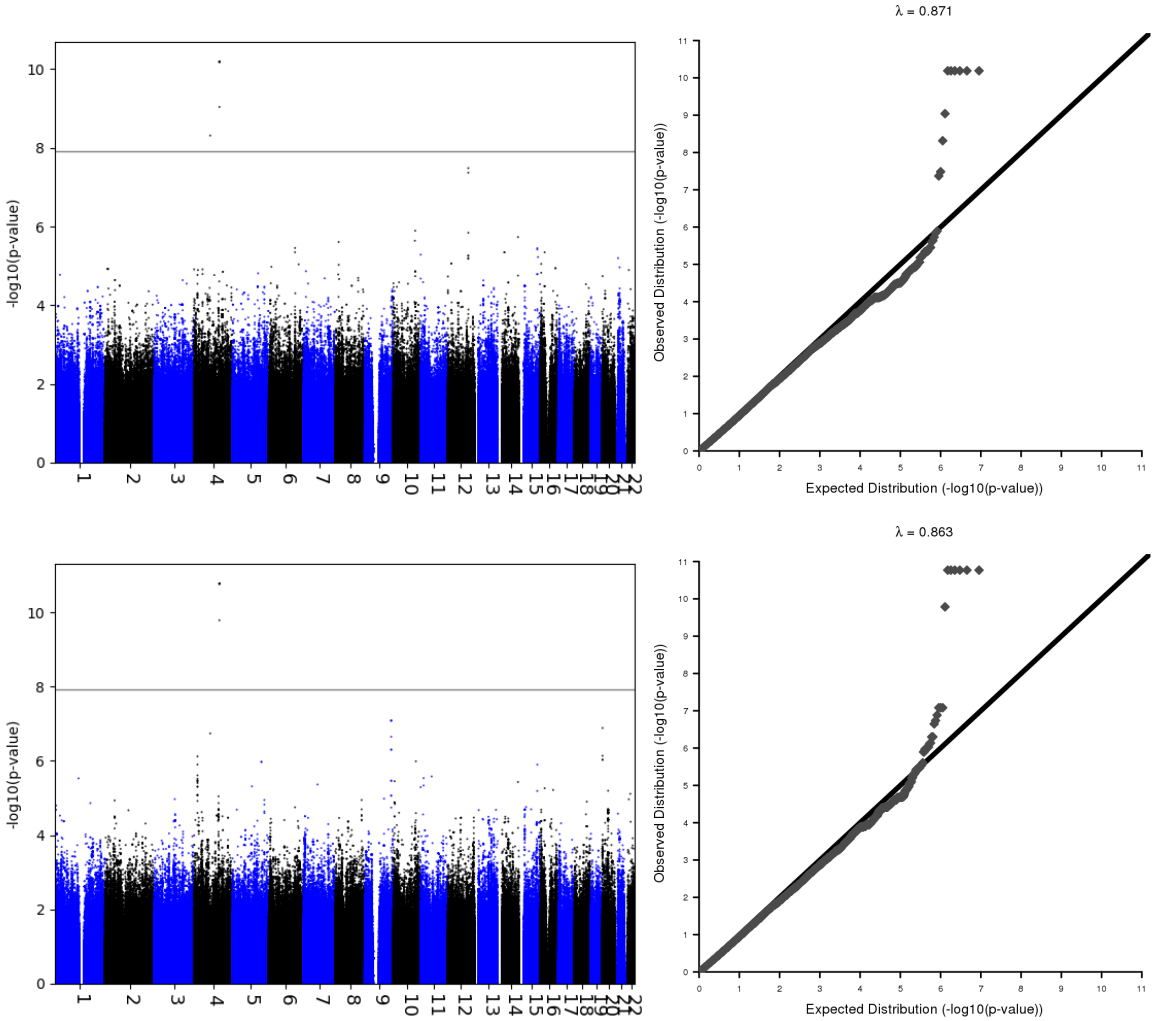

Figure 5. Imputation results of GWAS summary statistics for the change in integration phenotypes. Top plots represent the change in global efficiency Manhattan plot (left) and qq-plot (right), while the plots at the bottom represent the change in characteristic path length phenotype. Both qq-plots show a very little evidence of deviation before the tail of the distribution.

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Table 2. Significant associations between SNPs and global network metrics

SNP ID	Results are sorted according to p-value						
	Chr (Gene)	BP	Eff/Alt	Type	R2	P	Phenotype
rs144596626	5 (CDH18)	19473743	G/A	imputed	0.717	2.68e-10	Louvain
rs146631242	5	19396103	G/A	imputed	0.717	2.68e-10	Lovain
rs112039371	4	125809628	T/C	imputed	0.775	6.48e-11	G Efficiency
rs114045002	4	125825074	C/A	imputed	0.775	6.48e-11	G Efficiency
rs76699517	4	125820645	T/C	imputed	0.775	6.48e-11	G Efficiency
rs78276525	4	125811024	G/T	imputed	0.775	6.48e-11	G Efficiency
rs78538713	4	125821120	T/C	imputed	0.775	6.48e-11	G Efficiency
rs78570105	4	125828439	G/A	imputed	0.775	6.48e-11	G Efficiency
rs7657714	4	125814796	A/C	imputed	0.792	9.12e-10	G Efficiency
rs113323321	4 (ANTXR2)	79976465	C/T	imputed	0.743	4.85e-09	G Efficiency
rs112039371	4	125809628	T/C	imputed	0.775	1.7e-11	C P Length
rs114045002	4	125825074	C/A	imputed	0.775	1.7e-11	C P Length
rs76699517	4	125820645	T/C	imputed	0.775	1.7e-11	C P Length
rs78276525	4	125811024	G/T	imputed	0.775	1.7e-11	C P Length
rs78538713	4	125821120	T/C	imputed	0.77	1.7e-11	C P Length
rs78570105	4	125828439	G/A	imputed	0.775	1.7e-11	C P Length
rs7657714	4	125814796	A/C	imputed	0.792	1.64e-10	C P Length

Gene and Pathway Scores

Using the imputed GWAS association results - namely the p-values, we computed genome-wide gene scores, along with the pathway (gene set) scores. Here we used the PASCAL software[20]. Figure 6 and Fig. 7 are the gene scores obtained for brain segregation and integration phenotypes, respectively.

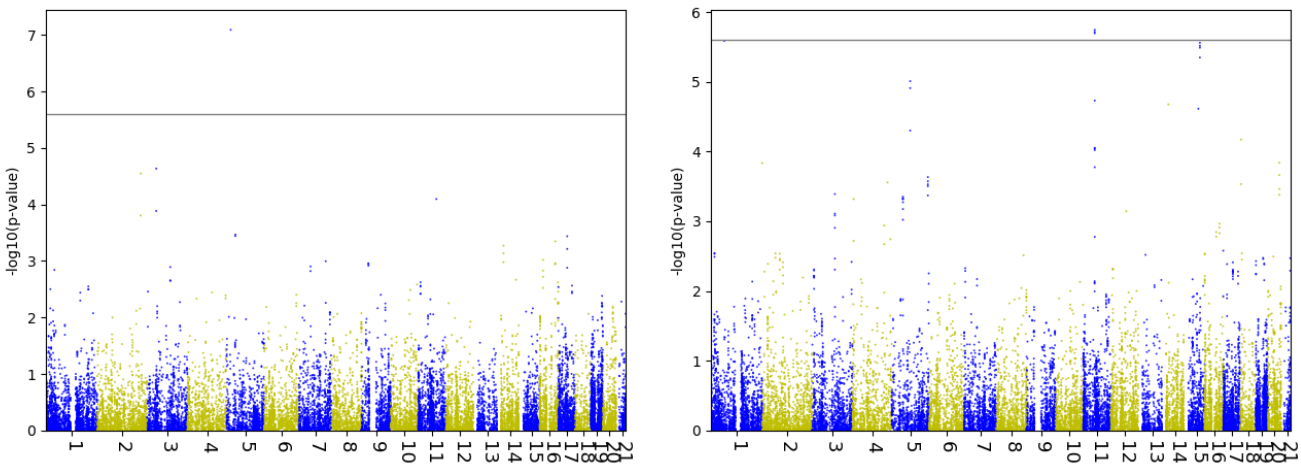

Figure 6. Manhattan plots of gene scores derived from imputed summary statistics for the change in segregation metrics. Lovain modularity appears in the left plot, and transitivity is illustrated by the right plot.

Using the total number of genes in the human genome, that is 20,000; we calculated the threshold. Therefore, we obtain the 5% gene-wide significance threshold by dividing the significance level by the total number of genes (or, tests), i.e.,

$$\frac{0.05}{20,000} = 0.0000025 = 2.5E-6,$$

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Table 3. Top 30 genes: Association results with global network metrics.

Gene	The dashed lines are the 5% and 10% significant thresholds.				
	Gene IDd	No SNPs	Chromosome	$P-value$	Metric
CDH18	1016	3974	chr5	$8.09359866E-8$	Louvain
OR5L1	219437	425	chr11	$1.79431531E-6$	Transitivity
OR5D13	390142	725	chr11	$1.9176502E-6$	Transitivity
OR5D14	219436	615	chr11	$2.00645586E-6$	Transitivity
IGF1	3479	446	chr12	$2.05728046E-6$	G Efficiency
JAK1	3716	670	chr1	$2.58354101E-6$	Transitivity
PSMA4	5685	306	chr15	$2.74836153E-6$	Transitivity
AGPHD1	123688	360	chr15	$3.03262918E-6$	Transitivity
CHRNA5	1138	410	chr15	$3.23116501E-6$	Transitivity
LOC100506100	100506100	133	chr9	$3.76839713E-6$	C P Length
ENDOG	2021	272	chr9	$4.17468163E-6$	C P Length
TBC1D13	54662	283	chr9	$4.18573966E-6$	C P Length
IREB2	3658	476	chr15	$4.47786255E-6$	Transitivity
C9orf114	51490	292	chr9	$4.50675833E-6$	C P Length
ZDHHC12	84885	134	chr9	$4.60713997E-6$	C P Length
PKN3	29941	174	chr9	$5.47820454E-6$	C P Length
ZER1	10444	262	chr9	$5.86368468E-6$	C P Length
LYSMD3	116068	263	chr5	$9.76915765E-6$	Transitivity
STK35	140901	625	chr20	$1.11193271E-5$	C P Length
POLR3G	10622	298	chr5	$1.22724816E-5$	Transitivity
CCBL1	883	394	chr9	$1.42623859E-5$	C P Length
OR5D18	219438	367	chr11	$1.85630017E-5$	Transitivity
SCFD1	23256	636	chr14	$2.10167199E-5$	Transitivity
CDCP1	64866	864	chr3	$2.31367611E-5$	Louvain
THSD4	79875	2560	chr15	$2.4273E-5$	Transitivity
MIR548F2	100313771	441	chr2	$2.82926063E-5$	Louvain
PHYHD1	254295	225	chr9	$3.73413736E-5$	C P Length
LRRC8A	56262	280	chr9	$4.16333012E-5$	C P Length
GPR98	84059	1991	chr5	$4.998E-5$	Transitivity
TMEM200C	645369	338	chr18	$6.73304265E-5$	Transitivity

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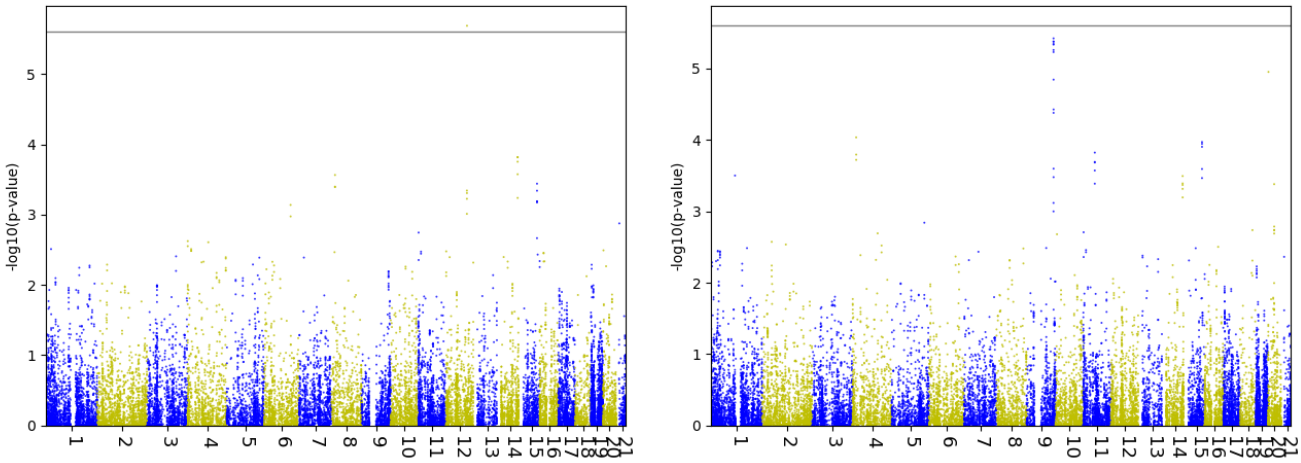

Figure 7. Manhattan plots of gene scores derived from imputed summary statistics for the change in integration metrics. Global efficiency is shown in the left plot, and characteristic path length is illustrated by the right plot.

If we consider less power (90%) and 10% significance level, we get a gene-wide threshold of

$$\frac{0.10}{20,000} = 0.000005 = 5E-6.$$

For each gene score result (and for both brain segregation and integration measures) we sorted our results and constructed a table that contains the top 30 genes, this is shown in Table 3. The table also shows the 5% and 10% significant genes.

In the pathway results obtained for each metric and each chromosome, the total number of pathways used at each step was 1078. Therefore, the 5% threshold is $0.000046382 = 4.6e-5$, while the 10% threshold is $0.000092764 = 9.28e-5$. The gene CDH18 contains 3974 genes as per the data, and was significantly associated with Louvain modularity change over time (p-value $\approx$ 8.09. Meanwhile, on chromosome 11 and chromosome 15, a number of genes were associated with the change in brain connectivity through transitivity, on the other hand chromosome 9 shows a number of significant association results with characteristic path length. Supplementary Table S5 reports all the significant results as well as the top 20 pathways along the whole genome and in all the four phenotypes. As it is shown in the table, REACTOME BIOLOGICAL OXIDATIONS pathway, which consists of genes involved in biological oxidationsat, was significantly associated with the change in Louvain modularity at 5% significance level (p-value=2.91E-5), on chromosome 10.

Discussion

Association studies of human genome variation and imaging features of the brain have led to new discoveries in AD disease susceptibility. Previous GWAS and Next Generation Sequencing (NGS) identified about 20 genetic loci risk factors associated with AD[22]. Moreover, cross-sectional studies of the GWAS of the brain connectome previously successfully identified some correlation between genetic variants and both AD and dementia[19]. Incorporating those imaging features in a longitudinal setting with genetic information facilitates the identification of more genetic risk factors which affect AD progression[23]. Here, we aim to identify the genetic variations which associate with AD brain neurodegeneration over time. The latter is measured as the change in global network metrics of the brain connectome of three clinical stages of AD.

In this study, we demonstrate the validity of a significant change in the global network metrics over time, through Wilcoxon test statistic (shown in Table 1). We tested the distribution of each metric before and after one year, and only the AD brain showed a difference, compared to controls. We proceeded with the analysis by conducting four quantitative genome-wide association tests, taking the absolute difference in the metrics of brain network integration and segregation as individual phenotypes. To our knowledge, this is the first study of its type, to compare longitudinal imaging features of the connectome to genetic information.

In this data, Louvain modularity reveals the SNP rs144596626 (p-value=2.68e-10), located at locus CDH18, to be the most significant SNP to manipulate the change in brain segregation (See Table S1 and Table 3). The CDH18 gene is a cadherin that mediates calcium-dependent adhesion, which plays an important rule in forming the adherens junctions that bind cells. The gene is located on chromosome 5, and it is reported to be highly expressed specifically in the brain, with higher expression in different parts of the Central Nervous System (CNS), including middle temporal gyrus, cerebellum and frontal cortex[24]. The

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gene is associated with several neuropsychiatric disorders, as well as glioma, the most common CNV tumor among adults[25]. Looking at glioma cells, and through in vitro and in vivo functional experiments,[25] et al. showed that CDH18 act as a tumor suppressor through the downstream gene target UQCRC2, and they suggested targeting CDH18 in the gliomas treatment discovery. Moreover, CDH18 was reported in a meta-analysis of depression personality trait association as the nearest gene to rs349475[26].

On the other hand, the change in weighted global efficiency metric over time was significantly affected by the ANTXR2 gene in chromosome 4 (see and 2), through the imputed SNP rs113323321 (p-value $= 4.85e-09$) with imputation accuracy of 0.743. ANTXR2 or ANTXR cell adhesion molecule 2 (also known as HFS; ISH; JHF; CMG2; CMG-2) is well-known to be involved in the development of Hyaline fibromatosis syndrome (HFS) through some mutations. HFS is a collection of rare recessive disorders forming an abnormal growth of hyalinized fibrous tissue; it affects under-skin regions on the scalp, ears, neck, face, hands, and feet. Moreover, some studies reported that ANTXR2 mutations manipulate the normal cell interactions with the extracellular matrix, and its deleterious mutations play an essential role in causing the allelic disorders Juvenile hyaline fibromatosis (JHF) and infantile systemic hyalinosis (ISH)[27,28]. Looking at gene-gene interactions, ANTXR2 interacts with the LRP6 (Low-Density Lipoprotein receptor-related protein 6) gene, which is located in chromosome 12, and is known for its genetic correlation with APOE. Together, their genetic variants, along with the alteration in Wntβ signalling, might be involved in the development of late-onset AD[29].

The segregation of the brain has shown a strong relationship with the olfactory receptor (OR) family 5 (specifically, OR5L1, OR5D13 and OR5D14 - see Table 3), located in chromosome 11, through the change in brain transitivity metric. The OR act together with the odorant molecules in the nose to produce a neuronal response that recognizes smell[30].

Our findings also suggest that the weighted global efficiency change over time significantly associates with the insulin-like growth factor 1 (IGF1) gene, as shown in Table 3. A previous study in mouse brain suggests neuroprotection in a mouse model can be obtained through chronic combination therapy with EPO+IGF-I and cooperative activation of phosphatidylinositol 3-kinase/Akt/GSK-3beta signaling. However, they did not test their model in humans[31].

At 10% significance level, we identified additional genes associated with Alzheimer's brain segregation and integration alterations. The gene ZDHHC12 (zinc finger DHHC-type containing 12), as many others in chromosome 9 - including LOC100506100, ENDOG, TBC1D13 and C9orf114, p-value= $3.76839713E-6$, $4.175E-6$, $4.186E-6$ and $4.507E-6$, respectively, showed a significant score (p-value=4.607E-6) in association with the change in characteristic path length (see Table 3). In an in vitro experiment,[32] showed that ZDHHC12 was able to alter amyloid β-protein precursor (APP) metabolism, and that the failure of AID/DHHC-12 in regulating the transportation or generation of APP in the neurons might result in the early development of AD[33].[34] also reported the Endonuclease G (ENDOG) to mediate the pathogenesis of neurotoxicity and striatal neuron death, through exposing the striatal neurons in mouse with Human immunodeficiency virus-1 (HIV-1) Tat_{1-72}.

Located in chromosome 1, Janus kinase 1 (Jak1) shows a significant score with the change in transitivity metric. The same phenotype was also reported with other significant gene scores, at 10% significance level, in Table 3, such as the proteasome subunit alpha 4 (PSMA4) on chromosome 15, and beside AGPHD1, CHRNA5 and IREB2 (see Fig 6). The dysregulation of the inter-cellular JAK-STAT signaling pathway, which activates Jak1 and Janus kinase protein family, is at the core of neurodegenerative diseases and other brain disorders[35]. The JAK2/STAT3 activation, in particular, was illustrated to protect the neuron, while alteration of the same pathway might play a role in developing neurodegenerative diseases.

We compared our results to previously identified genetic variants in association with Alzheimer's (specifically, SNPs), all genetic variants with p-values less than 0.01, in all global network metrics, are summarised in Table 4. We retrieved the AD SNP list from Ensembl Biomart online software[36]. Our sample reported rs6026398 (β =-0.6496, p-value=0.000814) to be the most significant SNP, and it associates with the change in brain segregation through Louvain modularity. The threshold we set here is $\frac{0.05}{1324}$, as we tested a total of 1324 pathways. None of the SNPs passed that threshold, however, our explanation for this is that those variants might play a significant role in developing AD, but do not contribute that much to its progression over time. A way to take this forward is to target all genes known to affect AD susceptibility and test, in a longitudinal study design, which of them contribute to the progression of Alzheimer's disease through the imaging features. Another recommendation is to consider studying the longitudinal association and consider whether any genetic variant has a biased contribution in different brain regions.

One of the main disadvantages of this work is the sample size. We suspect the underestimation that appears in our initial GWAS results for all four phenotypes excluding transitivity, is due to sample size (Fig. S5 and Fig. S4). In a larger sample, our result is expected to be more robust and to unveil more variants. However, to some extent, GWAS summary statistics imputation (Fig. 4 and Fig. 5) and PASCAL (6 and 7) improved this and unmasked some associations. Another concern here, is that our sample size was not sufficient to estimate the genetic correlation and heritability of our phenotypes. Most of the heritability estimation methods requires large sample sizes (at least $\approx$ 5k samples[37–39]) to yield robust estimates. Besides increasing the sample size, a good practice would be considering more time-points and studying the effect of genes in a survival analysis study design. In this work, we looked at the genetic variations taken at one time-point, and converted the longitudinal imaging

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information into a single measurement to study their association. A possible future focus would be to incorporate clinical and environmental factors such as hypertension and dementia score as well as the gene-gene and gene-environment interaction.

In summary, we conducted a longitudinal study and proposed a fast and straightforward way to quantify changes in the brain connectome through global connectivity measures of 1) segregation, that is Louvain modularity and transitivity, and 2) integration. For the latter, we used two metrics including the characteristic path length and the weighted global efficiency. We conducted a genome-wide analysis, starting with four quantitative GWAS, regressing the pre-mentioned global network metric on the whole-genome SNP, and then computed the gene scores by aggregating the GWAS summary statistics at a genome-wide level. In the ADNI sample we used here, and at a power of 95%, we identified significant SNPs and genes. The Louvain modularity change was affected by the ANTXR2 gene, while through transitivity, the change in brain connectivity is associated with OR5L1, OR5D13 and OR5LD14. On the other hand, the integration of the brain varies in relation to IGF1. A greater understanding of the genetic contribution and relationship of these genes and their effect over time through targeted studies, might facilitate the development of drug therapy to reduce the disease progression.

Methods

Datasets

Our analysis was conducted on the Alzheimer's Disease Neuroimaging Initiative (ADNI) dataset publicly available at (`adni.loni.usc.edu`). The initiative was launched in 2003 as a public-private partnership, led by Principal Investigator Michael W. Weiner, MD (see `www.adni-info.org` for updates). To match the aim of our study, we combined two types of ADNI datasets:

1) DTI volumes was taken at two-time points, at the baseline and after 12 months (we refer to this as follow-up). In this set, we used a cohort comprised of 31 Alzheimer's disease patients (age: 76.5 ± 7.4 years), and 49 healthy elderly subjects (77.0 ± 5.1) matched by age, as well as 57 MCI subjects (age: 75.34 ± 5.93).

2) The PLINK binary files (BED/BIM/FAM) genotypic data for AD, controls and Early MCI.

The DTI and T1-weighted were obtained by using a GE Signa scanner 3T (General Electric, Milwaukee, WI, USA). The T1-weighted scans were acquired with voxel size = $1.2 \times 1.0 \times 1.0\ mm^3$ TR = 6.984 ms; TE = 2.848 ms; flip angle=11°). DTI were acquired at voxel size = $1.4 \times 1.4 \times 2.7\ mm^3$, scan time = 9 min, and 46 volumes (5 T2-weighted images with no diffusion sensitization b0 and 41 diffusion-weighted images b=1000 s/mm^2).

Preprocessing of Imaging Data

Imaging data have T1 and DTI co-registered. To obtain the connectome; the AAL atlas[40] is registered to the T1 volume of reference by using linear registration with 12 degrees of freedom. Despite the AAL atlas has been criticized for functional connectivity studies[41], it has been useful in providing insights in neuroscience and physiology and it is believed to be sufficient for our case study centered on global metrics. Tractographies for all subjects were generated processing DTI data with the Python library Dipy[42]. In particular, a deterministic algorithm called Euler Delta Crossings[42] was used stemming from 2,000,000 seed-points and stopping when the fractional anisotropy was smaller than < 0.2. Tracts shorter than 30 mm, or in which a sharp angle (larger than 75°) occurred, were discarded. To construct the connectome, the graph nodes were determined using the 90 regions in the AAL atlas. Specifically, the structural connectome was built as a binary representation when more than 3 connections were given between two regions, for any pair of regions.

Brain Connectivity Metrics

To assess longitudinal changes, we evaluated the following global network metrics at the two time points, at the baseline and follow-up. We then computed the absolute difference between the two measures, at each of the network metrics.

To be in line with previous work on AD and connectomics[19,43,44], we focused on specific network segregation and integration features. Segregation represents the ability of a network to form communities/clusters which are well-organized[45]. While, integration represents the network's ability to propagate information efficiently[45].

1) Louvain modularity. This is a community (cluster) detection method, which iteratively transforms the network into a set of communities; each consisting of a group of nodes. Louvain modularity uses a two-step modularity optimization[17]. First, the method optimizes the modularity locally and forms communities of nodes, and secondly, it constructs a new network. The nodes of the new network are the communities formed in the previous step. These two steps are repeated iteratively until maximum modularity is obtained, and a hierarchy of communities is formed. For weighted graphs, Louvain modularity is defined as in Equation 1.

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Table 4. The top 22 (p-value < 0.01) association results of AD SNPs obtained from Ensembl BioMart

SNP	Results are sorted according to p-value							
	BP	Beta	Statstic	Chr	Eff/Alt	Type(R2)	P-vale	Metric
rs6026398	57180009	-0.6496	-3.544 (t)	20	G/A	gwas (1)	0.000814	Louvain
rs6665019	25328009	0.834	3.466 (t)	1	A/G	gwas (1)	0.00105	Louvain
rs2075650	45395619	0.6423	3.094 (t)	19	G/A	gwas (1)	0.0031	G Efficiency
rs78910009	86408183	NA	-2.9 (z)	16	G/T	imputed (0.83)	0.00368	C P Length
rs11218343	121435587	-1.025	-3.029 (t)	11	C/T	gwas (1)	0.00373	C P Length
rs4746003	71538292	-0.6693	-2.976 (t)	10	T/C	gwas (1)	0.00433	C P Length
rs8014810	36325030	0.7447	2.975 (t)	14	T/G	gwas (1)	0.00434	Transitivity
rs362389	73688861	1.284	2.93 (t)	14	C/A	gwas (1)	0.00492	Louvain
rs73310256	92438849	-1.179	-2.916 (t)	10	C/T	gwas (1)	0.00513	G Efficiency
rs4803760	45333834	-0.5974	-2.868 (t)	19	T/C	gwas (1)	0.00585	Transitivity
rs11218343	121435587	-0.9691	-2.838 (t)	11	C/T	gwas (1)	0.00635	G Efficiency
rs157582	45396219	0.522	2.836 (t)	19	T/C	gwas (1)	0.00641	G Efficiency
rs362384	73686310	0.9341	2.834 (t)	14	A/C	gwas (1)	0.00641	Transitivity
rs58920042	71981089	NA	-2.72 (z)	3	C/T	imputed (0.729)	0.00646	Louvain
rs117780815	124326227	-1.555	-2.793 (t)	6	T/A	gwas (1)	0.0073	Louvain
rs362393	73689629	0.924	2.788 (t)	14	A/G	gwas (1)	0.00732	Transitivity
rs1925690	87867063	0.8101	2.791 (t)	6	T/C	gwas (1)	0.00743	Transitivity
rs7364180	42218856	-0.5574	-2.775 (t)	22	G/A	gwas (1)	0.00754	G Efficiency
rs4746003	71538292	-0.6278	-2.765 (t)	10	T/C	gwas (1)	0.00772	G Efficiency
rs9969729	108631950	-1.04	-2.713 (t)	9	A/G	gwas (1)	0.00911	Louvain
rs117969561	101211189	-1.796	-2.702 (t)	13	T/C	gwas (1)	0.00935	C P Length
rs889555	31122571	-0.4928	-2.689 (t)	16	T/C	gwas (1)	0.00946	G Efficiency

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2) Transitivity. This also quantifies the segregation of a network, and is computed at a global network level as the total of all the clustering coefficients around each node in the network. It reflects the overall prevalence of clustered connectivity in a network[17]. Transitivity is mathematically defined by Equation 2.

3) Weighted Global Efficiency. This is a network integration feature, and represents how effectively the information is exchanged over a network. This feature can be calculated as the inverse of the average weighted shortest path length in the network, as shown in Equation 3.

4) Characteristic Path Length. This measures the integrity of the network and how fast and easy the information can flow within the network. The characteristic path length of the network is the average of all the distances between every pair in the network (see Equation 4).

$$Q = \frac{1}{2m} \sum_{ij} \left[A_{ij} - \frac{k_i k_j}{2m} \right] \delta(c_i, c_j), \tag{1}$$

where A_{ij} is the weight of the edge connecting nodes i and j from the adjacency matrix $\mathbf{A}$, k_i and k_j are the sums of weights of the edges connected to node i and j. respectively, $m = 1/(2A_{ij})$, c_i and c_j are the communities of nodes i and j, and δ is a simple delta function.

$$T^W = \frac{\sum_{i \in N} 2t_i^W}{\sum_{i \in N} k_i(k_i - 1)}, \tag{2}$$

where t_i^W is the weighted geometric mean of triangles around node i, and k_i its degree.

$$E^W = \frac{1}{n(n-1)} \sum_{i \in N} \sum_{j \in N, i \neq j} (d_{ij}^W)^{-1}, \tag{3}$$

d_{ij}^W, is the weighted shortest path length between node i and j, and n is the number of nodes.

$$L^W = \frac{1}{n(n-1)} \sum_{i,j \in N, i \neq j} d_{ij}^W. \tag{4}$$

where, d_{ij} be the number of links (connections) which represent the shortest path between node i and j

An illustrative example of global network connectivity metrics is shown in Fig. 8, the figure consists of segregated (left) and integration (right) network.

Integration of the two datasets

To quantify the longitudinal change in brain connectivity, we calculated the absolute difference between the baseline and follow-up, for each brain connectivity metric. We then merged the absolute differences with the PLINK fam file, matching the two datasets by the subject ID.

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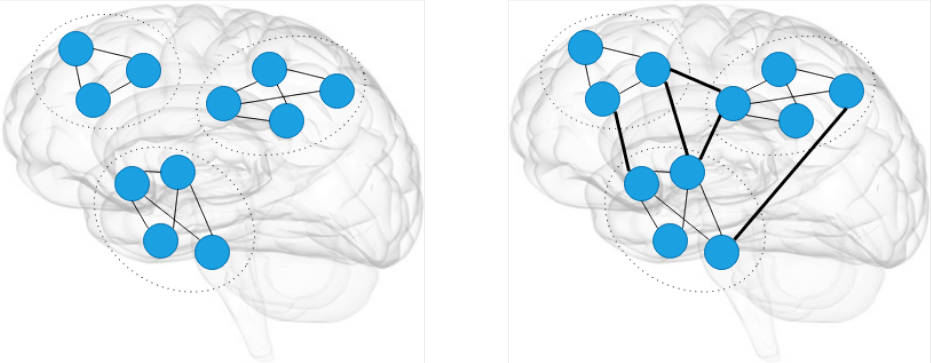

Figure 8. An illustrative figure of brain segregation (left) and brain integration (right)

Quality Control

Quality Control: Individuals

After merging the two datasets into PLINK files, we started to perform some quality control procedures. First of all, we applied quality control at individual-level and removed all poor samples. In order to identify those samples, we used PLINK software and the following criteria:

1) Sex-check - here we identified all samples with ambiguous sex and removed them. We used the flag –check-sex .

2) Identifying all the individuals with missing genotype data with the flag –missing. This is to check the missingness rate of genotype information for each individual. In our sample, the percentage of missingness for all individuals fell within the range (0.002834, 0.00544), since all subjects have passed the threshold of 10% missingness.

3) We ran one more step to identify Related Subjects (with Identity By Descent (IBD) > 20%), all subjects had IBD between 0.00 and 0.0526. We used a number of PLINK flags, including; –indep-pairwise 50 5 0.2, –extract, –genome, –min and –genome-full

After applying those quality control steps, we had a total of 57 subjects remaining for the rest of the analysis.

Quality Control: Genotypes

We ran quality control on the genotypes, by filtering them in terms of their minor allele frequency (MAF) with a threshold of 0.01. Here all SNPs with less than this threshold are considered rare SNPs and were removed from the analysis. We also removed all SNPs that had missingness more than 33.33 or Genotype Call Rate < 66.67% - this was done in such a way that keeps only SNPs with sample size no less than 38. In addition, SNPs which deviate from the Hardy-Weinberg Equilibrium (HWE) were removed, those are SNPs that have p-values of less than 5e-7 in the HWE test[46] (in total 351 SNPs do not satisfy the HWE). We used the flags, –maf, –geno and –hwe, and in total 7111195 SNPs remained.

Quality Control Correcting for Population Stratification

In this quality control step, we checked for the multiple presence of subpopulations in our sample. This is to make sure if we find significant variants, that the differences in allele frequencies is due to the trait under study and controlled for the different ethnic groups. Population stratification helps to avoid false positives[47]. Using multiple ancestry reference genotypic information, we compared the genotypes of each study sample and estimated its ancestry with the Multi-Dimensional Scaling (MDS) analysis[48]. We observed that most of our samples belong to the Caucasian population (CEU) and therefore, proceeded by only selecting the Caucasian samples in our study. In the figure, we show the genotypes of our samples compared with the reference data, before (left) and after (right) the population stratification correction. As a result of this step, we included all 57 samples as all belong to the CEU (Caucasian) ancestry. All previous quality control procedures used here followed the ENIGMA protocol[48].

Quantile Normalisation of Phenotypes

Supplemenrary Fig. S1 and Supplementary Fig. S3 indicate that our phenotypes are not symmetrically distributed, and there are potential outliers. Linear models assume asymmetric distribution of the response variable. Therefore, to allow the use of linear models and conduct quantitative GWAS for our traits, we first had to normalize our phenotypes. Here, we used PLINK2[49] (www.cog-genomics.org/plink/2.0/) to perform a quantile normalization[50] to our phenotypes, using the flag –quantile-normalized.

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Integrated Data Analysis

Genome-Wide Association Analysis

We performed four quantitative GWAS separately using PLINK software[21] (http://pngu.mgh.harvard.edu/purcell/plink/). A GWAS for each network connectivity metric - measured as the absolute difference between the baseline and follow-up – was performed with 57 individuals, and a total of 7111195 SNPs.

Statistical Thresholds

To correct for multiple testing, we rely on the Bonferroni correction[51,52], using the simple equation below,

$$\alpha^* = \frac{\alpha}{M},$$

where, M is the number of tests, and α is the desired significance level. The p-values are then compared with the threshold α^*.

Imputation of GWAS Results

More quality control was done before the imputation of GWAS summary statistics using Functionally-informed Z-score Imputation (FIZI) python tool (https://pypi.org/project/pyfizi/, https://github.com/bogdanlab/fizi). Using the munge function, where 4763 SNPs with duplicated rs numbers and 85757 SNPs with $N < 38.0$ were removed with a remaining number of 6792416 SNPs. We then imputed those summary statistics with ImpG-Summary - Imputation from summary statistics algorithm[53]. In this step, we rely on the European 1000 Genomes[54] haplotypes as a reference panel and performed the Gaussian imputation with FIZI. We then manage to impute additional 2222623 summary statistics.

Gene-Wide Scores and Pathway Analysis

After we obtained the GWAS association results, we used them as input for the PASCAL software[20] to aggregate SNPs at a gene level, and hence, compute gene scores for the four network measures. Along with the obtained association statistics; PASCAL uses a reference population from the 1000 Genomes Project to correct for linkage disequilibrium (LD) between SNPs. We set PASCAL to compute the gene score as well as the pathway scores, according to the max of chi-square statistics. We got a p-value for each gene, and for each gene set (or, pathway) provided that there were SNPs presents for that gene. Finally, we used Python to plot the Manhattan plot, and R studio[55] to plot the qq-plots. All steps are summarized in the pipeline shown in Figure 1.

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Author Contributions Statement

A.C. applied and obtained access to the data needed in this analysis from ADNI. A.C. ran all neuroimaging analysis, S.S.M.E. conducted the imaging genetic analysis and wrote the paper with A.C., N.J.M. and A.C gave continued feedback and closely followed-up the progress. E.R.C. gave constructive feedback on the analysis, and all authors proofread the final version of the paper.

Additional Information

Data Availability: The data used in this work is available at the ADNI repository (http://adni.loni.usc.edu/).
Supplementary information: Supplementary materials available for this paper.
Competing interests The authors declare no competing interests.