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A Framework to Diagnose Autism Spectrum Disorder Using Morphological Connectivity of sMRI and XGBoost

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Abstract. In this study, we automated the diagnostic procedure of autism spectrum disorder (ASD) with the help of anatomical alterations found in structural magnetic resonance imaging (sMRI) data of the ASD brain and machine learning tools. Initially, the sMRI data was preprocessed using the FreeSurfer toolbox. Further, the brain regions were segmented into 148 regions of interest using the Destrieux atlas. Features such as volume, thickness, surface area, and mean curvature were extracted for each brain region, and the morphological connectivity was computed using Pearson correlation. These morphological connections were fed to XGBoost for feature reduction and to build the diagnostic model. The results showed an average accuracy of 94.16% for the top 18 features. The frontal and limbic regions contributed more features to the classification model. Our proposed method is thus effective for the classification of ASD and can also be useful for the screening of other similar neurological disorders.

Keywords. Autism Spectrum Disorder, Structural Magnetic Resonance Imaging, Morphological Connectivity, Pearson Correlation, XGBoost

1. Introduction

Autism spectrum disorder (ASD) is a neurodevelopmental condition that adversely affects the social communication, behavior, and in some cases, even cognition of an

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individual [1]. Current diagnostic techniques rely mainly on subjective evaluations and may result in prolonged or misdiagnosis of the condition. Studies have shown that the structural and functional alterations of the brain are considered major biomarkers for the diagnosis of ASD [2]. Structural magnetic resonance imaging (sMRI) is a powerful technique that helps in the identification of these anatomical alterations. Many studies have used univariate analysis based on voxel-wise or local anatomical features like volume, thickness, and surface area of the various brain regions to analyze the ASD brain with the help of sMRI images [3]. However, these approaches fail to provide information on the inter-regional associations of the different brain regions. Morphological connectivity measures provide higher-order cortical information on the regions through interregional morphological relationships between pairs of brain regions that could be a valuable tool in the diagnosis of ASD [4]. Studies have also demonstrated the importance of morphological connectivity in classifying ASD and proved that it outperformed the morphological features [5]. The availability of a single 3D volume of sMRI per subject complicates the creation of morphological connectivity networks. To solve this problem, we proposed an approach that computed the morphological connectivity (correlated all the regions of interest) from morphological features of various brain regions using Pearson correlation. Furthermore, the performance of the morphological connectivity features on the diagnostic classification of ASD was tested using the XGBoost model.

2. Methods

The overall process pipeline followed in the study is shown in Figure 1.

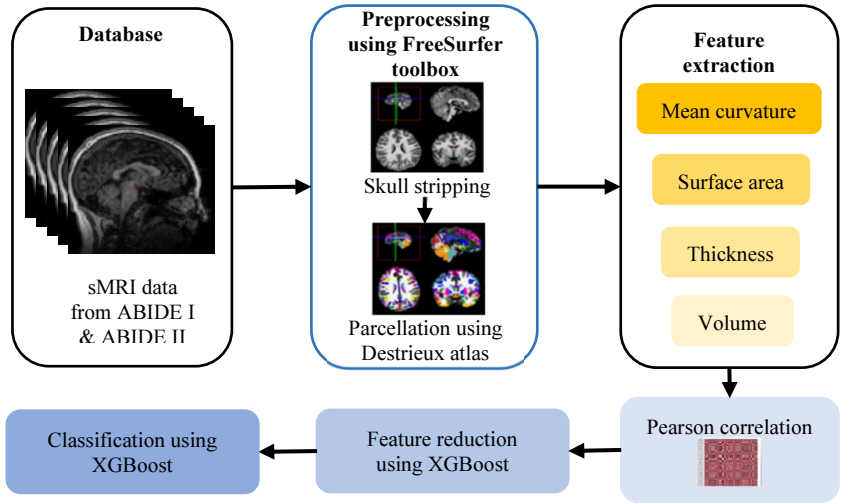


Figure 1. Process pipeline of the study

We obtained the raw sMRI data from the two open-access databases, ABIDE I & ABIDE II [6]. For our analysis, we considered the sMRI data from the Georgetown University (GU) site that contains 34 ASD and 40 typically developing (TD) individuals. We excluded two subjects (one ASD and one TD) from our analysis that contained incomplete data. The demographic information of the individuals selected for our

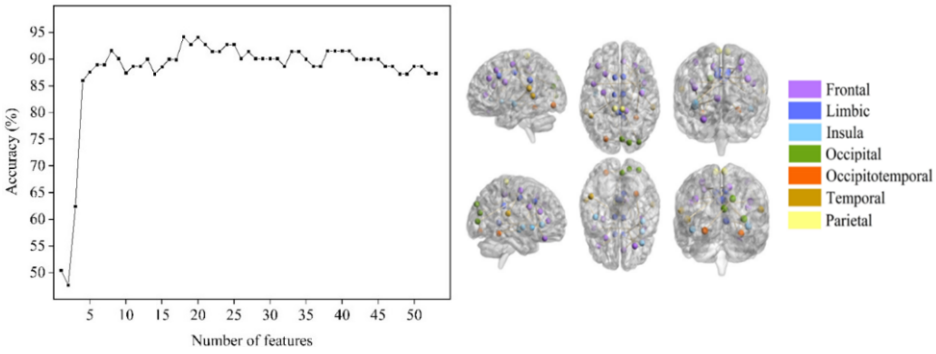
analysis from the GU site is given in Table 1. After preprocessing the data using the FreeSurfer toolbox, the brain regions were parcellated into different regions of interest (ROIs) with the help of the Destrieux atlas. The following features were extracted: volume, thickness, surface area, and mean curvature from these ROIs, and all the extracted features were then correlated to calculate the morphological connectivity using the Pearson correlation. A total of 74 regions from each hemisphere (148 ROIs in total) were selected, and we obtained a total of 10,878 (C_2^{148}) feature combinations of the ROIs. We used XGBoost for feature reduction, and the selected features were then fed into the XGBoost classifier with manual 5-fold cross-validation. We also tested the performance of different sets of the top 53 features that demonstrated a non-zero feature score (F-score) during feature reduction.

Table 1. Demographic information of GU site.

	TD (Mean±Standard Deviation)	**ASD** (Mean±Standard Deviation)
Number of subjects.	39	33
Gender (Males/Females)	21 /18	29 /4
Age (years)	10.69±1.79	11.28±1.29
Full IQ standard score (FIQ)	121.74±14.43	118.5±13.88

3. Results

Figure 2(a) shows the average accuracy of the XGBoost classifier for the different sets of top morphological connectivity features ranked based on their F-score. It can be noted that the top 18 features produced the highest average 5-fold classification accuracy, sensitivity, specificity, and f1-score of 94.16%, 95%, 94.28%, and 93.59%, respectively. Figure 2(b) shows the 3D representation of the brain regions of the top 18 features that contributed to the classification model. It can be noted that features from the frontal and limbic region of the brain contributed the most.



(a) (b)

Figure 2. a) Performance of classifier for different sets of morphological features, b) 3D representation of significant brain regions contributing to the classifier model

Figure 3 shows the pie chart representation of the Pearson-correlated features contributed by each lobe on the XGBoost model. It can be noted that the frontal, limbic, and insular

regions contribute the major percentage of features to the classifier. We can observe that the occipitotemporal and temporal regions also contribute a significant number of features to the classification model.

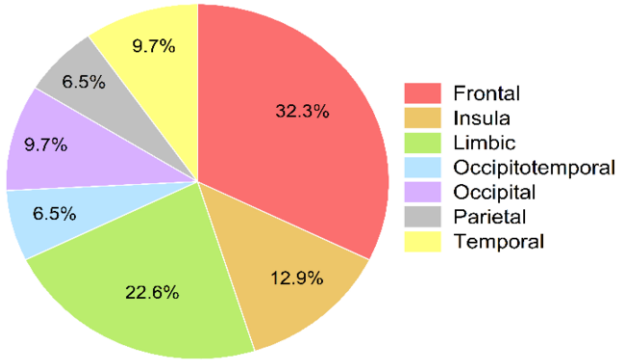


Figure 3: Pie chart representation of morphological correlated features from the brain lobes used in the XGBoost model for the GU site

4. Discussion

This research employed sMRI data to examine the impact of morphological connectivity via Pearson correlation on the diagnostic classification of ASD and TD individuals. The machine learning classifier XGBoost was employed, demonstrating proficient performance in discriminating between ASD and TD populations. The findings elucidated that an inadequate number of features utilized in the machine learning model resulted in suboptimal performance, underscoring the criticality of judiciously selecting an appropriate feature set. These results align with prior research highlighting the significance of a meticulous feature selection process in neuroimaging studies to enhance classification accuracy [7].

Furthermore, the study examined the effect of lobes on the classification models and identified that features from the frontal lobe region contributed significantly to the machine learning models in discriminating ASD and TD individuals. This finding aligns with prior research that has reported significant morphological differences in the frontal lobe of individuals with ASD compared to TD individuals [8]. The frontal lobe is known to play a crucial role in social cognition, which is impaired in individuals with ASD. Thus, the current study provides further evidence supporting the involvement of frontal lobe morphology in the classification of ASD [9].

5. Limitations and Future Work

The results of our study suggest that the morphological connectivity of various features is an effective method for classifying ASD and TD. However, our study has a few shortcomings; the performance of classifiers on features corresponding to zero F-score and other sites of the ABIDE database were not analyzed. The training dataset in this study is comparatively smaller and contains a less diverse population in terms of age. Moreover, we never compared the results with the non-correlated morphological features on the XGBoost classifier. This research can be extended to study the effect of morphological connectivity on different sets of morphological features. Furthermore, we plan to investigate the performance of structural and functional connectivity in addition to morphological connectivity for the diagnostic classification of ASD. These will also include different correlation methods and machine learning algorithms to improve the performance of the classification model.

6. Conclusion

In this study, we analyzed the effect of morphological connectivity features in the diagnostic classification of ASD. We computed the morphological connectivity using the Pearson correlation method and tested the classification using XGBoost. We achieved the highest average 5-fold classification accuracy, sensitivity, specificity, and f1-score of 94.16%, 95%, 94.28%, and 93.59%, respectively, using the top 18 features. The features from the frontal and limbic regions helped to achieve high classification accuracy. Our study proves that morphological connectivity can serve as an effective method to screen ASD subjects.

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