



Recognizing Brain Regions Of Schizophrenia Using Magnetitic Resonance Imaging And Machine Learning

Sadaf Qasim^{1*}, Dr. Nandita Pradhan²

^{1*}Electronics and Communication Engg. United University, Prayagraj, India. Email: sadaf.riya@gmail.com

²Electronics and Communication Engg. United University, Prayagraj, India. Email: nanditapradhan123@yahoo.com

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ABSTRACT

With the use of machine learning (ML) and neural images, one can find difference between schizophrenia (SZ) patients and normal controls (NCs).

The two useful techniques for conducting an inquiry into abnormalities in human brain are Functional MRI (fMRI) and structural MRI (sMRI) and with growing and fast development, the studies have revealed that these brain data can be a benchmark in the medical field for detecting such psychiatric disorder with high accuracy. There is no denying fact that Machine learning (ML) these days have been widely in a source of detecting neurobiological tendency and neuropsychiatry illness, with high degree of precision. To diagnose the affected area of brain in schizophrenia we can use the neural images which prove to be very beneficial and can be used to references in medical field. In this research article, sMRIs is used for detecting and comparing schizophrenia patient and normal controls. The techniques which are used here requires hyperparameter optimization of a neural network. This is called coarse-to-fine feature selection which is a Machine Learning substructure. For proposing this, it require two sample t-tests for pulling out the contrast feature within the group, after that inapplicable, irrelevant, and superfluous property is eliminated and lastly by considering the gray matter (GM) and white matter (WM) area selection, a decision model is built with the help of support vector machine (SVM). Here rather than focussing on group measure, this study is focussed on individual measure and have proposed a model that is widely used with high rate of interest unlike the previously modelled which reported differences of both group and individual measures leading to less involvement and application. By closely studying and demonstrating the result of experiment, here it is seen that the proposed structure determines highest accuracy of classification between schizophrenia (SZ) patients and normal controls (NCs) over up to 80%. With this proposed method, one can also determines various other disease with accurate results.

Keywords: schizophrenia; machine learning; structural MR images

Introduction

Schizophrenia (SZ) is a kind of psychiatric disorder which has unattended aetiology. Schizophrenia reports topmost chronicity among all the psychological disorder and is very challenging to work in this field. During the past few decades, schizophrenia has been reported as a pervasive illness in the structural region of brain [1]. At the same time, the terms and techniques used for their structural demonstration of brain images are partly perceived. SZ is a critical mental health issue identify by abnormalities like intuition, discernment, cogitative and limitation in the expression of emotion majorly effect 1% of natives. Over the recent study, it has been documented that the SZ patients exhibit configurational irregularities in the region of brains that includes frontal gyrus, temporal gyrus and corpus callosum [6-8].

The area involving brain formation and the biological study of nervous system processes is responsible for these compositional irregularities in brain play a pivotal role in the physiopathology of schizophrenia [2]. Moreover, the changes in the structure of brain are associated with prominent deranged indication which includes neuropsychology deficiency, paracusias, social strife in SZ. Currently, based on history, neural responses, and medical response of patient, doctor's assessments are the primary source for recognising and tracking

schizophrenia patient. The doctor's experience and medical knowledge plays a vital role in this filed for any kind of monitoring and diagnosis of SZ patient. Put differently, this subjective assessment could introduce uncertainty into the identifying and handling of schizophrenia. Neuroimaging techniques have been extensively employed to investigate brain anatomy, aiming to enhance diagnostic accuracy and gain valuable insights into potential physiopathology mechanisms. Because of its excellent in superior axial resolution, this imaging technique has emerged as the most favoured imaging technique. Most of the previous study has concentrated on employing traditional demographic inspection technique to examine distinctions between SZ and health controls through various classes experiments. Although, conventional demographic analysis methods can identify certain effected areas of brain in SZ, they are one variate in nature and frequently neglect the associated with the voxels, that may encapsulate crucial distinguishing information. Moreover, traditional demographic analysis solely focuses on disparities among groups, making it challenging to extend the diagnosis to individual patients in a universal manner [3].

ML techniques are employed to analyse neural images, aiming to address the limitations of traditional statistical analysis methods. These methods have the capability to derive consistent configurational patterns from neuroimaging data and hold promise in identifying noteworthy neuroimaging-derived signature molecules. Presently, encouraging outcomes have emerged in distinguishing between SZ patients and individuals without the condition [4]. The primary characteristic often utilized in structural MRI (sMRI) is brain tissue volume, acquired through voxel-based techniques. Nonetheless, an abundance of peripheral features can significantly diminish classification precision, particularly in neural investigations. The predilection of brain MRI data may include more than 100,000 non-zero. In contrast, the size of sample frequently falls below 1000. Therefore, the quantity of voxels surpasses sample size number by a significant margin. This challenge is a widespread issue in machine learning research. Several approaches have been suggested to leverage the constructional changes associated with schizophrenia for characterization utilizing the data of neural images.

Traditionally, machine learning algorithms have demonstrated the capability to classify mental disorders using this approach [7].

Notably, the support vector machine which is a form of supervised learning algorithm adept at observing chaotic patterns in multi-dimensional data, has emerged as the predominant choice for classifying schizophrenia. Features of this nature are conventionally derived through a blend of established disease attributes and feature selection algorithms. These characteristics might not fully capture the nuanced neurological distinctions linked with schizophrenia. Conversely, they could encompass excessive irrelevant data, necessitating further feature limiting. Recently, deep learning has surfaced as a novel method showcasing enhanced performance compared to traditional machine learning algorithms in classifying neural diseases using sMRI data. Convolutional Neural Networks possess the capability to acquire and encrypt the essential attribute required for grading, making them widely adopted in medical imaging investigation [9-11]. This characteristic renders CNNs particularly well-suited for tasks such as schizophrenia grading, where the precise selection of features can significantly influence model effectiveness.

The SVM is employed to train decision framework separately for white matter (WM) and gray matter (GM). Experimental findings show that the suggested approach can distinguish between SZ patients and Normal Controls with a peak accuracy of around 88%. Additionally, it can identify SZ molecular marker consistent with those identified in prior studies, encompassing regions such as postcentral gyrus, cerebellum [9].

This study contributes in the following ways:

- 1) From the study, a devised ML model aimed at distinguishing SZ patients from normal individuals. This model employs a coarse-to-fine strategy, initially reducing attribute spatiality through two-sample t-tests, followed by additional refinement using Recursive Feature Elimination (RFE). Hierarchical selection techniques aids in retaining informative features while discarding unnecessary ones. Moreover, the feature selection techniques like coarse-to-fine are straightforward to apply in identifying molecular marks, not limited to schizophrenia but extendable to other diseases, facilitating the taxonomy of patients and NCs dependent on structural MRI data.
- 2) The experimental findings indicate that the offered method outperforms other approaches in terms of classification productivity. Moreover, the biomarkers identified align with the results of previous relevant studies.
- 3) Past studies have predominantly concentrated on GM and have rarely delved into WM in individuals with schizophrenia. In this research, GM and WM are examined independently, revealing that those matter exhibits superior distinguishing capabilities compared to gray matter. This discovery offers valuable insights for healthcare evaluation [4].

1. Materials and Methods

1.1. Dataset: The data utilized in this study were drawn from the Centre for Biomedical Research Excellence (COBRE), an openly accessible neural images comprising fMRI and sMRI data from schizophrenia (SZs) and healthy controls, all of whom had complete clinical and imaging information available, which then gathered and shared by the Mind Research Network. For this research, a group of 71 paranoid SZ and 74 healthy controls was selected from the dataset [11]. To mitigate the influence of various subtypes of schizophrenia, we

specifically selected individuals diagnosed with irrationally anxious schizophrenia from the data. This set of schizophrenia represents the most prevalent subclass and typically exhibits a low progression of the disease, neurodegeneration, and a more favourable response to treatment. All participants underwent examination and were excluded if they had a chronicle report of neural illness, mental deceleration, traumatic head injury followed by memory loss of several minutes, or dipsomania or defencelessness within the past few months [5]. To eliminate the impact of handedness, we exclusively enrolled participants who were right-handed, so 16 participants were removed from the study. Taking into account different exclusion criteria, 14 participants with schizophrenia and 16 normal controls were eliminated during preprocessing of data and analysis. Thus, 57 SZ individuals 58 NCs were taken into account for the investigation purpose. The demographic details are presented in Table 1.

Table1: Demographic data pertaining to individuals with SZ and NCs.

Items	SZ	NC
Sample size	57	58
Gender (M/F)	46/11	41/17
Age range (year)	18-65	18-65
Age mean \pm SD	38.33 \pm 11.99	35.96 \pm 13.59

1.2. Data Acquisition:

The sMRI data was obtained using T1-weighted magnetization arrange fast acquired with MPRAGE sequences followed by the variable: TR of 2530ms, TEs 1:64 3.5, 5.36, 7.22, and 9.08 ms, TI of 900 ms, flip angle of 7°, FOV = 256 \times 256 mm, matrix = 256 \times 256, and voxel size = 1 \times 1 \times 1mm, slab thickness 176 mm.

1.3. Preprocessing and Segmentation

In this preprocessing step aims to enhance image quality, pursuing to minimize or eliminate unwanted image deformation and enhance specific image features conducive to segmentation. Subsequently, segmentation was executed to isolate the relevant information from the input data, facilitating subsequent extracting steps. Certain preprocessing steps, such as skull purging and standardization, were essential for brain tissue subdivision. Skull purging, serving as the primary stage in brain tissue segmentation, holds paramount importance for the precision of the scrutiny, preferable in structural MRI-based investigations focused on brain tissue. In the process of skull removal, external region of brain like braincase, skin and eyes are eliminated with the help of Brain Extraction Tool. The sMRI data underwent analysis using the voxel-based morphometry (VBM) within the Statistical Parametric Mapping (SPM) software package, specifically SPM8.

1.4. Machine Learning

Following preprocessing, feature selection was performed using a coarse-to-fine method used in reduction of feature amplitude. Initially, t-tests (2 samples) were employed to broadly for attribute selection, followed by Recursive Feature Elimination (RFE) [8]. Finally, a linear Support Vector Machine (SVM) classifier was utilized for the classification of SZ patients and NCs. The workflow of the suggested machine learning framework is depicted in Figure 1.

1.5. Feature Extraction and Feature Selection

Texture analysis aims to identify a unique method for capturing the fundamental characteristics of textures and representing them in a more straightforward and well-defined. The sMRI maps underwent sectionalisation into 246 ROI employing the Brainnetome-246 atlas encompassing 210 cortical and 36 subcortical subregions within the brain spectrum.

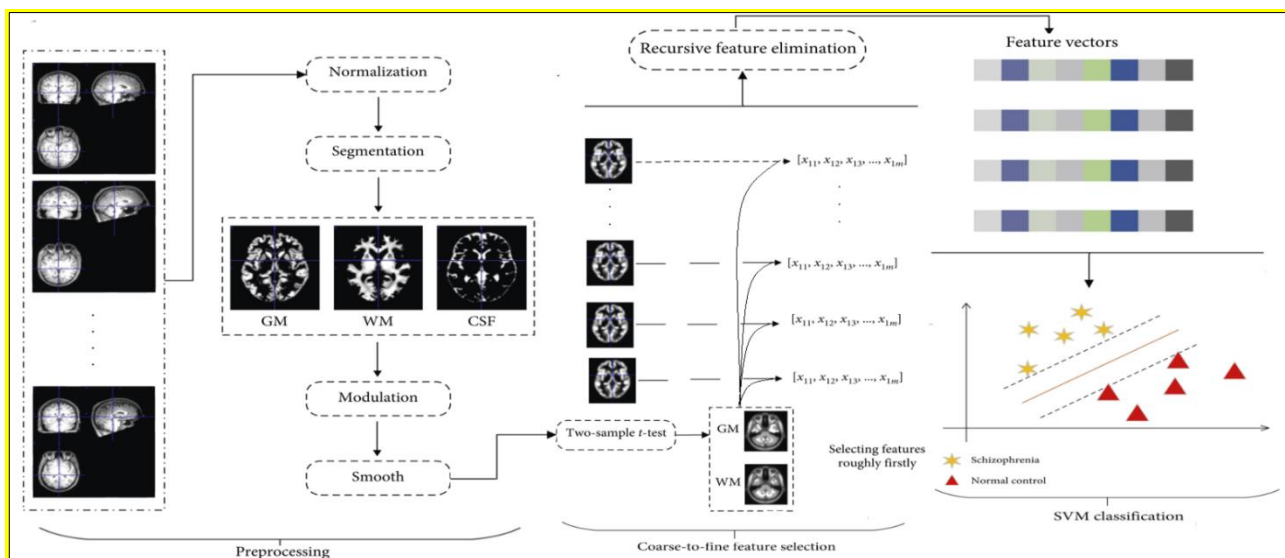


Figure 1: Diagram depicting flowchart consisting of 3 steps:(A) The preprocessing step, the process aligns the brains of diverse participants, and then smooths voxels for mitigation noise impact. (B) the feature selection model, employs a coarse-to-fine approach, utilizing t-tests and Recursive Feature Elimination (RFE); and (C) feature classification step

In pursuit of achieving effective classification performance, this paper employed two-sample t-tests for an initial rough selection. Subsequently, Recursive Feature Elimination (RFE) was utilized to further refine the selection of differential features [6].

Because of the abundance of information present in sMRI data, t-tests were employed at the beginning to mask the voxels. Serving as a analysis technique, t-tests (two samples) can extract remarkable differences between classes(set). Let a_1 and a_2 be the features mean of two classes. Their variance can be denoted by V_1^2 and V_2^2 respectively. Therefore, remarkable distinction between the two set can be calculated as:

$$C = \frac{|a_1 - a_2|}{\sqrt{\left(\frac{(S_1 - 1)V_1^2 + (S_2 - 1)V_2^2}{S_1 + S_2 - 2}\right) \cdot \left(\frac{1}{S_1} + \frac{1}{S_2}\right)}}$$

Where S_1 and S_2 are term as size of sample. The evaluation of a feature's ability to differentiate within two class set is determined by the value of C. A higher merit of C indicates a more selective attribute.

1.6. Recursive Feature Elimination

RFE, a desirous approach, aims to grade all features systematically to derive an ideal feature division for grouping purposes. In a machine learning baseline is designed for characterization or regression assign, that consist of columns and rows, like spreadsheet. This process involves training a machine learning model like SVM, grading all features based on criteria, and subsequently eliminating the features with the lowest grading. The process continues iteratively until all attributes are eliminated. Due to its versatility in removing a predetermined number or percentage of attributes according to user specifications and its robust capacity to elucidate distinctions, RFE has gained widespread popularity in neural study. At present, SVM stands out as one of the most renowned classification methods, offering computational dominance over other methods. Numerous prior studies have demonstrated the effectiveness of SVM, particularly in datasets with limited samples. To enable the classifier to normalize effectively to untouched data and mitigate overfitting issues, we incorporated the maximal margin classifier [10].

2. Result and Discussion

In the past demographic analysis of neural images has revealed various nervous tissues and practical distinctions between SZ patients and Normal Control. Machine learning has the capability to be utilized for individual-level prognosis and has demonstrated notable potential in diagnosing diseases on the basis.

For validating the efficiency of the proposed method, we conducted the subsequent experiments:

- Use of SVM straight on voxels
- Individual-level of selection attributes like RFE and SVM, 2T and SVM etc.
- Coarse to fine method as classifier

Prior MRI studies have consistently shown configurational abnormalities in SZ patients when compared to healthy controls.

Nevertheless, most studies have directed their focus towards DTI for the analysis of configurational alterations in SZ, with minimal detection of configurational disparities in sMRI. In this study, the GM and WM attributes identified through the proposed techniques offered valuable preferential insights into physiological irregularity observed in schizophrenia patient. In this current study, the method proposed showcased its capability to unveil precise and sensitive details regarding physiological irregularities within regions such as the frontal lobe, corpus callosum and central gyrus. Notably, it exhibited sensitivity in areas like the thalamus, cerebellum, and temporal lobe.

Numerous prior studies have noted alterations in the application of certain medium, like hydroxytryamine, within the amygdala and girdled cortex SZ. However, in this study, there was no configurational changes in these regions. One plausible explanation could be that shifts in hydroxytryamine concentration may not directly lead to structural irregularity.

3. Conclusion

Here, this paper explored a coarse-to-fine machine learning model was incorporated to distinguish between SZ and healthy control, as well as to identify potential signature molecules of SZ with the help of sMRI dataset. The experiments illustrated that attribute selection description can significantly enhance the performance of classifier. Employing coarse-to-fine selection method pull out more pertinent facts and figures and hence

notably enhanced the perfection. The experiments also revealed that the performance of classifier of white matter was markedly superior to that of gray matter. Hence, it can be inferred that SZ exerts a more pronounced effect on white matter. Moreover, this proposed coarse-to-fine attribute selection technique adeptly pinpointed aberrant brain area, offering valuable assistance for the medical investigation of SZ patient. Given its versatility, this framework could be expanded to determine various other disorder.

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