Autism Spectrum Disorder diagnosis using Multichannel Tri integrated Convolutional Neural Network with Attention

[1]Dr. Samriddhi M. Sharma, [2]S. J. R. K. Padminivalli V., [3]Naveen Mukkapati, [4]Mr. R. Sathishkannan, [5]Mrs. S. Jothimani, [6]Dr. S. N. Sangeethaa, [7]Dr. D. Stalin David

[1]MBBS, Jawaharlal Nehru Medical College, DMIHER, Sawangi(M), Wardha. samriddhisharma15@gmail.com

[2]Assistant Professor, Department of Computer Science and Engineering, R.V.R & J.C College of Engineering, Andra Pradesh. srivallivasantham@gmail.com

[3]Assistant Professor, Department of Computer Science and Engineering, Koneru Lakshmaiah Education Foundation- 522302. naveenkumar105@gmail.com

[4]Assistant Professor, Department of Computer Science and Engineering
Bannari Amman Institute of Technology, Sathyamangalam, 638401 India, kannancse255@gmail.com

[5]Assistant Professor, Department of Computer Science and Engineering, Bannari Amman Institute of Technology, Sathyamangalam,638401 Erode, Tamilnadu, India jothimanis.phd@gmail.com

[6]Associate Professor, Department of Computer Science and Engineering, Bannari Amman Institute of Technology Erode, Tamilnadu, India, dr.snsangeethaa@gmail.com

[7]Associate Professor, Department of Information Technology, Vel Tech Multi Tech Dr. Rangarajan Dr. Sakunthala Engineering College, Avadi, Chennai, India. sdstalindavid707@gmail.com

Abstract

The purpose of this research was to use deep learning procedures to detect people with autism spectrum disorder (ASD) using just their brain activity as a diagnostic criterion. We looked at ABIDE (Autism Brain Imaging Data Exchange), a global collection of brain scans from people with ASD. ASD is a neurodevelopment illness that is both difficult to treat and progressive in nature. Most current approaches rely on functional magnetic resonance imaging (fMRI) to make ASD diagnoses; however, these methods only in a limited number of situations, resulting in high accuracy but low generality. We set out to create a deep learning model for the automatic detection of ASD in this study. A multichannel Tri integrated Convolutional Neural Network with Attention Network (MTCAN) was developed to record the connections between different types of data using a combination of neural network layers, a method of attention, and feature fusion. The suggested MTCAN model was tested on a total of 809 participants from the repository. By combining three levels of brain functional connectomes with individual characteristic data, our model outperformed and reached state-of-the-art accuracy of 0.98 in ASD classification. To ensure that the proposed multichannel TCNN model is both generalizable and resilient, further k-fold cross validation was accomplished. The suggested model has an average accuracy of 98%. The suggested model has a sensitivity of 97%, an F1-score of 98%, and specificity 98%. The findings suggest that deep learning models may help automate the clinical diagnosis of ASD in the future.

Keywords -abide, Attention, Autism spectrum disorder, Cross model, Deep learning, multichannel

1. Introduction

ASD is one of a group of chronic growth diseases that involve reduced ability to express oneself socially and communicate and recurrent patterns of conduct [1]. One in every 160 children has autism spectrum disorder (ASD), according to a WHO estimate [2]. The specific cause of ASD is uncertain, but combined effects of heredity and surroundings have been implicated. Patients with ASD are often diagnosed using symptom-based clinical criteria, which in turn necessitates extensive behavioural tests. Structured examinations of the child's behavior, in-depth interviews with the parents, cognitive, speech and language, hearing, vision, and motor function tests, a physical assessment, an accumulation of medical and family histories, etc., are all part of the

current practice standards. Various research has pointed to difficulties in social interaction and communication as hallmarks of autism spectrum disorder. Yet the neuropathology underlying these signs and symptoms remains unproven. More study in this region can help shed light on the neurological dysfunction that affects people with ASD.

When an evaluation is delayed, the resulting behavioural symptoms are generally worse [3,4]. Diagnosis is often delayed despite the fact that symptoms are common in infants. Currently, a child's developmental history and behavior are discussed with the doctor during an interview to determine whether or not they have autism spectrum disorder [5,6]. Although these techniques are highly precise, they are time-consuming, labour-intensive, and may not be readily available at all hospitals due to the need for specialized personnel. Medical image analysis and illness detection have benefited greatly from recent advances in machine learning and image processing, with results that are practically on par with those of experienced specialists [9]. Additionally, one of the most active areas of study is the use of deep learning to healthcare [10]. The availability of vast quantities of data, in combination with ever-increasing processing power and freshly developed learning algorithms, is enabling these developments.

Limited ability to interact with others and a preoccupation with doing the same things again and over are hallmarks of autism spectrum disorders (ASD), a spectrum of severe, lifelong neurological disorders [11,12]. The signs of autism are present from a young age and go on into adulthood. There is still no clear understanding of what triggers autism, although studies point to interactions between environmental, genetic, brain structure/function, and developmental factors [13]. Currently, a patient's social behaviors and communication skills are assessed using a battery of tools designed to diagnose ASD. Although there are therapies that might help ease symptoms, ASD is difficult to diagnose due to its variability. An increasing number of studies [7] are now exploring the feasibility of computer-aided, robotic autism diagnostic, and [8] researchers are creating interactive technologies to aid in the recovery and therapy of autistic people. Such automated methods would increase diagnostic repeatability and accessibility while reducing subjectivity. Furthermore, it would be crucial in facilitating early diagnosis. Neuropsychiatric and neurodegenerative disorders can often be detected with magnetic resonance imaging (MRI).

There are three main problems with the use of neuroimaging-based machine learning in the past to automate diagnosis or describe biomarkers. First, they tend to narrow in on a single proposed predictive model, ignoring the hyperparameters of competing approaches and producing biased findings as a result. Second, they don't undertake a full analysis of the model once it's been created, thus we don't see any discussion of the neurophysiological relevance of the findings or disclosure of the learnt biomarkers. Third, they don't test their models on any other data, so their findings may be misleading if they're based on just one set of data.

Using a sizable ASD dataset, we compared and contrasted the efficacy of conventional, nonlinear, and deep learning models. Each model's hyperparameters were meticulously tuned to the same extent to exclude any potential for skewed outcomes. The improved models identified common brain regions useful for identifying autism spectrum disorders. Our best models' performance is on par with that of the state-of-the-art models in the current literature, and they're even simpler. We show that this improves their interpretability, resilience to overfitting training data, and generalization to novel datasets. The generality to new data, model consensus, and impartial optimization all lend credence to the reliability and accuracy of the discovered novel link markers.

Finding accurate, stable biomarkers that have been proven across numerous models and datasets strengthens the promise of deep learning as a diagnostic tool and a method of biomarker discovery, which in turn increases our underlying neurobiological understanding of ASD. High-efficiency overlapping filters were used in this study to improve photographs, get rid of noise in the eye-tracking route region, and capture the pathways of eye points that landed on the image. Integrating and fine-tuning these three individual CNN models yielded the Tri Integrated CNN (TICNN) model. The resulting TICNN model leverages the insights of all CNN models for better results. By combining multiple layers of neural networks, an attention mechanism, and feature fusion, the multichannel Tri Integrated CNN attention network (MTCAN) was created to capture the interactions in multimodality data

2. Related Works

In this section the various studies related to autism spectrum disorder are discussed. Vaishali R, et al. [14] established a method for diagnosing Autism using optimum behavior sets. In this study, a swarm intelligence

driven binary firefly feature selection wrapper was tested on a dataset for diagnosing autism spectrum disorder (ASD) that contained 21 features. The experiment's null hypothesis proposes that minimal feature subsets can improve a machine learning model's classification performance. Ten of the ASD dataset's twenty-one characteristics were found to be enough for making the distinction between Swarm intelligence-based binary firefly feature selection framework for people with autism spectrum disorder (ASD) and those without ASD. FadiThabtah et al. propose a machine learning adaptation-DSM-5 screening method for autism spectrum disorders [15]. One or more objectives in screening for ASD have been met through the use of a screening instrument. In this work, the author weighed the benefits and drawbacks of various approaches to classifying individuals with ASD using Machine Learning. The study author made an effort to draw attention to the inconsistency of existing ASD screening techniques and their reliance on the DSM-IV diagnostic manual.

M. S. Mythili et.al [16] employed classification methods in their research on autistic spectrum disorder. Finding the scope and severity of the autism problem was the major goal of this article. This Neural Network analyzes student behavior and social interactions using SVM and Fuzzy algorithms implemented in WEKA tools. For the purposes of autism diagnosis, J. A. Kosmicki1 et al. [17] have hypothesized a searching technique for a least set of features. The authors here analyzed the clinical diagnosis of ASD with the help of a machine learning technique. A group of children's behaviors that fall within the autism spectrum were subjected to the ADOS. Speech recognition, picture classification, machine vision, and natural language processing are just some of the many data analytics industries that have benefited greatly from deep learning [18]. Deep learning offers a new path for data analytic modeling by basing feature development on actual data. An increasing corpus of research published over the past several years lends credence to the effectiveness of deep learning methods for feature construction.

The reality that deep learning has been found to perform better than standard machine learning algorithms on numerous identification and classification tasks encourages scientists in the autism spectrum disorder community to use deep learning techniques to ASD categorization. In the past, rs-fMRI has been used in conjunction with DNNs to help identify people with ASD [19]. Using the FC matrix as characteristics for model training, their model improved accuracy to 70%. Using rs-fMRI data from 182 participants at NYU Langone Medical Center, a data location within the ABIDE repository, Kong et al. [20] built individual functional brain networks. All participants' networks were represented using FC characteristics, and then ranked using F-score. Then, a DNN model was created using stacked sparse autoencoders. When compared to two established algorithms, the proposed technique proved to be a significant performance enhancer.

To aid families and psychiatrists in making a diagnosis of autism, Ahmed, Z. A. et al. [21] developed a Web tool using deep learning for autism diagnosis using facial characteristics that have been empirically validated through experiments, employing a CNN with transfer learning and a flask structure. Pretrained models like MobileNet, Xception, and InceptionV3 were utilized for categorization. For the purpose of early autism detection, this study [22] created three AI methods: machine learning, deep learning, and a hybrid method combining the two.

An easy-to-use web tool built on a deep learning classification is used in this study [23] to aid communities and psychiatrists in empirically detecting autism based on face traits. For this categorization job, they employed pretrained models. In this article [24], we present a hybrid strategy that combines deep learning and Explainable Artificial Intelligence (XAI) to identify the most important aspects for the early and accurate diagnosis of ASD. CNNs, RNNs, and the bidirectional long short-term memory (BLSTM) model are all examples of deep learning methods that have been utilized or suggested for detecting autism in children [29, 30]. Recent years have seen an uptick in research towards the use of machine learning techniques for ASD diagnosis [28], in areas as diverse as brain imaging, biomarker evaluation, patient behavior, and clinical data processing

3. Materials and Methods

Data collection begins deep learning model training and testing. Medical, behavioural, and other autism data may be included. Data must be pre-processed before feeding deep learning models. Pre-processing may involve cleaning, removing outliers, normalizing, and more.CNNs can identify data's key features. After extracting features, train the deep learning model. Diagnose autism patients by analyzing the model's accuracy, precision, recall, and F1 score. Hyperparameters, model design, and regularization can reduce overfitting.
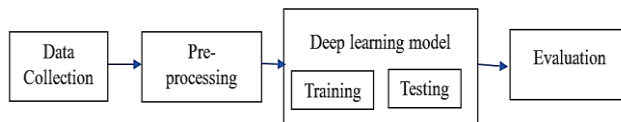
Fig.1. Proposed workflow which includes data pre-processing, training, testing, assessment, and ASD prediction using predefined models

Figure 1 depicts the suggested workflow, which includes data pre-processing, training, testing, assessment, and ASD prediction using CNN models. Python 3 is used for the implementation.

3.1. *Data Collection*

Brain imaging information gathered from people with ASD and neurotypical controls is shared through the ABIDE. It was created to promote collaboration and data sharing in autism research. The ABIDE dataset includes structural MRI, resting-state functional MRI, and diffusion MRI data from over 1,100 individuals, including over 500 with ASD and over 600 characteristically emerging controls. The dataset includes data from multiple sites across North America and Europe, and includes individuals ranging in age from 6 to 64 years old. From 17 locations, a total of 1,035 rs-fMRI data were obtained, 505 from individuals with autism spectrum disorder and 530 from healthy individuals serving as controls. The data set was retrieved from (http://preprocessed-connectomes-project.org/abide/) after being pre-processed.

Because ASD is more common in males, the samples are overwhelmingly composed of men; in fact, only 25% of the seventeen contributing sites include any women at all. For both total and verbal IQ, normal controls outperformed Autistic individuals by a significant margin (p 0.0001), while performance IQ was similarly higher, albeit with some variation (p = 0.067).

3.2. *Pre-processing*

Slice timing alteration, motion rearrangement, and intensity standardization are only some of the steps in the pre-processing pipeline used on all of the rs-fMRI data. Using bandpass filtering and global signal regression methods, we eliminated artifacts caused by the subject's own heart and breathing rates, head movement, and low-frequency scanner drifts (also known as "nuisance variables"). In addition, the functional to anatomical pictures were registered using the boundary-based rigid body and FMRIB's linear and nonlinear image registration methods. After that, we standardized the anatomical and functional pictures to the same reference coordinate system (MNI 152).

In this study, we retrieved functional connectomes from the brain on three different length scales. The Automated Anatomical Labelling (AAL) atlas, the Harvard-Oxford (HO) atlas, and the Craddock 200 (CC200) atlas were used to derive mean blood oxygen level dependent (BOLD) time-series signals. Pearson's correlation coefficient was used to
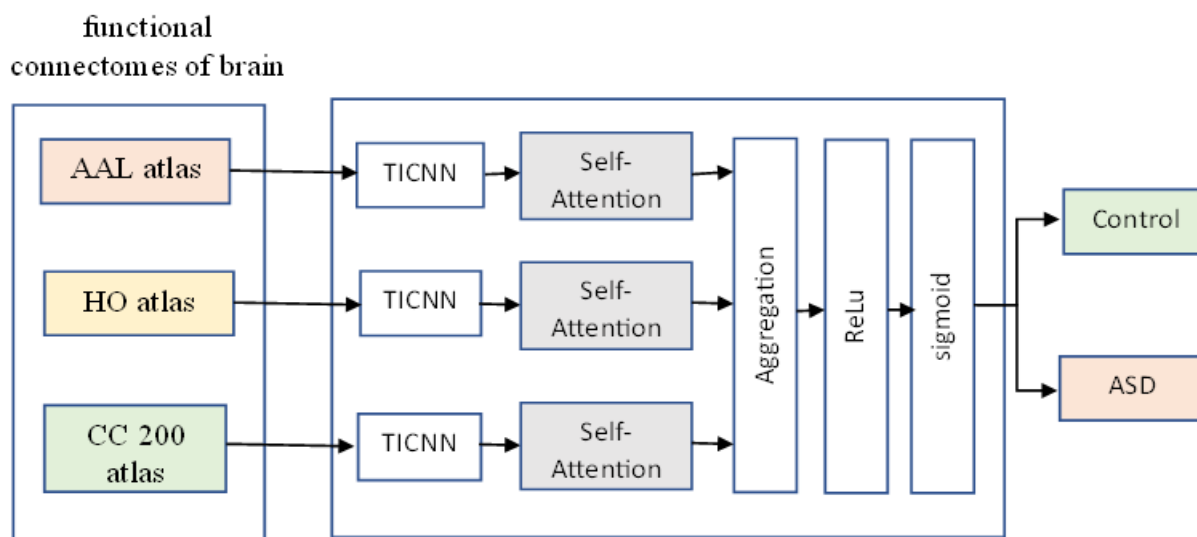

Fig.2. overview of the multichannel TICNN Attention Network (MTCAN) which classify the ASD and Control

establish the relative importance of any two regions of interest (ROIs) for the purpose of defining functional brain connectivity.

3.3. *Proposed methodology*

The basics of multichannel Cross Model Attention Network (MTCAN) are laid forth in Figure 2. Tri integrated CNN (TICNN) nodes make up its building blocks, together with attention to self, fusion, and aggregation. The subsequent sections elaborate on the various parts.

3.3.1 Convolutional Neural Network

Single-sample data is used as the input feature vector (X) for this network, which is then passed on to a convolutional layer. All the locations in X are iterated through by a filter K (or kernel), which is an array of integers (or weights). Since we are only working with a vector of one dimension, the height of K and X must also be 1. The K's receptive field is the area R across which it is now traveling. Element-by-element multiplication on K reduces the representation of R to a single integer. The connection among nearby connectomes can be detected in the provided data by employing the weight filter in this fashion. The resulting activation or feature map is a vector that encompasses every possible value for X. Therefore, the size of the activation map would be $1 \times Q - F_p$ if X a Q-dimensional vector is. Changing the Fs allows for an infinite number of possible feature maps. The size of the input feature vector is 1×16289, and the size of the convolutional kernel is 120 in our baseline CNN model, which uses 10 CF maps. It is generally known that this convolutional method is an effective local feature pattern finder. This convolutional technique will be able to detect patterns in the input data. The Rectified Linear Units (Relu) layer receives the output from our convolutional layer (CFs). The convolution layer is made up of a variety of trainable filters that can extract characteristics from raw data. The layer l , is expected to be recognized as z_b^c, whereas the layer c-1, mth has been chosen by z_b^{c-1} in the feature map. Following is the formula for determining z_b^c:

$$z_b^c = \sum_{r \in ij} a_{jr}^c * z_r^{c-1} + y_j^c \qquad (1)$$

where $|i|$ is the total number of mapping features in layer c, y_j^c is a biased term applied to all links leading to the j feature map, and ij is a collection of characteristic maps in layer $c - 1$ that are associated with unit j.

The expression for ReLU Functions activation $d(x)$ is as follows:

$$d(z) = max(o, z) \qquad (2)$$

where the range is from 0 to x. Following is a mathematical expression for the Maxpooling:

$$z_{b^{c+1}}r^{c+1}, s = \underset{0 \le b \le H, 0 \le r < K}{max} a_{b^{c+1}}^c * H + i, r^{c+1} * w + r \qquad (3)$$

An activation function like ReLU can help you simulate the intricate non-linear connection between your model's inputs and outputs. Relu uses a cheap thresholding function rather than an elaborate exponential one, in contrast to other activation functions like tanh and sigmoid. The Relu function may be written as,

$$f(r) = \begin{cases} r, & r \ge 0 \\ 0, & r < 0 \end{cases} \qquad (4)$$

In this case, r is an action potential entering a neuron. We know that every complicated relationship between input and output may be modelled by a CNN model with a sufficiently high number of neurons. However, in this case, our CNN model has a limited amount of training samples and is thus susceptible to overfitting. Therefore, a max pooling layer follows the Relu layer in order to down sample the input feature vector. To determine the maximum value of its input, a filter maximizes its receptive field. Pooling may result in
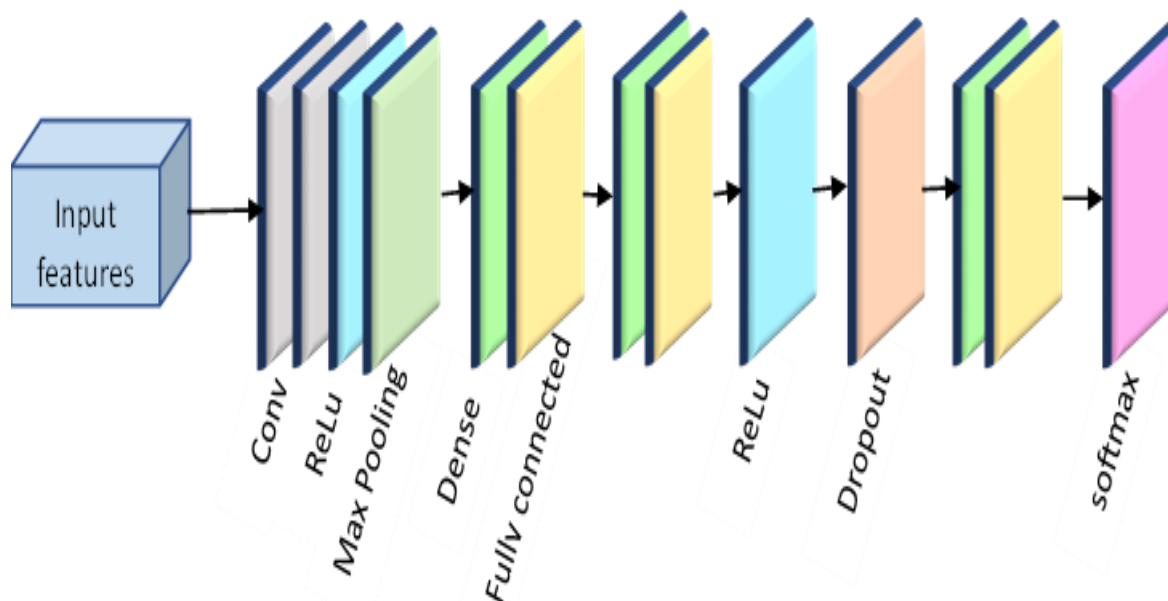
Fig.3. Basic Standalone CNN design for each data source. When training the multi-layer network, we take a backpropagation strategy. Feature vector size, output vector size from fully linked layers, and kernel sizes for each layer are all specified

some loss of information, but this is ultimately beneficial since it decreases the total parameters that need to be learned and so frees the model from the curse of overfitting. This layer also aids in making the model invariant to changes in the input data's translation, rotation, and scale. As a result, the CNN model as shown in the figure 3 benefits from improved generalization on the test data thanks to the pooling layer.

A fully connected (FC1) layer receives the results of our pooling layers as input. Each neuron in this layer is connected to the layer below it, and this layer's output is a simple matrix multiplication, represented as a one-dimensional vector. This vector has a size of 1250 in our lab setting. After this FC1 layer, we feed our input feature vector X into a second, more advanced fully connected (FC2) layer. This output is then passed on to a Relu layer and a Dropout layer before reaching a third fully connected layer (FC3). This is necessary since our network trains a large number of parameters with just a small number of training examples. The CNN model can be protected from overfitting thanks to the dropout layer's regularization strategy.

In this layer, nodes and their associated connections are lost at random. FC3 produces a 1 by 2 or 1 by 4-dimensional vector as its output. FC3 takes the output of FC2 and controls each of the high-level properties of X based on how strongly they correspond with a certain class. A softmax classification layer takes each value of FC3 as a prediction score for a given class and returns a probability score. Taking the prediction scores (x) and weights (y) from FC3, this layer uses them to build the softmax function. The following formula allows us to determine the likelihood of the pth class,

$$P(y = p|z) = \frac{e^{z^t x_p}}{\sum_{m=1}^{2} e^{z^t x_m}} \quad (5)$$

Adam, stated in Eq., is utilized as an optimizer, and the categorical cross entropy loss function is employed.

$$l(i) = l(p-1) - \gamma^* \frac{c(t)}{\left(\sqrt{a(t)} + \epsilon\right)} \quad (6)$$

3.3.2 Attention mechanism

An attention mechanism can be applied to a convolutional neural network (CNN) to enhance its performance by permitting the system to focus on significant regions or features in the input data. The attention mechanism helps the network allocate its resources effectively, emphasizing relevant parts of the input while suppressing irrelevant or noisy information.

The equation for an attention mechanism in a CNN can be described as follows:

$$Attention(X) = Softmax(ReLU(W_2 \cdot ReLU(W_1 \cdot X + b_1)) \cdot W_3 + b_3) \qquad (7)$$

Here, X represents the input feature maps of the CNN, and W_1, W_2, W_3 and b_3 re learnable weight matrices and bias vectors. The W_1 and b_1 linear transformation and subsequent ReLU activation function are applied to the input feature maps X. The goal of this process is to collect all of the pertinent data from the input. The W_2 and b_2 linear transformations are measured by a ReLU activation on the enhanced feature maps. This process is useful for recording the relative relevance of various parts of the feature maps. Another linear transformation is performed using W_3 and b_3 on the modified feature maps and the attention weights gained in the previous phase. At this point, the network is able to learn the optimal weighted mix of feature maps. The last step involves applying a softmax function to the previous phase's output to derive a probability distribution over the geographic locations or channels. Each location or feature's relative importance is reflected in this distribution.

3.3.3 Tri Integrated Convolutional Neural Network (TICNN)

We introduce a data-fusion model predicated on a deep convolutional neural network. Before making a final forecasting, this model combines the learnt deep features from many data sources.
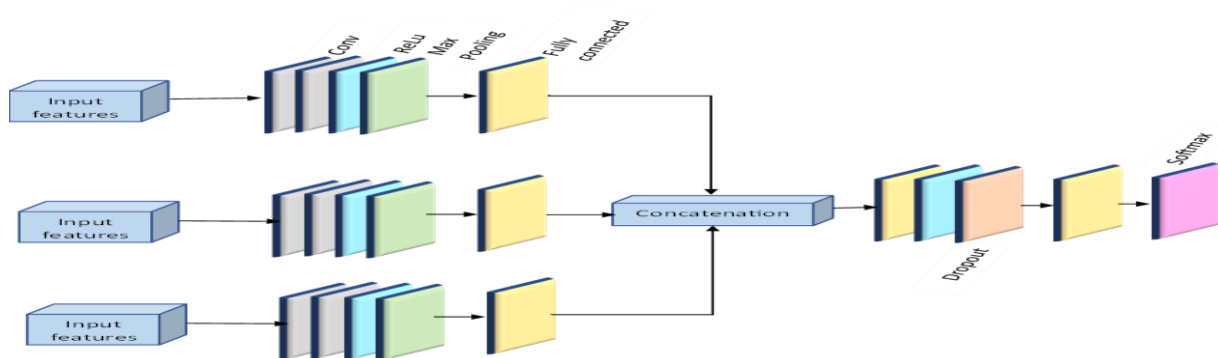

Fig.5. The Tri Integrated CNN Model's Detailed Architecture. A meta-learner model was utilized to produce the final classification after the output of each of the three base architectures that were mentioned before was piled on top of one another

Figure 4 depicts a stacked-ensemble model called the TICNN, which is an amalgamation of three separate basemodels. A meta-learner model was utilized to produce thefinal classification after the output of each of the three different base architectures that were mentioned before was piled on top of one another.The meta-learner algorithm learns from how accurately the other three fundamental systems forecast. The stacking ensemble method is the name that is most usually given to this methodology.

Using the keras concatenate package, the three core models were combined into a single model. The TiCNN model accepts form data in a number of different formats. The meta-learner model is a concatenation of two layers: a dense layer with ReLU activation and a dropout layer meant to mitigate overfitting. Both of these layers come after the concatenation step. An Adam optimizer was utilized in order to optimize the categorical cross-entropy loss, and a Softmax activation function was utilized in order to activate the output layer. The total number of weighted layers that make up TiCNN comes to 47.

3.3.5 Fusion and Aggregation

Combining the outputs of the three dense layer blocks, which are able to capture the correlation between the different types of spaces, results in the fusion output being created.

$$Fusion(F) = sigmoid\left(W^{(m_1)} y_{d_1} + W^{(m_2)} y_2 + W^{(m_3)} y_{d_3} + b^m\right) \qquad (8)$$

$$v = F \odot y_{d_1} + (1 - F) \odot y_{d_2} \qquad (9)$$

$W^{(m_1)}, W^{(m_2)}, W^{(m_1)} \in \mathbb{R}^{d_o}$ is the dimension of output d_o.

Concatenating, multiplying, or averaging the results of self-attention and fusion blocks yields an MTCAN comprised of thick layer, self-attention, and fusion. Our approach combines the results from the self-attention blocks with those from the fusion blocks, then uses a dense layer and a sigmoid layer to classify the data.

$$k_d = ReLu(W_d H + b_d) \qquad (10)$$

$$Final = sigmoid(W_c k_d + b_d) \tag{11}$$

H is the combination of output from the both attention and fusion layers.

Algorithm 1. multichannel TICNN Attention Network (MTCAN) to classify the ASD and Control

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Input:

        Dataset ABIDE $\{D_m\}$

Output:

        Autism, control

1. **Procedure** Pre-processing (D_m)
    a. **for** each file f_i in D_m **do**
        i. f_i ={cleaning, normalization, alignment}
        ii. **Extract** functional connectomes C_i where i=1,2,3.
        iii. **Divide** the functional connectomes into small patches
    b. **End for**
2. **Procedure** Split_Data (C_i):
    a. **For** each i in C_i
        i. Train, Test = Split $(C_i, label)$
        ii. Train, validation = (Train, label)
    b. **End for**
3. **Build** a parallel CNN model with multiple branches, with each branch processing a separate patch of the connectome.
4. **Procedure** Build_Model (Train, Test, Validation)
    a. Model1 = CNN (Train, label, Test, Validation)
    b. Model2 = CNN (Train, label, Test, Validation)
    c. Model3 = CNN (Train, label, Test, Validation)
5. **Procedure** Model_Training $(M_i, Train, Test, Validation)$
    a. **For** each model in M_i
        i. **Call** Split_Data (C_i)
        ii. **Train** the parallel CNN model on the training set.
        iii. **Evaluate** the model on the validation set
        iv. **Fine-tune** the hyperparameters for optimal performance.
    b. **End for**
6. **Procedure** Integrated_Model (Train, Test, Validation):
        i. TICNN = **Concatenate** (M_1, M_2, M_3)
        ii. TICNN.**Compile** (Adam, CategoricalCrossEntropy)
        iii. TICNN.**fit** (Train, Test, Validation)
        iv. TICNN.**Predict** (Test)
7. **Return** Autism, control

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4. Results and Discussion

4.1. Experimental Setup

Python 3.7 was used to implement the suggested MTCAN and deep learning representations. Using the Keras package and TensorFlow as a backend, we constructed models for deep learning. We used Sklearn 0.20's classic models for our analyses. Matlab 2019b was used for all of the statistical analysis. The workstation used for the studies

included a 64 GB RAM and 10 cores of Intel Core i9 processor. In order to speed up model training, we setup a single graphics processing unit to handle the intensive computations required by deep learning algorithms.

4.2. Performance Evaluation

The condition cannot be effectively managed without an early diagnosis of ASD. However, modern diagnostic techniques rely on the observation of disease-related behavioural abnormalities. The sickness has progressed to

a point where it can no longer be reversed. Therefore, it is crucial to make an early diagnosis of ASD through the use of medical imaging tools rather than relying on the observation of behavioural abnormalities. Here, we describe the results of an analysis of rs-fMRI data for the diagnosis of ASD.

The confusion matrix and classification report specificity, sensitivity, and accuracy are the metrics used to assess efficiency. The precision with which the model is trained will determine the outcome.

To determine a categorization model's efficacy in meeting a goal, performance metrics are necessary. Metrics for gauging how well a model classifies data from a given dataset are used to assess the classification model's performance. Metrics like confusion matrices, precision, recall, and false positive rates should all be considered when assessing a model's efficacy. The formulae below can be used to calculate various performance indicators.
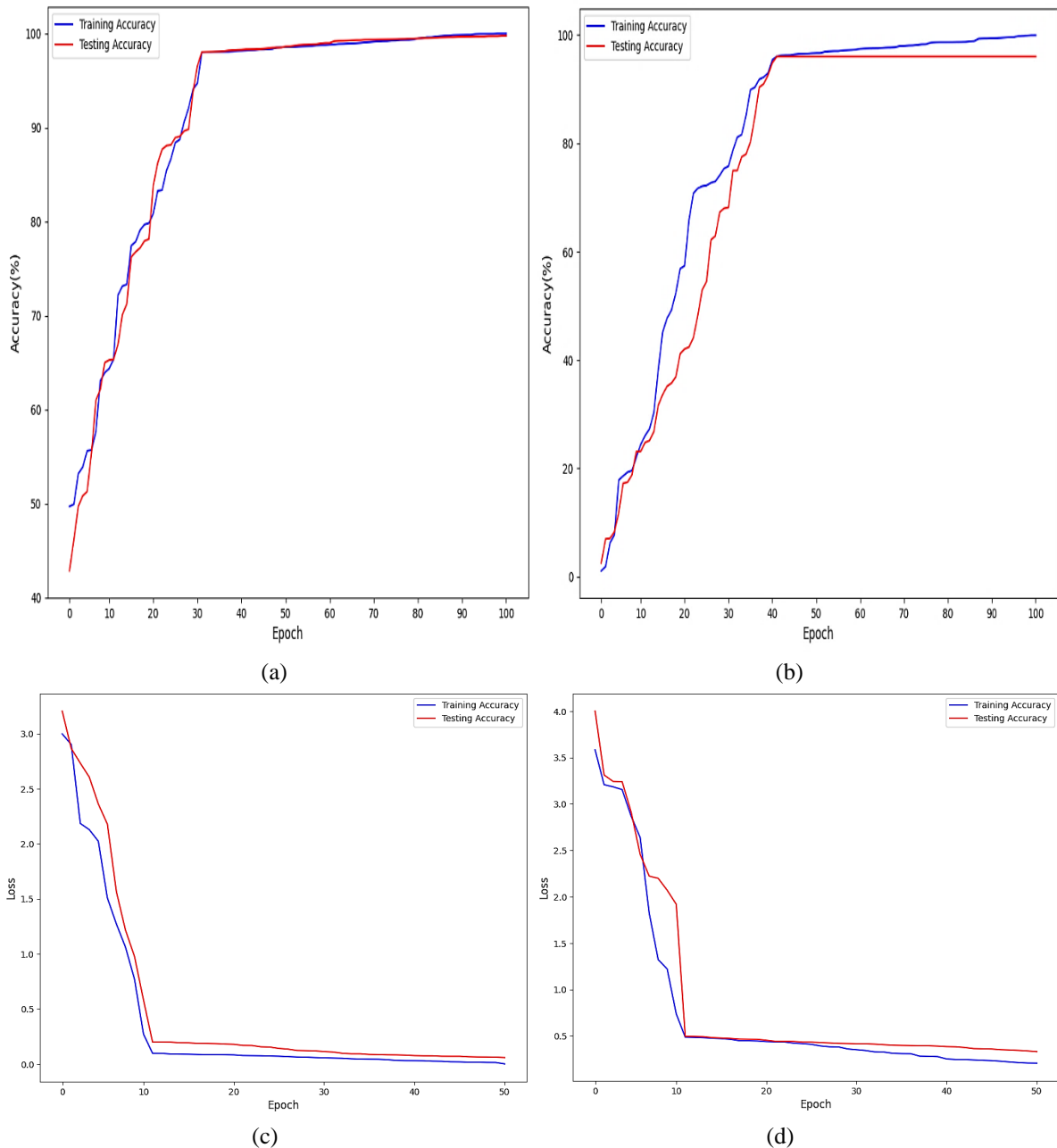

(a)

(b)

(c)

(d)

Fig.5. Accuracy and Loss of the Model MTCAN and CNN model on the Dataset ABIDE. (a) Accuracy of the model MTCAN (b) Accuracy of the model CNN (c) Loss of the model MTCAN (d) Loss of the Model CNN

$$Accuracy \ (A_{cy}) = \frac{Te_p + Te_n}{Te_p + Te_n + Fe_p + Fe_n} \ (12)$$

Figure 5 displays the suggested model's accuracy. The precision of the MTCAN and CNN models is depicted in Figures 5.a and 5.b. The model losses for MTCAN and CNN are shown in Figures 5.c and 5.d. Figure 5 shows that compared to other models, the MTCAN has superior performance.

$$Precision \ (P_{re}) = \frac{Te_p}{Te_p + Fe_p} \qquad (13)$$

$$Recall \ (R_{cl}) = \frac{Te_p}{Te_p + Fe_n} \qquad (14)$$

$$F1 - Score \ (F1_s) = 2 \times \frac{P_r * R_{cl}}{P_r + R_{cl}} (15)$$

The confusion matrix between the MTCAN and CNN is displayed in figure 6. The algorithm is sensitive enough to identify healthy pixels. The Abide dataset is evaluated on the models, CNN, AlexNet, EfficientNet and LSTM.
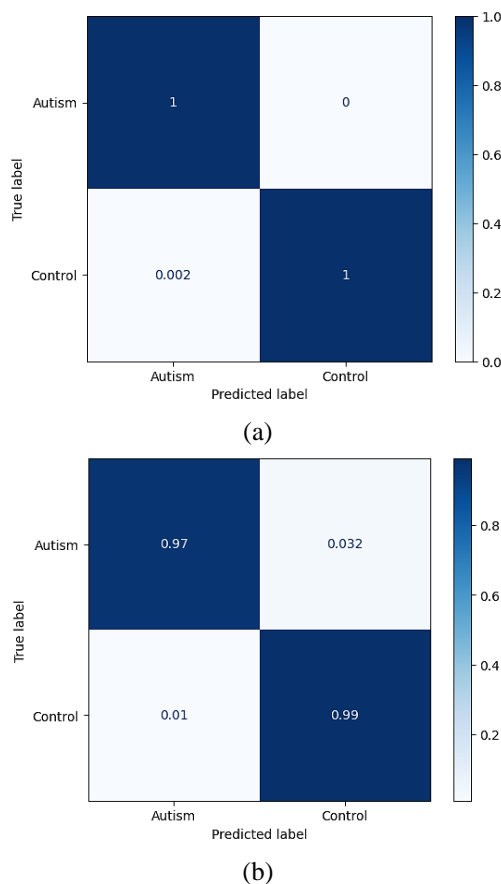

(a)

(b)

Fig.6. The confusion matrix of(a) MTCAN and (b)CNN. The MTCAN performs better than the single CNN model

Table 1 and figure 7 express the comparison outcomes of using the projected method to analyze normal and abnormal clinical images; the method has a sensitivity of 99 %, a specificity of 99%, and an accuracy of 100%. Accuracy on the original dataset ranged from (96%) to (100%) when evaluating several deep learning models for ASD diagnosis. The MTCAN was able to attain a classification accuracy of 100% (sensitivity 99.8%, specificity 99.5%) from the cross-validation folds, with each fold accuracy ranging from 99% to 100%.

Table 1. Performance comparison of the different models on the ABIDE dataset

Model	Sensitivity	Specificity	Accuracy	Recall	F1-Score
CNN	96%	96.2%	96.5%	0.96	0.96
MTCAN	99.8%	99.5%	100%	1.00	1.00
AlexNet	94.0%	94.8%	94.2%	0.93	0.94
EfficientNet	95.8%	95.5%	95.8%	0.95	0.95
LSTM	92.8%	92.7%	91.0%	0.92	0.91

According on the available research, this classification is the greatest level that has been reached thus far. The CNN classifier was able to achieve an average accuracy of 96% (sensitivity of 96% and specificity of 96.2%, 96% range). Using ABIDE multi-site resting-state brain activity find people that haveASD, the applied algorithm surpassed earlier research. The Additional materials provide results from the use of alternative brain parcellations. When compared to previous attempts at ASD classification using smaller participant examples, the current classification lost both specificity and sensitivity.
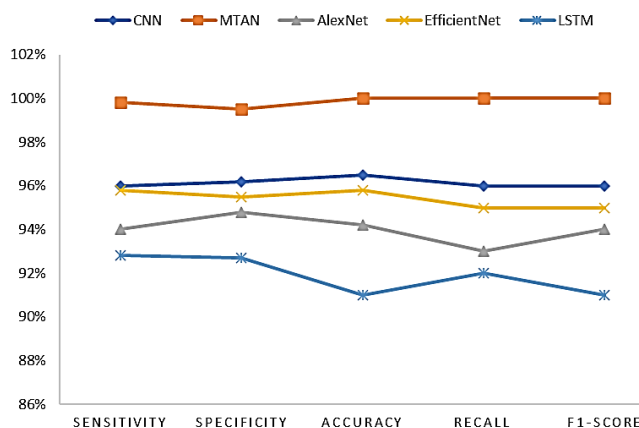

Fig.7. Result Comparison using the proposed method to other baseline model to analyze normal and abnormal clinical images

Classification accuracy improves when there are fewer site-wise differences or when no such variation exists in the dataset, but accuracy decreases when supervised algorithms are confronted with the problem of classification across numerous sites, as in ABIDE. Researchers using machine learning to analyze brain scans must contend with a growing number of dataset dimensions. It's possible that the dimensions are indicative of demographic differences that provide clinically significant information to the comprehension of a mental disease. Sensitive fluctuations in ABIDE data undermine site-to-site consistency. By taking these differences into account, deep learning techniques outperform their less sophisticated shallow counterparts.

5. Conclusion

This research put up a new scheme for utilizing fMRI to differentiate between children with ASD and classically emerging kids. For the purpose of automating the diagnosis of ASD, we constructed a multichannel MTCAN model using cutting-edge attention mechanism based deep learning systems. Our multichannel MTCAN outperformed several other machine learning models in a k-fold cross validation trial, achieving perfect

accuracy. Individual data methods, such as the brain functioning connectome, were shown to have discriminative power in trials utilizing different combinations of data modalities.

This points to the need for further integration of other data modalities in order to advance machine learning applications towards therapeutic use of ASD CAD tools. Due to the selection of a cohort consisting mostly of teenagers and young adults for whom the diagnosis of ASD was established at a younger age, the current work is limited in its capacity to be extrapolated to a larger population. In a follow-up investigation, we want to retrain the model with information from participants of varying ages. To further refine this model, researchers will collect more data from psychologists who have diagnosed children throughout the age spectrum with autism. The use of such a tool will aid in the ASD diagnosis process for both parents and mental health professionals. Children with autism may benefit from a more accurate diagnosis and subsequent treatment plan

Conflicts of Interest

The author(s) declare(s) that there is no conflict of interest regarding the publication of this paper.

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