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Brain Size Analysis System Using Algorithm

Monisha R[1], Iraniyapandiyan M[2], Kumaran M[3]

Student, Department of CSE, Jaya Engineering College, Chennai, India[1]

Assistant Professor, Department of CSE, Jaya Engineering College, Chennai, India[2]

Professor, Department of CSE, Jaya Engineering College, Chennai, Country India[3]

Abstract: Many studies of monozygotic (MZ) twins have revealed evidence of genetic influences on intellectual functions and their derangement in certain neurologic and psychiatric diseases afflicting the forebrain. Relatively little is known about genetic influences on the size and shape of the human forebrain and its gross morphologic subdivisions. Using MRI and quantitative image analysis techniques, we examined neuroanatomic similarities in MZ twins and their relationship to head size and intelligence quotient (IQ).

ANOVA were carried out using each measure as the dependent variable and genotype, birth order, and sex, separately, as between-subject factors. Painvise correlations between measures were also computed. We found significant effects of genotype but not birth order for the following neuro anatomic measures: forebrain volume (raw, p 5 0.0001; normalized by body weight, $p = 0.0003$); cortical surface area (raw, $p = 0.002$; normalized, $p = 0.001$); and callosal area (raw, p 5 0.0001; normalized by forebrain volume, $p = 0.02$). We also found significant effects of genotype but not birth order for head circumference (raw, $p = 0.0002$; normalized, p 5 0.0001) and full-scale I& ($p = 0.001$). There were no significant sex effects except for raw head circumference ($p = 0.03$). Significant correlations were observed among forebrain volume, cortical surface area, and callosal area and between each brain measure and head circumference. There was no significant correlation between I& and any brain measure or head circumference.

These results indicate that: 1) forebrain volume, cortical surface area, and callosal area are similar in MZ twins; and 2) these brain measures are tightly correlated with one another and with head circumference but not with I& in young, healthy adults.

Keywords: Monozygotic twins (MZ), Intelligence quotient (IQ), Brain size analysis, Algorithmic analysis, Neuroimaging, MRI scans, Computational neuroscience, Brain structure, Automated analysis, Medical research, Cognitive conditions, Neurological disorders, Brain health, Data processing, Computational methods, Research applications, Brain development, Neuroinformatics, Image processing, Neurological insights, Precision measurements, Advanced technology.

I. INTRODUCTION

The human brain is an astonishing organ, responsible for our thoughts, emotions, and actions. Understanding the intricate details of brain structure and function has been a fundamental pursuit in neuroscience and medical research for decades. One crucial aspect of this understanding is the analysis of brain size, as it can provide valuable insights into various cognitive and neurological conditions.

Advancements in technology and computational methods have revolutionized the field of neuroimaging, allowing researchers to collect vast amounts of data related to brain structure. However, the sheer complexity of these datasets and the need for precise measurements call for robust and efficient algorithms to extract meaningful information from them. The Brain Size Analysis System Using Algorithm (BSASUA) represents a groundbreaking approach to address this challenge. This innovative system leverages state-of-the-art algorithms and computational techniques to analyze and quantify various aspects of brain size from magnetic resonance imaging (MRI) scans. By automating and enhancing the brain size analysis process, BSASUA opens up new possibilities for both clinical and research applications.

In this introduction, we will explore the significance of brain size analysis, the limitations of manual methods, and the potential benefits of using advanced algorithms to study brain structure. We will also highlight the key features and objectives of the BSASUA system, underscoring its potential to contribute to our understanding of brain health, development, and disorders.

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II. PROPOSED SYSTEM

Head circumference was a highly significant genotype effect for both raw head circumference (F (9,9) = 14.84, p = 0.0002) and head circumference normalized by body weight (F (9,9) = 16.80, p 5 0.0001). No birth order effects were found (raw, F (1,9) = 0.71, p = 0.42; normalized, F (1,9) = 0.70, p = 0.42). There was a sex effect for raw head circumference but not for normalized head circumference (raw, F (1,8) = 7.48, p = 0.03; normalized F (1,8) = 0.11, p = 0.75).

For all brain measures, there were highly significant genotype effects but no significant birth order effects, indicating that total forebrain volume, total cortical surface area, and callosal cross-sectional area varied far more across unrelated pairs than within co-twins. Consistent with the results of previous twin studies, co-twins were also more similar than unrelated pairs with respect to head Circumference' and I&. "." Genotype effects were not attributable to sex differences across unrelated pairs.

Brain size:
The present in vivo brain measurements (see the table) correspond well with those previously obtained and in vivo.10,11,27,28,48-80 For example , the range of our 20 volume measurements (963 to 1,439 cm3) overlaps the range found by Zilles et al.47 (851 to 1,329 cm3) in 60 cadavers. The range of our cortical surface area measurements (1,685 to 2,264 cm2) lies within that of previous postmortem measurements (1,469 to 3,031 cm2).33,40 Likewise, our midsagittal callosal area measurements (5.7 to 8.8 cm2) match those found in previous postmortem studies. Unified conscious experience relies on colossally mediated interactions between cortical neurons in the left and right cerebral hemisphere^. ^^ The strong correlation between cortical surface area and callosal cross-sectional area found in the present study suggests constancy in the proportion of cortical neurons that send projections from one hemisphere to the other. Based on our measurements of total cortical surface area (mean, 1,906 cm2) and previous estimates of 105 neurons per 750 pm2 of cortical surface57 and 200 million fibers per adult callosum,58 we estimate that approximately 1% of cortical neurons project contralaterally in humans. Head size is routinely measured in pediatrics and obstetrics to assess brain development, and micro and macrocephaly have long been known as signs of underlying brain pathology.59 However, the relationship between head size and brain size in healthy adults remains uncertain. We found strong correlations between head circumference and forebrain volume and between head circumference and cortical surface area in our 18- to 43-year-old population.

III. METHODOLOGY

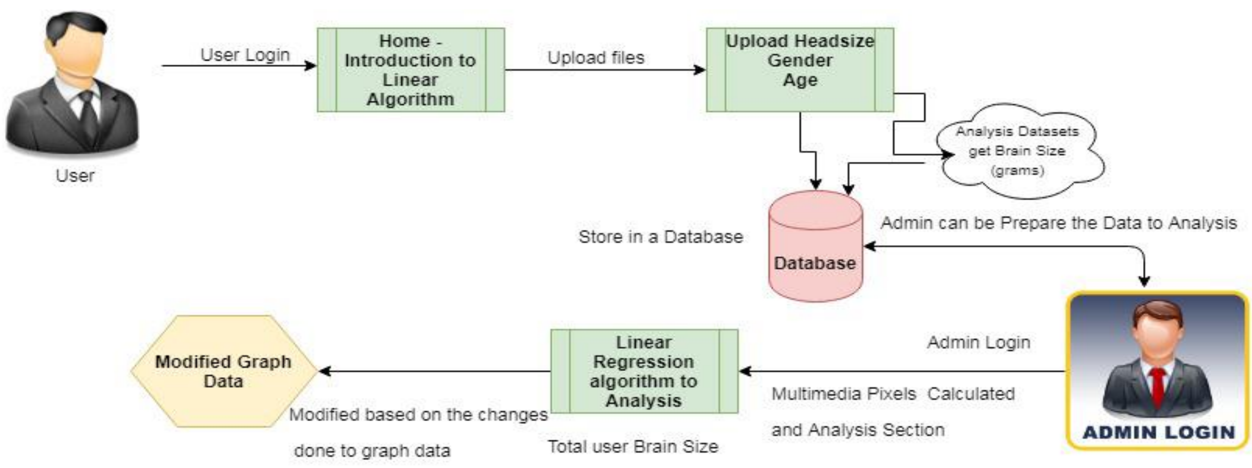

Figure 1.1: Architecture of Linear Regression Algorithm.

Linear Regression:
Linear Regression is a supervised machine learning algorithm where the predicted output is continuous and has a constant slope. It's used to predict values within a continuous range, (e.g. sales, price) rather than trying to classify them into categories (e.g. cat, dog). It is used to estimate real values (cost of houses, number of calls, total sales etc.) based on

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continuous variable(s). Here, we establish relationship between independent and dependent variables by fitting a best line. This best fit line is known as regression line and represented by a linear equation Y= a *X + b. The best way to understand linear regression is to relive this experience of childhood. Let us say, you ask a child in fifth grade to arrange people in his class by increasing order of weight, without asking them their weights! What do you think the child will do? He / she would likely look (visually analyze) at the height and build of people and arrange them using a combination of these visible parameters. This is linear regression in real life! The child has actually figured out that height and build would be correlated to the weight by a relationship, which looks like the equation above.

Simple Linear Regression
Multiple Linear Regression

Simple Linear Regression**:**

We discussed that Linear Regression is a simple model. Simple Linear Regression is the simplest model in machine learning. A linear regression algorithm is called simple linear regression if it is having only one independent variable. Simple linear regression uses traditional slope-intercept form, where m and b are the variables our algorithm will try to "learn" to produce the most accurate predictions. x represents our input data and y represents our prediction.

Y = mx+b

m – Slope

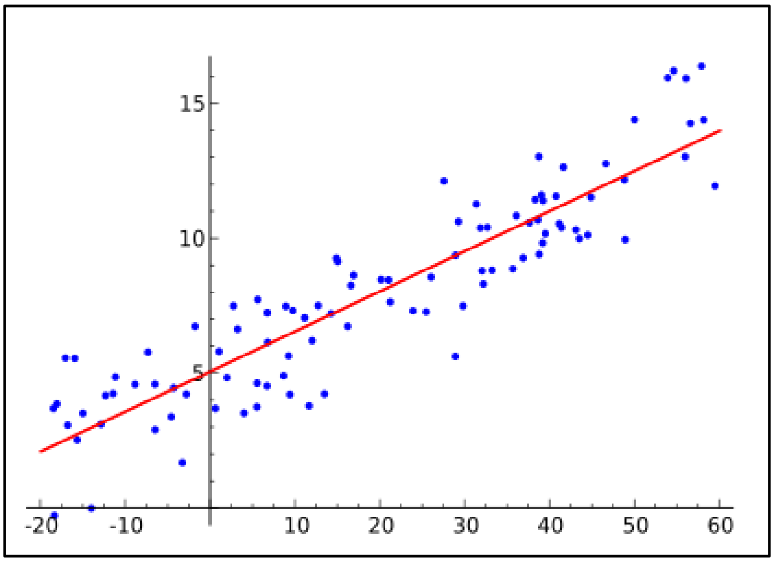
X – Independent variable

b – Intercept

Y – Dependent Variable

Ordinary Least Square Method:

Earlier in this post we discussed that we are going to approximate the relationship between X and Y to a line. Let's say we have few inputs and outputs. And we plot these scatter points in 2D space, we will get something like the following image. And you can see a line in the image. That's what we are going to accomplish. And we want to minimize the error of our model. A good model will always have least error. We can find this line by reducing the error. The error of each point is the distance between line and that point. This is illustrated as follows.



1.2: A scatterplot of Ordinary Least Square Method.

Multiple Linear Regression:

A linear regression algorithm is called multiple linear regression if it is having more than one independent variable. A more complex, multi-variable linear equation might look like this, where w represents the coefficients, or weights, our model will try to learn. Multiple Linear Regression is a type of Linear Regression when the input has multiple features(variables).

$$f(x, y, z) = w1x+w2y+w3z$$

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The variables x, y, z represents the attributes, or distinct pieces of information, we have about each observation. For sales predictions, these attributes might include a company's advertising spend on radio, TV, and newspapers.

Model Representation:
Similar to Simple Linear Regression, we have input variable(X) and output variable(Y). But the input variable has nn features. Therefore, we can represent this linear model as follows;

$$Y=\beta\ 0+\beta\ 1\ x\ 1+\beta\ 1x\ 2\ +...+\beta\ nx\ n$$

IV. CONCLUSION

Our findings of co-twin similarity in both brain size and I& combined with the absence of a correlation between brain size and I& suggest that intellectual similarities in MZ twins cannot be accounted for by genetically based neuroanatomic similarities using a straightforward "bigger is better" hypothesis. It remains plausible, and we believe likely, that genetic influences on brain organization (i.e., how the brain is put together, not just how big it is) underlie intellectual similarities in MZ twins. For example, genetic influences on brain organization may be manifested at the gross morphologic level by similarities in the local geometry of folds in the left cerebral cortex,15 which in the vast majority of humans governs language and abstract reasoning-the cognitive skills that distinguish our species in primate evolution and that contribute most to I& test performance. The notion that genetic influences on intellectual functions might be reflected in regional measures rather than, or in addition to, global measures of brain size resonate with the prevailing view80-s2 that intellect emerges from the concerted action of functionally specialized neural systems distributed within specific regions of the forebrain.

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