Classification of Autism Spectrum disorder using computer vision with deep learning and the ABIDE dataset

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The current work seeks to use deep learning algorithms to categorize Autism Spectrum Disorder (ASD) patients using the multi-site brain imaging dataset known as ABIDE (Autism Brain Imaging Data Exchange). We examined Autism Spectrum Disorder patients' brain imaging data from ABIDE, a global multi-site database. Autism Spectrum Disorder is a neurological condition marked by social difficulties and repetitive activities. Convolutional Neural Networks (CNN) have made important advances in voice recognition, picture classification, automotive Autism Spectrum Disorder software engineering, and neuroscience. This tremendous success is primarily due to a mix of algorithmic innovations, computational resource advancements, and access to a massive quantity of data. We describe the findings and highlight the regions of the brain that contributed the most to distinguishing ASD from normally developing controls using our deep learning model. The suggested CNN model does not involve feed-forward convolution; instead, we used concatenation of many convolution layers, and the whole result set obtained is sent to the multilayer perceptron (MLP) to finish classification.

I. Introduction

Autism spectrum disorder (ASD), a form of neurological illness, impacts communication abilities and social interaction in children aged 6 to 17. According to the WHO, one out of every 160 children has ASD, and these children frequently present with additional illnesses such as melancholy, anxiety, and attention deficit hyperactivity disorder (ADHD). Early detection during childhood is critical for improving the social skills and communication challenges of children with ASD, as well as their overall quality of life. An early diagnosis is critical for controlling and treating this condition. Functional magnetic resonance imaging (fMRI) is a technique for studying the brain and its architecture. It may be used to detect linked oscillations in blood oxygen level-dependent (BOLD) signals from brain areas, which can then be used to classify ASD patients. In the research of ASD, biomarkers and blood oxygen levels are investigated. ASD is predicted using neuroimaging and phenotypic data derived from ABIDE. The ABIDE dataset (ABIDE I) combines neuroimaging and phenotypic information from 17 worldwide imaging locations, and it includes 539 ASD patients and 573 individuals. The ABIDE dataset is made up of structural and resting-state fMRI data, as well as phenotypic information. ASD alters functional connections between brain areas, affecting global brain networks. The primary purpose of this endeavor is to categorize ASD and control participants based on functional connectivity brain patterns[1].

To precisely forecast the categorization, we will utilize CNN in our model. CNN has gotten a lot of interest in the classification and representation learning fields. CNNs are strong classifiers with excellent accuracies in a wide range of applications and a large number of free parameters. Furthermore, CNN models have improved feature extraction accuracy and can handle many free parameters. An activation function, convolutional layers, fully connected layers, normalization layers, and pooling layers are all part of the CNN model. Using fMRI, the CNN approach can analyze brain biomarkers in ASD patients. ASD biomarkers are critical in early diagnosis and therapy[2]. To diagnose early biomarkers of ASD, the proposed multi-channel convolutional neural networks are based on a patch-level data-expanding method, multivariate and high-dimensional data are reduced to two-dimensional features, and the functional connectivity pattern associated with ASD is investigated using a variational autoencoder (VAE).

II. Dataset description

The current study made use of resting state fMRI data from the Autism Imaging Data Exchange (ABIDE I). ABIDE is a partnership that provides previously acquired resting state fMRI ASD and matched controls data for scientific data exchange. The NIH Clinical Center NMR Research Facility used a GE Signa 3T whole-body MRI scanner to acquire functional MRI data. A high-resolution T1-weighted anatomical picture (MPRAGE) was acquired for everyone. We

	Voxel size (mm^3)	Flip angle (deg)	TR (ms)	TE (ms)	T1 (ms)
CALTECH	1	10	1,590	2.73	800
CMU	1	8	1,870	2.48	1,100
KKI	1	8	8	3.7	843
LEUVEN	0.98× 0.98×1.2	8	9.6	4.6	885.145
MAX MUN	1	9	1,800	3.06	900
NYU	1.3 × 1.3	7	2,530	3.25	1,100
OHSU	1	10	2,300	3.58	900
OLIN	1	8	2,500	2.74	900
PITT	1.1 × 1.1 × 1.1	7	2,100	3.93	1,000
SBL	1	8	9	3.5	1,000
SDSU	1	45	11.08	4.3	NA
STANFORD	0.86 × 1.5 ×0.86	15	8.4	1.8	NA
TRINITY	1	8	8.5	3.9	1060.17
UCLA	1 ×1× 1.2	9	2,300	2.84	853
UM	1.2 × 1 × 1	15	250	1.8	500
USM	1 ×1× 1.2	9	2,300	2.91	900
YALE	1	9	1,230	1.73	624

Fig. 1 Different parameters in structural MRI imaging for each site in ABIDE I.

used data from 539 people with ASD and 573 matched controls (typical controls, TC). The ABIDE datasets were gathered at 17 distinct imaging sites and comprise resting state fMRI pictures, T1 structural brain scans, and phenotypic data for each patient. The data includes essential phenotypic information such as the gender and age distribution of ASD and TC, as well as the ADOS score for ASD participants and the Mean Framewise Displacement (FD) quality measure. In general, ABIDE 1 is a difficult data set to work with. Many machine learning techniques, whether shallow or deep, fail to generalize effectively over the whole ABIDE I data set. As a result, a machine learning algorithm that performs well throughout the whole ABIDE 1 may be able to handle with changes in scanner setups and phenotypic differences and may be acceptable for generalization in real-world clinical situations. [**?**] Resting-state functional MRI gives neural measures of the functional connection between brain regions. Rs-fMRI data is very beneficial for studying clinical populations. It enables research of disrupted brain networks without the extra complication of variance associated with task-related brain activity. Low frequency fluctuations in resting-state fMRI are caused by changes in blood oxygenation or flow. It is a manifestation of the brain's functional connection. A correlation is generated for the average of the time series of the regions of interest to explore brain connection. A connection matrix is constructed using the correlation which is then fed to the neural networks for ASD classification.

A. Data Preprocessing

The Preprocessed Connectomes Project (PAC) (`http://preprocessed-connectomes-project.org/`) preprocessed the ABIDE I data. The data came from the C-PAC preparation pipeline. Slice time correction, motion correction, and voxel intensity normalization were applied to the fMRI data. The elimination of nuisance signals was accomplished using 24 motion parameters and CompCor with 5 components. As regressors, low-frequency drifts (linear and quadratic trends) and global signal are used. Functional data was band-pass filtered (0.01-0.1 Hz) and spatially registered to a template space using a nonlinear technique (MNI152)[3]. For each subject, the meantime series for regions of interest was extracted. To minimize the size of the features vector, the CC400 functional parcellation atlas of the brain was employed. This atlas was created using a data-driven parcellation of the whole brain into 400 geographically near areas of homogenous functional activity[4, 5].

III. Project Description

A. Description

Autism is a diverse developmental condition with a wide range of symptom expression patterns, and rs-fMRI may help explain why this is true. Regardless of the efficacy of rs-fMRI as an ASD diagnostic biomarker, classifier approaches are still useful tools for studying brain circuits in ASD. Biomarkers are desperately needed to increase diagnostic accuracy when behavioral symptoms are ambiguous and to detect newborns or early children who may be at risk for ASD before reliable behavioral symptoms show. [6] Rs-fMRI is a particularly intriguing approach since it can examine the concept that ASD includes the disturbance of large-scale brain networks in a task-independent way. fMRI has the potential to discover functional biomarkers of neuropsychiatric diseases, however the data is noisy and has a high dimension. These multivariate approaches have revealed new useful brain characteristics and offered convergent evidence on brain abnormalities that underpin ASD. We can expose the critical ROIs that play important roles in classification by visualizing image classification models learnt using deep Convolutional Networks or ConvNet [7]. We investigated the effect of classifier algorithm and ROI set on the classification accuracy of rs-fMRI applied to ASD in this study. We used Recursive Feature Elimination (RFE) with stratified-10-fold cross-validation for the top performing classifiers to discover which rs-fMRI characteristics were most predictive of ASD or TD categorization.

Our CNN model's architecture is as follows: Each linear layer is followed by a tanh activation function after one completely linked hidden layer.[8, 9] Parallel filters with dimensions ranging from 1x392 to 7x392 operate on rows representing brain regions. As a result, we consider 400 filters of length 1 and wide 392-400 filters of length 7 and width 392. In this case, the weight sizes in the convolutional neural network are identical to the representation matrix. To decrease the amount of features and avoid overfitting, the hidden layer is utilized, followed by max-pooling. A dropout regularization follows the max-pooling layer, retaining just 25% of the nodes for training.

Finally, the output node is combined and completely linked to a dense layer, which is then utilized for classification. In addition, the model is trained for 300 epochs with a batch size of 32 and a learning rate of 0.005. created with a 10-fold cross-validation approach

Feed-forward convolution is not included in the suggested CNN model. Concatenation of many convolution layers was used, and the resulting result set was transferred to the multilayer perceptron (MLP) to finish the classification.

B. Difference in approach

We created connectomes, or functional connectivity matrices, for the identification of ASD classes in this study. This symmetric matrix depicts the relationship between the mean values of time series derived from a ROI. The Pearson correlation coefficient is shown in each column of the matrix, and the ROI is represented in each row. A 10-fold cross-validation approach is used to create the model. To address the weariness caused by storing many models during 10-fold cross validation, we created a memory flushing mechanism that emptied the memory. This forced us to just save the final accuracy attained on each fold's test set. We also tried the RMSProp optimizer, which yielded 52.68% accuracy, while the steepest descent optimization yielded 49% accuracy.

C. Difference in Accuracy

After including the memory management element, our work reached an accuracy of 58.16% on the 10 folds, with the best accuracy of 67.81% on one of the folds. On 10-fold cross validation, the author of the work we cited attained an accuracy of 70.22%. The author of the study acquired the above-mentioned results with the NVIDIA RTX 3050 Titanium as opposed to the Tesla K80 model GPU.

IV. Analysis

CNN is increasingly widely used for dataset classification. We developed a CNN model for automated ASD detection using the ABIDE I dataset. We used preprocessed neuroimaging data from the ABIDE I dataset in our study. Following preprocessing, the ABIDE I dataset was reduced to 871 individuals (539 with ASD and 573 typical controls). During training, the learning rate was set to 0.005, with batch sizes of 32 and 400 epochs. A 392x392 matrix is supplied into the network, with each row representing one of the brain's regions. In our CNN design, we used 400 filters ranging in size from 1 392 to 7 392. In general, the breadth of the filter can be any size. The relationship between the related area and the other brain areas is represented by each row of the connection matrix. We tested the RMSProp optimizer and the steepest descent optimization, but we remained with the Adam optimizer since it performed better. To reduce the

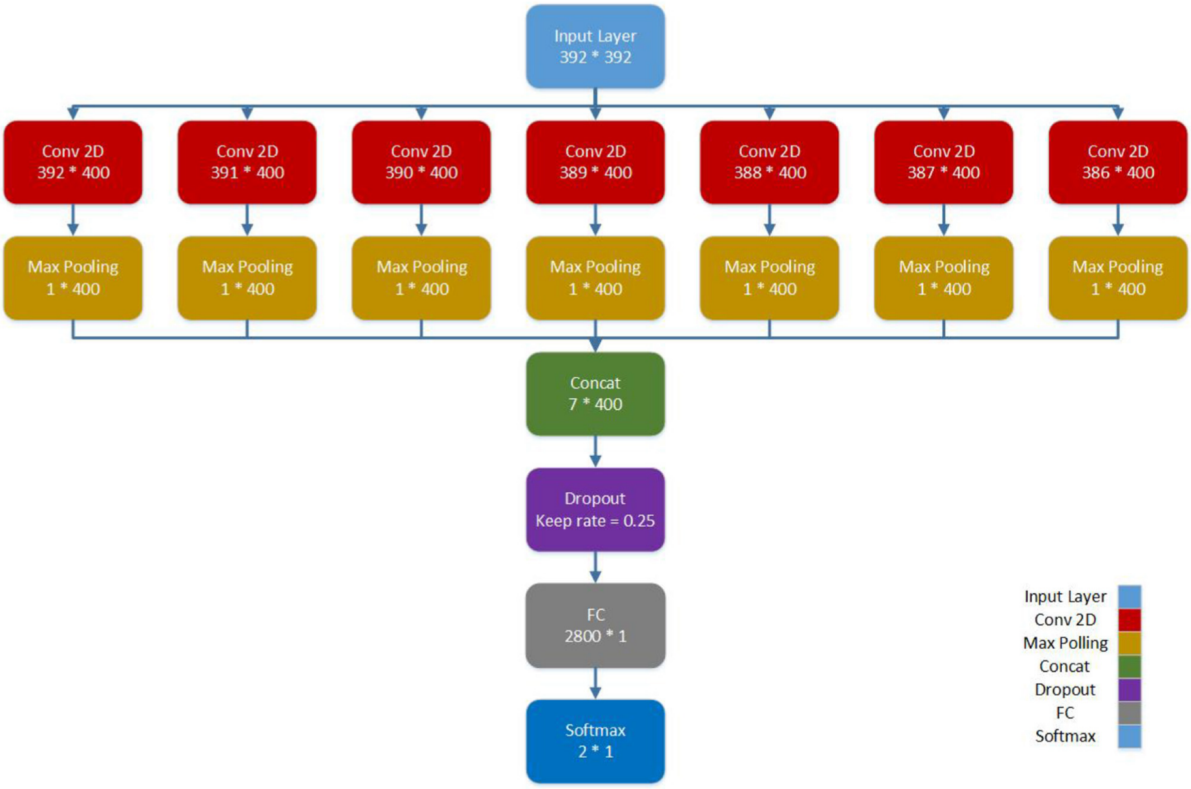

Fig. 2 Proposed CNN architecture for automated detection of ASD.

number of parameters for faster training, 400 units in the MLP's dense layer were tested instead of 2800 units, but this resulted in poor accuracy.

The table compares the automatic identification of TC and ASD classes performed by different studies using the same database. When compared to other cutting-edge treatments, our results were close to average, according to the comparison table.

A. What did we do well

The algorithm implemented for flushing the memory and storing only the required result for each fold improves the performance of the training due to lower utilization of memory. The improvements observed in the performance of our training lead us to believe that this can be incorporated across many learning applications.

B. What could we have done better

Using 10 fold cross validation with grid search to obtain optimal hyper parameters could have resulted in improvement in the model accuracy using RTX 3050 Ti GPU which is highly efficient as compared to the GPU used for this study.

C. What is left for future work

fMRI data has a high potential for use as biomarkers in the diagnosis of autism spectrum disorder. Instead of utilizing correlation to detect signal transmission from one neural connection to another, the performance of specific brain areas should be studied. Using deep learning algorithms, we can detect the pattern of signal transmission in an autistic patient vs a regular control patient.

References	Protocol	Best method	Accuracy (%)
Nielsen et al. (2013)	NA	Multiple bins and leave- one-out classifier	60
Parisot et al. (2017)	10-fold CV	Graph Convolutional Networks (GCN)	69.5
Dvornek et al. (2017)	10-fold CV	LSTM32	66.8
Parisot et al. (2018)	10-fold CV	Graph Convolutional Networks (GCN)	70.4
Aghdam et al. (2018)	10-fold CV	Deep belief Network (DBN)	65.56
Xing et al. (2018)	5-fold CV	CNN with element-wise filters (CNN-EW)	66.88
Kazeminejad and Sotero (2019)	Leave-one-site-out	Deep learning and PCA	66
Sharif and Khan (2019)	Leave-one-site-out	Multi-Layer Perceptron (MLP) and Feature Selection	56.26
Abraham et al. (2017)	10-fold CV	SVC-l1 and SVC-l2 Networks	67
Heinsfeld et al. (2018)	10-fold CV	SVM	65
Heinsfeld et al. (2018)	10-fold CV	Deep Neural Networks (DNN) and transfer learning	70
Study referenced	10-fold CV	CNN	70.2
Our work	10-fold CV	CNN	58.16

Fig. 3 Comparison of our work with other research papers.

V. Conclusion

In this work, we presented a CNN architecture for detecting and categorizing ASD patients and controls in this paper. The results show that our model's average accuracy while using test data is 58.16%. Keeping this in mind, we may be able to train our model with less parameters and achieve greater accuracy than the best-performing models. Our proposed model is less difficult and quicker than prior similar models since it has fewer parameters. In addition, each row of the connection matrix was examined as a representation of the association between the related area and the other brain areas in our model. Additionally, the memory flushing technique reduces memory use. As a result, our proposed model is simpler, faster, and more efficient than current equivalent models. Furthermore, we examined each row of the connection matrix as a representation of the relationship between the linked area and the other brain areas in our model.

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