

Global-To-Local Segmentation and Genotypic Analysis Of Brain Shape Asymmetry

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Abbreviations

3D three-dimensional

AD Alzheimer's disease

ADHD attention-deficit / hyperactivity-disorder

AI asymmetry index

ANOVA analysis of variance

ASD autism spectrum disorder

BD bipolar disorder

CCA canonical correlation analysis

CNS central neural system

D-V dorsal-ventral

DA directional asymmetry

DK Desikan-Killiany

DNA deoxyribonucleic acid

DOF degree of freedom

FA fluctuating asymmetry

FDR false discovery rate

GLM generalized linear model

GO gene ontology

GPA generalized Procrustes analysis

GRM genetic relationship matrix

GSEA gene set enrichment analysis

- GWAS** genome-wide association studies
- HCP** Human Connectome Project
- HSC** hierarchical spectral clustering
- L-R** left-right
- LD** linkage disequilibrium
- LDSC** LD score correlation
- LDSC-SEG** LD score regression applied to specifically expressed genes
- LDSR** LD score regression
- LFC** language functional connectivity
- MAF** minor allele frequency
- MDD** major depressive disorder
- ML** machine learning
- MRI** magnetic resonance imaging
- MSS** mean sum of squares
- mvGWAS** multivariate genome-wide association study
- NMI** normalized mutual information
- NPC** neuroepithelial cell
- OCD** obsessive/compulsive disorder
- PC** principal component
- PCA** principal component analysis
- PD** Parkinson's disease
- PLSR** partial least squares regression
- R-C** rostral-caudal
- RGC** radial glial cell
- RNA** ribonucleic acid
- RSS** residual sum of squares
- SNP** single nucleotide polymorphism
- SVD** singular value decomposition
- TF** transcription factor

Abstract

The overall purpose of this thesis has been to complement the existing bibliography on the detection and examination of the genetic associations of brain shape asymmetry. Asymmetry components are computed based on the brain magnetic resonance imaging dataset provided by UK Biobank database. A data-driven approach is followed, where the brain surface is partitioned in an unsupervised manner, through hierarchical spectral clustering, a technique that allows for a coarse-to-fine segmentation. Aggregated asymmetry measurements are retrieved from the segments, whose genetic association is examined through a multivariate genome-wide association study statistical analysis. Recognized significant single nucleotide polymorphisms were then analyzed individually or in groups, through comparison with existing results and databases. The genetic overlap with neurodevelopmental disorders and traits, that have been reported to exhibit phenotypic associations with brain structure asymmetry, such as autism, Alzheimer's disease or intelligence, were examined. Functional annotations of variants associated with the genes where significant single nucleotide polymorphisms were detected were obtained, offering an insight into the functional reasoning behind the brain shape asymmetry existence.

Chapter 1

Introduction

1.1 Biomedical and anatomic principles

1.1.1 Bilateria lineage

Cerebral bilateral symmetry is a universal quality of organisms belonging to the Bilateria lineage [? ?], the phylum incorporating all species with a single plane of symmetry, in contrast with their sister group, Cnidaria (??). Bilateral symmetry is a byproduct of the activity of two separate developmental processes. Those produce two axes of polarity [?], and therefore a symmetry plane. Firstly, the formation of primary body axis, that corresponds to the long anatomical dimension of the animal, called rostral-caudal (R-C) (i.e., head-to-tail), is primarily dictated by highly conserved controlled activation of HOX genes during cell differentiation. Secondly, the shaping of a secondary body axis, orthogonal to rostral-caudal, named dorsal-ventral (D-V) (i.e., back-to-front), is attributed to a variety of genes, such as the chromatin organizer CTCF, the left-right determination factor Nodal and central HOX genes [?]. The remaining axis, left-right (L-R), is the one along which the symmetry pattern is manifested. On account of the high biodiversity that bilateria group includes, only the subgroup of vertebrates is examined in the following literature study. In addition, any reference to symmetry or asymmetry from now on corresponds to the left-right direction, unless explicitly mentioned otherwise.

This study makes an effort to statistically identify the genetic origins of a complex structural phenotype. Hence, examining, based on existing research, the main brain developmental stages is essential to discern the processes that induce bilateral symmetry. An important vertebrates (and bilateria) common characteristic is the germ line **triploblasticity**: the embryo begins as a flat disk, through a process called **gastrulation**, with three distinct cell layers; **endoderm**, **mesoderm**, and **ectoderm** [?]. Of significance in the neural system formation is the ectoderm, which is initially equivalent to one of the flat disk sides. Under the context of this study, although a fact not directly connected to the brain's cortex, it is necessary to mention that the perfect bilateral symmetry pattern appears to break even before gastrulation. In *Xenopus* (frog species) embryos, during fertilization and the initial 4-cell cleavage of the fertilized egg, the **cytoskeleton microtubules** appear to asymmetrically

localize the ion channels proteins, whose RNA has been passed on by the mother, with a preference for the right side of the complex [?]. Chick embryos also exhibit a similar pattern. The occurrence of asymmetry at this extremely early time point underlines the significant role it has on the embryo development, species fitness, and, concomitantly, the conservation potential of this trait drivers [?]. Another cellular component that is considered to enhance asymmetry, during gastrulation, is the motile cilia, hair-like organelles on the cell surface with the ability to beat [?]. Their movement is by construction asymmetric, causing a leftward flow of extraembryonic fluid and, subsequently, asymmetric distribution of exogenously introduced proteins [?]. Both studied phenomena point to early initiation of asymmetric genes expression.

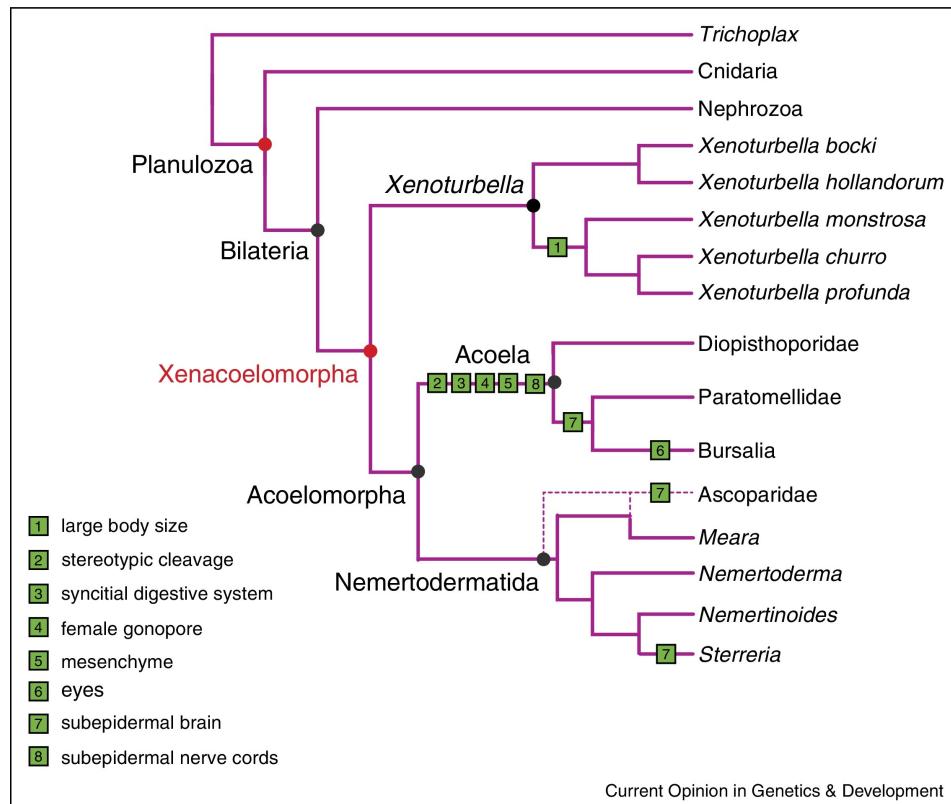


FIGURE 1.1: Species phylogenetic tree subset, displaying bilateria clade, its sister clade, Cnidaria, and the direct children[?]. Of great importance on the evolutionary studies of bilateral symmetry is the Xenacoelomorpha clade.

1.1.2 Symmetry during CNS formation

Shortly after gastrulation, the disk folds, in such a way that the central region of the ectoderm, called neural plate, forms a tube-like shape, the **neural tube**, which acts as the neural system precursor, under a process called **neurulation**. All bilateria have a central neural system (CNS), which entirely develops from the neural tube walls [?]. The next pivotal step in the brain development, **differentiation**, leads to the creation

1.1. Biomedical and anatomic principles

of three distinct compartments along the rostral-caudal axis, at the neural tube rostral end, the **prosencephalon** (forebrain), which develops into the brain cerebrum, the **mesencephalon** (midbrain), and the **rhombencephalon** (hindbrain), that is later attached to the spinal cord in vertebrates. For the subsequent mechanisms and terminology to be compatible with human cerebrum related literature, the focus is shifted on the mammals' phylum and, spatially, on the prosencephalon. The differentiation proceeds, with two pairs of lumps extruding symmetrically from the prosencephalon, the **telencephalic** vesicles, the predecessors of cerebral region, and the optic vesicles, the precursors of optic nerves and retinas, while the central remaining, linking structure is called **diencephalon** [?]. The formed symmetry plane is called **midsagittal**. The telencephalic vesicles continue to grow, expanding also caudally and in parallel with the diencephalon, gradually assuming the form of the two hemispheres, while a new pair of vesicles appears on the rostral part of the diencephalon, giving rise to the **olfactory bulbs**. The neural tube shape also reacts to the changes, forming four distinct **ventricles** along the neural tube, with two of them, named **lateral ventricles**, being mirrored inside each of the telencephalic vesicles. The earliest stage where asymmetry is noted in an anatomic level inside the human brain is during the end of the first trimester of gestation [?]. Specifically, the choroid plexus, a specialized cell network that lies inside the ventricles, attached to the diencephalon, and produces most of the **cerebrospinal fluid** in the central neural system, develops asymmetrically in each lateral ventricle. The cerebrospinal fluid is of great value for the developing brain, as the main source of nourishment, waste removal and protection [?]. Such an asymmetry manifestation at a macroscopic level, therefore, may be the progenitor of other forms of asymmetry at a later developmental stage [?], even at the brain surface. Cerebral bilateral symmetry therefore begins breaking down during fetal development, producing an asymmetric brain (??), and giving rise to partial functional disassociation, called **brain lateralization**. Lateralization becomes visible when examining organisms' behavior, with the most studied trait in humans being handedness and language [? ?]. To better understand why and how the inner functions are related with the external brain cortex development, the underlying cellular processes of **neurogenesis** and **neuron migration**, active throughout differentiation, need to be identified, before introducing the reader to the anatomy of the fully grown brain. For this purpose, a further focus on the primates' phylum is needed, given the differences exhibited when comparing different mammals, such as rodents[?].

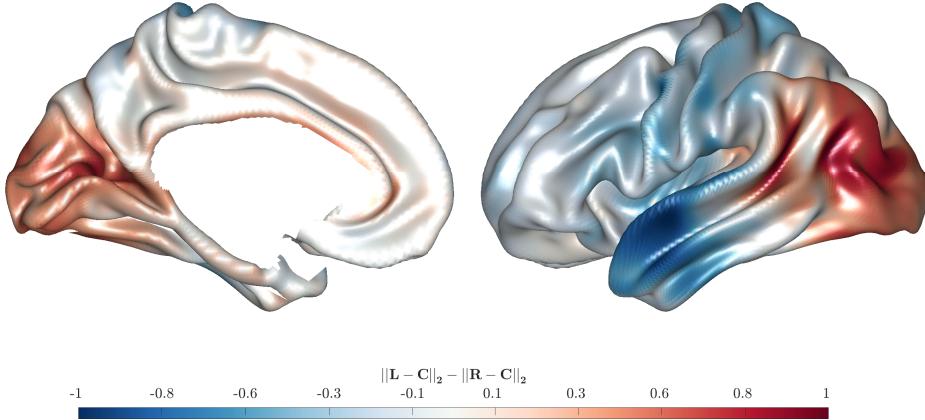


FIGURE 1.2: Illustration of human cerebrum brain asymmetry. Normalized differences of the distances of each hemisphere rescaled, rotated and averaged surface landmarks from the center of mass. See ?? for more details on the preprocessing.

1.1.3 Neurogenesis, neuronal migration and plasticity

The cells initially comprising the neural tube walls are named neuroepithelial cells, and exhibit similar properties with stem cells, that is limited multipotency (i.e., they can differentiate into multiple cell types) and limited self-renewing (i.e., they can divide symmetrically into new neuroepithelial cells a finite number of times), while also properties of epithelial cells, that is polarity (i.e., asymmetric cellular organization, with distinct basal and apical surfaces) and attachment (i.e., junctions tightly connect adjacent cells) [?]. This cells array is contained between the basal and apical laminae, lipid membranes lateral to each other, with the apical lamina facing the neural tube lumen [?], and the cells being radially distributed. During anatomical differentiation, around the 7th gestational week in humans [?], self-renewing is activated, leading to cells proliferation and central neural system bilateral expansion, while attachment is hindered, gradually exchanging the neuroepithelial cells with radial glial cells, the fate-restricted progenitors of neurons, marking the initiation of **neurogenesis**[?]. A radial glial cell acts as the main building block of the brain, from which a single neuron or a neural progenitor, that later divides symmetrically in neurons, is generated. Radial glial cells' pivotal role does not end here. As it can be seen in ??, RGCs are stretched during development, with processes connected to the surface of neural tube successor ventricles and to the outer cortical region surface, forming thread-like scaffolds. Newly formed neurons, generated from the RGCs main, oval body, which remains close to the ventricles, use this structure as a guide to move towards the outer region of the cortex, under a process named **neuronal migration**[?]. This type of movement implies that the newly formed neurons head towards the brain surface, building the brain in an

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inside first, outside last fashion [?]. At later stages of human gestation, around week 19, studies have shown that a morphological transition happens, where the majority of radial glial cells stops being attached to the **pial surface**, the outer surface of the brain, limiting the migration ability of neurons [?] and affecting the way new layers are formed. Human neurogenesis extends to the third gestation trimester, being suppressed in case of premature birth [?]. Postnatal neurogenesis is therefore presumed to be quite limited for primates [?], despite the fact that the postnatal brain dramatically increases in size, with that attributed to a rapid increase in neuronal connections and glial cells (i.e., cells that provide physical and metabolic support to neurons) number [?]. The environmental factors that may affect brain lateralization are mainly detected before or during birth, with epigenetics and birth complications appearing to be mostly correlated with handedness [? ?]. However, the human brain exhibits high **plasticity**, namely the ability of intrinsic or extrinsic factors to change the neurons connectivity, setting aside the genetic predisposition, a property that has been proven to particularly affect the brain surface asymmetry in studies with monozygotic twins [? ?]. In general, though, the more complex the phenomenon and the closer it is to humans, the higher the uncertainty and the greater the ethical implications. Only recently, non-invasive imaging and transcriptomic techniques have given out further details regarding the brain development sequence, with genetic studies indirectly identifying the landscape of the underlying genes that affect different brain regions formation and symmetry [?]. Moving on the literature study path and getting closer to the studied phenotype, the fully grown human brain cerebrum is subsequently anatomically described.

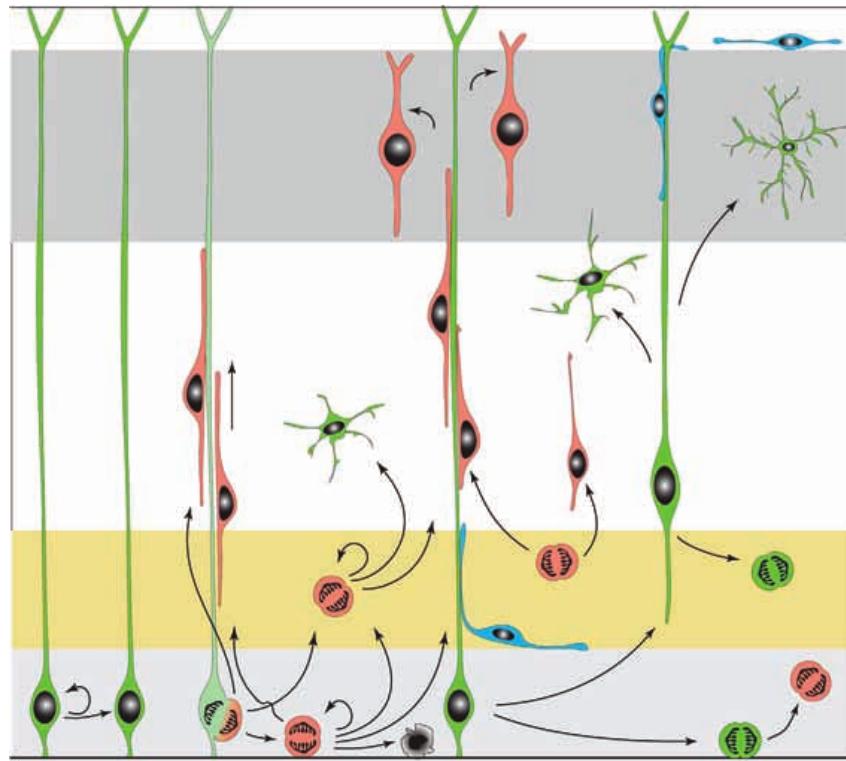


FIGURE 1.3: Illustration of a classical model of radial glial cells complex nonlinear division processes and neuronal migration [?]. From left to right: NPCs (green) originally divide symmetrically; During differentiation, NPCs become RGCs, which divide asymmetrically, generating neurons or neural progenitor cells (orange). Neural progenitor cells eventually divide symmetrically into neurons. The majority of neurons in humans is produced by neuronal progenitors. A part of the generated neurons migrate radially towards the cortical plate, by attaching on the RGCs projections; Eventually, after brain maturation, most RGCs in humans undergo apoptosis (i.e., cell death) or generate neurons-supporting cells, such as astrocytes.

1.1.4 The adult human cerebrum anatomic and functional properties

The human cerebrum is the center of sensations and thinking. The following excerpt provides a summarized anatomic [?] and functional [?] perspective. As aforementioned, the cerebrum is entirely produced from the telencephalon during fetal development, with the telencephalic vesicles ending up becoming the two hemispheres, that remain connected through what is known as the **Corpus callosum**. The side view of each hemisphere is named **lateral**, and the view of the inner side is called **medial**. The human cerebrum outer covering surface is called **cerebral cortex**, the region on which the current study focuses. The human cerebrum appears distinctly different from other organisms, mainly due to the **sulci** (i.e., grooves) and **gyri** (i.e., bumps), with them being the result of the tremendous expansion of the cerebral

1.1. Biomedical and anatomic principles

cortex surface area during fetal development, folding and wrinkling in order to fit the skull. The precise pattern of gyri and sulci varies significantly across populations, rendering the brain surface unique per individual. Under a biopsy dissection or a magnetic resonance imaging scan, the cerebrum appears to consist of two distinctly colored types of matter, implying changes in composition and consistency; the gray matter, at the outer part of the cerebrum, which contains the cell bodies, dendrites and the axon terminals, where all synapses are, and the white matter, at the inner part, made up of myelinated (i.e., biologically insulated) axons, which connect different parts of gray matter to each other (??). Protective layers on top of the gray matter, called **meninges**, ensure that the brain does not come in contact with the outer bone, with the one attached on and marking the outer borders of the gray matter named **pial surface**. In this study, the midthickness surface is examined, a term referring to the surface halfway between the pial and white matter surface.

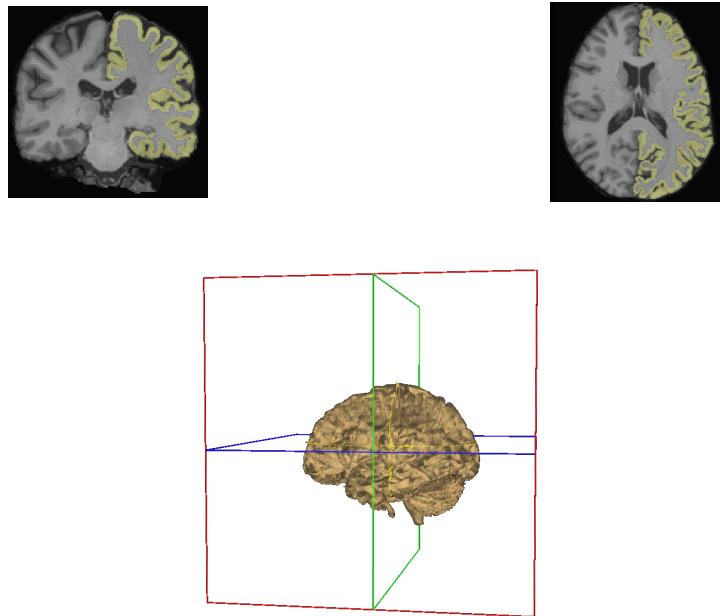


FIGURE 1.4: Gray and white matter as seen from different sections, in an magnetic resonance imaging screening of a sample from Human Connectome Project [?], as visualized using Freesurfer freeview routine. The gray matter is annotated with yellow color in the right hemisphere. Non brain regions have been removed. At the bottom, a three-dimensional representation of the sections is displayed, with the green rectangle corresponding to the coronal (top left) and the blue rectangle to the axial (top right) section.

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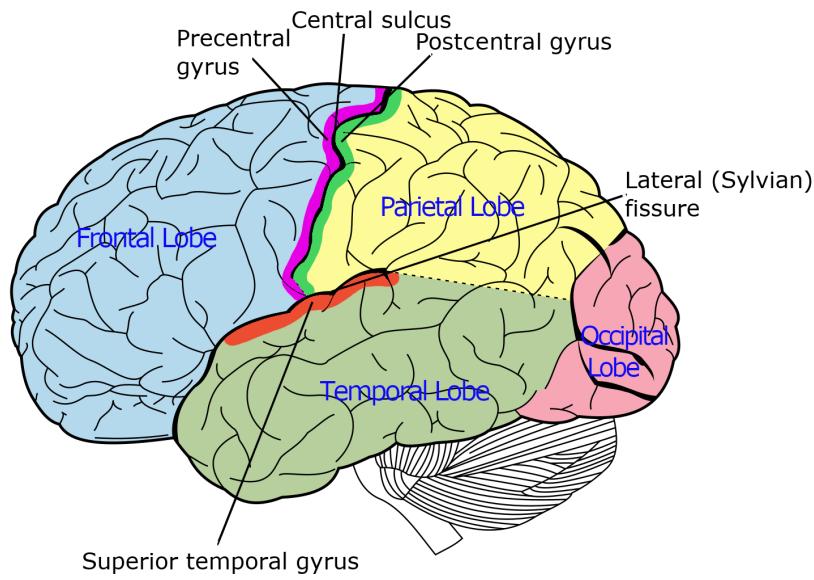


FIGURE 1.5: Cerebrum lobes (blue font) and main gyri, sulci and fissures approximate positions (black font). (Adapted from Wikimedia)

Efforts of partitioning the brain have been numerous throughout the years of medicine, with diverse resolution and purpose. Crudely, the cerebrum hemisphere is divided into lobes, that are named, by convention, after the bones of the skull that lie over them (??). A more detailed approach is based on the identification of the functional processes that take place in each part of the cortex, with Korbinian Brodmann being the first person constructing a 52-partitions experimentally based approximation of the hemisphere [?] (??). Each partition is being represented by an identifier BA##. The main regions identified are:

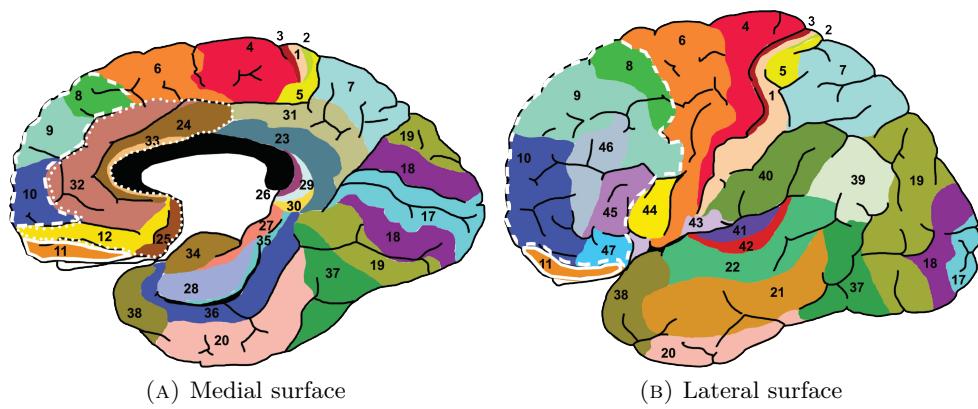


FIGURE 1.6: Brodmann map of functional partitions.

- Sensory areas:

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- Somatosensory cortex (areas 1-3): the post-central gyrus (??). It is responsible for the body-wide sensory information processing, such as touch, temperature and pain.
 - Visual cortex (areas 17-19): occipital lobe surface. It constitutes the center of processing of visual information, as received from the optic nerve.
 - Auditory cortex (areas 41,42): rostral posterior part of the temporal lobe. It processes auditory information, identifying fundamental sound characteristics, such as frequency and loudness.
 - Gustatory cortex (area 43): An area behind the temporal lobe, responsible for taste signals processing.
- Motor areas, that are related to movement planning and manifestation:
 - Primary motor cortex (area 4): The precentral gyrus (??). It is the center of voluntary movements execution, generating the electrical signals required for the neural impulses to be transmitted to the body muscles.
 - Premotor cortex and supplementary motor area cortex (area 6): rostral part of the frontal lobe, anterior to the primary motor cortex. They are the center of motion planning and control, determining the sequence of movements required for a simple task to be performed.
 - Association areas, which are related to perception, memory and thought processes:
 - Prefrontal cortex (areas 8-14,24,25,32,44-47): anterior part of the surface of the frontal lobe. It is centrally involved in cognitive control functions, spanning attention, salience detection, inhibitory control, working memory (i.e., short-term temporarily stored memory, related to a certain task), cognitive flexibility, empathy and pain processing [?]. Areas 44 and 45, referred to as **Broca's region**, are responsible for speech production. Human prefrontal cortex remains one of the least functionally demystified parts of the cortex , presenting difficulties in every level of study, as it exhibits a higher relative size, higher cellular type variety, more complicated neuronal migration and denser connectivity patterns than other animals.[?]
 - Inferior temporal cortex (areas 20,21): caudal part of the temporal lobe cortex. It is responsible for the aggregation of the processed visual information towards a meaningful interpretation, supporting object recognition.
 - Posterior parietal cortex (areas 5,7): posterior part of the parietal lobe surface. It processes sensory information produced from all six senses to construct a semantic representation of the person's surroundings, leading to motion planning and spatial reasoning.
 - Cingulate gyrus (areas 23-24,28,33): an arch-like fold rostrally to corpus callosum. It is the conscious part of the **limbic system**, which is the center of emotions, instinct and reflex responses.

Recently, with the advance of imaging methods, maps have been manufactured, to automatically partition the magnetic resonance imaging extracted three-dimensional cortical surface into 68 partitions, based on morphological characteristics. One such gyral-based atlas, Desikan-Killiany, is derived from the changes in curvature under an expert-driven model of gyri locations [?] and provides automatic **cortical parcellation**, aligned to the Brodmann functional partitioning (??). This atlas is going to be used throughout the proceeding analysis for the quality control of applied segmentation techniques.

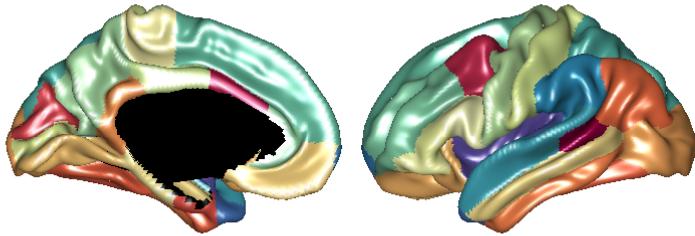


FIGURE 1.7: Desikan-Killiany atlas, mapped on the midthickness surface of the left hemisphere, with the medial (left) and the lateral (right) views displayed.[?] Different colors represent different partitions. The black region has not been mapped or is referring to sub-cortical parts.

1.1.5 Reported general human cortex symmetry traits

Although the human cortex exhibits roughly symmetric structure, the symmetry is systematically suppressed, not only due to the environment, with plasticity playing a central role, but also because of genetic factors, as explained in the previous sections. An asymmetric pattern is manifested across adult individuals, irrelevantly of their upbringing, comprising, therefore, a characteristic of the human species, while general abnormalities in this pattern are related to the occurrence of mental disorders, such as autism or developmental language disorder [? ?]. Some of the most prominent asymmetric traits across healthy individuals are the following:

- Yakovlevian torque (??): the right hemisphere prefrontal lobe and the left hemisphere occipital lobe tend to cross the midsagittal plane, extending towards the other hemisphere [?]. This creates a phenomenon of counter-clockwise warping, making the whole brain appear slightly leftwards rotated, while also making an impression on the inner part of the skull, called **petalia**. Increased left hemisphere occipital lobe extension, possibly caused by enlarged left lateral ventricle, is correlated with bipolar disorder[?]. Rising absence of the torque during aging is connected to schizophrenia and other mental disorders [?].

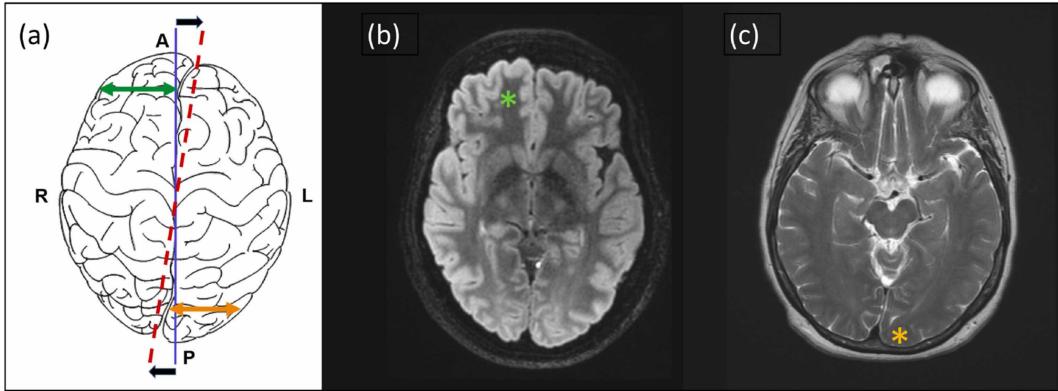


FIGURE 1.8: Yakovlevian torque schematically illustrated (a), along with its manifestation in different axial sections for a single individual (b,c) [?].

- Peri-Sylvian asymmetry: the left Sylvian (lateral) fissure is longer and sharper than the right one, while the right Sylvian fissure exhibits a more visible leftward curve, in the part where temporal lobe meets the parietal lobe, that is the auditory cortex, also called **planum temporale** [?]. The increased thickness of the right superior temporal lobe, that reduces the lateral fissure steepness, is attributed to increased white matter volume. Such trait has been reported to be gender-related, with males exhibiting greater asymmetry than females, as noted in previous studies, with steroid hormone receptor activity and steroid metabolic process related genes [?].
- Central sulcus asymmetry: the right hemisphere central sulcus is deeper and larger [?]. Larger asymmetry appears to be correlated with attention-deficit / hyperactivity-disorder [?].
- Motor areas asymmetry: the motor areas are generally larger on the left hemisphere.

Statistical modeling of the observed symmetry pattern can provide a hint on the significance of genetic and environmental factors contribution[?]. The current study focuses on the genetic component, which has been diversely investigated across literature.

1.1.6 Evolutionary studies

From an evolutionary perspective, it is extremely rare for the right conditions to occur, in order for any soft tissue specimen to be preserved, across a considerable amount of time. The only known way is through mineralization [?]. This fact renders a mammal's ancestor brain almost impossible to retrieve. Nevertheless, endocranial imprints have been used as a proxy to describe the relationships between hominids and their ancestors [? ?]. The reason behind this phenotypic delegation is purely practical. The brain size and shape follow the container volume restrictions.

Although such studies support the theory of propagating asymmetry among studied individuals, with the most evident signs in human skulls, little information about the surface shape can be retrieved, as only the convex hull shape of the brain can be delineated from such process. Through the association of brain asymmetry with DNA, a universal code among organisms, it becomes possible to deploy tools used by evolutionary geneticists, to identify the phylogenetic tree of this complex trait, locating conserved regions among organisms and their predicted divergence in time, under a pleiotropic model [?].

1.2 Genetics of multivariate quantitative traits

1.2.1 Single nucleotide polymorphisms (SNPs) and linkage disequilibrium

Single nucleotide polymorphisms (SNPs) are characterized by single nucleotide base-pairs positions where two or more different alleles (i.e., variants of nucleotide bases) are observed, with the second most frequent allele appearing with a frequency, called minor allele frequency, higher than 1%, a property that sets this term apart from the more general notion of a single-nucleotide variant. Being the most common type of polymorphism in the human genome, single nucleotide polymorphisms were popularized on account of their considerable effect on influencing transcription. Apart from the direct case, where a single nucleotide polymorphism belongs to an exon and the alternate allele corresponds to a non-synonymous (the translated amino-acid differs) or a nonsense (the codon stops translation) mutation [?], the majority of registered single nucleotide polymorphisms (88%) reside in non-coding regions. They can have an impact on the physio-chemical properties and conformation of docking positions for deoxyribonucleic acid-binding enzymes, such as transcription factors, causing binding affinity changes, influencing transcription regulation and, ultimately, altering biological pathways relevant to dependent phenotypic traits [?]. As a matter of fact, 31% of the known deoxyribonucleic acid elements, as reported by the ENCODE project, the human genome encyclopedia, appear to be part of transcription factors binding domains [?].

Linkage disequilibrium (LD) effect on single nucleotide polymorphisms

The genetic information for each individual is only represented by a certain amount of single nucleotide polymorphisms, called **tag** single nucleotide polymorphisms, based upon the principle of high linkage disequilibrium (LD) [? ?]. Linkage disequilibrium, the non-random association between alleles at different loci, is attributed to mutations, genetic drift and, concomitantly, selection [?] that has rendered certain combinations of alleles, named **haplotypes**, more beneficial for the survival and reproduction of a population than others, increasing therefore its **fitness**. These combinations are also more likely to occur topologically close, with recombination events (i.e., events that cause deoxyribonucleic acid strands to break and recombine, altering the haplotype) being less frequent the smaller the genetic distance [?]. Tag single

nucleotide polymorphisms reduce the amount of information required to process pheno-to-geno associations, however the larger the effective population size(the part of the population that reproduces with viable offspring), the weaker the linkage disequilibrium phenomenon [?].

1.2.2 GWAS

Genome-wide association studies (GWAS) aim to relate genetic information, usually extracted from single nucleotide polymorphisms (SNPs) markers arrays, with a phenotypic trait. When the trait is dichotomous, measured by its presence or absence, then genome-wide association studies are applied on a case-control fashion, where two cohorts, an affected (case) and an unaffected (control), are compared. [?] In the present work, the focus is directed to quantitative traits, whose measurement takes continuous values.

Genetic association modeling

Phenotypic differences among individuals, described by the trait variance V_p , are the result of genetic variation V_g , known as **heritability**, environmentally induced variation V_e and developmental noise V_d (the deviations observed when environment and genetics are controlled), formally denoted as $V_p = V_g + V_e + V_d$ [?]. The genetic information content V_g is *approximated* by the amount of variation in tag single nucleotide polymorphisms that is translated to variation in the studied trait properties. The presence of a minor allele signifies divergence from the general population characteristics, and hence implies that information is contained in that single nucleotide polymorphism. The relationship of each single nucleotide polymorphism with the phenotypic trait is statistically represented by a certain genetic model. Under the assumption of an **additive model**, if a certain minor allele occurs in both deoxyribonucleic acid strands, i.e., the allele is homozygous at that locus, then its effect is double compared to the heterozygous case, independently of which strand is carrying it. This hypothesis requires no prior knowledge and makes no further assumptions regarding the alleles dynamics, that is the degree of dominance of each allelic variant. The described model, for a single quantitative trait (dependent variable) and a single nucleotide polymorphism with a single minor allele (assumed independent variable), assessed on a sample with size N after controlling for covariates, can be formulated using a univariate linear regression $y = \mu + \beta x + \epsilon$, with x the allele's occurrences number, y the phenotypic trait, β the single nucleotide polymorphism effect and ϵ the part of non-controllable factors, referring to environment and developmental noise.

Contradicting no association

A single nucleotide polymorphism is considered to be significant, if its effect contradicts the null hypothesis H_0 of no association ($\beta = 0$). For the subsequent analysis, under a biological setting, it is assumed that the phenotypic trait follows a normal distribution. Under the reduced model of H_0 , the residual sum of squares

equals $RSS_R := \sum (y - \bar{y})^2$, with \bar{y} the observed mean value of the phenotype, and the degrees of freedom being equal to $N - 1$. Under the full model of alternative hypothesis H_a , the residual sum of squares equals $RSS_F := \sum (y - \hat{y})^2$ with \hat{y} the estimated trait, with $N - 2$ degrees of freedom. In an analysis of variance setting, the F-statistic $\frac{MSR}{MSE} := \frac{RSS_F - RSS_R}{RSS_R / (N-2)}$ is defined, as MSR and MSE follow a χ^2 distribution with 1 degree of freedom and $N-2$ degrees of freedom respectively under H_0 , which can be used to contradict the null hypothesis.

An alternative to the aforementioned hypothesis test can be made by considering an H_0 that the coefficient β , scaled by the standard error (i.e., standard deviation), follows a standard normal distribution. The hypothesis then can be contradicted by comparing that quantity with the corresponding z-score. An advantage of the latter approach is that the distribution compared is two-sided, meaning that the effect can be given a positive or a negative sign. However, no consideration for the uncontrolled factors is made, a fact that could potentially influence the computed score and render it less interpretable, compared to the analysis of variance case.

Measuring single nucleotide polymorphism significance

By assigning a minimal probability to the event that no association is observed, namely defining a p-value cutoff threshold, a single nucleotide polymorphism is found to be significant if the p-value from the corresponding F-test is less than the explicitly defined cutoff [?]. Greater sample size means lower MSE, larger F-statistic and, consequently, lower p-value. Thus, greater sample size increases the chance of discovering significant single nucleotide polymorphisms and low sample size raises the type I error of the detection, namely the presence of false negatives that actually confirm H_a .

The probability threshold is derived based on an empirical value, fixed to 0.05, corrected using the Bonferroni correction for multiple independent tests, hence $\frac{0.05}{N_t}$ with N_t the number of single nucleotide polymorphisms. The method is rather conservative, therefore usually cutoffs are computed by replacing the number of tests with the amount of independent common single nucleotide polymorphisms for a given population. Based on the findings of the International HapMap Project, this amounts approximately between 200,000 to 1 million tag single nucleotide polymorphisms [?]. Therefore, the proposed cutoff threshold 5×10^{-8} is used. The p-values are most commonly converted to values proportional to significance, by applying the $-\log_{10} p$ transformation. The linkage disequilibrium phenomenon, being often locally observable, causes seemingly continuous p-value spikes to appear when plotting the data points, with the lead single nucleotide polymorphism, that is the one with the greatest local significance (i.e., the lowest locally recorded p-value), being ‘supported’ by lesser significant single nucleotide polymorphism in its vicinity. The resulting scatter plot, with single nucleotide polymorphisms $-\log_{10} p$ values placed by bp position on x axis, resembles the Manhattan city landscape (??).

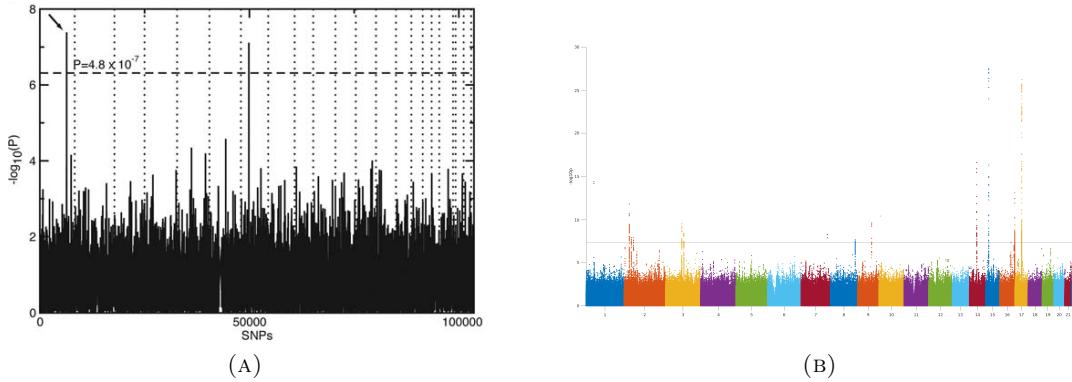


FIGURE 1.9: Examples of genome-wide association studies. In (A), the first recorded genome-wide association studies Manhattan plot [?] is displayed, where the single nucleotide polymorphism in chromosome 1 (black arrow) with the most significant effect, related to Complement H Factor Polymorphism, was identified to affect age-related macular degeneration disease propensity, one of the major causes of blindness among elderly. In (B), a genome-wide association studies scatter plot from the present work is shown, where the single nucleotide polymorphisms spikes signal, attributed to linkage disequilibrium, is evident.

Major advantages and disadvantages of univariate genome-wide association studies

There are several benefits and limitations of such a study design. genome-wide association studies have been successful in revealing novel relationships between genes with known properties and a variety of observed phenotypic traits and clinical applications, presenting evidence of possible biological mechanisms related to genes with unknown function [?]. They also empower population-specific comparative studies, at the level of how ethnicity or other kinds of population stratification affect a certain trait, while accommodating the possibility to investigate the effect of an allele no matter how frequently it might appear in the studied sample [?]. On the other hand, it has been generally observed that each single nucleotide polymorphism can only explain a small part of the heritability of a certain trait, with a large amount of the signal hidden in gene-to-gene interactions, that are not captured in this method, and possibly in single nucleotide polymorphisms whose contribution has not been considered significant enough [?]. To remedy the latter issue, larger sample size is ideally required. Due to the fact that the largest amount of single nucleotide polymorphisms is located in intronic regions, it has also been difficult to assess the causality of those variants, which genes they affect and how they do it. Additionally, too many, possibly unrelated, hits may be involved in a genome-wide association studies result, due to linkage disequilibrium. [?] Recent studies have deployed advanced post-genome-wide association studies statistical and machine learning approaches to account for identifying the causality and the functional behavior of significant single nucleotide polymorphism [? ?].

Multivariate genome-wide association studies (mvGWAS)

When the analyzed phenotype is described by more than one measurements, as is the case in this work, where it is expressed as the combination of different three-dimensional landmarks composing the cortex of each individual, genome-wide association studies require a methodological change to accommodate this fact, as univariate regression cannot be used as is. Also, a single genetic locus may exhibit more than one minor allele. The goal, consequently, is to incorporate multi-allelic SNPs and, more importantly, multivariate phenotype, in a single hypothesis test per single nucleotide polymorphism, leading to what is called multivariate genome-wide association study (mvGWAS). In general, there is an abundance of strategies on how to perform a multivariate genome-wide association study, ranging from direct methods, that approximate the inputs relation either in an unbiased manner or making certain educated guesses, to more complex techniques, that increase statistical power by transforming the inputs, at the expense of explanatory ability [?]. There are also methods that are based on the meta-analysis of outcomes from univariate studies, commonly used to juxtapose experiments from separate sources, for which the original data is missing, the experimental setup, mainly sample size, across studies varies, marking the studies data ‘incompatible’, or a single study is computationally intractable [? ?]. These approaches combine the test-statistics produced from the individual studies and produce an estimate of the multiple trait test-statistic. Which approach performs best mainly lies on the dataset properties and the nature of the scientific question. Factors such as low sample size [?], genes pleiotropic effects [?] (i.e., a gene affects multiple phenotypically independent biological pathways) or within-study variability [? ?] tend to handicap the statistical modeling and increase the type I and II errors of the corresponding hypothesis tests. In this study, canonical correlation analysis was chosen due to the high capacity in efficiently reducing the inputs dimensionality while preserving most information regarding their correlation, and the same sample size across analyzed traits, an approach that has provided successful results in similar efforts of brain shape and face shape analysis [? ?]. An additional strength of this method is that a single test is performed per single nucleotide polymorphism, not requiring further multiple test correction over the number of phenotypic traits, thus having increased statistical power than meta-analysis techniques.

1.2.3 Generalizing to genes - Functional association

The next natural step to perform, once significant variants have been identified for a specific phenotype, is to investigate how such an association is realized, ultimately supporting and extending the assembly of the complex relationships graph between genetics and actual observations. No matter if there is effect on regulatory elements or on the gene product itself, this kind of venture is largely obfuscated, given the little amount of knowledge that exists to fill the relational path, which may include a great number of steps and interactions. The majority of single nucleotide polymorphisms reside in intronic regions [?]. A great number of them is also

likely to exhibit *cis*-acting effects. Surprising is also the event that single nucleotide polymorphisms mapped on an exon of a known gene can be actually manifesting significant correlation with a trait, such as obesity [?], through the interaction with a different gene. Resolution of genome-wide association studies in discovering causal genes is also being limited by the number of studied individuals, the genotyping arrays technologies and the existence of linkage disequilibrium [?], with the lead single nucleotide polymorphisms not necessarily being the functional source of the association signal. Even by ignoring the ambiguous relationships and by knowing the start and end of an association path, the probabilities are thin that the exact trajectory, implicating selective messenger ribonucleic acid translation throughout development, can be derived.

Nevertheless, active research is being performed, to approximate and model the underlying dynamics. Highly trait-specific and exhaustive wet-lab ablation studies, that include genome editing, can profoundly reduce the functional analysis complexity, particularly when little evolutionary and ethical barriers exist, and the analyzed trait has low dimensionality [?]. In the general case, though, modeling and approximations need to be performed, in order to deal with the task. Population stratification and ethnic group variation has shown little interference in common variants analyses [?], at least when considering genome-wide association studies on various diseases, a fact that points to highly frequent and widely distributed causal alleles and may support a form of simplification for the described, seemingly physically and computationally intractable task, possibly allowing for the unification of results from diverse ethnicity experiments. In addition, a gradual incorporation of multiple knowledge sources is taking place to support this undertake; findings from ribonucleic acid expression profiling (such as RNAseq and scRNAseq), also known as eQTL analysis, [? ?] or epigenetic regulation studies (such as ATACseq and CHIPseq) [? ?], that could potentially provide snapshots of genes expression during development, are cross-tested against genome-wide association studies. Through identification of cell types by genetic expression profiles clustering and association between tissues and identified clusters, localized analyses can be more accurate in extracting single nucleotide polymorphism-to-gene relationships [?].

The key approximation required to combine information is to map the underlying data onto the same space. The most elementary jointly studied structure in these relational analyses is genes, due to the recurring need for actual, known, gene product concentrations to be detected. For the generalization from single nucleotide polymorphism to gene, the intermediate detection of lead single nucleotide polymorphisms needs to take place, as aforementioned, under a process called **fine-mapping** [?], which is tackled in various ways, from application of basic heuristics to regression and Bayesian modeling, by incorporating priors fitted on the data. It is frequent practice to assume that lead single nucleotide polymorphisms reside in the captured and imputed data, therefore overlooking the event of no registration, when investigating rather common phenotypic traits. Once the lead single nucleotide polymorphisms have been pinpointed, they are matched to existing maps of annotated genes, after also considering surrounding non coding regions, such as the transcription start sites, as well as other information, retrieved from curated databases [? ?]. A great part of

the generalization is susceptible to underlying biases, with each gene having distinctly different size and possibly overlapping with others [?].

Functional association is then made possible under the framework of gene set enrichment analysis [?]. Being a well-established and extensively used method by a variety of different bioinformatics tools [? ? ?], with its first application dating back to 2003 [?], gene set enrichment analysis is realized by considering gene expression or epigenetic profiles, namely sets of significantly up and down-regulated genes, from different cell types or tissues, and statistically comparing the relation degree, i.e., enrichment, with the genes identified in genome-wide association studies. This process can also be applied ubiquitously, from deriving connections with literature-specific gene annotated knowledge, such as gene ontology terms [?] and publications [?], to back-projecting the genome-wide association studies results to identify shared regulatory domains [?] or enriched transcription factors motifs [?]. A main disadvantage of gene set enrichment analysis, other than the great number of assumptions required to retrieve genome-wide association studies gene sets, is the fact that the compared genes are lacking any prioritization or score, so their contribution is assumed uniform [?].

1.3 Related studies and contribution

The current work is meant to complement existing literature on the derivation of a statistical and genetic basis of cortical surface asymmetry on reportedly healthy individuals [? ? ? ?]. However, the deployed methods are largely correlated with what has been done by [?] and [?]. Initially, a presentation of other association studies is given, and, afterwards, the contributions of this work are summarized.

1.3.1 The current landscape of cortical asymmetry genome-wide association studies

In the work of [?], Desikan-Killiany atlas parcellation was used to extract widely-used asymmetry phenotypic features, called asymmetry indices (AIs) [? ? ? ? ?], that are calculated as the scaled difference of the contra-lateral segments areas, or volumes, depending on the nature of the research. The described quantity, for surface studies, is mathematically formulated as:

$$AI_i = \frac{S_{li} - S_{ri}}{S_{li} + S_{ri}}$$

with S_{li} and S_{ri} being the areas of the left and right hemispheric i-th segment of the atlas, respectively. Although the application of this method has brought forward plausible and promising results, regarding, for example, blood flow discrepancies [?], sex preference studies [?], Alzheimer's disease effect evaluation [?], or depression phenotypic traits detection [?], it has also met skepticism, relatively to the implied assumptions statistical validity [?]. [?] considered only the regions with significant single nucleotide polymorphism heritability ($FDR > 0.05$), as calculated using restricted maximum likelihood estimation [?], while at the same time controlling for

age, ethnicity, data collection and other covariates. Subsequently, they performed a multivariate genome-wide association studies using a meta-analysis tool, called MetaPhat [?], on the filtered areas. MetaPhat joins the univariate genome-wide association studies per asymmetry index results, through the application of canonical correlation analysis, extracting the first canonical correlation coefficient r_i , along with a p-value of the hypothesis of all canonical correlation analysis coefficients being 0. The steps of SNP-to-gene and functional annotation were performed using FUMA toolbox [?], that makes use of a large variety of databases and other tools, including the single nucleotide polymorphism annotation tool ANNOVAR [?] and the gene-set enrichment tool, MAGMA [?]. The lead single nucleotide polymorphisms filtering and functional characterization was specifically done with brain-related provided eQTL and chromatin datasets [?]. Additional temporal developmental analysis was made feasible, once again through FUMA, and the authors identified high genetic enrichment during the early weeks of brain development, albeit with limitations in the dataset size and time resolution [?]. From the described pipeline, ?] were able to identify 21 genetic loci, implicated in microtubule organization and prenatal brain development. Furthermore, single nucleotide polymorphism-level significant similarities were identified with regards to schizophrenia, autism and educational attainment[?]. Because of the fact that a multivariate genome-wide association studies was conducted, the authors argue that no LD score analysis, could be performed. The dataset used to perform genome-wide association studies was the self-proclaimed white European cohort of UK Biobank, amounting to 32,256 individuals [?].

In the work of ?], the performed phenotypic measurements remained similar, enhanced with cortical thickness asymmetry statistics. However, the target goal did not implicate genetic factors at all and was conversely related to the first part of the current study, that is the statistical understanding of asymmetry across partition segments. The authors identified high asymmetry index dependency on age, sex and intercranial volume, raising awareness about the need of such covariates control. They managed to validate, through their analysis, global patterns of asymmetry in the inferior frontal gyrus, transverse temporal gyrus, parahippocampal gyrus, and entorhinal cortex [?], sub-regions of the inferior temporal and prefrontal cortices. ?] extended their research in performing genome-wide association studies on a global proxy of asymmetry, the Yakovlevian torque effect as measured using the skewness coefficients extracted from the three-dimensional affine transformation matrix required to align a real asymmetric brain shape onto a template symmetric cortex, by merging a variety of different datasets, including UK Biobank. The authors were able to identify significant associations, without considering underlying genetics, between handedness and horizontal or vertical brain skewness, strengthening the position that functional lateralization follows structural asymmetry. Skewness also showed significant correlations with cognitive ability, behavior, language skills and mental health. The place and the country of birth appeared highly correlated with the observed asymmetry, without them being controlled prior to the correlation analysis. BMI was also found to be considerably associated. On a genetic basis, ?] identified high polygenicity, low heritability and genetic overlaps with autism

spectrum disorder, though without detecting any significant genetic correlation with skewness.

By far the most complete reported study on cortical asymmetry was performed by [?]. They focused on local geometrical features and the alteration of brain torque during development, by considering contiguous brain slices along with skewness coefficients and average landmark asymmetry differences on regions defined by automatic parcellation Destrieux atlas [?], collecting 348 features per individual. To handle the temporal factor, specialized datasets for studying brain development during adolescence, ABCD [?], PING [?] and PNC [?], came into play [?]. By using meta-analysis applied on univariate genome-wide association studies, they were able to identify only 2 significant lead single nucleotide polymorphisms, in chromosomes 1 and 10, from the originally discovered 86 lead single nucleotide polymorphisms, after adjusting p-values for the number of traits under a strict Bonferroni threshold. Without considering this adjustment, they identified significant genetic correlations under moderately high positive r_g (>0.2), with Alzheimer's disease, attention-deficit / hyperactivity-disorder, and under negative r_g (<-0.2) with bipolar disorder, educational attainment, intelligence and schizophrenia [?].

1.3.2 Present work contributions

The current work aims to provide a data-driven approach of studying cortical asymmetry, under a coarse-to-fine segmentation strategy. The scientific goal is to fundamentally identify the underlying factors that give rise to this phenotypic trait throughout the different regions of the cortex, both in the general, statistical context, as well as in the more specific genetic landscape. To this end, two stages of analysis take place.

The first stage consists of a non-parametric statistical analysis, that demarcates the degree different effects have on asymmetry, using a 2-way permutation analysis of variance, on landmark-defined brain regions. It closely follows the analysis performed by [?] on the facial asymmetry, as firstly introduced by [?]. The outcomes pinpoint the degree under which different regions in the average brain are asymmetric, referring to the average genetic effect, and the degree under which being a different individual affects the shape of the average hemisphere, which is related to the individuals' upbringing, as well as their specific genetic background. Lastly, the interaction between the effect of sides and individuals is assessed, to offer an understanding of whether being a different individual affects the underlying asymmetry. To our knowledge, no similar analysis has been applied in the past, and an anatomic analysis of the outcomes is being provided by [?].

The second stage dissects the genetic background of cortical asymmetry, by identifying the variants on healthy individuals that are most likely to affect different brain regions, under the regimen of a 4-level partitioning, performed in a bifurcating manner. The phenotype analyzed is the principal components of the difference of coordinates of contra-lateral landmarks of the normalized hemispherical shapes. Hence, no prior assumptions on anatomical regions, global morphology and geometry are made, in contrast to relevant studies [? ?]. For each identified partition,

the following analysis is performed. Canonical correlation analysis linearly relates the multivariate phenotypic features contribution with covariates adjusted multi-allelic single nucleotide polymorphisms, making the minimal assumptions that the distributions of the studied variables are multivariate normal and that the underlying phenotypic differences are linearly correlated. The genome-wide association studies design power of generalization is evaluated by considering two different datasets and comparing, qualitatively and quantitatively, the extracted results. The results from these analyses are subsequently combined, to increase the statistical power and to identify originally underrepresented associations. The heritability of the analyzed phenotypic traits is consecutively measured, following the work of [?]. Next, functional, developmental, tissue and cell-type specific analysis is applied on each partition, to identify the genetic correlation of cortical asymmetry with other traits, diseases, biological pathways and age, in a similar format as [?], enhanced with the methods suggested by [?] and [?]. Last but not least, the genes that are found to correspond to identified lead single nucleotide polymorphisms have their functional relations distinguished and clustered, their conservation among hominids closely related to humans are assessed, and significantly enriched publications are retrieved, using the work of [?]. The results of this study are compared to the ones in the literature, particularly to the results reported by [?], being the only known authors to have published their genome-wide association studies scores to date. No such detailed, and at the same time inclusive analysis is known to have been performed on the cortical asymmetry phenotypic trait, like it has successfully been applied on other traits, such as brain shape [?] and face [?].

Chapter 2

Materials and Methods

In ?? a brief overview of the processes applied in this work is displayed. In the coming sections, each compartment will be separately analyzed.

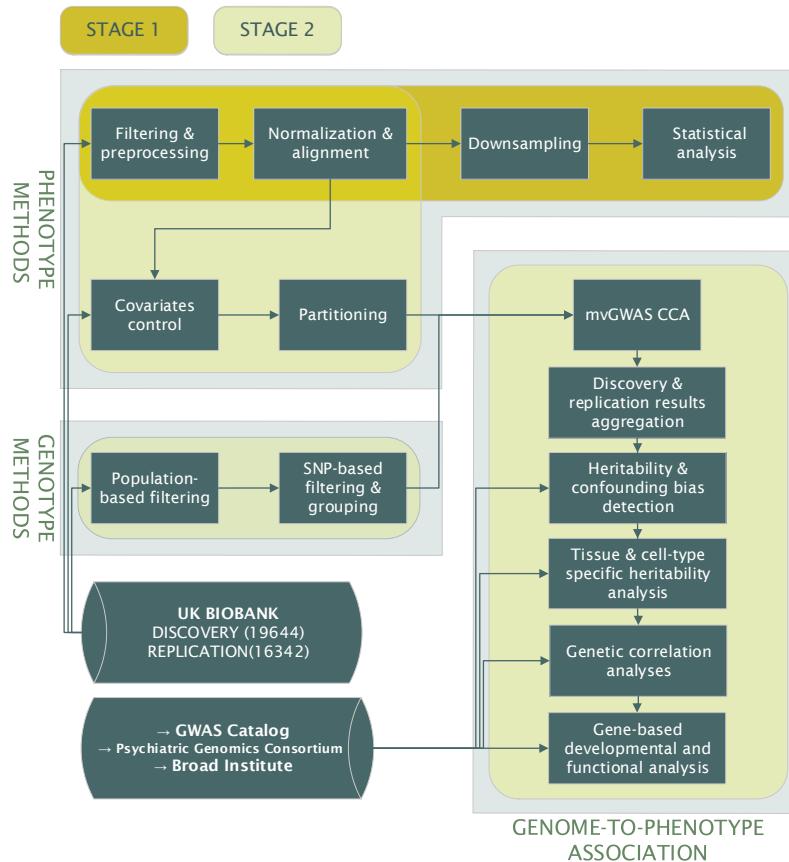


FIGURE 2.1: Visual overview of the applied methods and used materials. Stage 1 corresponds to the statistical analysis of brain shape asymmetry. Overlapping stage 2 refers to the steps performed in the genetic and functional studies.

2.1 Data description

2.1.1 Primary Data Source

With the advent of technology capable to collect and process genomes from different individuals in relatively high speed, vast databases targeting human physiology have been constructed. One of the main players in the data collection has been UK Biobank [?]; a large-scale database from a randomized consortium of 500,000 individuals, whose genome has been collected, from whom 48,000 subjects had also participated in brain magnetic resonance imaging collection process, as of December 2020 [?]. Participants are male and female, with the age range spanning 40 to 69. Apart from magnetic resonance imaging scans and genetic information, of interest are general individual biomarkers that were collected, such as age, height, weight, BMI and blood pressure, as well as information about the imaging process, like date of acquisition, seat height, head (x,y,z) coordinates inside the scanner, and diagnostic center. Those are considered as covariates in the genetic analysis and their effect is assessed and removed. The present study focuses on healthy self-reported white individuals of European ancestry, filtering and preprocessing them based on the work of ?]. Specifically, the discovery dataset, amounting to 19,644 individuals and 9,705,931 single nucleotide polymorphisms, of the present work is identical to the one used in their study. In addition to that dataset, a smaller one, coming from a different, collected at a later time but under the same protocol, batch of 16,342 individuals is used as a replication dataset during genome-wide association studies.

2.1.2 Other sources

A 20 samples test-retest magnetic resonance imaging dataset from Human Connectome Project was collected to simulate replications during symmetry analysis. Various other sources are directly used during the meta-analysis, mainly to collect external genome-wide association studies scores. Those were selected from GWAS Catalog [?] or the Psychiatric Genomics Consortium and are summarized in the following tables:

2.1. Data description

	# Cases	# Controls	Ancestry
ADHD[?]	20,183	35,191	Undefined
AD[?]	24,087 late-onset 47,793 with family history	383,378	European
ASD[?]	18,381	27,969	Danish
BD[?]	41,917	371,459	European
Handedness[?]	31,856	299,181	British
MDD[?]	7,264	49,373	European
OCD [?]	2,688	7,037	European
PD [?]	2,978	653168	European & East Asian
Red Hair [?]	15,731	328,153	European
Schizophrenia [?]	36,989	113,075	European & Asian

TABLE 2.1: Qualitative traits genome-wide association studies sources.

	# Individuals	Ancestry
Cortical surface asymmetry[?]	32,256	European
Cortical surface shape[?]	19,644	European
Educational attainment[?]	405,072	European
Intelligence[?]	78,308	European
LFC[?]	32,186	European
Neuroticism[?]	329,821	European

TABLE 2.2: Quantitative traits genome-wide association studies sources.

Maybe something surprising presented in ?? is the red hair trait, which was assessed with data from the UK Biobank [?]. The reason of its inclusion is that, as the current work’s approach is data-driven, significant signal is observed in the gene-based analysis, regarding this trait, raising questions about subpopulation stratification and leading to a deeper investigation of this association. As a global reference genome for identifying the linkage disequilibrium structure and comparing genome-wide association studies from different sources, 1000G (Phase 3) data is used [?], with the same reference having been utilized during the phasing (ie. the haplotype inference) and imputation process of UK Biobank genotyping [?], . For epigenetic studies, the chromatin data from Roadmap Epigenomics [?] and ENCODE [?] projects are utilized, proposed and preprocessed by ?] and offered by Broad Institute, amounting to 489 different tissues. Lastly, the out-of-the-box tools FUMA [?] and STRING[?] use their own abundant sets of resources.

2.2 Methods applied on phenotype

2.2.1 Initial filtering and preprocessing

T1-weighted MRI scans are analyzed. The analysis is performed by initially converting the raw DICOM MRI volumetric images to well-defined 3D surface triangular meshes through the pipeline applied by FreeSurfer ‘recon-all’ [?] and Ciftify ‘ciftify-recon-all’ commands [?], on a space of 32 thousand vertices, with the average edge length being 2mm. Subsequently, the mid-cortical surface is arbitrarily selected, enabling the distinction of sulci and gyri without over-representing their geometry [?]. After quality control, the vertices from the sub-cortical part of the surface, referring to corpus callosum connection points, are removed based on a mask derived from the Conte69 atlas [?], getting reduced to 29,759.

2.2.2 Magnetic resonance imaging Shapes normalization and alignment

The current work applies principles from general symmetry studies to model cortical asymmetry. For any of these analyses to occur, the aberrations of three-dimensional shapes produced from magnetic resonance imaging scans need to be considered. Magnetic resonance imaging output is affected by the subject positioning and technical error [?]. Volumetric differences also increase the level of discrepancies among magnetic resonance imaging samples. To prevent positioning and volume deviations from gravely affecting shape comparisons, a normalization is required[?]. The samples of the derived 3D triangular mesh are represented as a set of vertices \mathcal{V}_S of predefined dimensionality P, with a single landmark coded in the format of (x,y,z) coordinates. Those are joined together with a predefined faces matrix \mathcal{E}_S , with each of its elements containing three indices referring to \mathcal{V}_S , with the additional constraint that S is a multiple-connected structure, namely a graph in which there is at least one path joining any two vertices. Shapes normalization is performed through the application of generalized Procrustes analysis. Generalized Procrustes analysis is an algorithm that iteratively performs translation, scaling and rotation on a given set of structures S , given initially a reference S_0 , aiming to minimize the Euclidean distance of corresponding points and the average shape. The translation is performed in such a way that the centroid C, defined by $\frac{\sum_{\forall i} \mathcal{E}_{S_i}}{P}$, becomes the system origin. The scaling is such that the centroid size of the normalized S structure, defined by $\sqrt{\sum_{\forall i} \|\mathcal{E}_{S_i} - C\|_2}$ becomes equal to 1. The transformed samples then belong to what it has been coined as Kendall Space [?]. Under the framework of cortical surface analysis, a single hemisphere is considered to be one of the S structures. To apply any symmetry analysis, therefore, one of the individual hemispheres needs to be mirrored on the other side of the midsagittal plane, and then generalized Procrustes analysis is applied to align all hemispheres at once. The mirroring is performed by normalization of right and left hemispheres sets separately, and, then, x coordinate sign inversion of the right hemisphere landmarks. Aligning, finally, the entire dataset marks the end of the shapes normalization for the two tasks, statistical asymmetry

analysis and genome-wide association studies, resulting into left (H_L) and mirrored right (H_R) shapes. In the case of genome-wide association studies, the difference between the left and right landmarks of the aligned shapes $D_A = \mathcal{E}_{H_L} - \mathcal{E}_{H_R}$ is computed, a proxy of directional asymmetry defined in ??, before being reshaped to merge the dimensions of L landmarks and coordinates, resulting in an array with size $N \times 3L$. This structure plays the role of the asymmetry phenotype in further analysis.

2.2.3 Downsampling

An intermediate step is followed when performing cortical symmetry statistical analysis, in order to reduce the computational burden of the process. An algorithm, in MATLAB context, has been derived, that computes the subset of indices of a given shape S , *approximately* with a given factor, that best describe the downsampled shape M provided from the proprietary function ‘reducepatch’ output [?]. With this method, the analyzed shapes are downsampled by a factor of 10, with the average shape retaining most morphological characteristics. The key idea is to find the one-to-many correspondence between faces from the two meshes. Let \mathbf{Cn}_T be the centroids of each face of a shape T . The faces correspondence is found by firstly identifying for each face $x \in \mathcal{E}_M$ a part S_x of S , with $\mathcal{E}_{S_x} \subset \mathcal{E}_S$, joined to the closest, to x , face of S with index $y_{min}(x) = \arg \min_{\mathbf{Cn}_S} \|\mathbf{Cn}_S - \mathbf{Cn}_M\|_2$, through a path of utmost 10 edges, that is the desired reduction rate. The faces of S_x are having non-zero entries in the 10th power of the S ’s adjacency matrix, at the y_{min} -th row. Then, the optimal vertex correspondence is found by taking all the vertices corresponding to the faces subset \mathbf{V}_{S_x} and identifying which of them is the closest to each of the vertices of x . The resulting downsampled shape R then has the faces of M , but projected on the vertices of S . This mapping allows for instant, although naive and of reduced quality, downsampling of 29,759 to 3,098 landmarks (??).

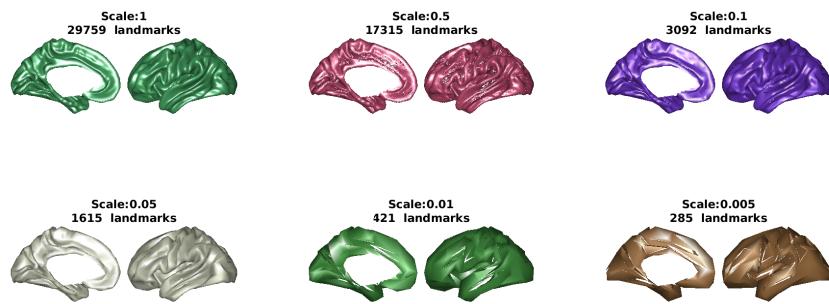


FIGURE 2.2: Downsampling indices of original average template using the novel algorithm and specific reduction scales ($1/r$). As no inter-face edge connectivity criterion is being considered, artifacts occur in the approximated shape, in the form of scars.

2.2.4 Symmetry statistical analysis

Bilateral asymmetry is mainly described using three components in literature [?][?]. Directional asymmetry (DA), the main focus of this study, corresponds to the hemispheric side effect, namely how the intrinsic (i.e., genetic) properties of the studied population are manifesting across individuals. Antisymmetry, which is related to the effect where sidedness is random in a population (i.e., left-right pattern is mirrored to a right-left pattern), is not observed in the human cerebral cortex, in contrast to other internal organs positions, or organisms [?]. The third component, fluctuating asymmetry (FA), encompasses any random developmental and environmental effects, that cannot be explained with the existing knowledge. The observed deviations can be statistically linearly modeled as products of two effects, the hemisphere side studied and the individual specimen analyzed, as well as their interaction [?]. Given that the analysis is performed on a pair of symmetric objects, and not on a single symmetric object, this configuration is named **matching asymmetry analysis**. Formally, based on [?] assuming the presence of replications for each observation per individual, to account for technical error, a mixed linear model representing the aforementioned dependencies is defined as:

$$Y_{ijk} = \mu + \beta + I_i + S_{ij} + E_{ijk} \quad (2.1)$$

where Y_{ijk} is the phenotype of the i-th individual, from the j-th side, under the k-th replication, μ and β are the fixed intercept and fixed side effect respectively, $I_i \sim \mathcal{N}(0, \sigma_{ind}^2)$ is the random individual effect, $S_{ij} \sim \mathcal{N}(0, \sigma_{FA}^2)$ is the random side and individual specific effect, matched to fluctuating asymmetry, and $E_{ijk} \sim \mathcal{N}(0, \sigma_{ME}^2)$ is the measurement error. Given this definition, a way to measure the statistical significance is performed through an F-test applied on a 2-way nonparametric permutation-based analysis of variance, to relate the residual sum of squares ratios of effects to observable error terms, and of fluctuating effect to the measurement error. Extra care needs to be given on the determination of the degree of freedom of each term, given the preprocessing applied to bring the hemispheres surfaces into Kendall shape space [?]. Specifically, the constructed F-ratios, for each pair of contralateral landmarks coordinates separately, on N individuals and R replications, are:

$$F_I = \frac{RSS_I}{RSS_S}, F_{DA} = (N - 1) \frac{RSS_D}{RSS_S}, F_{FA} = \frac{2(R - 1)N}{N - 1} \frac{RSS_S}{RSS_E}$$

RSS_I , RSS_D , RSS_S and RSS_E are the rows, columns, interaction and error residual sum of squares respectively, as computed by MATLAB ‘anova2’ function on the $NR \times 2$ array that contains in each group of R rows information about each individual. Replications are necessary in such analysis, in order to distinguish the fluctuating asymmetry effect from measurement error, and manage to detect F_{FA} . To this end, an magnetic resonance imaging test-retest subset of 20 individuals from HCP is retrieved [?], and the preprocessing mentioned in ?? is performed. For each landmark and coordinate, and for each hemisphere separately, the mean observed replication variance across individuals is computed. Subsequently, assuming that the technical measurement error is normally distributed, an augmented dataset is

produced for the magnetic resonance imaging samples in the UK Biobank dataset. Three ($R = 3$) replications per individual are generated by sampling from the identified distributions.

While simple analysis of variance bases the F-score significance on the assumption of normality, permutation-based analysis of variance makes no assumptions on the underlying distribution [?]. Instead it bases significance of a F-statistic on the number of permutations which resulted in F-scores equal or higher than the F-statistic measured in the simple analysis of variance scenario on the original data, divided by the total number of permutations [?]. By definition, the observable p-value resolution is the reciprocal of the permutations number. This is introduced in the fraction described before by adding 1 to the nominator and denominator, namely considering the non-permuted case as well. Let N be the number of individuals. A reshaping operation is performed, after which the set of size L landmarks becomes a set of size $3L$ coordinates per individual per side, in other words a three-dimensional dataset. The permutations are generated considering each time the dimension being investigated, pursuing biologically feasible result when possible; for assessing the individual effect and computing RSS_I , the hemispheres are randomly shuffled across individuals (N^{3RL} possible orderings); for the side effect test and RSS_D measurement, landmarks of each individual are reassigned a random side (2^{NRL} configurations); for the fluctuating effect, quantified by RSS_{FA} , the whole dataset is randomly permuted ($(6NRL)!$ orderings). As it can be foreseen, a handicap of the method is the largely unequal size of the possible permutations among the components analyses. This fact renders the last test more sensitive to assign low p-values to each landmark, as the configuration that could possibly produce a better f-score is exponentially less likely to be selected. However, it is worth noting that in all tests the possible cases number is prohibitively large, and that analyses in Monte Carlo simulations, suggest the size of 1000 replications as good enough [?].

The consecutive analysis has also been demonstrated in the work of ?]. 1000 replications are selected to test the significance of each asymmetry component, which means that the analysis is computationally intensive, but facilitated by the downsampling described in ?? . Five random subsets of 50 samples are collected from the discovery dataset. The number of samples is chosen experimentally, as it was observed that the size of 1000 replications is actually not enough for larger datasets and the method is generally sensitive in assigning high significance (p-value<0.05) to each landmark, the larger the set size assessed. A number of different random subsets is selected, so that to reduce the effect of cherry-picking. The final counts are computed to be the average of the experimental iterations.

2.2.5 Covariates control

In the case of genome-wide association studies, variance caused because of non-genetic factors needs to be excised from the underlying data. To this end, covariates adjustment is performed, by retrieving the residue of a partial least squares regression [?] describing D_A relatively to the factors mentioned in ?? , along with the 20

genetic principal components, to account for population stratification and reduce confounding biases (??).

age(1)	age squared(1)
height(1)	weight (pre-imaging)(1)
diastolic blood pressure(1)	systolic blood pressure(1)
date of measurement(1)	genetic principal components (20))
volumetric scaling from T1 head image to standard space(1)	
X-position of center-of-gravity of brain mask in scanner coordinates(1)	
Y-position of back of brain mask in scanner coordinates(1)	
Z-position of center-of-gravity of brain mask in scanner coordinates(1)	
Z-position of table/coil in scanner coordinates(1)	
one-hot encoded assessment location (21)	
left & right hemisphere centroid sizes prior scaling (2)	

TABLE 2.3: Covariates used to control phenotype, totaling 57. Numbers in parenthesis show the dimensionality of each covariate.

2.2.6 Shapes partitioning

The present work evaluates the brain asymmetry genetic landscape in a coarse-to-fine segmentation, through hierarchical spectral clustering (HSC). The technique has been used in a number of different related phenotypic studies [?][?], yielding results that are in accordance with the underlying anatomic features. The main reason behind this partitioning is the intrinsic complexity of the studied phenotype, eliciting expected differences in the genomic profiles of each cerebral cortex region. This type of distance-based clustering is governed by the least quantity of assumptions, regarding the shape or form of the cluster [?]. The partitions' genetic juxtaposition is valuable for identifying which regions share similar significant genetic loci, highlighting the corresponding genes contribution, or showcasing the specialization of certain regions that share little to no similarities with their neighbors.

Hierarchical spectral clustering is an unsupervised method of iterative partitioning, that makes use of the distance matrix eigenvectors [?]. The distance matrix between pairs of rows of D_A , across individuals, is constructed using RV coefficients [?], a generalization of Pearson correlation in N-dimensional space. The resulting matrix gets enhanced pairwise similarities, by becoming sharper through the application of the Laplacian transformation dictated by the Shi-Malik method [?]. The eigenvectors of the matrix are computed and Kmeans++ clustering [?] is applied with 2 clusters. The process is repeated on each cluster for a desirable amount of levels, resulting into a binary tree structure (i.e., each parent shape is partitioned into two children). In the current study, a level-4 partitioning is performed, resulting into a tree of 31 partitions, with the root partition, the entire hemisphere, included. This specific partitioning depth was arbitrarily selected, considering the trade-off of finer results resolution with the computational resources required for the subsequent analyses. Consequently, the rows of D_A corresponding to each of those

partitions are transformed by principal component analysis, keeping maximally 500 principal components that explain at most 80% of the variance, resulting into a structure P_A that contains 31 arrays, $P_{Ai}, i = 1..31$, one for each partition, with varying dimensionality. The last step is not only performed for reasons of dimensionality reduction and computational efficiency, but also to ensure that the resulting phenotypic traits are orthogonal with each other, and therefore compatible for LD score correlation analyses, discussed in ???. The partitioning is derived by the discovery dataset only, so that the genome-wide association studies results between discovery and replication datasets correspond to the same partitions and are directly comparable. The computed clustering is subsequently compared to the Desikan-Killiany atlas parcellation, through a symmetric measure of similarity called normalized mutual information. Let $U := \{\mathbf{v}_i\}, i = 1..n_{DK}$ and $V := \{\mathbf{v}_j\}, j = 1..31$ be the supersets of sets of indices in \mathcal{V}_S associated to partitions by Desikan-Killiany atlas and hierarchical spectral clustering respectively. Then, the normalized mutual information score is:

$$\text{NMI}(U, V) := \frac{1}{S} \sum_{i=1}^{|U|} \sum_{j=1}^{|V|} \frac{|U_i \cap V_j|}{N} \log \frac{N|U_i \cap V_j|}{|U_i||V_j|}$$

where in this study the normalizing factor S , generally variable [?], is defined as the square root of the product of the sets entropies, namely

$$S := \sqrt{\sum_{i=1}^{|U|} (|U_i| \log |U_i|) \sum_{j=1}^{|V|} (|V_j| \log |V_j|)}$$

This score is by definition independent on the ordering and the number of the labels. However, a differential number of labels which is expected between the measured labels affects the maximally possible result. Therefore, the score is further normalized by scaling it by the approximate (based on integer division) theoretical maximum score that can be observed, if each lesser partitioning does not ‘share’, in correspondence, any labels of the greater partitioning, apart from a single placeholder label, to account for integer division.

2.3 Methods applied on genotype

2.3.1 Population-based filtering

principal component analysis, using as reference data the 1000G (Phase 3) [?], is applied to select European individuals only. First, single nucleotide polymorphisms in linkage disequilibrium, as computed by PLINK 1.9 with parameters 50 variant window-size, 5 variant step size and $0.2 r^2$, are excluded from the reference dataset. KMeans algorithm is fitted on 25 principal components of the reference dataset. Then, only individuals from discovery and replication datasets that are included in the clusters with a EURO label are considered. The individuals identifiers of the genotype are consecutively matched to those in the phenotype.

2.3.2 SNP-based filtering and grouping

In addition, single nucleotide polymorphisms referring to indels, with low genotyping rate (<50%), low minor allele frequency < 1% (i.e., corresponding to rare alleles), or not in Hardy-Weinberg equilibrium ($P < 10^{-6}$) are excluded from the analysis. Subsequently, the linkage disequilibrium filtering applied on the reference dataset is also done for the remaining single nucleotide polymorphisms of the discovery and replication data. The filtered discovery and replication datasets contain 9,705,931 and 8,305,363 variants respectively. The multi-allelic single nucleotide polymorphisms rows are grouped together, so that single association test is applied.

2.4 Genome-to-phenotype association

2.4.1 mvGWAS CCA

For each i -th partition, canonical correlation analysis is applied between each single nucleotide polymorphism and P_{A_i} . To accelerate the genome-wide association studies process, missing values on snp-level were substituted with the mean observed value. The reason behind the acceleration resides in the way canonical correlation analysis finds the vectors \vec{a}, \vec{b} that maximize $\text{corr}(a^T X, b^T Y)$, or, alternatively, the linear combinations of the input random variables that have maximum correlation. A step of this process is the calculation of the singular value decomposition of both X and Y matrices. If X and Y are the phenotype and genotype respectively, the matrix corresponding to X remains the same throughout the per-single nucleotide polymorphism canonical correlation analysis, if no missing values exist in the dataset, so the singular value decomposition is required to be computed only once. On the other hand, if missing values are considered in Y , the singular value decomposition of a subset of X needs to be computed for every different single nucleotide polymorphism ‘missingness pattern’, which was identified to be of the order of magnitude of the sample size for the discovery dataset, given the large sample size. Under a theoretical framework, assuming that single nucleotide polymorphisms are missing completely at random (MCAR) cases, a simple mean substitution distorts the j -th variant underlying distribution variance by a factor of $(n^j - 1)/(n - 1)$, with n^j the number of available cases [?]. The mean amount of missingness across studied alleles was found to be less than 1%, therefore this simple method was selected. Experiments on eigenvector decomposition techniques has also shown that, under a sparse missingness hypothesis, the methods remain robust to such simplification [? ?]. The mean substitution greatly affects the computational resources and time required to perform the analysis, reducing them by at least twenty-fold, without an observable effect on the quality of the results, as discussed in ???. The canonical correlation analysis operation is repeated for both discovery and replication datasets. The produced χ^2 scores are transformed into the quantity dictated by multivariate LD score correlation analysis. The resulting P values are transformed into -log10P values and the genome-wide association studies results are compared qualitatively, as well using LD score correlation genetic correlation analysis.

2.4.2 Discovery and replication results aggregation

Once the comparisons between the results from discovery and replication datasets are made, they are aggregated into a single output, with the p-values combined using Stouffer's method. This method is applied by first projecting the p-values corresponding to the i -th sample into z-scores, through the calculation of the complementary inverse error function erfc^{-1} of $p_i = \{p_{i1}, p_{i2}\}$. The combined p-value p_{ci} then is:

$$p_{ci} = \text{erfc} \left(\frac{\sum_{k=1}^2 \text{erfc}^{-1}(p_{ik})}{\sqrt{2}} \right)$$

Apart from this, the χ^2 scores are summed, under the theoretical basis that the sum of two independent χ^2 values with d_1 and d_2 degrees of freedom respectively follows a χ^2 distribution with $d_1 + d_2$ degrees of freedom.

2.4.3 Heritability and confounding bias detection

The linkage disequilibrium between two alleles A and B from different loci is generally quantified using one of the following values:

- the coefficient of linkage disequilibrium \mathcal{D} :

$$\mathcal{D} := p_{AB} - p_A p_B$$

with p_{AB} referring to the haplotype AB frequency and p_i to the frequency of allele i . This coefficient is scaled by theoretical maximum \mathcal{D} , \mathcal{D}_{max} , to render it independent of the per-pair frequencies magnitudes, producing \mathcal{D}' .

- the genetic correlation r^2 , a proxy of the Pearson coefficient, defined by:

$$r^2 := \frac{\mathcal{D}}{p_A(1-p_A)p_B(1-p_B)}$$

Based on simulations, it has been shown that \mathcal{D}' is inflated when the sample size is small or the minor allele is rare [?], thus genetic correlation is generally preferred. In a seminal research work from [?], it was found that there is a closed mathematical expression that connects the j -th allele χ^2 expected value with the average heritability explained per single nucleotide polymorphism h and its linkage disequilibrium score, defined by $\sum_k r_{jk}^2$, r_{jk}^2 being the r^2 of the j -th with the k -th allele:

$$E[\chi^2 | l_j] = \frac{Nh^2 l_j}{M} + N\alpha + 1$$

α is the contribution of population-related effects, such as population stratification, that are not being controlled, known as confounding biases. The gains from this regression are dual; a measurement of heritability can be obtained by estimating

the slope, and the confounding bias effect can be measured by the intercept. This formula, which originally referred to a univariate phenotype, was extended in [?] to incorporate D-dimensional multivariate traits:

$$E \left[\frac{\chi_j^2}{D \left(1 + \frac{\chi_j^2}{N} \right)} \right] = \frac{N-1}{P} \left(\frac{\sum_{d=1}^D h_d^2}{D} \right) l_j + 1 + O \left(\frac{1}{N} \right)$$

where $O(1/N)$ term is corresponding to the confounding biases effect. Therefore, this tool is used to estimate heritability and confounding biases, per partition, from the combined genome-wide association studies results. The basic underlying assumptions, or limitations, of such a model are:

- The single nucleotide polymorphism heritability follows a uniform distribution, i.e., it is on average the same genome-wide. Extensions have been made to relax this, generally wrong [?], assumption, by considering partitions of single nucleotide polymorphisms separately and doing what is known as stratified LD score regression [? ?].
- Each single nucleotide polymorphism effect is assessed independently from the rest, therefore no between-single nucleotide polymorphisms interactions can be included in the computation.
- The covariance matrix of the phenotype equals the identity matrix multiplied by N, that is the studied traits are orthogonal to each other.

Another limitation of LD score regression is that the heritability is under-estimated when the effective sample size is small[?]. The analysis is performed on the meta-analyzed combined dataset, as it has been similarly used in other studies [? ?]. This approach remains in accordance with the underlying theoretical framework, by reviewing another result by ?], corresponding to the case of computing the expected χ^2 -statistic of variant j from a meta-analysis on two sub-studies with sample sizes N_1 and N_2 respectively ($N = N_1 + N_2$) and samples from the same underlying population, without genomic control:

$$E \left[\chi^2 | l_j \right] = \frac{h_g^2}{M} \frac{\left(\frac{N_1}{\lambda_1} + \frac{N_2}{\lambda_2} \right)^2}{N} + \frac{1}{N} \left(\frac{N_1}{\lambda_1} + \frac{N_2}{\lambda_2} \right), \text{ with } \lambda_1, \lambda_2 = 1$$

2.4.4 Tissue and cell-type specific heritability analysis

As mentioned in ??, extensions have been devised to account for different heritability profiles of disparate biological and functional regions. ?] incorporate the notion of chromatin regulation and gene expression profiles in LD score regression applied to specifically expressed genes. Let m be the number different gene expression profiles, each on a separate tissue or a cell type, an annotation class. For each of those a set of genes, corresponding to a set of single nucleotide polymorphisms K_j , ($j = 1..m$),

has been found to be significantly enriched, relatively to the rest of the comparison group. The discussed extension is of the form:

$$E[\chi_i^2] = N \sum_j \tau_j l(i, j) + N\alpha + 1$$

with the linkage disequilibrium score of the i-th single nucleotide polymorphism for the j-th genes cluster $l(i, j)$ being defined as $\sum_{k \in K_j} r_{ik}^2$. τ_j is the estimated coefficient per annotation class and explains the signed effect of each class on the heritability of the observed phenotype. In other words, the coefficient τ_j relates the cumulative linkage disequilibrium effect of the j-th set of single nucleotide polymorphisms with the observed capacity of the i-th single nucleotide polymorphism to affect the phenotypic trait.

Under this framework, in the present study, a significant association is sought between chromatin regulation studies related to gene expression, to identify the degree under which the identified significant single nucleotide polymorphisms effects are also likely to be regulated by epigenetic modifications, using the same dataset used by [?], as mentioned in [??].

2.4.5 Genetic correlation analyses

[?] also invented a way to utilize genome-wide association studies scores produced for two different traits as a proxy to relate the genetic correlation of these traits, namely the extent over which the two characteristics are being regulated by similar genetic drivers:

$$E[z_{1j}z_{2j}|l_j] = \frac{\sqrt{N_1 N_2} \rho_g}{M} l_j + \frac{\rho N_s}{\sqrt{N_1 N_2}}$$

The conversion between χ^2 with 1 degree of freedom and z score values is straightforward, as, by definition, the square of a standard normal distribution follows the χ^2 one with 1 degree of freedom. In other words, the equation above retrogresses to the LD score regression one, if traits 1 and 2 are considered the same. With LD score correlation, seemingly independent phenotypes can be compared, testing for pleiotropic single nucleotide polymorphism effects and discovering novel biological pathways [?]. However, a main limitation of the canonical correlation analysis multivariate genome-wide association study analysis does not contain information about the direction of the effect of a variant on a trait, and such an event is not considered during the derivation of the aforementioned equation [?]. Instead, Spearman correlation can be used, to relax the check by testing for monotonic, and not linear, relationships. To this end, LD blocks from the work of [?], retrieved from haplotypic information occurring in the 1000G (Phase 3), are used to perform an average aggregation of the p-values observed per trait and subsequent monotonicity assessment based on Spearman correlations. A P-value for the correlation process is also produced by comparing bootstrapping spearman correlation variance with the observed correlation.

The aforementioned method, also applied by [?], is used to relate the genome-wide association studies scores presented in [??]. One of those comparisons is done

versus the work from [?], with the aim to quantitatively relate the results presented there to the current study. In addition, as an internal measure of similarity, it is applied to measure the degree of concordance between the results presented by the discovery and the replication dataset, and the effect of mean-vs-no single nucleotide polymorphism substitution on the discovery dataset.

2.4.6 Gene-based developmental and functional analysis

Last but crucial step, analyses at the gene level are performed. The focus is mainly shifted on 5 partitions; the entire hemisphere, and the 4 ones on the second level, as greater discrepancies in genome-wide association studies are identified among partitions at that level relatively to others. The subsequent analysis refers to the process applied on each partition separately. FUMA toolbox SNP2GENE utility is used [?] for lead single nucleotide polymorphism detection and initial single nucleotide polymorphism-to-gene reduction.

Lead single nucleotide polymorphisms are retrieved by considering the genetic relationship matrix (GRM), that is the symmetric matrix produced by computing r^2 for each single nucleotide polymorphism pair from the neighborhoods of significant single nucleotide polymorphisms, selected by imposing a 5×10^{-8} threshold on the produced p-values p_c . [?]. Then, after applying a genetic relationship matrix r^2 upper cutoff of 0.1, a lead single nucleotide polymorphisms is assigned to each separate region, based on the lowest observed p-value.

Underlying gene sets are retrieved, in the exact same way as it was done by [?], by accumulating the outputs of positional, eQTL and chromatin interaction mapping, with default parameters and only taking into consideration brain-related samples when deemed necessary [? ?]. A further extension of the gene sets is achieved by using GREAT tool [?], supplying it with the identified lead single nucleotide polymorphisms. This tool models possible gene regulatory domains based on empirical evidence and assigns single nucleotide polymorphisms in such intronic regions to the corresponding genes [?].

Leveraging the power of another statistical tool through FUMA, MAGMA, a time-dependent analysis is performed, identifying the degrees under which identified genes are enriched in genetic expression profiles from brain tissues from different developmental stages [?]. MAGMA gene-set analysis uses the full distribution of single nucleotide polymorphism p-values, hence it is fundamentally different from a gene set enrichment analysis kind of test. However, long-range relationships, assessed and introduced by the methodologies of FUMA and GREAT, defined above, are not considered. Instead, MAGMA process examines the joint association signals of all single nucleotide polymorphisms within a given gene, in a 100kb region, while considering the linkage disequilibrium between those single nucleotide polymorphisms [? ?].

The resulting gene set is supplied to the FUMA GENE2FUNC process, where a variety of gene set enrichment analysis takes place [?], extracting functional relationships with gene ontology terms, biological pathways, GWASCatalog traits and differentially expressed tissue-specific gene sets. Concurrently, the identified

2.4. Genome-to-phenotype association

gene set protein interactions are graphically represented and significantly enriched publications are identified using STRING suite [?]. Reactome GO enrichment through PANTHER statistical over-representation test [?], with Fisher’s exact test without correction, is used to annotate large clusters identified in STRING proteins network, produced using MCL algorithm with inflation 2.

Chapter 3

Results

3.1 Statistical brain shape analysis

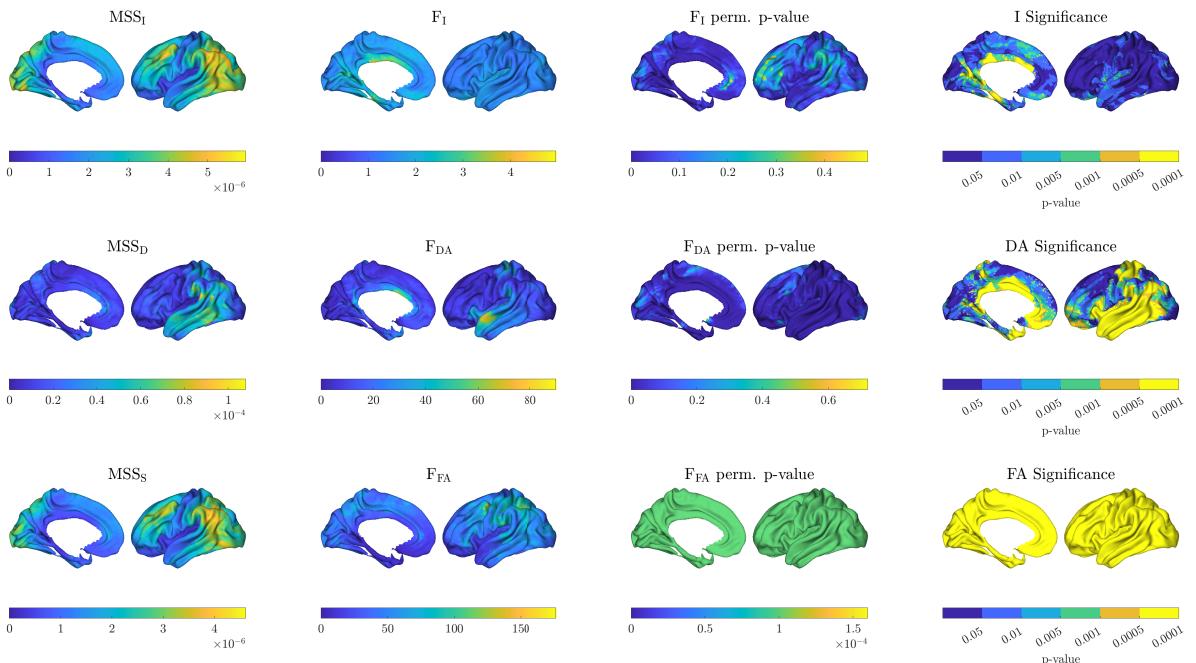


FIGURE 3.1: Asymmetry components significance analysis. Information about each landmark has been used to fill the three-dimensional average shape of the left hemisphere, displayed medially and laterally. The MSSs are produced by dividing RSSs with the appropriate degrees of freedom. Both the first and the second column refer to information retrieved from the non-permuted data. The last column is derived by applying various thresholds (shown in the colorbar) on the p-value response presented on the third column. As explained in ??, first row refers to the individual effect, second row to directional asymmetry and last row to fluctuating asymmetry, attributed to developmental factors and the environment.

Prior to the genetic studies, a statistical analysis purely on the phenotypic trait was done, to reveal existing symmetric patterns. The main results from the 2-way permutation analysis of variance are summarized in ?? and are also being more formally medically analyzed by ?]. The individual effect (first row), which corresponds to the average shape variability across individuals, exhibits greater variation in the medial surface, particularly in the middle-anterior and middle-posterior parts of the cingulate gyrus and sulcus (\subseteq BA28, processing emotions and behavior regulation), the rostral part of the cuneus (\subseteq BA17, processing of visual information), the parahippocampal gyrus (\subseteq BA27, memory encoding and retrieval), and the fusiform gyrus (\subseteq BA37, recognition of faces).

Directional asymmetry (second row), the focus of this study, relevant to the general aptitude of individuals to exhibit certain asymmetric traits, is found to be highly significant in almost half of the studied surface. In line with the general identified asymmetry patterns presented in ??, it is greatly localized around the peri-sylvian fissure and the temporal lobe (see peri-sylvian asymmetry). Also, it occurs in the medial surface, and the occipital lobe, implying relationship with the Yakovlevian torque, although lower significance of the effect is demonstrated on the prefrontal lobe.

Fluctuating asymmetry effect (last row), which, as a reminder, is related to environmentally and developmentally induced variations, has been found generally significant across the cortical surface. This finding can be partly justified to the large combinatorial space from where permutations are collected (see ??), as well as the overall exhibited plasticity of the human cortex (see ??), as raised by ?]. However, a comparison across regions is possible by inspecting F_{FA} instead, where, in the caudal part of the middle frontal gyrus (\subseteq BA40, phonological processing and emotional responses), the superior part of the precentral gyrus (\subseteq BA07, space localization), and the caudal part of the superior frontal sulcus and gyrus (\subseteq BA08, planning complex movements) greater effect of fluctuating asymmetry is exhibited.

3.2 Covariates control

The existing available metadata was used to exclude variability in the dataset that is not attributed to genetic factors. In ??, the average covariates explained variance on each segment of Desikan-Killiany atlas is observed as retrieved from partial least squares regression. The largest part of the frontal lobe, with greater impact on the inferior frontal, the inferior parietal gyrus and the parahippocampal gyrus appear to be more correlated with the collected metadata, shown in ?? . The results point to less observed explained variation around the area of the sylvian fissure and the temporal lobe, and also raise a degree of uncertainty on the significant response observed during the statistical shape asymmetry analysis, regarding the medial surface and the inferior part of the frontal lobe.

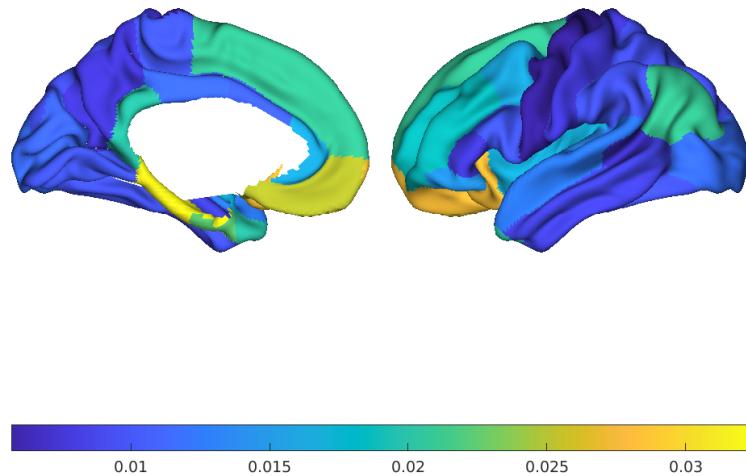


FIGURE 3.2: Explained variance from the covariates on each Desikan-Killiany atlas segment, as retrieved from partial least squares regression, mapped on the average left hemisphere medial and lateral side.

3.3 Partitioning and PCA

To perform a coarse-to-fine analysis, hierarchical spectral clustering was applied on the preprocessed phenotype. In ??, the partitioning produced from the application of hierarchical spectral clustering is displayed. On the first level, although the cross-section follows the sylvian fissure on the lateral part and partitions the frontal lobe from the rest of the hemisphere, on the medial surface it appears to split the precuneus in half (\subseteq BA07). On the second level, the occipital lobe is separated from the temporal lobe, while the central gyrus appears to be dissected from the frontal lobe, while inspected the lateral surface. On the medial surface, the paracentral gyrus (\subseteq BA04) is approximately separated from the superior-frontal, whereas another cross section appears to share its boundaries with the temporal pole (\subseteq BA38). In general, the unsupervised clustering follows the functional partitioning, validating the close relationship between function and morphology of each cortical region. The calculated normalized mutual information score for the partitioning, compared to the Desikan-Killiany atlas is displayed in ?? for each level. Although the finer the partitioning, the further away from the theoretical maximum value, quantitatively the two clusterings highly agree.

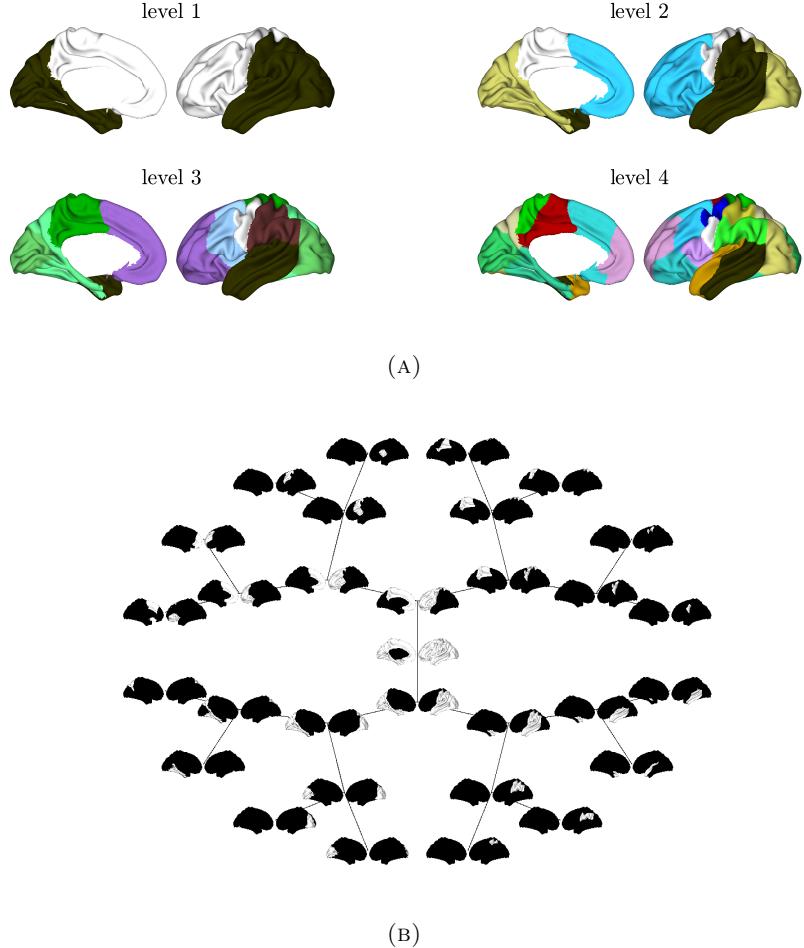


FIGURE 3.3: 4-level brain shape partitioning based on cortical asymmetry, using hierarchical spectral clustering. Shown in 2 different versions, on a level representation (top), and as a polar dendrogram plot, annotated with white color against black background (bottom). Those representations are used across the coarse-to-fine analysis in this study.

	NMI	NMI_{max}	ratio
Lvl 1	0.37	0.48	0.78
Lvl 2	0.49	0.66	0.74
Lvl 3	0.55	0.79	0.71
Lvl 4	0.62	0.90	0.69

TABLE 3.1: Normalized mutual information scores across hierarchical spectral clustering partitioning levels, comparing Desikan-Killiany atlas with computed partitioning levels. NMI_{max} is an approximate maximal value, given the different number of partitions in each clustering, and ratio is the scaled normalized mutual information using that value.

The required number of principal component analysis features per partition given the constraints, as computed by assessing the discovery dataset, is displayed in ???. A significant dimensionality reduction was achieved, given that the original total number of landmark coordinates per individual was 89367.

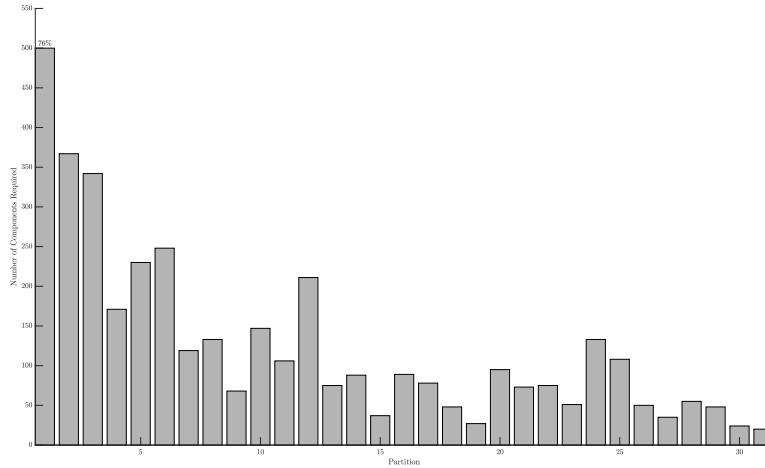


FIGURE 3.4: Number of principal components for each hierarchical spectral clustering cortical surface partition, required to explain 80% of its variance, relatively to the discovery dataset. For the first partition, the upper limit of 500 components was reached and only 74% of its variance is explained.

3.4 GWAS

By combining the aforementioned processed phenotypic and genetic features under the framework of canonical correlation analysis, insights were provided into the genetics of asymmetry. The resulting multivariate genome-wide association study Manhattan plot on the entire hemisphere exhibits distinct peaks, that slightly differ between discovery and replication dataset (??). In ??, the identified single nucleotide

polymorphisms are shown for the discovery and replication datasets genome-wide association studies, as well as the meta-analysis genome-wide association studies union and the ones reported in literature [?]. 22 lead single nucleotide polymorphisms with p-value less than 5e-8, versus 21 reported in literature [?], are retrieved from the meta-analysis union, six of which have also been exactly identified by ?] (??). Further comparisons with literature are provided in ??.

For each separate partition genome-wide association studies, the number of significant variants after Bonferroni correction is reported in ??, with the overlaid Manhattan plots shown in ???. A different chromosome-based response is observed when inspecting the second level of partitioning, namely partitions 4-7. Furthermore, partition 6, which corresponds to the frontal lobe cortical asymmetry, appears to be quite less genetically determined and agrees with the findings from the statistical analysis, where directional asymmetry did not appear to be, in general, significant in that region, whereas fluctuating asymmetry did (??). An additional observation is that partitions do not necessarily share the genetic signature of their parents, for example partition 8 exhibits a significant peak at chromosome 21, while that chromosome has not been identified elsewhere to exhibit significant genetic effect on cortical asymmetry. Chromosome 15 exhibits the highest peak, namely the single nucleotide polymorphism rs2033939 ($P=2e-50$).

To confirm that mean substitution of missing genotypes (i.e, variants that, even after imputation, had not been assigned a value) did not considerably affect the results, Spearman correlation was measured between the genome-wide association studies scores produced from the discovery dataset, with and without mean substitution. The produced values clearly suggested that mean substitution had little to no effect on the overall monotonicity (table ??).

3.4. GWAS

DISCOVERY			REPLICATION			UNION			SHA ET AL.		
CHR	SNP	P	CHR	SNP	P	CHR	SNP	P	CHR	SNP	P
15	rs1080066	4.10e-28	15	rs4924345	1.41e-27	15	rs2033939	2.09e-50	10	rs41298373	5.00e-38
17	rs10775404	5.12e-27	17	rs9910683	2.42e-20	17	17:44243312_C_G	3.91e-44	17	rs35853889	1.00e-20
14	rs160459	2.57e-17	9	rs7023465	3.74e-18	14	rs160459	3.58e-28	17	rs80103986c	5.00e-16
1	rs6658111	3.05e-15	14	rs74826997	3.02e-14	9	rs7023465	1.40e-25	9	rs911934	2.00e-15
16	rs111398992	1.17e-12	14	rs160459	6.57e-13	1	rs6658111	4.31e-25	17	rs55938136	5.00e-15
2	rs7575465	1.57e-12	1	rs6658111	8.08e-12	14	rs74826997	3.36e-22	16	rs111398992	6.00e-15
16	rs9939914	7.01e-12	10	rs41298373	2.10e-11	16	rs72813426	3.78e-21	17	rs568039055	8.00e-15
10	rs41298373	3.66e-11	16	rs35769864	1.40e-10	10	rs41298373	9.26e-21	16	rs72813426	2.00e-14
17	rs62063672	1.40e-10	12	rs10783306	7.41e-10	16	rs111398992	1.66e-20	14	rs160459	5.00e-12
3	rs35124509	2.71e-10	2	rs7575465	7.75e-10	2	rs7575465	1.80e-20	12	rs10783306	1.00e-11
14	rs76341705	3.81e-10	16	rs111398992	9.24e-10	3	rs35124509	1.26e-15	2	rs12617392	4.00e-11
9	rs911934	4.71e-10				16	rs11640500	2.84e-15	1	rs6658111	1.00e-10
3	rs2399037	4.21e-9				12	rs1057548	1.71e-13	2	rs62130503	1.00e-10
7	rs117766132	6.39e-9				16	rs12711472	4.61e-12	2	rs368536282	1.00e-10
2	rs2691112	1.29e-8				2	rs7601767	8.67e-11	6	rs7781	2.00e-10
2	rs7601767	1.88e-8				7	rs151218739	1.76e-10	14	rs201816193	4.00e-10
8	rs7000137	2.60e-8				8	rs10106820	1.80e-10	19	rs11672092	6.00e-10
						2	rs13021393	6.80e-10	21	rs7283026	8.00e-10
						21	rs7283026	3.01e-9	3	rs2279829	1.00e-9
						8	rs442103	3.43e-9	5	rs869219775	3.00e-9
						15	rs8026370	4.49e-9	20	rs6135555	7.00e-9
						21	rs4819075	5.01e-9	X	rs12400461	1.00e-8
						2	rs2287283	1.38e-8	6	rs9385385	1.00e-8
						2	rs7609463	1.38e-8	17	rs35908989	1.00e-8
						17	rs930119	3.02e-8	4	rs9307052	2.00e-8
						11	rs2251662	3.41e-8	22	rs9615351	3.00e-8
									7	rs6947352	4.00e-8

TABLE 3.2: Identified lead single nucleotide polymorphisms for the entire hemisphere across the different datasets, along with a comparison with [?]. In gray, single nucleotide polymorphisms with significance less than 1e-8 but greater than 5e-8 are reported. In bold are displayed the variants identified both in the present study and in the work of [?].

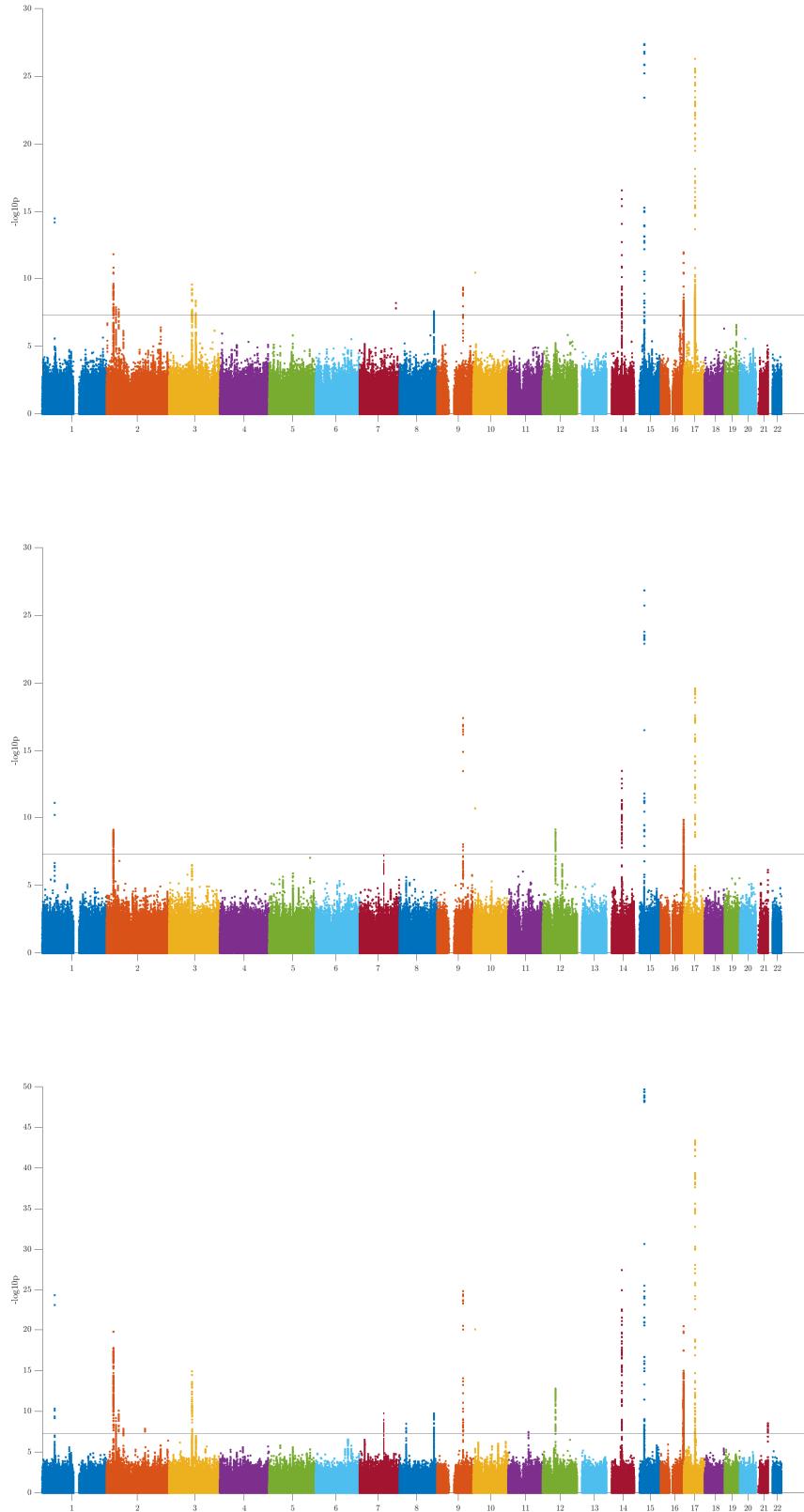


FIGURE 3.5: Multivariate genome-wide association study of the entire hemisphere shape asymmetry computed on the discovery (top) and the replication (middle) dataset, along with the meta-analysis union based on Stouffer's method (bottom). The genome-wide threshold of 5×10^{-8} is also being displayed as a horizontal line.

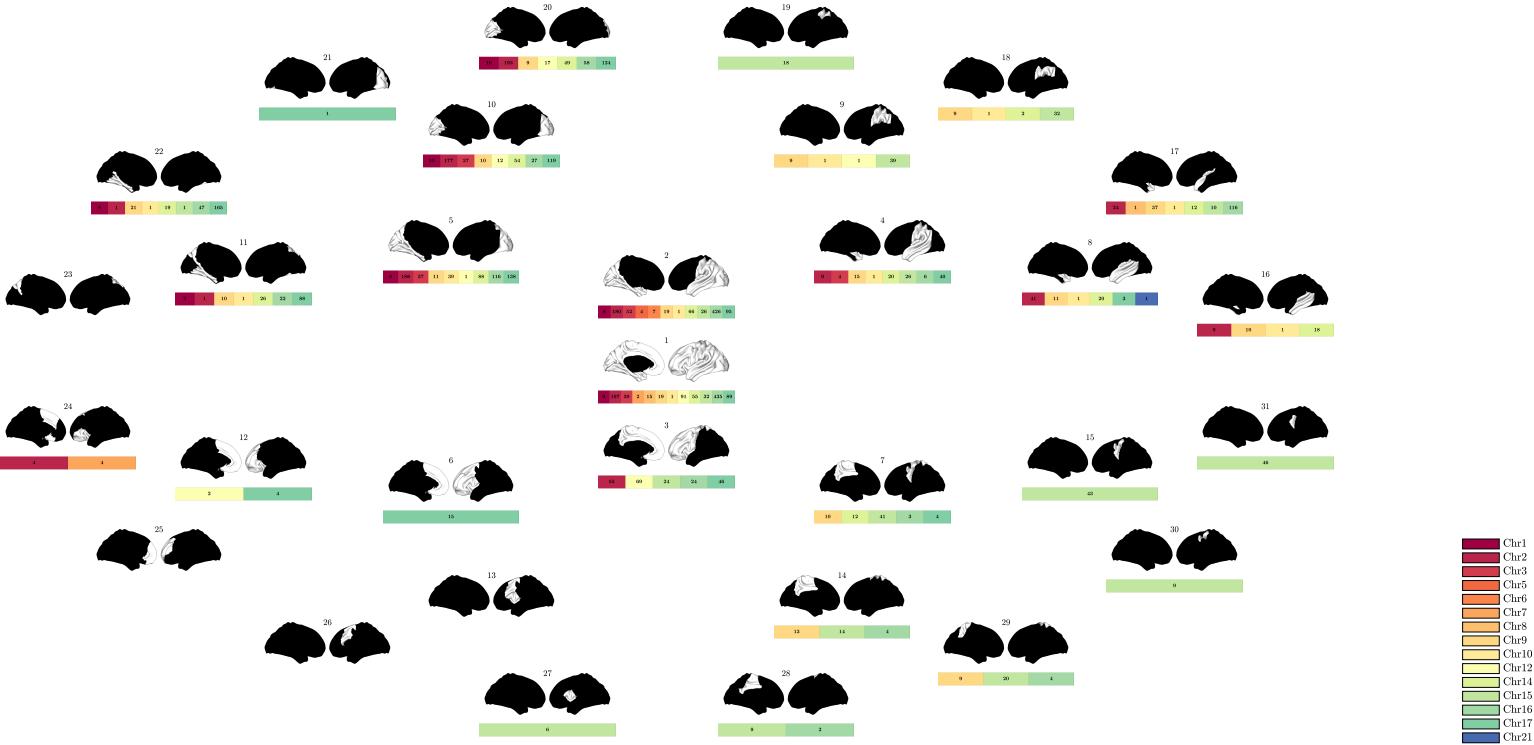


FIGURE 3.6: Number of significant single nucleotide polymorphisms per chromosome after Bonferroni correction across partitions. The variants number per chromosome is shown inside boxes of a different color, as displayed in the legend on the right.

3.5 LDSR

Another important question to be answered was how much of the variability of cortical symmetry is attributed to genetic factors. The observed heritability is generally below 0.3 across the different partitioning levels (figure ??), as expected from the effect of plasticity on human cortex. The heritability estimates minima and maxima grossly agree with the results of [?]. Comparably more heritable than in other regions appears to be the asymmetry on the temporal lobe, on the auditory cortex and the basal surface of the temporal lobe. The confounding bias is found to be considerably low, with the LD score regression intercept being close to 1 [?] (figure ??), so little to no evidence is presented regarding subpopulation stratification.

3.6 Cross-trait correlation

To examine whether cortical asymmetry is genetically related with other indications, and potentially reason about the universal patterns among individuals, statistical tests for cross-trait monotonicity followed.

3.6. Cross-trait correlation

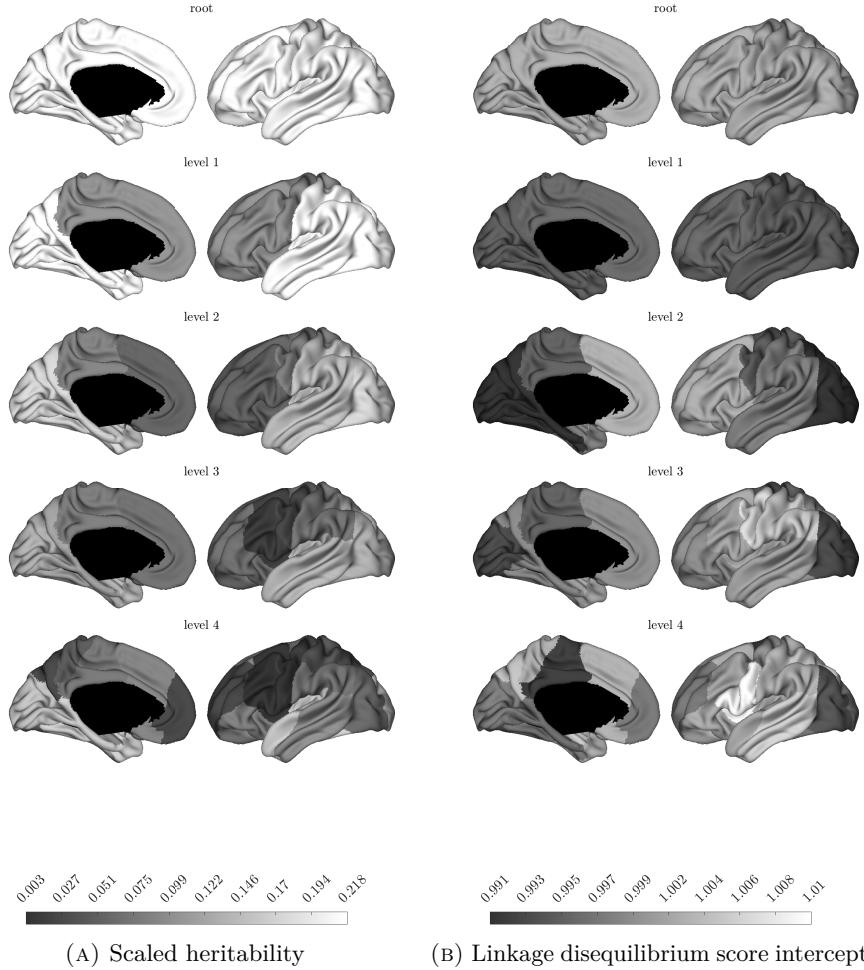


FIGURE 3.7: LD score regression results on the entire hemisphere and each partitioning level.

By inspecting the results from Spearman cross-trait correlation with the univariate traits mentioned in ?? (?? and ??), language functional connectivity exhibits the strongest relationship, for the entire hemisphere and partition 17. Educational attainment also appears to be strongly correlated with cortical asymmetry, with the strongest sign occurring on the 2nd partition, which includes most sensory areas. Obsessive/compulsive disorder exhibits strong correlation with cortical asymmetry with partitions 14 and 26. Partition 11 from the 3rd level and its child partition 22 from the 4th level point to correlation with handedness. Furthermore, intelligence exhibits significant genetic correlation with partitions 9 and 11, both exhibiting genome-wide association studies peaks on chromosomes 9 and 15 (??). Moreover, Parkinson's disease appears to be genetically correlated with the cortical asymmetry observed on partition 20. No monotonicity between cortical asymmetry p-values and the genome-wide association studies scores of the following traits was identified

3.6. Cross-trait correlation

for acfadhd, autism spectrum disorder (ASD), Alzheimer's disease (AD), bipolar disorder (BD), major depressive disorder and schizophrenia.

Investigating the relations of cortical asymmetry with another trait related to cortical structure, specifically the average mid-cortical surface per individual, coined as brain shape, and the corresponding 8-level hierarchical spectral clustering partitioning and genome-wide association studies performed by ?] in a similar fashion to the present study, it is apparent from ?? that there is a quite strongly supported genetic relationship. Such correlation stands not only for the entire hemisphere (partition 1 and shap1 respectively), but also for other pairs, with observed P-values getting as low as 10e-59, and Spearman correlation values as high as 0.34.

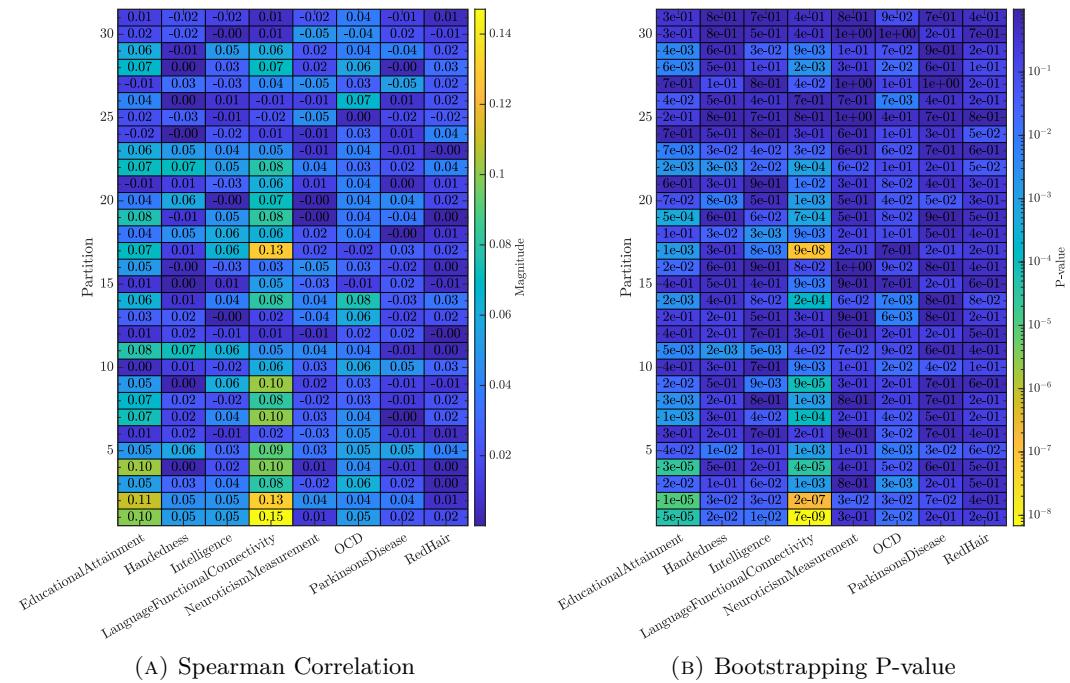


FIGURE 3.8: Cross-trait correlation stats across partitions in a tabular format.

3.6. Cross-trait correlation

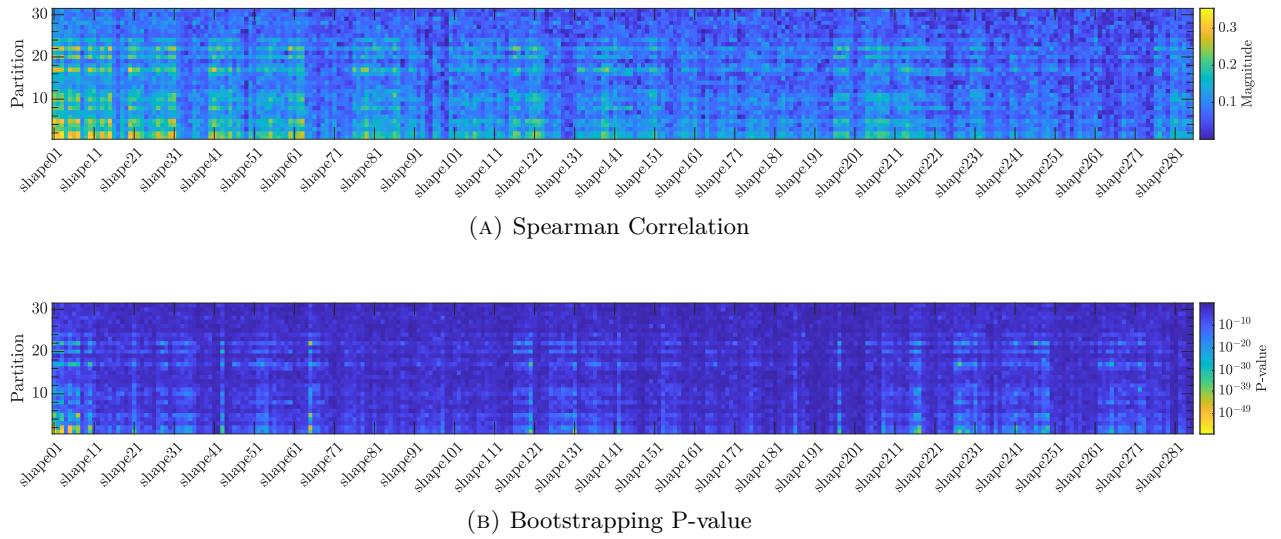


FIGURE 3.9: Brain shape partitions (x-axis) genome-wide association studies scores, as derived by [?], compared against cortical asymmetry partitions (y-axis) genome-wide association studies scores of the present study.

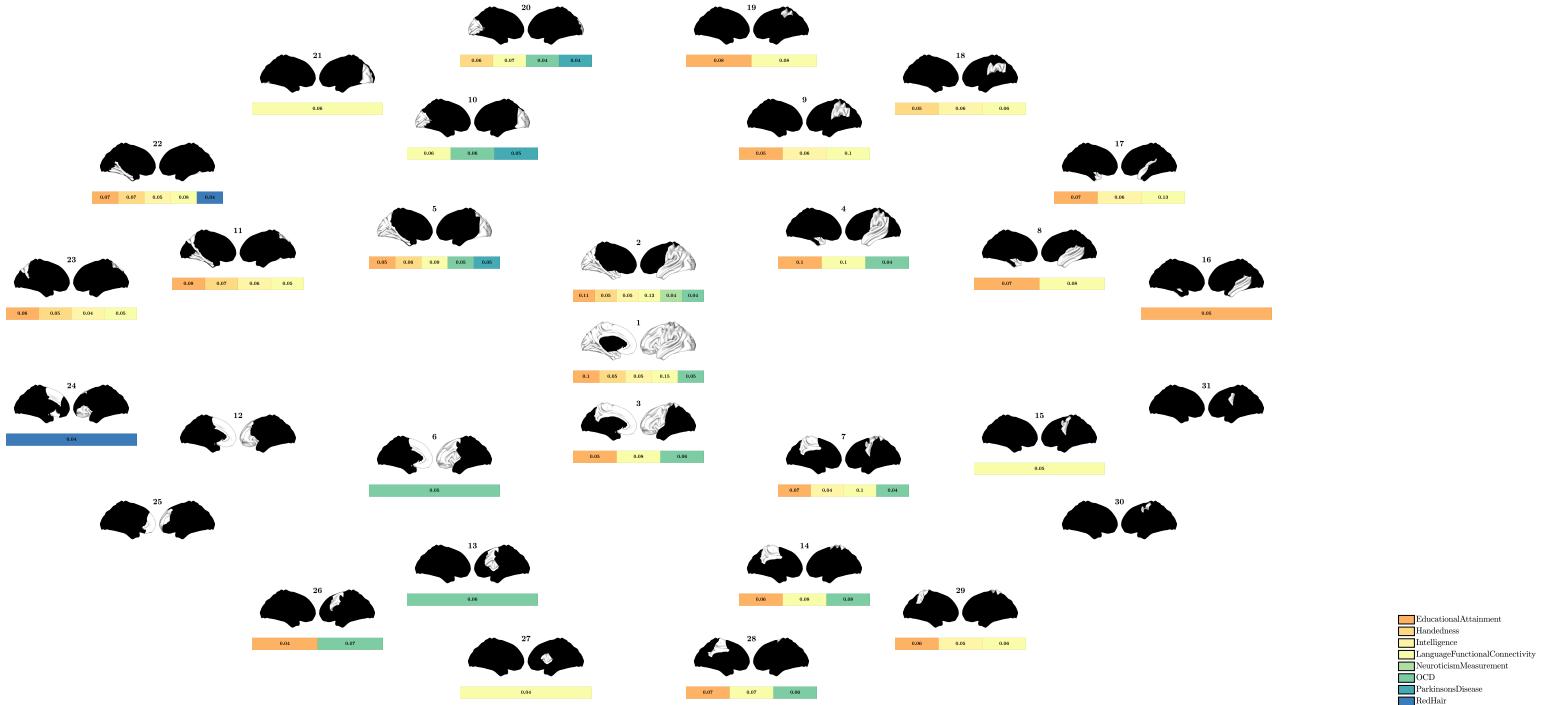


FIGURE 3.10: Cross-trait correlation with asymmetry in a polar diagram. Only correlations with p-values less than 0.05 are shown.

3.7 LDSC-SEG

After having determined the genetic factors that drive cortical asymmetry, it is of interest to examine the amount of epigenetic regulation affecting them, by investigating profiles of different types of tissues. In ?? chromatin accessibility enriched regions for specific adult or developing tissues were found to be related with cortical asymmetry heritability. Out of the 489 tested tissues, mainly those related with the brain, and in particular with the fetal brain, exhibited more significant relationship with the studied population. The strongest significance was displayed by the fetal brain female tissue, versus the male analog, suggesting that female fetuses may exhibit increased asymmetric heritability. However, these results need to be taken with a grain of salt, as the underlying population used to collect the samples was comprised only by a few individuals, at different time periods, so it is quite possible that uncontrollable factors and sample bias obscure the results. Another observation is that partitions that ‘reacted’ to this analysis are mainly localized on regions that had already been found to have increased heritability in ?? and figure ??.

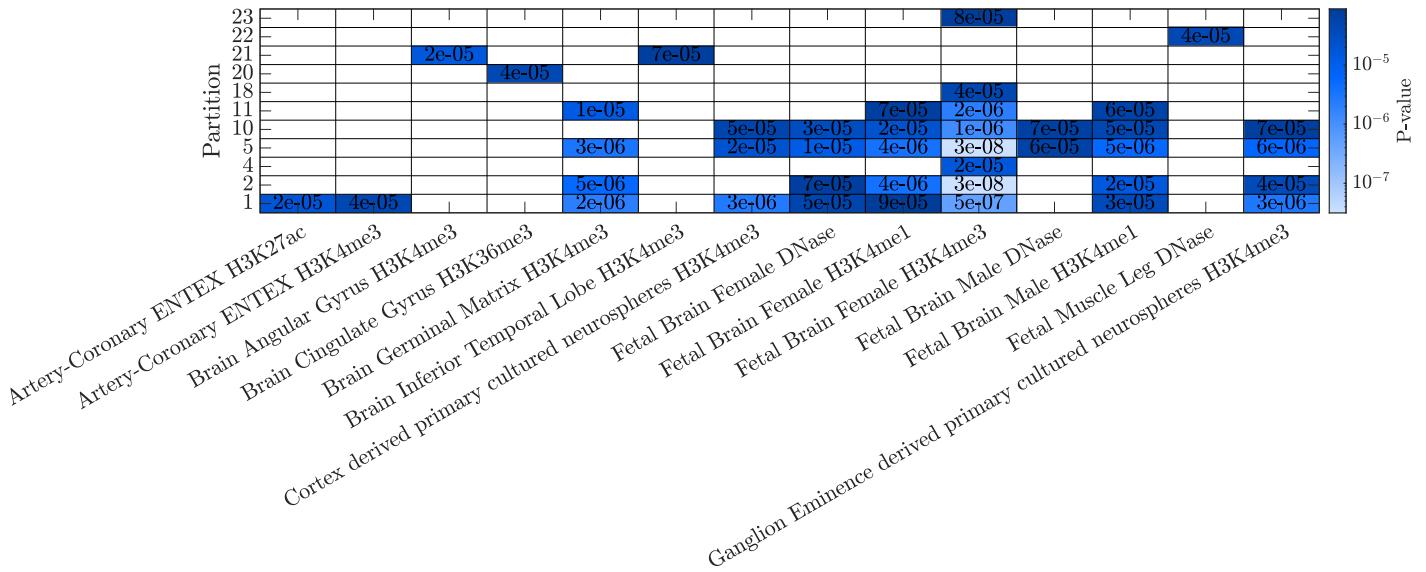


FIGURE 3.11: Significance of heritability affected by different tissues enriched chromatin accessibility profiles, across partitions. Unavailable(white) values and missing partitions mean that the LD score regression applied to specifically expressed genes algorithm failed to identify strong relationships in these cases. H3K27ac, H3K4me3 and HeK4me1 are each different epigenetic modifications on histones, the molecules that compose the deoxyribonucleic acid packaging, and are used as markers of gene regulation.

3.8 Developmental analysis

For the following analyses, only the genome-wide association studies scores produced by assessing the entire hemisphere and the 2nd level partitions are assessed, considering

3.8. Developmental analysis

their distinct genetic signature. In ??, genetic loci that have been found strongly in connection with the existence of cortical asymmetry appear to be developmentally regulated, with their activity primarily detected in the early weeks of gestation, while the stringent regulatory mechanism, which is activated after the 2nd month of gestation, appears to ‘relax’ during adolescence. The variability of the regulatory pattern on different partitions does infer that not all structural characteristics develop at the same time across the human cortex.

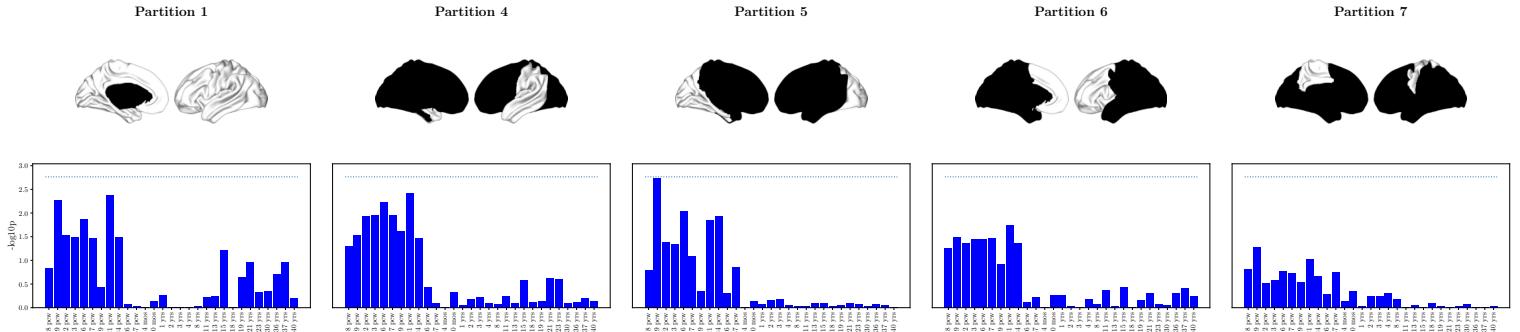


FIGURE 3.12: MAGMA analysis on age specific brain tissue enriched genes, on the genome-wide association studies of the entire hemisphere and the 2nd level partitions. Samples were densely collected from tissues during gestation, ranging from 8 to 37 post conception weeks (pcw), and also from individuals aged up to 40 years old.

Partition 1 84 genes			Partition 4 43 genes			Partition 5 68 genes			Partition 6 32 genes			Partition 7 34 genes	
AGBL5	FOXD2	SHFM1	ALCAM	RP11-368I7.4		ACTR10	GAS8	TIMM9	ARL17A			ARL17A	
ARL17A	FOXL1	SLA	ARL17A	SFMBT2		AGBL5	ITIH5	TMEM214	ARL17B			ARL17B	
ARL17B	FOXN2	SLC25A13	ARL17B	SPATA33		ARHGAP27	KANSL1	TOMM20L	C17orf58			C16orf3	
C16orf3	GALNT12	SPATA33	C16orf3	SPIRE2		ARL17A	KCNA5	TRABD2B	CRHR1			C17orf58	
C16orf95	GAS8	SPATS2	C17orf58	SPPL2C		ARL17B	KHK	TUBB3	DHH			CENPBD1	
CDK10	ITIH5	SPIRE2	CENPBD1	STH		C16orf3	L3HYPDH	VPS9D1	DNAJC22			CRHR1	
CENPBD1	KANSL1	SPRED2	COL15A1	TCF25		C17orf58	LHCGR	WNT3	FMNL3			DAAM1	
CGREF1	KHK	STRN	COL18A1	THBS1		CDK10	LHPP	ZNF276	GTF2A2			DBNDD1	
CHMP1A	KMT2D	TCF25	CRHR1	TIMM9		CENPBD1	RRRC37A		KANSL1			DEF8	
CMPK1	LMBR1L	TENM4	DAAM1	TUBB3		CGREF1	RRRC37A2		KMT2D			FANCA	
COL15A1	LRRC37A	THBS1	DACT1	VPS9D1		CHMP1A	LRRC37A3		LMBR1L			GAS8	
COL18A1	LRRC37A2	TIMM9	DBNDD1	WNT3		CMPK1	MAPRE3		LRRC37A			KANSL1	
CPNE7	LYPD6	TMBIM6	DEF8	ZNF276		COL15A1	MAPT		LRRC37A2			L3HYPDH	
CRHR1	LYPD6B	TMEM214	EPHA3			CPNE7	MC1R		MAP2			RRRC37A	
DAAM1	MAPRE3	TRABD2B	FANCA			CRHR1	METTL10		MAPT			RRRC37A2	
DACT1	MAPT	TROAP	GALNT12			DAAM1	NR2F1		MC1R			MAPT	
DBNDD1	MC1R	TUBA1A	GAS8			DACT1	NSF		MEIS1			MC1R	
DEF8	MEIS1	TUBA1B	ITIH5			DBNDD1	NTF3		NSF			NSF	
DHH	NSF	TUBA1C	KANSL1			DEF8	OST4		PRKAG1			rs4924345	
DLX6	OST4	TUBB3	KCNK16			DPYSL5	PLEKHM1		RHEBL1			rs7023465	
DNAJC22	PLEKHM1	VIT	KIF6			EMILIN1	PREB		SPATS2			rs72813426	
DPYSL2	PNMA2	WISP1	RRRC37A			EPHA3	RP11-12J10.3		SPPL2C			rs75267789	
DPYSL5	POFUT2	WNT3	RRRC37A2			FAM175B	RP11-368I7.4		SPRED2			rs76341705	
EMILIN1	PREB	ZNF276	LYPD6			FAM53B	RTN1		STH			RTN1	
EPHA3	PRKAG1		LYPD6B			FANCA	SFMBT2		TCF25			SPATA33	
FANCA	QPCT		MAPT			FMNL1	SPATA33		TMBIM6			SPIRE2	
FBXO11	RASGRP1		MC1R			FNDC4	SPIRE2		TROAP			SPPL2C	
FBXO31	RHEBL1		NSF			FOXD2	SPPL2C		TUBA1A			STH	
FMNL3	RP11-368I7.4		POFUT2			FSHR	STH		TUBA1B			TCF25	
FOXC2	RTN1		RASGRP1			GALNT12	TCF25		TUBA1C			THBS1	

TABLE 3.3: Identified gene sets using FUMA and extended with GREAT, for the entire hemisphere and the 2nd level partitioning genome-wide association studies. In bold, the genes that do not occur in other gene sets are displayed. Lead single nucleotide polymorphisms that have not been mapped to a gene are also displayed with their rs-id.

3.9 Functional association

The extrapolation of the identified lead single nucleotide polymorphisms to the gene abstraction level, using FUMA and GREAT produced the genes sets presented in ???. It is evident that there are differences, and even certain genes appear to be related with cortical asymmetry only in certain partitions. By examining FUMA functional association with gene ontology terms, a tight connection of the identified gene set is demonstrated with the cytoskeleton and particularly with the microtubules function and biological processes (?? and ??), in line with literature [?]. Furthermore, testing the identified gene set versus gene differential expression of diverse tissues, cerebral and cerebellum tissues displayed the greatest enrichment (??), whereas thyroid and female gender related tissues, namely uterus and ovary ones, exhibit mostly downregulated genes enrichment. By investigating the gene set enrichment on traits reported in genome-wide association studies catalog (?? and ??), behavior-related traits, such as alcohol use disorder, handedness, and phenotypic traits closely related to the exoderm, such as sun tan response, male baldness and the red hair

trait, appear highly correlated with the identified asymmetry gene sets. Canonical pathways enrichment analysis (?? and ??) reveals connections with NMDA receptors pathways, particularly on the frontal lobe, known to control synaptic plasticity and memory function in mammals [?].

3.10 Proteins set network analysis

Last but not least, through the analysis of the computed STRING proteins network on the genome-wide association studies of the entire hemisphere, densely connected clusters were identified and their functional identity was researched through gene enrichment analysis (??). The results showcase four main pathways, governing cytoskeleton formation at diverse abstraction levels, with the first cluster related to the left-right axis formation [?], the second cluster to the dorsal-ventral axis formation [?], the third participating in the intracellular cytoskeleton structure and the fourth in the extracellular matrix formation. Enriched publications were mainly related to chromosome 17 and Koolen de Vries syndrome, a genetic disease that is recognizable in an magnetic resonance imaging scan by highly asymmetric ventricles, often giving rise to increased cortical asymmetry [?].

3.10. Proteins set network analysis

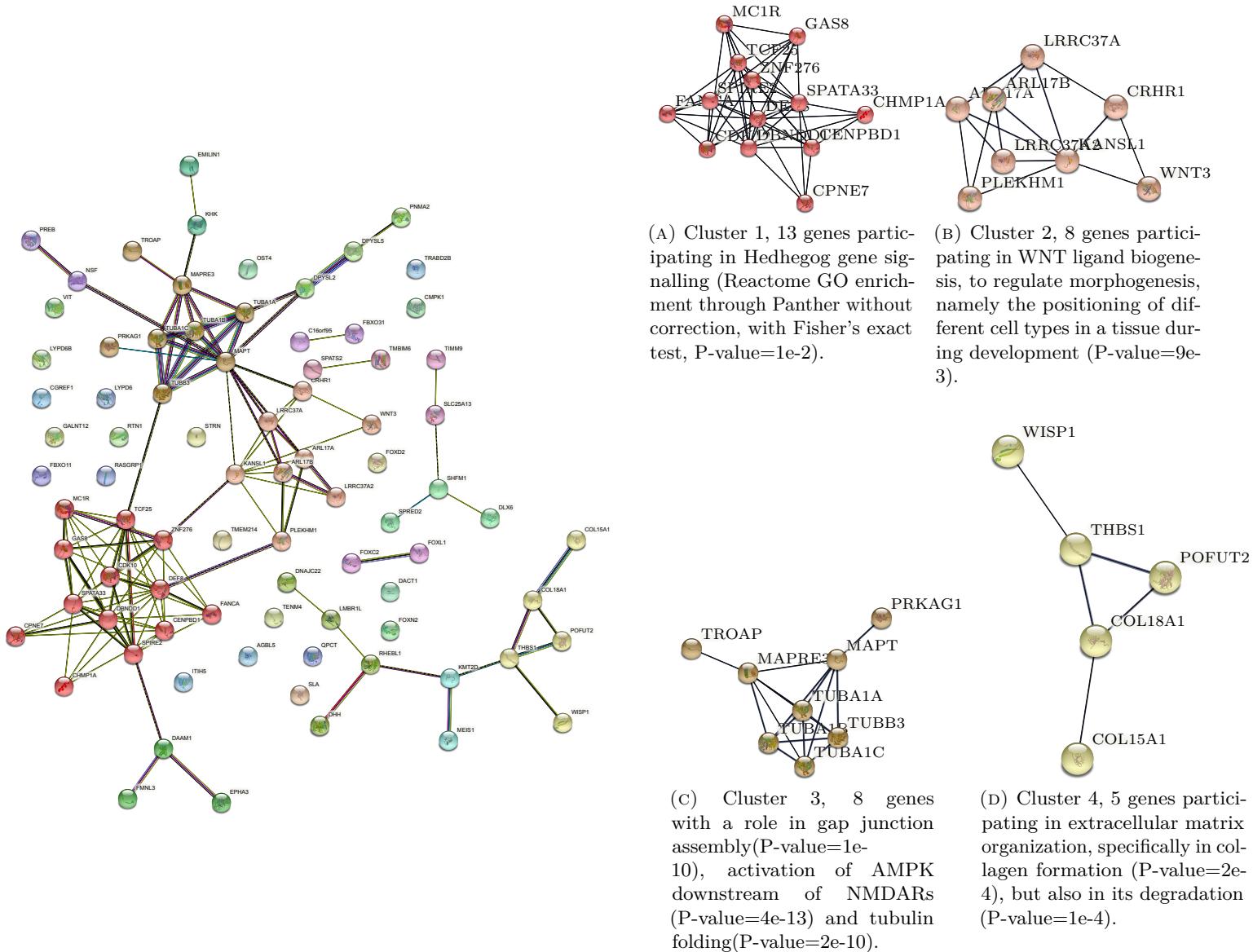


FIGURE 3.13: STRING protein-protein interaction network from the entire hemisphere genome-wide association studies gene set. Each cluster is annotated using PANTHER (cf. ??).

Chapter 4

Discussion

4.1 Comparison with literature

4.1.1 Associations with brain morphology

Cortical symmetry is a phenotypic trait exhibiting both global and local properties. It has been extensively anatomically studied in the past as large deviations present great medical value. Situs-inversus, the condition where antisymmetry in the organs placement is exhibited for an individual, is not observed in the asymmetric nature of the cortex, indicating the significance of counter-clockwise torque and other global traits in health and survival. Furthermore, the universality of common sulci and gyri asymmetries, such as the one observed for the central sulcus, implicate genetic factors also in a local setting. [?] mainly analyze features that have already been extensively studied in the literature, following carefully expert supervised anatomical parcellation of the human cortex, neglecting regions identified to have low heritability, based on the GCTA software, mainly located in the vicinity of the motor cortex and occipital lobe. They identified lead variants by inspecting the meta-analyzed univariate genome-wide association studies, on each DK atlas-specific region, and then traced back the results to each region separately, using phenotypic decomposition[?]. Therefore, localized analysis was performed only in an indirect manner, with a predefined parcellation. Other studies focus on modeling specific cortical asymmetric traits, without considering the general structure [? ? ?]. In contrast, the present study followed a data-driven, multi-level analysis, similar to the work presented in [?] and [?], focusing on capturing the entire variability of each hierarchical spectral clustering partition. Statistical shape analysis mostly agreed with past anatomical studies on cortical symmetry [?], although the global pattern of Yakovlevian torque, namely the counter-clockwise warping of the brain, was not detected, most likely due to the shape normalization and alignment process applied on the two hemispheres [?].

The applied multivariate genome-wide association study on the collected phenotypic features, following the steps of [?], with certain simplifications for computational reasons, led to novel extended findings that also partially validate with greater support the results retrieved from [?]. Out of the lead single nucleotide polymorphism

4.1. Comparison with literature

set difference, of interest is chromosome 15 implication, which had not been detected by [?] and that exhibits the highest peak in the current study, corresponding to single nucleotide polymorphism rs2033939 ($P=2e-50$). That variant resides closest to C15orf53 gene, with a long non-coding ribonucleic acid (lncRNA) transcript and a disputed role of being a genetic etiologic factor of Schizophrenia [?]. [?] reported the most significant single nucleotide polymorphism, rs41298373 ($P=5e-38$), to be located at chromosome 10. In the present study that chromosome peak, although exhibiting the exact same lead single nucleotide polymorphism, did not rank in an equally high degree of significance. In general, several differences with the primary results reported by [?] are observable, even from a qualitative viewpoint. There is also generally more confidence reported over common identified lead single nucleotide polymorphisms, characterized by lower p-values in the present study than the ones reported in literature [?]. A more fine-grained, quantitative comparison is also performed by applying Spearman correlation, in the way mentioned at ?? [?] (cf. ??). The degree of agreement is non-negligible, and most partitions exhibit significant monotonic relationship with the results from [?]. The greatest (0.16) and most strongly supported ($P=1e-11$) correlation is observed relatively to the entire hemisphere (partition 1). Furthermore, substantial heritability was detected throughout the studied partitioning levels, in line with literature [?]. At the gene level, significant correlations with cytoskeleton formation, morphogenesis and other prenatal developmental stages were observed, similarly to literature [?], while at a protein-protein interaction level, connections with principal symmetry axes determination were detected. An additional observation relates region-specific differential gene inhibition, due to epigenomics, with cortical asymmetry development.

Having taken into account that, prior genome-wide association studies, covariates control had been applied and any controllable gender effect had been removed from the analysis, through the ablation of the sex chromosome, it would have been expected that no gender-specific differences would be detectable. However, the results reported in ??, particularly when superimposed with the observations in the separate analysis of partitioned chromatin accessibility heritability in ??, point to differential cortical structure characteristics between male and females, caused by distinct epigenetic regulation. Furthermore, male-pattern baldness is a trait that shares a significant amount of genes with cortical asymmetry, as it can be observed in the gene set enrichment analysis (??). That observation is anatomically supported by literature, with males generally exhibiting greater asymmetry than females [?]. The fact that [?] report a significant lead single nucleotide polymorphism on the X chromosome further corroborate such a dependency at the deoxyribonucleic acid-replication level. More direct comparisons with related studies to cortical asymmetry were not applicable, due to the distinct phenotypic segmentation and the scarcity of similar research with published results, connecting genetic factors and cortical symmetry.

4.1.2 Associations with other traits

Through the genome-wide association studies-based monotonicity analysis, various insights were retrieved about the relationship of cortical surface asymmetry with other traits. Genetic associations with language functional connectivity were identified on a segment that corresponds to the superior temporal lobe, a part of the auditory sensory system (BA41, BA42), and BA22, involved in auditory short-term memory and the production of speech. Studies performed on functional magnetic resonance imaging (fMRI) stream by [?] have shown that different asymmetric patterns of activity on that region are observed, depending on language proficiency. Obsessive/compulsive disorder was found to exhibit genetic correlation with cortical asymmetry on regions that correspond to the dorsolateral prefrontal cortex, an area broadly recognized as relevant to obsessive/compulsive disorder pathology [? ?]. A weaker genetic correlation with Parkinson's disease ($P\text{-value}=0.05$) was localized on BA17 and BA18, which are part of the occipital lobe. Being the center of visual processing, this region has been identified to be significantly affected by this disease, leading patients to suffer from hallucinations [?], while asymmetric cortical atrophy on that region has been mainly reported for late stage patients [?]. Connections with autism spectrum disorder were not directly made, in contrast to what has been reported in previous work [?]. A controversial finding is handedness, whose correlation with cortical asymmetry has received mixed reception in the literature [? ?]. In the current study, it was found to be genetically related with asymmetry at BA20 and BA37, which contain the fusiform and the inferior temporal gyri. Fusiform gyrus is known to encase neurons functionally allocated to the encoding of details of human body parts [?]. In addition, evidence from fmagnetic resonance imaging studies shows asymmetric activation of fusiform, correlated with manual dexterity [?]. Intelligence was identified to be genetically related with the asymmetric shape of partition 9, which represents the posterior parietal cortex, an association area that participates in motion planning and spatial reasoning. However, connection of intelligence with asymmetric structure on that region is not supported by existing literature. Finally, brain shape [?] was identified to strongly genetically correlate with cortical asymmetry at a multi-level fashion, a finding that acts as solid evidence for structural asymmetry to be considered as an extension of the overall brain shape structure, genetically bridging the two related phenotypes.

The single nucleotide polymorphism to gene reduction returned the genes displayed in ?? for the entire hemisphere and the focused partitions. By inspecting the sets differences, some additional observations can be made. For example, on the entire hemisphere, the forkhead box (FOX) family of transcriptions factors, namely FOXC2 (CHR16), FOXD2 (CHR1), FOXL1 (CHR16) and FOXN2 (CHR2), is uniquely mentioned. This family of genes has been found to participate in embryonic developmental processes and known to regulate cellular proliferation [?]. For partition 5, which includes the lower midsagittal part of the temporal cortex, the genes FAM53B (CHR10), METTL10 (CHR10) and FAM175B (CHR10) have been identified in literature to be related to hippocampal volume [?] (??). The hippocampus resides underneath the studied partition, thus there are indications

4.1. Comparison with literature

that, locally, asymmetry is genetically adjusted for the hemisphere to host a larger hippocampus. Unfortunately, the corresponding study did not discriminate between left and right hippocampal measurements, so that further links with subcortical asymmetry can be made. Partition 7, on the other hand, exhibited a strong relationship with blood measurements (??), because of the genes SPATA33, WNT3, CRHR1 ARL17A and ARL17B. However, those also occur in most of the other partitions as well, an observation implying that the gene set enrichment analysis on a limited amount of genes might give rise to spurious results. The fact that in the current study the identified genes are only few leads to question the validity of certain gene set enrichment analysis results. Only on the specific group of APOE ϵ 4-carriers, namely individuals that carry a mutation at APOE gene that increases the risk of Alzheimer's disease at an early age [?], genetic relations between Alzheimer's disease and cortical asymmetry were identified. Although neither at a single nucleotide polymorphism nor at a gene level significant connections with Alzheimer's disease among a more general consortium were identified, this finding associates brain disorganization with Alzheimer's disease and infers that magnetic resonance imaging scan measurements could serve as a feature in empowering prediction on individuals exhibiting signs of the disease. That is also supported by [?], where a longitudinally surging increase of cortical asymmetry caused by thinning of the cortex is observed among patients, thus such evidence brings forward the prognostic capacities of this imaging technique applied for Alzheimer's disease. Connections with bipolar disorder, brought forward by other phenotypic-based studies [?], were only made at the gene set enrichment analysis level. In addition, correlations with behavioral and cognitive traits were an insightful finding. Alcohol use disorder exhibited a significant signal across the hemisphere, which partially agrees with the results presented by [?], where addiction on substances had shown aberrations in volumetric asymmetry of the basal forebrain. Lastly, reaction time was also found to be significantly correlated with cortical asymmetry. However, testing this quality usually entails hand and finger movements [?]. Such actions have been found to be differentially affected by handedness [?], hence reaction time is likely to be genetically correlated with handedness.

Despite the observation that region-based characteristics, namely hair color, skin pigmentation and tan response, are related to cortical asymmetry based on the gene set enrichment analysis, the intercept value identified during LD score regression suggests no existence of subpopulation structures. Indeed, this connection appears to be indirectly made due to genetic alternative splicing. When inspecting the identified gene sets in the functional analysis (??), MC1R (CHR16) appears to be correlated with the entirety of population-specific traits, while at the same time it is connected with obsessive/compulsive disorder. This gene codes for melanocortin 1 receptor and plays a pivotal role in the production of melanin, affecting skin and hair color [?]. Alarmingly, MC1R and TUBB3, an instrumental gene in microtubule formation, share the same coding region, with alternative splicing happening on an included poly(A) site [?](??). Other associated genes to cortical asymmetry and race-specific traits are FANCA (CHR 16), also relevant to chronotype, an expression of individual circadian rhythmicity [?](??), SPIRE2 (CHR 16), implicated in cell division, and SPATA33 (CHR16), participating in spermatogenesis. Mutations to those genes increase the

risk of exhibiting a rare disease called Fanconi anaemia, which, among developmental atrophy and high probability of cancer occurrence, is characterized by non-uniform melanin deposition on the skin [?]. The aforementioned genes are all located at approximately the same neighborhood in chromosome 16, with a maximum pairwise distance of 10 kb (??). Based on the observed proximity, it is likely that the identified ambivalent cross-trait connections may be spurious. Nonetheless, the peak exhibited at SPIRE2 and the ‘stretch’ of significant single nucleotide polymorphisms along the FANCA may call for a stratified linkage disequilibrium score regression study on the loci of interest, to assert the assumption of single nucleotide polymorphism heritability uniformity made by LD score regression [?].

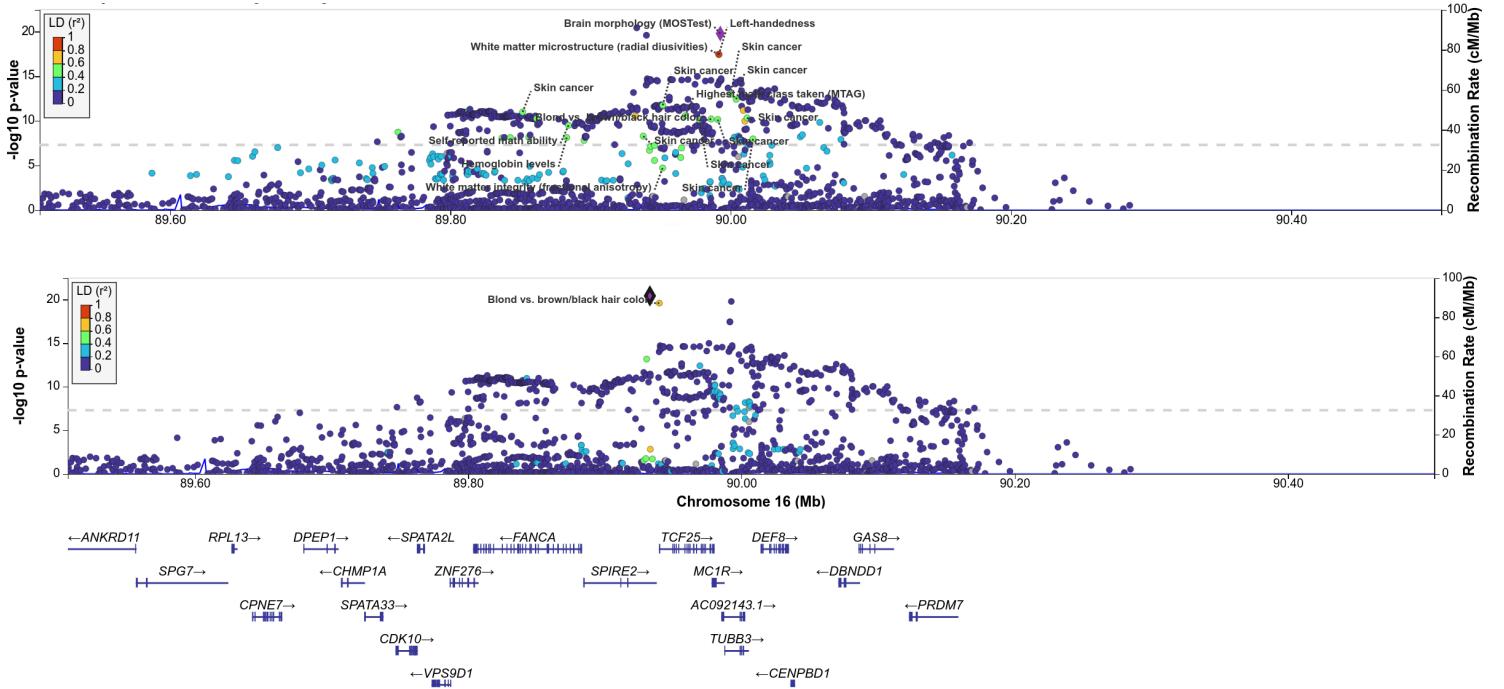


FIGURE 4.1: Scores from the entire hemisphere genome-wide association studies for chromosome 16 TUBB3 and SPIRE2 lead single nucleotide polymorphisms neighborhood. $-\log_{10}P$ values, corresponding LD r^2 scores and cross-trait single nucleotide polymorphisms annotations are shown, as retrieved by LocusZoom tool [?]. With a purple rhombus shape the point corresponding to the reference single nucleotide polymorphism for LD computation is displayed, rs111398992 (TUBB3) and rs72813426 (SPIRE2) on the top and middle graph respectively. At the bottom, a genes mapping, based on the GRCh37 build, is displayed for that region.

4.2 Contributions

In the current study, a detailed data-driven multi-level analysis statistically elucidated the origins of cortical asymmetry, a complex multivariate phenotypic trait, on healthy individuals of European origin from the largest known magnetic resonance imaging database to date, UK Biobank [?]. The degree to which plasticity effect

is dispersed throughout the brain was statistically mapped using 2-way analysis of variance and genetically quantified, through heritability studies. A coarse-to-fine data-driven segmentation identified homogeneously symmetric regions, without any prior anatomic knowledge. Novel causal region-specific genetic variants were identified after multivariate genome-wide association study on the derived partitions, complementing the existing literature [?]. Different spatially-dependent genetic profiles were identified. Connections with biological pathways, concerning intra- and extra-cellular organization and the formation of symmetry axes, were made, by examining protein-protein interactions. The effect of a strong regulating, spatially dependent epigenetic effect on development was determined. Furthermore, gender-controlled epigenetic modifications appeared to affect cortical asymmetry. Gene- and single nucleotide polymorphism-level associative studies with other genetically-driven traits led to the establishment of a tight genetic connection between brain shape and asymmetry, while strong single nucleotide polymorphism-level genetic correlation was detected relatively to intellectual skills, handedness, obsessive/compulsive disorder, Parkinson’s disease and neuroticism. At the same time, computational acceleration was achieved, without observable loss in accuracy, through the application of simple operations, such as the average shape downsampling discussed in ?? that made the statistical analysis feasible, and the mean substitution of the single nucleotide polymorphisms, that permitted a significant speed up of the canonical correlation analysis analysis.

4.3 Limitations and possible extensions

4.3.1 Limitations

First stage

Several limitations were detected during the conduction of this study, some of which could potentially be avoided by an extended future research. As far as the first stage of the analysis is concerned, lack of access to a test-retest dataset from UK Biobank and the disproportionate permutation spaces of 2-way analysis of variance increased the error margin of the results, and the total variability of the data was not captured, because of the small sample size used, despite the three experimental iterations aggregation. In addition, covariates control prior to the statistical analysis could potentially provide a more consistent shape normalization and improve results quality. Furthermore, adaptive remeshing, by performing non-rigid group-wise registration, in place of the used naive method, would possibly have increased the results resolution, in exchange for greater computational demands.

Second stage

At the second stage, the absence of a signed statistic from multivariate genome-wide association study did not allow to deduce whether identified single nucleotide polymorphisms’ presence contributes positively or negatively to cortical asymmetry, while also prohibiting the application of LD score correlation during cross-trait

analysis. Another step of multivariate regression, possibly in the form of canonical correlation analysis, using the lead single nucleotide polymorphisms as covariates and the phenotype as predicted variable, could produce signed effects for each significant variant.

Furthermore, 1000G project Phase 3 single nucleotide polymorphism filtering greatly reduced the amount of significant genes, with p-values lower than 5e-8, approximately by 82% for the entire hemisphere genome-wide association studies (table ?? and ??), while certain partitions lost all the single nucleotide polymorphisms for at least one chromosome, whose p-value is lower than the Bonferroni threshold of 5e-8/31 (table ??). Although UK Biobank makes use of the 1000G Phase 3 project as the reference genome to perform phasing and imputation [?], in the current study, the high percentage of significant single nucleotide polymorphism pruning implies that non-significant single nucleotide polymorphisms relationships are mostly driving the correlation studies and the LD score analysis.

It is also noteworthy to mention that the initial single nucleotide polymorphism-based filtering (cf. ??) has pruned away variants, which could potentially have a great impact on the studied phenotypic trait. However, studying the complementary case is difficult and highly error-prone, heavily relying on the sequencing technologies. Including rare variants and indels requires a denser genotyping, feasible through whole genome sequencing (WGS) [? ?], a technology to-be applied on UK Biobank anticipated dataset update [?].

4.3.2 Further extensions

A possible extension would be to expand the gene-based meta-analysis on the entire set of identified partitions (i.e., not only on the second level ones), and develop a hierarchy-dependent gene set enrichment analysis, to promote cohesive results and remove false positives. Enriching the Spearman cross-trait correlation analyses with a larger amount and variety of traits' genome-wide association studies scores would, in addition, offer a better support of the identified correlations. Gender-based studies, after the extension of multivariate genome-wide association study on X chromosome, could derive, using sex as a covariate in a regression setting, the degree of variance explained by gender for each gene [?]. Partitioned-based heritability analysis, centered at the regions of interest, could provide an answer to whether localized subpopulation structures exist. Lastly, modeling the cortical asymmetry heritability profile through epistasis analysis and even statistical shape modeling, extending existing ideas [? ? ?], could make an approximate measurement of cortical plasticity in a spatially dependent manner possible, providing grounds for a personalized method of cortical structure anomaly detection and diagnosis of related diseases.

Appendix A

Genome preprocessing and filtering

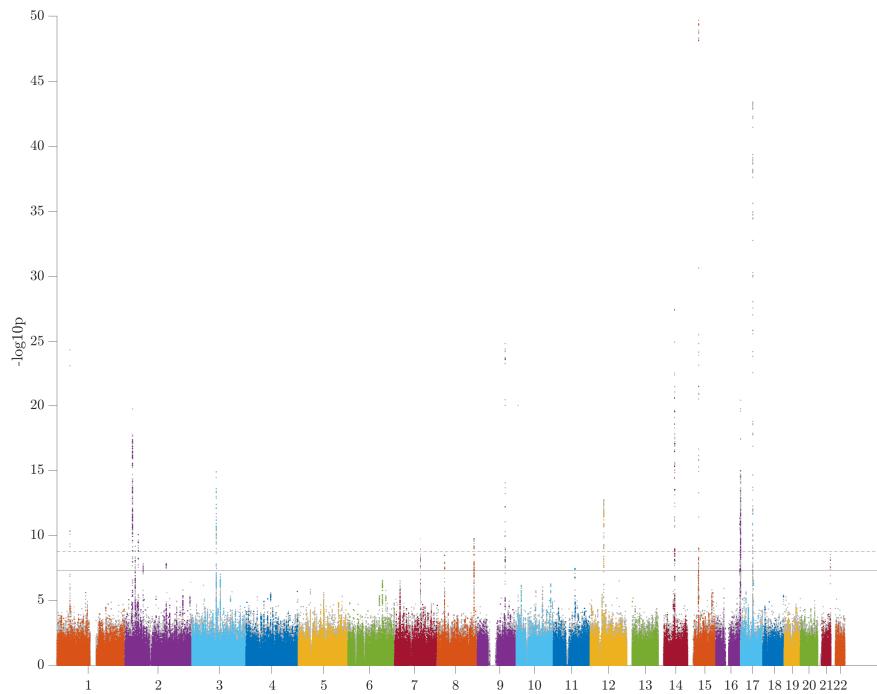


FIGURE A.1: Entire hemisphere genome-wide association studies, with grayed out the single nucleotide polymorphisms removed when filtering with 1000G phase3 single nucleotide polymorphism set data.

Chr.	# Removed	# Kept	Rem. Percentage	Removed Min. P-value	Kept Min. P-value
1	5	1	83.33%	4.31e-25	4.56e-11
2	175	74	70.28%	1.80e-20	4.30e-18
3	34	11	75.56%	3.48e-15	1.26e-15
7	48	6	88.89%	1.76e-10	1.13e-9
8	31	16	65.96%	1.97e-10	1.80e-10
9	28	10	73.68%	1.40e-25	1.81e-24
12	79	20	79.80%	1.71e-13	4.89e-13
14	51	16	76.12%	1.09e-25	3.58e-28
15	46	9	83.64%	2.09e-50	3.94e-50
16	467	56	89.29%	3.78e-21	1.04e-15
17	99	5	95.19%	3.91e-44	8.20e-31
21	5	2	71.43%	3.01e-9	7.89e-9
Total	125	1068	82.53%		

(A) Overview of the entire hemisphere significant, based on the European threshold 5e-8, single nucleotide polymorphism filtering.

Chr.	Partition	# Removed	Removed Min. P-value	Kept Min. P-value
16	4	6	1.61e-11	1.67e-8
17	4	40	4.87e-11	1.73e-8
16	7	3	9.24e-16	2.51e-9
17	12	4	4.10e-10	3.38e-9
16	14	4	1.18e-13	6.73e-9
8	17	1	1.54e-9	1.74e-9
15	22	1	8.42e-10	5.65e-9
16	28	2	4.98e-10	3.43e-8

(B) Partition-chromosome pairs that had the entirety of Bonferroni significant single nucleotide polymorphisms (P-value<5e-8/31) removed.

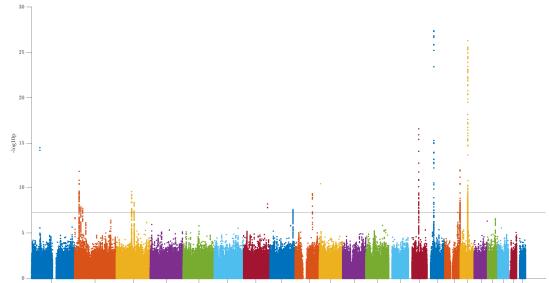
TABLE A.1: Effect of 1000G Phase3 filtering on meta-analyzed genome-wide association studies scores

Appendix B

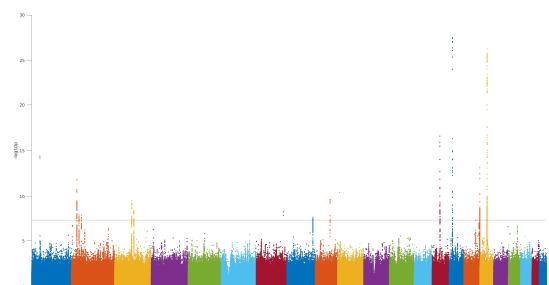
GWAS results

Partition	Spearman Correlation
1	0.9996
2	0.9997
3	0.9989
4	0.9997
5	0.9997
6	0.9994
7	0.9997
8	0.9994
9	0.9997
10	0.9997
11	0.9996
12	0.9996
13	0.9997
14	0.9997
15	0.9997
16	0.9996
17	0.9997
18	0.9997
19	0.9997
20	0.9995
21	0.9997
22	0.9997
23	0.9997
24	0.9997
25	0.9997
26	0.9996
27	0.9997
28	0.9996
29	0.9996
30	0.9996
31	0.9997

(A) Spearman correlation assessing mean substitution effect



(B) With substitution



(C) Without substitution

FIGURE B.1: Graphs assessing the quantitative (across partitions) and qualitative effect (on the entire hemisphere) of mean SNP substitution on the discovery dataset GWAS.

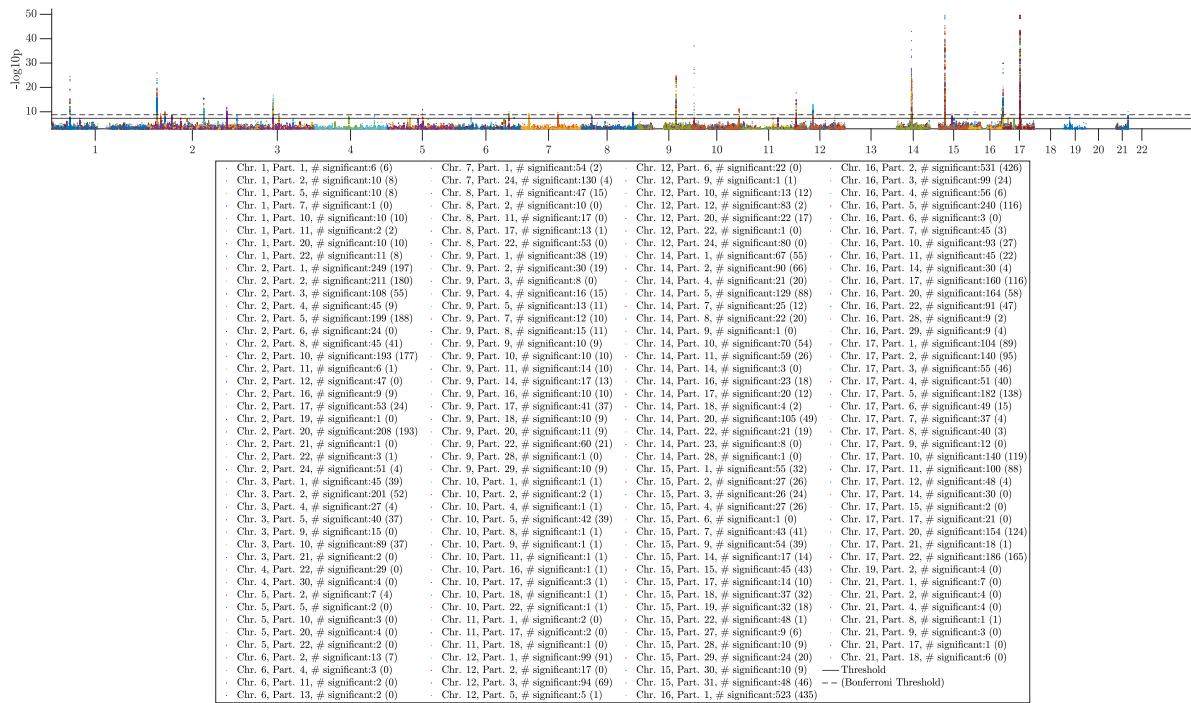


FIGURE B.2: Combined Manhattan plots across different partitions, showing the number of significant single nucleotide polymorphisms below the threshold of 5e-8 and with the Bonferroni correction, inside parentheses.

Partition	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
Correlation	0.16	0.13	0.14	0.12	0.1	0.1	0.08	0.13	0.06	0.06	0.11	0.1	0.05	0.09	0.04	0.1	0.15	0.05	0.04	0.03	0.04	0.15	0.08	0.16	0.02	0.05	0.02	0.08	0.07	-0.02	0.01
P-value	1.2e-11	1.1e-8	2.6e-11	4.3e-7	7.5e-5	1.7e-5	9.6e-4	5.1e-8	6.9e-3	1.8e-2	4.3e-6	1.1e-5	4.0e-2	2.2e-4	6.0e-2	1.5e-5	1.4e-9	1.8e-2	8.4e-2	1.0e-1	4.0e-2	5.1e-10	2.9e-3	4.3e-11	2.6e-1	2.8e-2	1.9e-1	8.2e-4	5.0e-3	7.6e-1	3.7e-1

TABLE B.1: Spearman correlation of the mvGWAS on each partition with the results from [?], and the corresponding bootstrap p-values.

Appendix C

Heritability

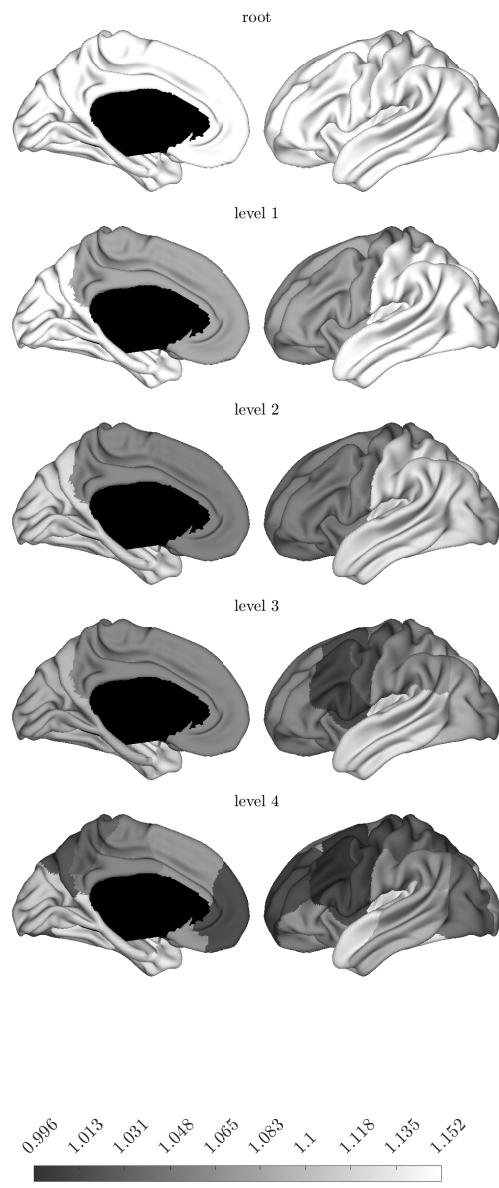
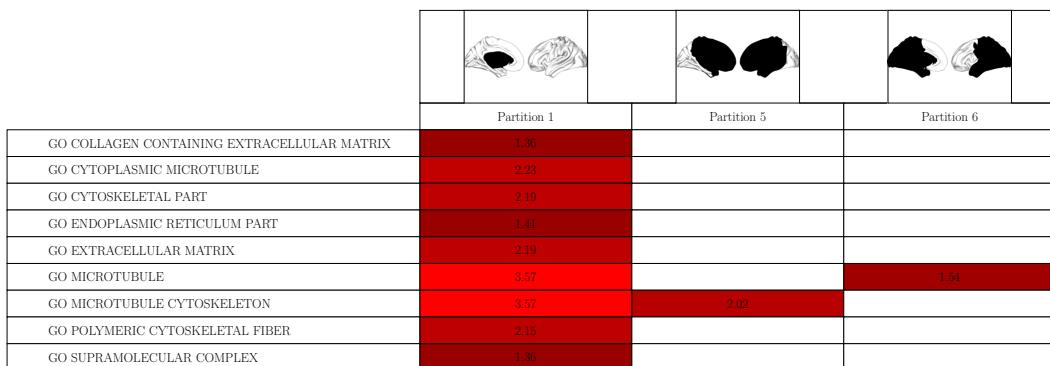


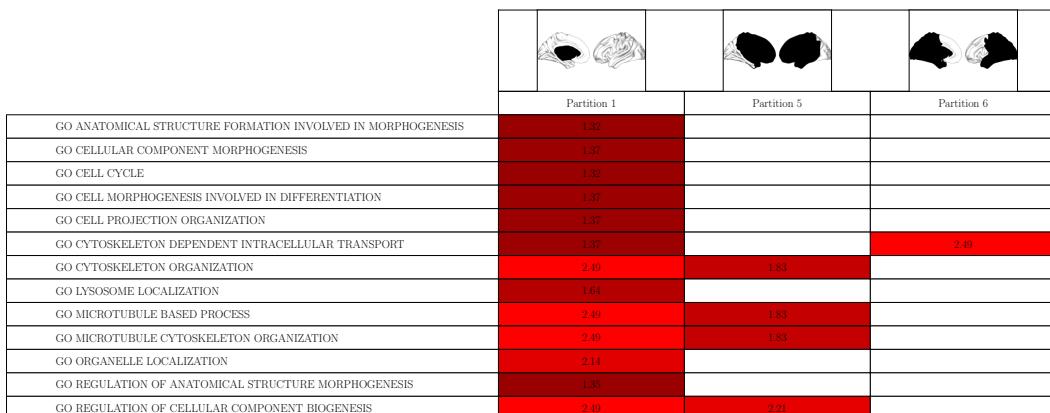
FIGURE C.1: λ_{GC} coefficient, as computed by LD score regression. The observed χ^2 value is close to the expected one at all studied partitions, with their ratio being close to 1.

Appendix D

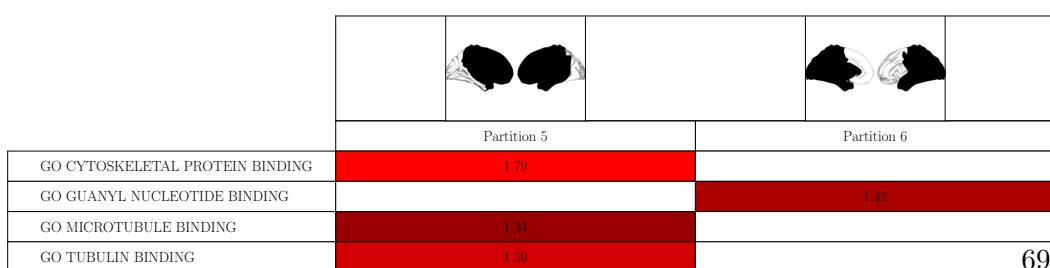
Functional analysis



(A) Cell components



(B) Biological processes



(C) Molecular function

FIGURE D.1: Gene ontology terms enrichment analysis -log10 P-values (the higher value and the darker color, the more significant), as computed by FUMA, with the gene set augmented by GREAT. For all three cases, the entire hemisphere and the four 2nd level partition were assessed, however not all of the tests displayed a significant signal with gene ontology terms.

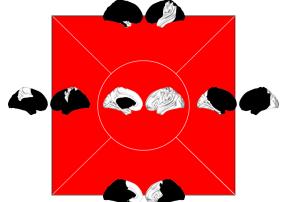
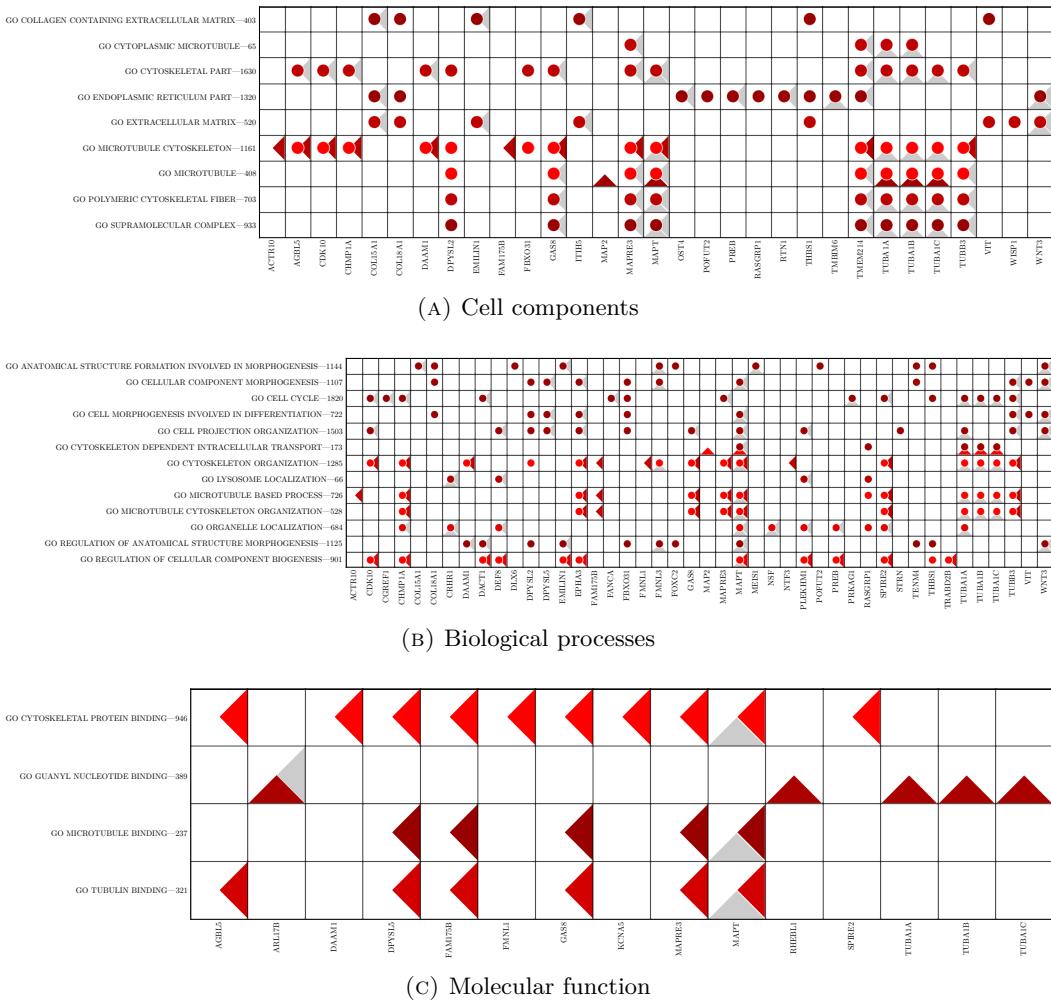


FIGURE D.2: Gene ontology terms enrichment analysis genes (the higher value and the lighter color, the more significant). For all three cases, the entire hemisphere and the four 2nd level partitions (ie. P1 and P4-P7) were assessed. With gray, genes are shown that, although intersecting with the trait gene set, were not enough for FUMA to identify significant correlation, based on the underlying gene sets sizes ratios. The partition information per cell is coded as shown in the shape at the bottom right. Next to the name of the category, the total number of related genes is displayed.

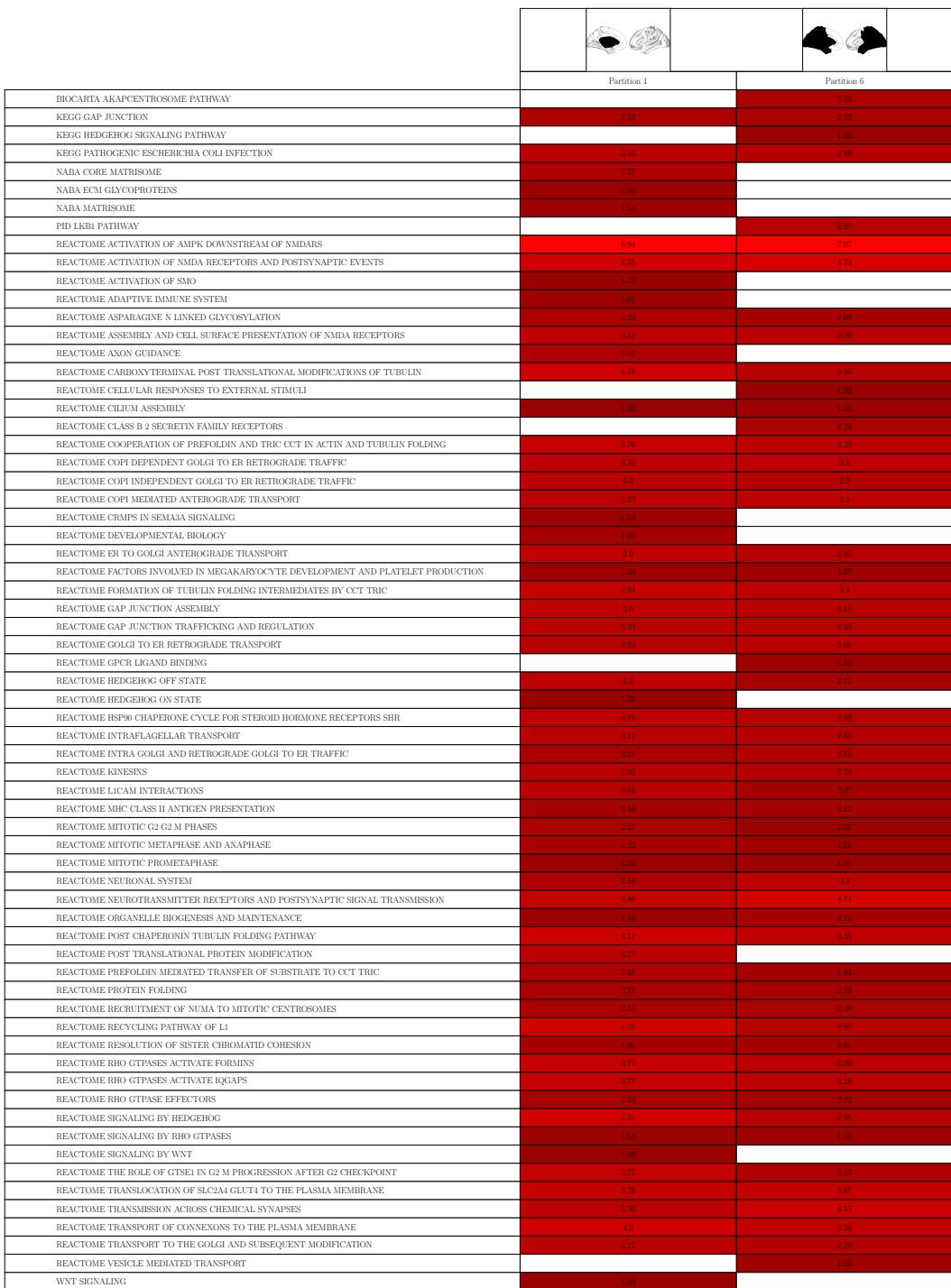


FIGURE D.3: Differential gene set enrichment analysis performed on various canonical pathways reported by KEGG and Reactome, as computed by FUMA. Displayed -log10 P-values have increased lightness the higher the value.



FIGURE D.4: Differential gene set enrichment analysis performed on various canonical pathways reported by KEGG and Reactome, as computed by FUMA. Displayed cells have increased lightness the higher the value. The entire hemisphere and the four 2nd level partitions (ie. P1 and P4-P7)) were assessed. With gray, genes are shown that, although intersecting with the trait gene set, were not enough for FUMA to identify significant correlation, based on the underlying gene sets sizes ratios. The partition information per cell is coded as shown in the shape at the bottom right. Next to the name of the category, the total number of related genes is displayed.

	Partition 1	Partition 4	Partition 5	Partition 6	Partition 7
Adipose Visceral Omentum	1.34	0.45			
Artery Aorta	0.27				
Artery Coronary	0.82				
Artery Tibial	0.39	0.08	1.53		
Bladder			0.15		
Brain Amygdala	0.28		0.51		
Brain Anterior cingulate cortex BA24	0.28		0.11		
Brain Caudate basal ganglia	0.0				
Brain Cerebellar Hemisphere	0.77	2.09	4.21	1.82	3.94
Brain Cerebellum	1.36	1.5	4.03	2.01	4.18
Brain Cortex	0.49		0.8		
Brain Frontal Cortex BA9	0.21				
Brain Hippocampus	0.09				
Brain Hypothalamus	1.56	0.32			
Brain Nucleus accumbens basal ganglia	0.48				
Brain Putamen basal ganglia	0.28				
Brain Spinal cord cervical c-1	0.43				
Breast Mammary Tissue	0.43				
Cells Cultured fibroblasts	1.07	0.65	3.7		1.07
Cells EBV-transformed lymphocytes	0.24	0.44			
Esophagus Gastroesophageal Junction	2.23	0.56	1.29	0.1	0.31
Esophagus Mucosa	0.57				
Esophagus Muscularis	1.76	0.52	2.33		0.07
Heart Left Ventricle			0.11		
Liver	0.07				
Lung	0.19		0.22		
Muscle Skeletal			0.06		
Nerve Tibial	0.16	0.65	0.18		0.67
Ovary	1.45		1.88	0.15	
Pancreas	0.09				
Pituitary	0.82		0.09		0.48
Prostate	0.1				
Skin Not Sun Exposed Suprapubic	0.36	0.19	1.96		
Small Intestine Terminal Ileum			0.17		
Spleen		0.75			
Thyroid	2.5		1.01		
Uterus	1.43	0.76	0.91	0.35	0.78

FIGURE D.5: Differential gene expression enrichment analysis performed on different tissues. Displayed -log10 P-values, as computed by FUMA using the identified partition-specific gene sets, are displayed in blue if the relation favors downregulated genes, red if it favors upregulated ones, or gray, if both downregulated and upregulated gene subsets are significantly enriched.



	Partition 1	Partition 4	Partition 5	Partition 6	Partition 7
Alcohol use disorder (total score)	6.89	10.78	11.69	11.83	12.47
Alzheimer's disease in APOE e4- carriers	3.43	4.69	4.08	5.12	5.44
Bipolar disorder	1.86			3.75	
Blond vs. brown/black hair color	1.51	1.35	1.97		1.88
Brown vs. black hair color	3.58	2.99	4.2	1.46	3.55
Chronotype	1.62				
Cognitive ability				1.31	1.49
Cognitive function	2.29	2.01	5.74	2.23	2.54
Dentate gyrus granule cell layer volume			4.08		
Dentate gyrus molecular layer volume			3.97		
Facial pigmentation	1.98	2.59	2.35		2.96
General cognitive ability				2.23	
General factor of neuroticism	3.17	4.09	5.21	5.18	5.58
Hair morphology traits	1.71	2.33	2.05		2.7
Handedness (Left-handed vs. non-left-handed)	10.1	14.88	16.54	18.87	16.28
Handedness (Right-handed vs. non-right-handed)	10.57	15.4	17.41	16.63	16.8
Headache		1.53		1.64	1.9
Hematocrit		1.38			1.9
Hemoglobin concentration		1.61			2.14
Hippocampal subfield CA1 volume			4.15		
Hippocampal subfield CA3 volume			4.26		
Hippocampal subfield CA4 volume			4.08		
Hippocampal tail volume			6.22		
Idiopathic pulmonary fibrosis	2.84	8.28	7.39	8.85	9.24
Intracranial volume	1.98	5.06	4.58	5.34	5.62
Intraocular pressure				1.5	
Laterality in neovascular age-related macular degeneration			2.35		
Low tan response	8.17	7.77	8.98		8.74
Lumbar spine bone mineral density	1.66				
Lung function (FEV1)	1.35	2.17	1.71	2.37	2.7
Lung function (FVC)		2.33	1.71	1.41	1.66
Macular thickness	1.35			1.46	
Male-pattern baldness	6.89	9.99	19.89	11.29	11.9
Monobrow			1.68		
Mood instability	1.52	2.33	1.92	2.57	2.88
Multiple system atrophy	4.39	3.61	3.18	3.9	4.17
Neuroticism	2.65	4.13	5.94	4.66	5.08
Obsessive-compulsive disorder or autism spectrum disorder	1.71	2.33	2.05		2.7
Parkinson's disease	3.41	6.7	9.69	7.51	8.08
Primary biliary cirrhosis				1.34	1.51
Pulse pressure				1.57	
Reaction time	9.89	10.25	8.98	13.4	11.73
Red blood cell count					1.41
Red cell distribution width					1.45
Red vs. brown/black hair color	12.82	10.5	14.27	1.88	11.77
Rosacea symptom severity		1.61			2.14
Sense of smell	4.01	5.94	7.39	6.35	6.7
Sex hormone-binding globulin levels			1.46		
Skin pigmentation traits	3.72	4.72	4.26		5.34
Squamous cell carcinoma	2.64	3.57	3.14		4.13
Subcortical brain region volumes	1.44	4.11	3.67	4.39	4.67
Systolic blood pressure				1.39	
Total hippocampal volume			3.52		

FIGURE D.6: Differential gene set enrichment analysis performed on various traits reported by GWAS catalog, as computed by FUMA. -log10 P-values are shown, with increased lightness the higher the value.

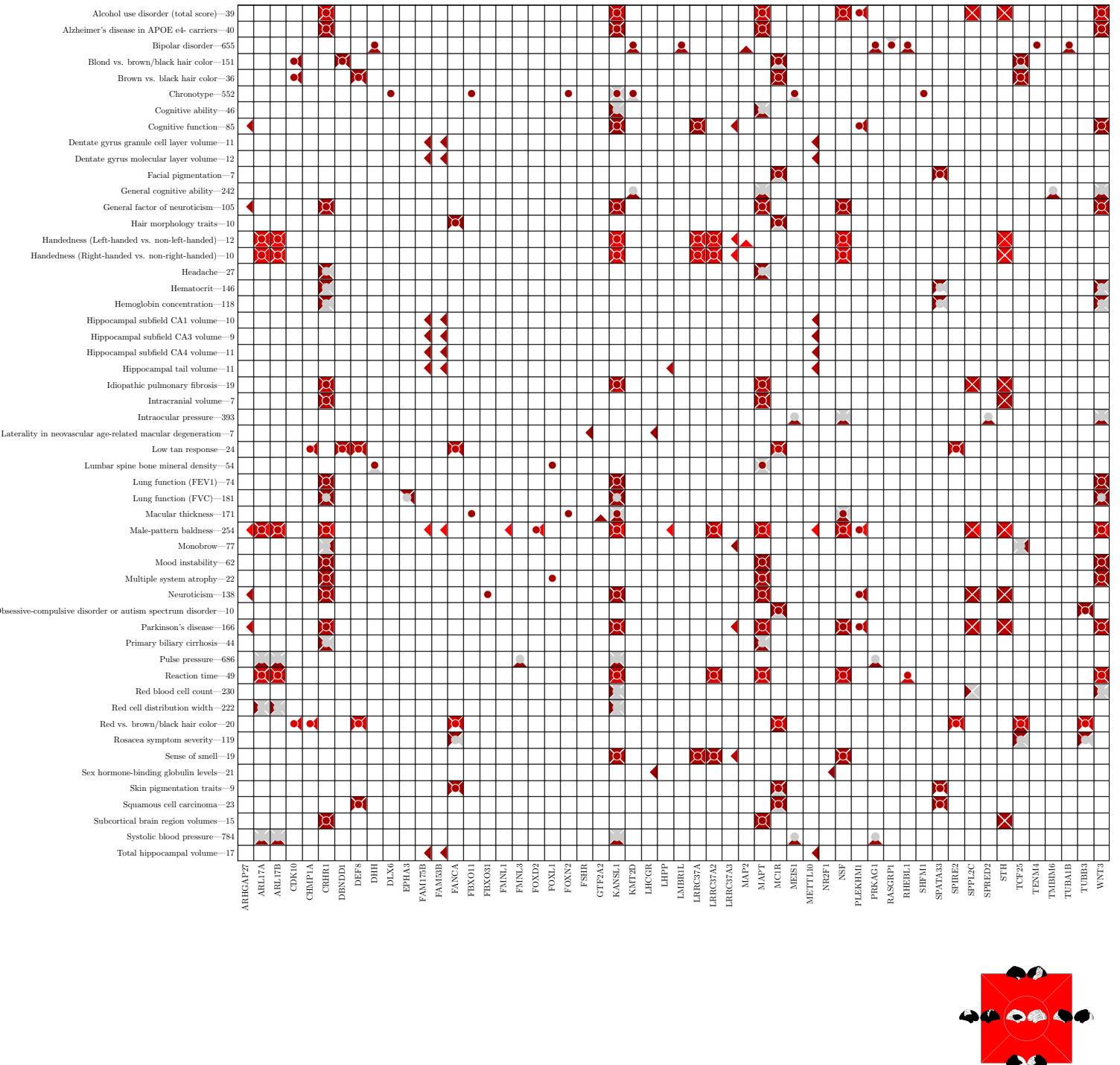


FIGURE D.7: Differential gene set enrichment analysis performed on various traits reported by GWAS catalog, as computed by FUMA. Displayed cells have increased lightness the higher the value. With gray, genes are shown that, although intersecting with the trait gene set, were not enough for FUMA to identify significant correlation, based on the underlying gene sets sizes ratios. The partition information per cell is coded as shown in the shape at the bottom right. Next to the name of the category, the total number of related genes is displayed.

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Popularized Summary

The overall purpose of this thesis is to complement the existing bibliography on the detection and examination of the genetic associations of brain shape asymmetry. Our body generally exhibits bilateral symmetry, namely our sides are mirrored images of each other. However, if someone pays close attention, not one feature is completely symmetric on each side of our body. In this thesis, we seek the genetic roots of this intrinsically complex trait, investigating the brain surface on healthy individuals of European origin from UK Biobank database. Cortical asymmetry has been found to be correlated with a variety of brain-related diseases, such as OCD, neuroticism and bipolar disorder, and an early detection of the accountable genetic variants could be used for personalized diagnosis and treatment. Furthermore, brain asymmetry does not display the phenomenon of situs-inversus, that is internal organs occurring mirrored at certain individuals, which leads us to believe there is evolutionary pressure on this trait manifestation. Therefore, substantial heritability, namely phenotypic variation explained by genetic changes, is expected.

To this end, asymmetry statistical analysis was performed based on brain MRI scans, detecting regions with high affinity to display genetically inscribed asymmetry. A data-driven approach was then followed, where the brain surface was partitioned in multiple hierarchical levels, without any prior anatomic knowledge. Aggregated asymmetry measurements, retaining most of the included variation, were retrieved from the segments, whose genetic correlation was then examined through a multivariate genetic statistical analysis. Recognized significant variants were then compared against reported traits from other databases, based on monotonicity. Functional annotations were constructed, associating genetic variants to genes, offering an insight into the functional reasoning behind the brain shape asymmetry existence. The degree on which plasticity effect (that is the amount of variation not explained by the genome, but by environmentally affected development) is dispersed throughout the brain was statistically mapped and genetically quantified, through genetic heritability studies. Novel causal region-specific genetic variants and increased heritability was identified throughout the entire hemisphere and the derived partitions, extending the related literature. Different spatially-dependent genetic profiles were identified. Connections with biological pathways, concerning intra- and extra-cellular organization and the formation of biological symmetry axes, were made, by examining protein-protein interactions. The effect of a strongly regulating, spatially dependent epigenetic effect on development was determined. Furthermore, gender-controlled epigenetic modifications appeared to affect cortical asymmetry. Lastly, associative studies led to the establishment of a tight, strongly supported, genetic bridge between brain shape and asymmetry.