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Implementation of Machine Learning and Deep Learning Models Based on Structural MRI for Identification of Autism Spectrum Disorder

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ABSTRACT

Autism spectrum disorder (ASD) is a developmental disability resulting from neurological disparities. People with ASD frequently struggle with communication, social interaction, and limited or repetitive interests or behaviors. People with ASD may also have unique learning, movement, and attention styles. People living with ASD can be interpreted as 1 in every 100 individuals in the globe having ASD. The abilities and requirements of autistic individuals vary and may change over time. Some autistic individuals can live independently, while others have severe disabilities and require lifelong care and support. Autism frequently interferes with educational and employment opportunities. Additionally, the demands placed on families providing care and assistance can be substantial. Important determinants of the quality of life for persons with autism are the community's attitudes and the level of support provided by local and national authorities. Autism is frequently not diagnosed until adolescence, even though autistic traits are detectable in early infancy. This study will discuss the identification of Autism Spectrum Disorders using Magnetic Resonance Imaging (MRI). MRI images of ASD patients and MRI images of patients without ASD were compared. By employing multiple machine learning and deep learning techniques, such as random forests, support vector machines, and convolutional neural networks, the random forest method achieves the utmost accuracy with 100% using a confusion matrix. Therefore, this technique can optimally identify ASD through MRI.

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1. INTRODUCTION

Autism, or Autism Spectrum Disorder (ASD), is a developmental disorder in children that causes impaired communication and socialization skills in children [1]. Until now, the cause of autism is not known with certainty. However, the risk of developing autism disorders can increase if genetic and environmental factors include exposure to toxins, cigarette smoke, infections, drug side effects, and the mother's unhealthy lifestyle during pregnancy. Disorders that are included in ASD are Asperger's Syndrome, pervasive

developmental disorder (PPD-NOS), autistic disorder, and childhood disintegrative disorder. Based on data compiled by the World Health Organization (WHO), autism occurs in one in 160 children worldwide [2]. Meanwhile, in Indonesia, until now, there is no definite data regarding the number of people with autism. The prevalence of autism in the world is increasing day by day. Until before 2000, the prevalence of autism was 2-5 to 15-20 per 1,000 births, 1-2 per 1,000 world population. Based on data from the Autism Society of America (ASA) in 2000, it was 60 per 10,000 births, with a population of 1:250.

Based on data from the Centers for Disease Control and Prevention, USA (CDC), in 2001, it was one in 150 residents, and in some areas in the USA/UK, it was among 100 residents. In 2012, CDC data showed that 1:88 children had autism; in 2014, it increased by 30%, namely 1.5% or 1:68 children in the USA have autism. There are no actual data for people with autism in Indonesia; referring to the Incidence Prevalence of ASD, there are two new cases per 1,000 population per year and 10 cases per 1,000 population [2]. Meanwhile, Indonesia's population is 235.5 million, with a population growth rate of 1.14%. So it is estimated that people with ASD in Indonesia are 2.4 million people with the addition of new people with 500 people/year. Typical findings include increased brain volume before the age of six years and increased volume in the frontal and temporal lobes. Several inconsistent findings include the longitudinal trajectory of brain volume across development. Future studies should consider using larger datasets by combining data from multiple sites or using available datasets and 3T scans, which may be needed to detect more subtle brain changes. A well-fitted and generalizable model can yield more accurate estimates of the likely diagnosis of ASD and predict clinical outcomes. Research conducted by [3] related Machine learning methods for brain tissue classification: Application for the diagnosis of autism using cortical morphological networks. This study presents the results of the competition and describes the computational approaches of the top 20 ranked teams. This paper provides a comprehensive comparison and characterization of various ASD/NC ML classification methods on cortical morphological networks and interprets the performance of each method. Feature Extraction Techniques Principal Component Analysis (PCA) and Linear Discriminant Analysis (LDA) are typical examples of feature extraction methods in machine learning. The PCA method generates features in new feature space by projecting a sample of data onto a predefined axis. LDA aims to find new feature axes where the samples are most spread out but also tries to group data samples from the same class. Feature Selection Techniques such as SelectKBest, Variance Threshold, Minimum Redundancy Maximum Relevance (MRMR), and Recursive Feature Elimination with Cross Validation (RFECV) are categorized as feature selection methods. Each has different criteria to determine the importance of features.

The MRMR algorithm takes the basis of the correlation between features and labels of sample data for space reduction rather than scoring those features depending on specific metrics or score generators. The RFECV method differs from the three because it needs to use a learning model because of its wrapper-based characteristics. The journal [2] evaluated the performance of the ML pipeline for ASD/NC classification using results obtained from a subset of public and private tests. The public test kits are partially accessible to competitors during the competition so they can check the accuracy of their models. The private ones were hidden to judge the model's generalizability after the competition. All participating teams are ranked in three ways, each based on one type of average measurement. The result displays the classification results for the 20 competitors.

The Autistic Brain Project is a Kaggle competition to design an ML framework for ASD diagnosis. T1-w structural MRI-derived cortical morphology networks were used in this competition. This competition aims to design a robust and accurate ML framework for ASD. Many studies are conducted in neuroimaging involving non-invasive brain imaging modalities such as functional MRI (fMRI) and diffusion MRI (dMRI) for diagnosis. However, morphological brain connectivity derived only from structural T1-w MRI is rarely used, despite the new insights it may provide about ASD. In this study, Researchers organized a Kaggle challenge in the classroom to fill a gap in utilizing cortical morphological networks for ASD diagnosis—research conducted by [3] related to Autism Classification Using Brain Functional Connectivity Dynamics and Machine Learning. This study aimed to identify autism using machine learning techniques and resting state brain imaging data, utilizing the temporal variability of the functional connections (FC) as the only information. Researchers estimated and compared FC variability across brain regions between healthy and typical subjects and autistic populations by analyzing brain imaging data from a multi-site worldwide database called the Autism Brain Imaging Data Exchange (ABIDE). Temporal variability in resting-state fMRI (rs-fMRI) and task-fMRI BOLD signals, and their aberrations in brain disorders. Often, the sliding-window technique is used, where functional connections are estimated within each temporal window. This study examined changes in node variability in the autistic brain concerning the typical brain. It further uses node variability as a feature to train a machine-learning model for autism identification in a world-vast, multi-site functional MRI dataset.

Machine learning model training and testing were conducted using the open-source machine learning tool kit - Weka. We defined two distinct feature sets when training the model using variability: (1) all 200 nodes and (2) nodes exhibiting < 0.9 variabilities in typical subjects. Researchers trained the model using Naïve Bayes, Random Forest, Support Vector Machines, and the Multilayer Perceptron algorithm. For intra-site, model evaluation was tested using a K = 5 cross-validation scheme. Two scenarios were tested: (1) data from all sites were combined, keeping their original proportions intact, and (2) subjects from each site were removed proportionally to create a more balanced subset. For inter-sites, we used a leave-one-out-site approach which involved training the classifier at all sites except those left for testing. To evaluate each classifier, accuracy, sensitivity, and specificity were estimated.

Subsequent research was conducted by [4] on Classifying Autism Spectrum Disorders Using Temporal Statistics Resting-State Functional MRI Data With 3D-CNN. This study aims to maintain complete and spatial resolution as input by summarizing the temporal dimension per voxel as a single number. The neuroimaging literature informed most of the summary measures we used. This journal has an update, as previous research has yet to attempt to use these measures extensively using deep learning algorithms. This study used the ABIDE I + II dataset, a collection of structural (T1w) and functional (rs-fMRI) brain images collected at 29 institutions. It included 1,028 participants with a diagnosis of autism, Asperger's or another pervasive-unspecified developmental disorder (called ASD) and 1,141 participants who usually progressed (CON). Nearly all ASD participants were high functioning (99.95% with IQ > 70), and most of the included participants were adolescents (mean age 13 years, range between 5 and 64 years). The previous research discussed in this literature review was carried out by [5] and related Improve autism diagnosis with optimized machine learning models and personal characteristics data. This study aims to determine the optimal ASD classification performance with personal characteristic data (PCD) as a feature. With additional discriminatory features (e.g., neuroimaging), machine learning models could eventually enable automated clinical diagnosis of autism. Researchers selected six interesting PCD features from the ABIDE I Preprocessed Database. Age at testing, gender, disposition, full-scale IQ, verbal IQ, and performance IQ were included. Of the 851 subjects, 430 were typical non-ASD controls, and 421 had a confirmed ASD diagnosis. Using a two-tailed Student's t-test (unequal variances), we identified significant differences between ASD patients and healthy controls.

From some of the problems described above, this study aims to carry out the process of identifying ASD through MRI brain images. By combining MRI images with machine learning and deep learning methods, it is expected to be able to create a new tool to speed up the process of diagnosing ASD. There are several contributions that can be made such as the use of machine learning and deep learning methods in identifying ASD through MRI brain images which can become a new tool to support diagnosis by doctors so that it can speed up the identification process.

2. METHODS

2.1. Research Flowchart

Fig. 1 depicts the progression of the research conducted for this study. At this stage, the derived images will be subjected to a process of feature extraction using multiple techniques, including Global Features Extraction from Images, discrete cosine transform (DCT), and discrete radon transform (DRT). At this stage of the classification process, machine learning and deep learning techniques will be used to classify image data. In the third stage as well as the final process, namely the evaluation using the Confusion Matrix to determine the accuracy of the algorithm utilized in this study, results are obtained. After obtaining the highest level of accuracy from one of the methods utilized in this study, this method is the finest method in this study.

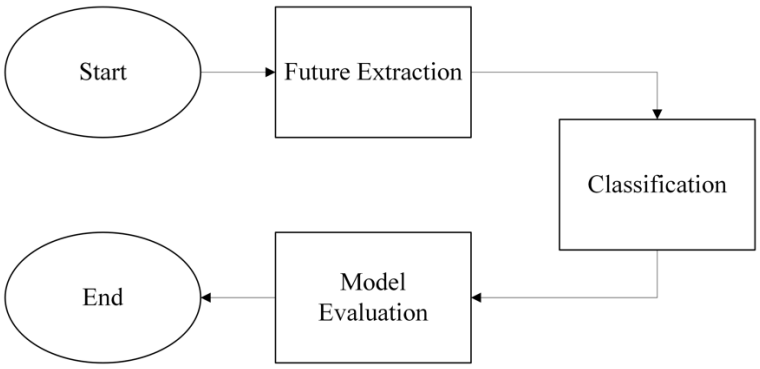

Fig. 1. Research Flowchart

2.2. Data Collection

The data used in this study uses data from http://fcon_1000.projects.nitrc.org/indi/abide/abide_II.html. ABIDE I demonstrated the viability and utility of aggregating MRI data across sites. Nonetheless, the complexity of the connectome, the considerable heterogeneity of Autism Spectrum Disorder (ASD), and the preliminary results of ABIDE I data analyses highlight the need for even more significant and better-characterized samples. ABIDE II was established to promote further the scientific discovery of the brain connectome in ASD. ABIDE II has aggregated over a thousand additional datasets with enhanced phenotypic characterization, especially in measures of core ASD and associated symptoms.

Moreover, two collections contain longitudinal data samples from 38 individuals at two time points (1-4 year intervals). Ten charter institutions and seven new members have contributed 1114 datasets from 521 individuals with ASD and 593 controls to ABIDE II. (age range: 5-64 years). In June 2016, these data were publicly available to the scientific community. According to HIPAA regulations and 1000 Functional Connectomes Project / INDI protocols, all datasets are anonymous and do not contain any protected health information. Fig. 2 is a sample image that we used in this research.

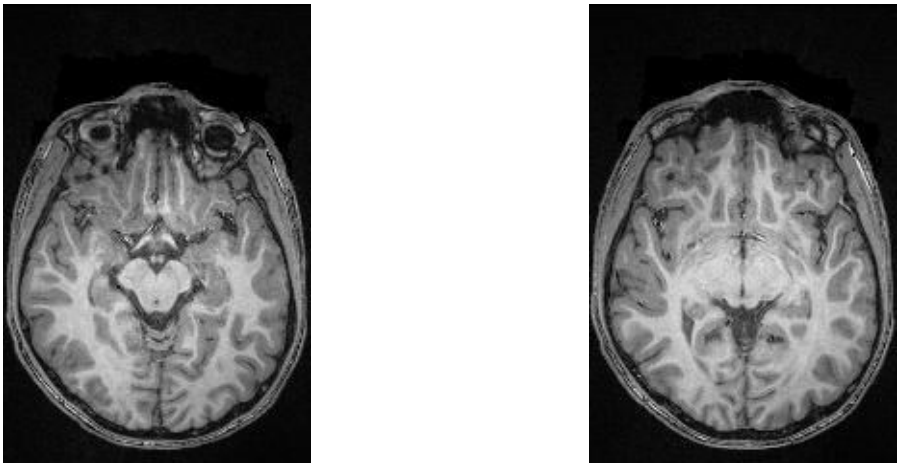

Fig. 2. Dataset Sample Image

The selection criteria for datasets used in studies utilizing the Autism Brain Imaging Data Exchange II (ABIDE II) vary depending on the research question and study design. However, some standard criteria are typically used to ensure the quality and comparability of the data across different sites. One crucial criterion is the inclusion of individuals with a clinical diagnosis of autism spectrum disorder (ASD) based on standardized diagnostic criteria such as the Diagnostic and Statistical Manual of Mental Disorders (DSM) or the International Classification of Diseases (ICD). This ensures that the individuals in the study represent the ASD population and that the study results are relevant to this group. Another criterion is the availability of high-quality brain imaging data, including both structural and functional imaging data. The data should be of sufficient quality for reliable analysis and interpretation of the results.

In addition, many studies using ABIDE II aim to control for potential confounding factors that could affect the imaging data, such as age, sex, and IQ. Therefore, the selection of datasets may also consider the participants' demographic characteristics, such as age range, gender balance, and IQ distribution. Overall, the criteria used to select datasets for studies using ABIDE II are designed to ensure that the data is of high quality and is representative of the ASD population while also controlling for potential confounding factors that could affect the results.

2.3. Magnetic Resonance Imaging

Magnetic Resonance Imaging (MRI) is a radiological scanning technique that uses magnets, radio waves, and computers to produce images of body structures. The MRI machine is shaped like a tube surrounded by a giant circular magnet [6]. In an MRI examination, the patient is placed on a bed and inserted into a magnetic hole. A strong magnetic field will be formed to align the hydrogen atoms' protons, which are then exposed to radio waves. The result is a signal that is detected by the receiver on the MRI machine. The computer will then process the recipient's information and generate an image. The images and resolution of MRI are detailed enough and can detect small changes in structures in the body. In some procedures, a contrast material is used to improve image accuracy [7].

2.4. Feature Extraction

Home Feature extraction is used to get a pattern from an image being tested. The feature extraction method has three methods, one of which is feature extraction. Feature extraction is an initial process to perform an image classification and interpretation process [8]. This extraction process is related to the characteristics of the appropriate image values. One of the methods used in this extraction is the First Order and Second Order Statistical Feature Extraction method [9]. First, Order Feature Extraction is a feature retrieval method based on the characteristics of the image histogram (The histogram shows the probability of occurrence of the grey level value of pixels in an image).

Meanwhile, Second Order Feature Extraction is performed using a co-occurrence matrix, an intermediate matrix image representing the neighboring relationship between pixels in the image at various orientation directions and spatial distances. The features in the first order are Mean, Skewness, Variance, Kurtosis, and Entropy. At the same time, the second order has several features, such as Angular Second Moment/Energy, Contrast, Correlation, Variance, Inverse Different Moment (IDM), and Entropy. When using machine learning, these features will be used in classification [10].

2.5. Machine Learning

During the rapid development of artificial intelligence (AI) technology today. Few know that AI has several branches, including Machine Learning (ML). Artificial Intelligence in its application is broadly divided into seven branches, namely Machine Learning, Natural Language Processing, Expert Systems, Vision, Speech, Planning, and Robotics [11]. The branch of artificial Intelligence is intended to narrow the scope when developing or learning AI because AI has a comprehensive scope. ML technology is a machine developed to learn by itself without direction from the user. Machine learning is developed based on other disciplines, such as statistics, mathematics and data mining, so that machines can learn by analyzing data without needing to be reprogrammed or ordered [12]. ML is divided into four (4) different lessons.

2.5.1. Supervised Learning

Supervised Learning is an algorithm in ML that uses labeled data, for example, input, where the output is known. There are several methods, including Logistic Regression [13], K-Nearest Neighbor [14], Support Vector Machine [15], Naïve Bayes [16], Decision Tree [17], and Random Forest [18]. Typically, this learning is used in an application that predicts future events based on stored data [19].

2.5.2. Unsupervised Learning

Unsupervised Learning is learning that is the opposite of supervised learning. This method has data to be processed but not a label, and the system needs to know the correct answer or output. The main objective of this study is to explore the data and find its structure. Several methods include *K*-Means Clustering, *K*-Means-Mode and Hierarchical Agglomerative Clustering [20].

2.5.3. Reinforcement Learning

Reinforcement Learning is a learning that is used for robotics, game creation, and navigation [21]. With this learning method, the algorithm can find the action or treatment that produces the best output from the results of repeated trials (trial and error). There are three main components to this learning, namely agents (decision makers), environment (whatever agents interact with), and action (what agents can do). The main objective of this study is for the agent to determine what action maximizes the result in the allotted time [22].

2.6. Support Vector Machine

The Support Vector Machine (SVM) algorithm uses nonlinear mapping to convert the original training data to higher dimensions. In this algorithm, each data item is plotted as a point in n-dimensional space (where n is the number of features), with the value of each feature being a specific coordinate value. Then, the classification is done by looking for a hyperplane that distinguishes the two classes very well so that the examples from the separate categories are divided by a clear gap that is as wide as possible [23]. The new examples are then mapped into the same space and predicted to fall into categories based on their side of the gap. A hyperplane H in *n*-dimensional space is the set of points $(x_1, x_2, \ldots, x_n)$ that satisfies the linear equation [24].

$$a_1x_1 + a_2x_2 + \cdots + a_nx_n \quad (1)$$

For SVM, there can be an infinite number of separate hyper fields (Table 1). The best one should be found, with minimum misclassification on previously unseen tuples [25].

Table 1. Pseudo Code Support Vector Machine

```
candidateSV = { closest pair from opposite classes }
while there are violating points, do
find a violator
candidateSV = U candidateSV
        S
violator
if any α_p < 0 due to the addition of c to S, then
        candidateSV = candidateSV\p
        repeat till all such points as pruned
end if
end while
```

2.7. Random Forest

Random Forest (RF) is an unprotected classification or regression tree collection caused by bootstrapping training data samples using random feature selection in the tree induction process. Predictions using RF are made by combining in the form of a majority vote for classification or the average regression value of the ensemble prediction. RF generally shows a substantial performance improvement compared to a single tree classifier such as the C4.5 Algorithm. RF can also fail when the training data set throws the tree out of balance. RF is built to minimize the overall error rate, which tends to focus more on the prediction accuracy level of the majority class, which often results in poor accuracy for the minority class [15][16]. According to the Table 2, the pseudo code is describe the process of random forest based on the mathematics formula (2). Entropy is a set teory, n is the number of partitions S and p_i: the proportion of S_i to S.

$$Entropy = \sum_{i=1}^{C} - p_i * log_2(p_i) \quad (2)$$

Table 2. Pseudo Code Random Forest

```
For each branch in split:
    Calculate the percent branch represents #Used for weighting
    For each class in the branch:
        Calculate the probability of class in the given branch.
        Multiply probability times log(Probability,base=2)
        Multiply that product by -1
        Sum the calculated probabilities.
        Weight each branch based on the baseline probability.
        Sum the weighted entropy for each split.
```

2.8. Convolutional Neural Network

Artificial Intelligence has witnessed tremendous growth in bridging the gap between human and machine capabilities [28]. Researchers and enthusiasts work on different aspects of the field to make extraordinary things happen. One of these many areas is the Computer Vision domain. The agenda of this field is to enable machines to see the world as humans do, understand it in the same way, and even use the knowledge for many tasks such as Image & Video recognition, Image Analysis & Classification, Media Recreation, System Recommendations, Natural Language Processing, etc. [29]. Advances in Computer Vision with Deep Learning have been built and refined over time, primarily through one particular algorithm — Convolutional Neural Network (CNN) [30]. CNN is a Deep Learning algorithm that can take input images, assign importance (learnable weights and biases) to various aspects/objects in the image, and distinguish one from another [31]. The preprocessing required in CNN is much lower compared to other classification algorithms. While in primitive methods, filters are engineered by hand, with sufficient training, CNN can learn these filters/characteristics [32]. The CNN architecture is analogous to the connectivity pattern of Neurons in the Human Brain and is inspired by the organization of the Visual Cortex. Individual neurons respond to stimuli only in a limited visual field region known as the Receptive Field. These sets of planes overlap to cover the entire visual area [33]. Adding a Fully Connected layer is a (usually) inexpensive way to study the nonlinear combination of higher-order features represented by the output of the convolution layer [34]. The Fully Connected Layer studies the possible nonlinear functions in that space.

Convolutional = $$z^l = h^{l-l} * W^l \quad (3)$$

Max Pooling = $$h_{xy}^1 = max_{i=0..s,j=0..s} h^{l-l}\,(x+i)(y+j) \quad (4)$$

Fully-Connected Layer = $$z_l = W_l * h_{l-1} \quad (5)$$

ReLu (Rectifier) = $$ReLu(z_i) = \max(0, z_i) \quad (6)$$

Softmax = $$Softmax(z_i) = e^{zi} / \sum_j e^{zj} \quad (7)$$

Where z^l is the pre-activation output of layer l, h^l is the activation of layer l, $*$ is a discrete convolutional operator, and W is the learnable parameters. We can see the implementation of the mathematics formula on Table 3 as the pseudo code of CNN.

Table 3. Pseudo Code Convolutional Neural Network

set the required parameters and complete the initialization work
while t < max_time and **L(t) > target_error**
    For all trainingSet:
        train_p (prediction of the label) is calculated according to train_x and forward calculation formula 3-7
    end for
    L(t) is re-calculated as $L(t) = \frac{1}{2}\sum_{n=1}^{N}(train\_p(n) - train\_y(n))^2$, N is total number of trainingSet.
    $\boldsymbol{\Delta w^l, \Delta b^l, \Delta w_{ij}^{-1}, \Delta b_j^{-1}}$
    $\boldsymbol{w^l(t), b^l(t), w_{ij}^{-1}(t), b_j^{-1}(t)}$
    $\boldsymbol{t}$++
end while

2.9. Confusion Matrix

Confusion Matrix is a method that is usually used to calculate the accuracy of the methods used in the classification process [35]. The value-sharing process is described in Table 4, Confusion Matrix.

Table 4. Confusion Matrix [36]

Prediction \ True Values	True	False
True	True Positive	False Positive
False	False Negative	True Negative

According to Table 4, True Positive is the number of positive data the system classifies correctly. True Negative is the number of negative data correctly classified by the system. False Negative is the number of negative data classified incorrectly by the system. False Positive is the number of positive data classified as wrong by the system. Based on the values in Table 4, it can produce values of accuracy, precision, recall, and F1-Measure [37]. The formulas for calculating the value can be explained as follows

Accuracy = $$\frac{TP + TN}{TP + TN + FP + FN} \quad (8)$$

Precision = $$\frac{TP}{FP + TP} \quad (9)$$

Recall = $$\frac{TP}{FN + TP} \quad (10)$$

$$\text{F1-Score} = 2 \times \frac{Recall \times Precision}{Recall + Precision} \quad (11)$$

Accuracy is a predictive value with the actual value obtained based on the results of all values in each prediction. Precision is an accuracy value between the information requested by the user and the answer given by the system. Recall is the value of the success rate of a system in finding back information. F1-Measure is one of the evaluation calculations in information retrieval that combines recall and precision. Recall and Precision values in a situation can have different weights. The measure that displays the reciprocity between Recall and Precision is the F-Measure which is the weight of the harmonic mean, recall and precision.

3. RESULTS AND DISCUSSION

3.1. Preprocessing

The dataset will be fully processed using Python. Before the data is classified, the data needs to be preprocessed to get a numeric form. Preprocessing using LabelEncoder and MinMaxScaler [38]. The LabelEncoder is a significant challenge an analyst faces in converting text/categorical data into numeric data and creating algorithms/models to make sense of it. Neural networks, the basis of deep learning, expect input values to be numeric. This straightforward approach involves converting each value in the column to a number. Consider a bridge data set with a column name of bridge type, which has the values below. Although there will be many more columns in the data set, we will focus on only one categorical column to understand label encoding. We can apply MinMaxScaler to a dataset directly to normalize input variables. The research will use the default configuration and scale values to the ranges 0 and 1. First, the MinMaxScaler instance is defined with the default hyperparameters. Once defined, we can call the fit_transform() function and pass it to our dataset to create a transformed version of the dataset [39].

3.2. Feature Extraction

The Hough transform can extract Global Features Extraction from images, Discrete Cosine Transform (DCT), Discrete Radon Transform (DRT), etc. [40]. However, in this paper, we use two methods, namely DRT, and it is proposed to extract projection-based images. Features (Horizontal and Vertical projection). Radon transform is the image intensity projection along a radial line oriented at a certain angle. The Radon transform of a function $f(x, y)$ states that $g(s)$ is defined as its line integral along the slanted line with an angle from the y-axis and at a distance s from:

$$g(s, \theta) = \int_{-\infty}^{\infty} f(s\ cos\theta - u\ sin\theta, s\ sin\theta + u\ cos\theta) du, \quad (12)$$

where

$$s = (x\ cos\theta + y\ sin\theta) \quad (13)$$

$$u = (-x\ sin\theta + y\ cos\theta) \quad (14)$$

The radon function calculates the image matrix projection along with predefined directions. The one-dimensional vertical projection feature vector can be extracted by assigning a value of 0 degrees for and 90 degrees for the horizontal projection feature vector.

3.3. Model Evaluation

Two different methods are used in the classification process: Random Forest and Support Vector Machine. Both methods are made using the Python programming language. Then, in evaluating the model, the confusion matrix (CM) calculation is used. In CM, the results that will be displayed are accurate. The results on RF, SVM, and CNN have different results. Look at Table 5 for the evaluation results of the two methods.

Table 5. Results of the Model

Model	Accuracy (%)
Random Forest	100
Convolutional Neural Network	89.58
Support Vector Machine	88

Any study has several potential sources of error or bias, including those that utilize neuroimaging data to identify autism spectrum disorder (ASD). Here are some potential sources of error or bias that researchers should be aware of:

1. Data Acquisition: Neuroimaging data can be affected by various factors, such as motion artifacts, scanner differences, and image quality. These factors can lead to data variability and affect the results' accuracy. Therefore, it is essential to carefully select and evaluate the imaging protocols used in the study to ensure high-quality data
2. Sample Size: The size of the dataset used in a study can significantly impact the generalizability and reliability of the findings. Small sample sizes can lead to overfitting and a lack of statistical power, while large sample sizes can be computationally intensive and expensive. Therefore, researchers should carefully consider the sample size needed to address the research question and ensure it is sufficient for the proposed analysis.
3. Feature Selection: The choice of feature selection methods can also affect the accuracy and interpretability of the results. Some feature selection methods may be biased towards certain features or not capture the most informative features for the problem being addressed. Therefore, researchers should carefully evaluate the performance of different feature selection methods and choose the most appropriate one for the addressed problem
4. Generalization: Generalizing the proposed methods to new datasets or populations is essential. Methods that perform well on a specific dataset may not generalize well to new datasets, especially if there are significant differences in the imaging protocols or populations. Therefore, researchers should carefully evaluate the generalizability of the proposed methods to ensure that they can be applied to new datasets or populations.

In future studies, researchers can improve the proposed methods by addressing some of these potential sources of error or bias. For example, they can use more significant and diverse datasets to ensure the generalizability of the methods, carefully evaluate the imaging protocols and feature selection methods used, and use cross-validation or other statistical tests to ensure the reliability of the results. Additionally, they can explore new feature extraction and selection methods, such as deep learning, that may be better suited for capturing the complex relationships between neuroimaging data and ASD.

4. CONCLUSIONS

This article summarises an analysis of the health system and the issues and problems faced by the world's health systems. This article makes the following contributions to supporting knowledge. The study of the developing brain remains limited in several respects, given the inherent methodological and experimental problems. Quality control procedures are essential to ensure the biological correctness of MRI observations. High-field MRI will also be an exciting and promising perspective for mapping delicate structures in development. This is a hot topic that several collaborative research and clinical groups are beginning to tackle. A crucial current perspective concerns a multi-modal approach that combines brain MRI measures with clinical and behavioural markers or electrophysiological indices such as those provided by electroencephalography. The application of AI in images is expected to accelerate the process of identifying an abnormality to obtain the expected results. Based on the results, the best model for the identification of ASD is Random Forest with 100%, then the convolutional neural network with 89.58 % and the last is the support vector machine with 88%.

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