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A System for Diagnosing Alzheimer's Disease from Brain MRI **Images Using Deep Learning Algorithm**

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ABSTRACT

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In addition to their vulnerability, the complexity of the operations, and the high expenses, disorders of the brain are one of the most challenging diseases to treat. However, because the outcome is unpredictable, the procedure itself does not need to be successful. One of the most prevalent brain diseases in adults, hypertension, can cause varying degrees of memory loss and forgetfulness. Depending on each patient's situation. For these reasons, it's crucial to define memory loss, determine the patient's level of decline, and determine his brain MRI scans are used to identify Alzheimer's disease. In this thesis, we discuss methods and approaches for diagnosing Alzheimer's disease using deep learning. The suggested approach is utilized to enhance patient care, lower expenses, and enable quick and accurate analysis in sizable investigations. Modern deep learning techniques have lately successfully demonstrated performance at the level of a human in various domains, including medical image processing. We propose a deep convolutional network for diagnosing Alzheimer's disease based on the analysis of brain MRI data. Our model outperforms other models for early detection of current techniques because it can distinguish between different stages of Alzheimer's disease.

Keywords: Alzheimer's condition, Magnetic Reasoning imaging, Deep learning, Brain disorder

I. INTRODUCTION

The neurological disorder. Older aged is more susceptible to Alzheimer's disease (AD), which affects around 46 million individuals globally. The first symptom of the illness is a forgetfulness of prior conversations or occurrences. As the condition worsens, it results in a substantial loss of memory and functional ability. The damage occurs years before any symptoms develop, but it first shows up in the part of the mind that regulates memory. As more parts of the brain begin to lose neurons, the brain finally becomes much smaller. Following are the stages of the illness: Mild, Severe, and Medium. Some of the more common

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early symptoms of Alzheimer's disease include memory loss, emotional changes, poor judgment, social withdrawal, and vision problems. This happens as a result of Alzheimer's disease harming the hippocampus, an area of the brain important for remembering. Every three seconds, a new dementia patient is found somewhere. In both the hippocampus and the entorhinal, two regions of the brain essential for recall, the first consequences frequently include the death of neurons and the connections that connect them. Therefore, it is necessary to do study and analysis in order to understand the alterations in the neural network. This environment uses MRI images as input. The deviations revealed by various measures (AD) are also examined using a machine learning technique to determine whether Mild Mental Impairment (MCI) evolves into Alzheimer's disease. One could then take the necessary prescriptions if changes in such elements arise and be conscious of them. The initial phase, often known to be the mild stage, is characterized by difficulties in using the proper word or name as well as missing or misplacing priceless items. The third and longest stage is the intermediate phase, which involves losing one's own past, being unclear of one's whereabouts, and remembering what day of a week it is. The late stage, often known as the severe stage, is characterized by changes in one's physical capacities and communication challenges. With more than 4 million people suffering from Parkinson's and various types of dementia, India has the third-highest caseload in the world, behind China and the United States. In India, there will likely be roughly 7.5 million dementia and Alzheimer's patients by the year's end of 2030. Whenever a disease can be detected in advance, the risk of death is decreased. Several methods are used for putting the illness's categorization into action.

Fig 1 specifies difference between healthy and Alzheimer brain structures.



Fig 1: Normal Brain Vs Alzheimer Brain II. RELATED WORK

Gang chen, et.al,...[1] Alzheimer's disease (AD), There is a mechanism in place for the seventh most frequent cause of death in the US. Research on the cause and pathology of AD, the development of animal models of AD, and the development of AD therapeutics have all made important strides. It is highly desirable to create verifiable biologically based markers that could be used to identify AD, track its progression, and determine the likelihood that AD will occur. Finding early AD markers has been done through reclined magnetic resonance (MR) scanning. Subjects in an investigation are said to be in a "resting state" if they don't perform any tasks or respond to any inputs while imaging. Practically specialized neural networks and their linkages are revealed by new information on the connections between physically diverse brain structures in resting-state functioning magnetic resonance (MR) imaging.

A novel viewpoint on network collapse in neurological disorders has been proposed. Earlier studies focused on specific hypothesis-driven evaluation, such as those on the hippocampus network, typical systems, and the tiny world network. Since asleep workable MR pictures may provide additional information about how structurally separate as well as operationally specialise brain networks interact with one another, it is believed that disease neurological connections underlying this very same interactive pathological processes during in the neurobiological neurodegenerative diseases could be recognised. This



study used LSN analysis to categorise individuals into cognitively normal (CN), amci, and people with AD.

Taheo jo, et.al,...[2] Deep learning techniques have been used however they need a lot of data to perform as well as needed. The hybrid approaches that combine conventional machine learning techniques for diagnostic classification with deep learning for feature extraction demonstrated increased performance in the currently limited neuro imaging data, and they can be a useful choice to handle the sparse data. An autoencoder (AE) was used to decode the original picture values, correlate them to the actual image, and then incorporate those as inputs in order to appropriately employ the small amount of brain imaging information. Although mixed methods have typically led to favourable results, they do not fully take use of deep learning, which automatically extracts characteristics from vast numbers of brain images. CNN, which specialises in identifying features from images, is the most widely used deep learning approach in vision research. The use of 3D CNN models and heterogeneous PET scans (FDG-PET and florbetapir PET) has improved the classification of AD/CN and the prognostication of the development of MCI to AD.

Silvia basaia, et.al,...[3] implemented A timely diagnosis of AD is essential for effective therapy. As an outcome, multiple investigators have devoted a lot of effort into developing a computer-assisted technique that can precisely and independently identify AD in its early stages. In this study, using a single cross-sectional brain structural MRI scan, we constructed and assessed a deep learning system that could forecast the specific diagnoses of AD and MCI that could proceed to AD. The results show that our CNN can accurately predict whether a patient will become AD after 36 months and is pretty good at discriminating AD or MCI patients from healthy controls. Importantly, our approach performed well across a broad range of imaging modalities and scanners and didn't necessitate any particular feature design in advance, proving that it can be used by inexperienced operators and may be portable to patient data that was not previously observed. There are numerous limitations that need to be considered. First, we are unable to entirely rule away the development of c-MCI in patients with s-MCI. In fact, a longer clinical evaluation could improve clinical diagnosis and, thus, the efficacy of our strategy. Secondly, the model needs to be assessed in conjunction with medical, cognitive, genetic, PET, and CSF indications in order to improve the estimation of the emergence of full-blown dementia in those suffering from MCI. Third, it's crucial to keep in mind that AD is a condition with a variety of clinical manifestations. Effective methods of diagnosis should be used to treat atypical AD presentations such as the logopenic type of primary progressive aphasia and posterior cortical atrophy. Not to mention, neurode gradation associated with AD begins years, if not decades, before symptoms appear. The techniques accuracy in identifying people in the early phases of the illness and whether it may be implemented as a tool for dementia screening in the general population will need to be investigated further.

Yubrajgupta, et.al,...[4] The approach for predicting Alzheimer's disease (AD) includes the moderate cognitive impairment (MCI) stage, which may or may not progress into Alzheimer's disease (AD). MCI is the form of memory that is most prevalent. It is critical to precisely identify people at this stage because AD may or may not develop during the MCI stage. At this phase, anticipating outcomes is essential. Many investigations had thus far focused their attention on a specific biomarker method for the diagnosis of AD or MCI. According to recent research, an amalgamation of one or maybe more distinct indications may provide more details for diagnosis, but it also increases the accuracy of classification by discriminating between different groups. Using an amalgamation of four different biomarkers-CSF protein levels, systemic magnetic resonance imaging (smri), fluorodeoxyglucose positron emission (FDG-PET), and Apolipoprotein-E (APOE) genotype-we propose an innovative machine



learning-based structure in this paper to differentiate between participants with AD or MCI. A multiclass support vector machine (SVM) classifier was used in this instance, and it was supported by a novel gridsearch technique. Before passing the generated data to the classifier, we dimension-reduced high-dimensional features into lower-dimensional features using the truncate single value decomposition (Truncated SVD) method.

Nick bryan, et.al,...[5] implemented the analysis system It is impossible to overstate the significance of Alzheimer's disease (AD) for both individuals and society. The most common type of dementia in the United States, which affects 14% of those over 70 and is becoming more prevalent as the general population ages, is one among the more expensive diseases. (1). When considering the standard medical approach to disease care, the requirement for an effective diagnostic test would appear to be of the utmost importance. Contrary to popular belief, a large number of scientific research, and unconfirmed rumours, there is currently no accurate test for this sickness. A publication by Collij et al. on an imaging technique that once again focuses on cerebrovascular flow of blood (CBF) for the diagnosis of AD comes after this assertion (2). But is it true that there are no trustworthy tests available for AD? Will this new test meet the requirement if not? For AD, there are many reliable diagnostic tests available. The diagnostic efficacy of the normal cutoff criterion can be increased with the right When further family history, regular blood tests, and brain magnetic resonance imaging (MR) are taken into account, the clinical diagnosis increases to 90%. Cognitive test results for the Mini-Mental State Exam are around 85%. This demonstrates that there is no need for additional diagnostic tests (dementia) for an AD patient who, in accordance with the diagnostic criteria, exhibits clinically substantial cognitive impairment. At this stage of the disease, treatment rather than diagnosis is the problem. Despite the enormous efforts of the psychiatric research

community, there is no cure for mental disorders, though there are several treatments that have received approval from the US Food and Drug Administration. help momentarily decrease sensations that are mild through medium.

Sanjay m, et.al,...[6] the central nervous system of the human body, the examined brain areas, were put into practice. The brain is an advanced organ, with between 50 and 100 billion neurons. Any abnormal cell formation within or around the brain is referred to as a brain tumour. There are two basic types of brain tumours: benign and malignant. Non-cancerous or benign tumours are those that aren't malignant. A benign tumour typically fails to spread and remains in one place on the body. The majority of benign tumours are treated successfully. Compared to benign tumours, tumours that are malignant are more harmful. Malignant tumours are tumours. They typically defy therapy and can spread to other body regions. Malignant growths fall into two categories: primary tumours or secondary tumours. The malignant tumour grows rapidly, infiltrating further brain tissues, and worsening until it is fatal. The unique anatomy of the brain makes identifying brain tumours a very challenging task. It is challenging for researchers to identify tumours because of the diverse characteristics of their boundaries and outward appearance. Understanding brain tumours, their different kinds, and various techniques for recognising and dividing them form the main goals of this study. This review article's goal is to describe a variety of algorithms for extracting cancerous segments from brain MRI data.

Sergio pereira, et.al,...[7] examined brain Segmentation of the brain tumor is crucial for therapy planning and post-treatment assessment. But it requires a long time, and there is inter- and intra-rater variability. As a result, efficient and reliable processes are favoured. However, segmenting brain tumours is a challenging task because of their inconsistent shape, appearance, and placement. In recent years, modern conclusions were established utilising CNN-based techniques. It is difficult for feature construction to



detect complex patterns, such as the characteristics of brain tumours, but CNN scan can learn them with just the right amount of data. In this paper, we investigate the recombination and reevaluation of fms. Instead of only lowering the fms number during recombination, we mix the information using line area expansions followed by compression. We also look into how recalibration is implemented in FCN. All of the contextual information from the FM is collected via global average pooling in the sub block. Instead, we argue that dilated convolution is better suited for the recalculation block in FCN. As a result, this study makes three key points. First, we advise combining fms into lines for reduction and elongation. In the second section, we examine FM adjustment with regard to FCN. We recognise that the initial SE block is not ideal for FCN and offer a superior alternative. Third, we assess our segmentation of brain cancer proposal using data that has been easily accessible to the general population.

Pereira, et., al,... [8] Gliomas are most prevalent and dangerous brain tumors, with a relatively short life span in their maximum grade. This method was developed to predict the many types of brain illnesses, such as brain tumours. Therefore, preparing for treatment is crucial to enhancing the quality of life for cancer patients. The amount of data produced by magnetic resonance imaging (MRI), despite being a widely used imaging technology for detecting malignant tumours, limits the application of reliable quantitative assessments in clinical practise. Due to the high anatomical and spatial heterogeneity among brain tumours. automated segmentation is difficult, necessitating the development of trustworthy techniques. In this paper, we investigate micro 3 kernels to create a convolutional neural network (CNN)-based auto-segmentation method. Utilising smaller kernels allows for the construction of a deeper architecture while also assisting in the prevention of over-fitting because there are fewer weights in the network. Brightness normalisation was examined as a step that happened before dividing brain tumours in

MRI scans. Despite being atypical among CNN-based classification techniques, this methodology was highly successful when combined with the addition of data.

Ali iúõna, et.al,...[9] developed this strategy to evaluate brain cancer, which is thought to be the result of the body's unregulated, abnormal cell division. A lump referred to as a brain tumour develops when this abnormal cell division and development occur inside the brain tissue. Although their rarity, tumours are among the most deadly forms of cancer. Brain tumours can be classified as primary or metastatic based on where they first appeared. While the cells that make up the original tumour come from the tissue of the brain, in migratory tumours the malignant cells might initially appear in any part of the body before spreading to the brain. Brain tumours of the glioma type are derived from glial cells. They constitute the primary type of brain tumours, and they are the subject of almost all of current study into tumour division. High-grade (grade IV) gliomas range in intensity from decreased gliomas such astrocytomas or oligodendrogliomas to high-grade (grade IV) gliomas, with glioblastoma multiform (GBM) being the most aggressive and often occurring primary malignant brain tumour. Gliomas are treated with surgery, chemotherapy, and radiotherapy-often in conjunction. Because deep learning techniques generate cutting-edge results and are more successful than earlier strategies at resolving this problem, they have recently become more popular for automatic segmentation. Deep learning algorithms can also be used to process the enormous amounts of magnetic resonance image data effectively and evaluate them impartially. There are currently many review articles that focus on traditional methods for segmenting MRIbased brain tumour pictures.

El-dahshan, et.al,...[10] analyzed When tissue delineation is required, magnetic resonance (MRI) is frequently the preferred medical imaging technique. This is especially true for any attempts to classify the brain's tissues. The suggested hybrid technique has



three stages: classification, dimension reduction, and picture augmentation. We were successful in retrieving the early stage (DWT) MRI image characteristics using discrete wavelet-based processing. In the second stage, the method known as principal component analysis (PCA) was used to retrieve the most crucial components of magnetic resonance pictures. The classification process has resulted in the creation of classifiers. Both the first classifier and the second classifier use artificial neural networks (FP-ANN) that are based on feedback backward propagation. Classifiers were initially used to categorise people in MRI images as defective or normal. In the collection's grayscale images, the foreground is always in the centre. The skull is photographed from several angles, allowing us to view the tumours' size and placement from a variety of angles. The size differences amongst the tumours make tumour diagnosis difficult. In actual practise, the knowledgeable medical professional is aware of the MRI image's direction. Convolutional models' learning process is similar to that of humans, so we decided to build up the sophisticated neural networks in a humanlike setting. We found that using a single network to find tumours in all photographs does not produce accurate findings.

III.BACKGROUND OF THE WORK

Alzheimer's disease (AD) depends on factors associated with the diabetes sickness. It is vital to select those factors and features with an efficient manner in order to improve the precision of forecasts. Effective feature selection and categorization will increase the clinical reliability of the diagnosis as well as decrease the cost of identifying the disease. By choosing a smaller sample of relevant variables from Diabetic data, the feature selection (FS) method improves the accuracy of classification while utilising fewer features. To improve system efficiency, a significant feature of these features was selected using the technique of feature engineering. Segmenting images is the most difficult and important step in the image processing process. A picture is segmented into its distinct components or regions, and visual elements with similar characteristics are grouped together. Segment serves a number of purposes in the processing of digital pictures, include compression as well, automatic handwriting analysis, remote sensing, arthritis diagnosis from joint images, and medical image processing. The clustering algorithms may divide any image into several groups according to similarity criteria like texture or colour. The present system uses the technique of K-means clustering, which divides the image into K groups based on how similar the pixels in each cluster are.

The basic flow diagram for disease prediction as specifies in fig 2.



Fig 2: Brain Abnormality detection

Several methods for machine learning, such as the Support Vector Machine and the KNN classification method, may be used to perform the categorization.



IV. NEURAL NETWORK BASED ALZHEIMER'S DISEASE PREDICTION

The chance of death of Alzheimer's disease is decreased with early detection. To either directly or through indirect means examine the pharmacology, structure, or function of the brain, scanning or brain scans is used. The brain is scanned using magnetic resonance imaging (MRI) and positron evoked potentials (PEEP). In order to measure the electrical activity in the brain, an EEG method is applied to the scalp on the head. An EEG measures the electric activity in your mind using a few electrodes that are affixed to the head. An electrical flow can enter or escape through a connection. These devices transmit data from your brain to an apparatus that gathers and stores the data. Brain tumour segmentation is the development of a simple method for determining the size and shape of a tumour in a brain MRI image. An MRI or CT scan can be used to diagnose a condition and typically displays the structure of the brain architecture. Using the popular clustering method known as K-means, the data is separated into K distinct groups. This approach relies largely on the early identification of objects that appropriately reflect the clusters because clusters are set in before. A fuzzy C-means clustering strategy was also developed. This method, however, is unable to handle the complex structure of the brain's tissues.

The model was created using CNN, a prominent deeplearning technique. Deep learning refers to artificial neural networks that take raw input images and extract a hierarchy of information from them. In excess of five layers are frequently present in these networks of neurons. Deep learning, which extracts complex, highlevel properties from the images and trains a sizable amount of data, increases accuracy. Due to the considerably enhanced GPU processing power, deep learning approaches allow us to train a huge amount of imaging data and improve accuracy notwithstanding variances in photos.

CNN, a well-known Deep learning technique, was used to develop the system. The phrase "deep learning" refers to neural networks that construct a pyramid of information from unprocessed input images. More than five layers are frequently present in these networks of neurons. Deep learning, which extracts complex, superior qualities from the photos subsequently trains with a significant quantity of data, produces greater accuracy. Due to the significantly enhanced GPU processing capacity, deep learning approaches allow us to work with a large amount of imaging data and improve accuracy despite variances in images.

Only a few of the layers that make up CNN and have different purposes pooling, convolution, are stimulation, and completely linked layers. The convolutional layer produces map features by convolutionally resampling the input images over the kernel. The output from the previous convolution layer has been extracted at a rate using the highest number or mean of each defined neighbourhood inside the pooling layer as the value to be conveyed to the following layer. The rectified unit (ReLU) and the leaky ReLU, a variation of ReLU, are neither of the most widely used activation functions. The ReLU transforms data nonlinearly by clipping bad input values to zero and sends only the good input data as outputs.



Fig 3: Proposed Framework



DATASETS ACQUISITION

An MRI can be used to assess the condition of the brain and provide predictions about abnormalities and brain activity. In this study, an Automatic Diagnostic Tool (ADT) was developed with the goal of examining and categorising MRI signal patterns from the normal and Alzheimer classes. Data from MRI images can be entered using this module. A collection of MRI scans from young people with incurable Alzheimer's disorder make up this Kaggle dataset. Subjects were monitored for up to several days after stopping anti-Alzheimer medication in order to summarise the information they submitted and evaluate whether they qualified for a surgical operation.

PREPROCESSING

Data preliminary processing, a crucial step in the data mining process, is the altering or wiping of data prior to usage in order to ensure or improve performance. The adage "garbage in, garbage out" is particularly relevant to initiatives using data and machine learning. The lack of proper control in data collection methods leads to anomalous data, impossible information combinations, data that's missing, etc. Inadequately checking for these issues could lead to erroneous optimistic data analysis outcomes. Therefore, an assessment of the accuracy or arrangement of the information must come before each analysis. Particularly in the field of computational biology, the single most crucial phase of a machine learning project is often preparing the information. A rolling time frame is used to first divide serial EEG recordings in earlier stages without crossing over. A wavelet transformation is then used to the EEG data to create a group of signals.

FEATURES EXTRACTION

In this module, we can extract the temporal or frequency domain features from processed data. It includes "mean," "variety," "kurtosis," "skewness," and other characteristics that will follow identification. The average value of an N-sample signal from an EEG is what is meant by the word "mean."

$$\mu = \frac{1}{N} \sum_{i=1}^{N} Y_i$$

Standard deviation: A standard deviation is the variation in data from a signal's mean value.

$$\sigma = \sqrt{\frac{1}{N-1}} \sum_{i=1}^{N} (Y_i - \mu)^2$$

Kurtosis: Time series data have a peaked quality due to a statistical phenomena. Kurtosis is a result of

$$k = \frac{1}{N} \sum_{i=1}^{N} (\frac{y_{i-\mu}}{\sigma})^4$$

Skewness: It measures the degree of symmetry of the spatial distribution of a signal that is produced as

skewness =
$$\frac{1}{N} \sum_{i=1}^{N} (\frac{y_{i-\mu}}{\sigma})^3$$

CLASSIFICATION

A number of remark operations must be performed on the outputs of a training Deep CNN in order to obtain the offer upgraded again for test MRI scan image in the manner of diagnosing Alzheimer's disease using MRI recordings. Input, a layer, and numerous buried layers make up a CNN. Convolution, pooling, and fully connected layers are typically seen in a CNN's layers that are concealed. The outcome of a convolutional layer's operation on the input is passed on to the next layer. The process of convolution simulates a single neuron's reaction to visual stimuli. In convolution networks, local or global layers for pooling can be used to integrate the output of a neural cluster at one level with a nerve cell from a higher level. The mean value from each brain cell in the preceding layers is used in mean pooling. Every neuron in one layer can communicate with every other layer's neuron through fully connected layers. Conceptually, the CNN and the traditional multi-layer feed-forward neural network



are identical. In comparison to conventional classifiers, CNNs are without a doubt superior for the analysis of high-dimensional data. Convolutional layers of CNNs use a parameter-sharing technique to regulate and lower the total number of variables. The introduction of a pooling layer gradually lowers the network's variable and computation count while also improving fitting control, as different studies have shown for the representations.

Constructing the CNN Model

function INITCNNMODEL (θ , [n-5]) layerType = [convolution, max-pooling, fullyconnected, fully-connected]; layerActivation = [tanh(), max(), tanh(), softmax()] model = new Model(); for i=1 to 4 do layer = new Layer(); layer.type = layerType[i]; layer.inputSize = *ni* layer.neurons = new Neuron [*ni*+1]; layer.params = θi ; model.addLayer(layer); end for return model: end function

Training the CNN Model

Initialize learning rate, maximum iterations, minimum errors, and training batches. training BATCHES, batch size SIZE, etc.;

Compute *n*2, *n*3, *n*4, *k*1, *k*2, according to *n*1 and *n*5; Generate random weights θ of the CNN; cnnModel = InitCNNModel(θ , [*n*1–5]); iter = 0; err = +inf; while err >ERRmin and iter<ITERmax do err = 0; for bach = 1 to BATCHEStraining do [$\nabla \theta J(\theta)$, $J(\theta)$] = cnnModel.train (TrainingDatas, TrainingLabels), Update θ err = err + mean($J(\theta)$); end for err = err/BATCHEStraining; iter++; end while

Save parameters θ of the CNN

As a result, our suggested study uses extraction of features to overcome the separation of outliers in MRI data categorization. We can forecast both the normal and symptoms of Alzheimer's according to classification.

I. EXPERIMENTAL RESULTS

Numerous performance measures, such as accuracy, sensitivity, specificity, error rate, and precision, can be established in order to analyse the system's performance.

Number of genuine positives - the best possible positive forecast

False positives (FP) are the number of inaccurately predicted positive outcomes.

Amount of genuine negatives - perfect forecast of a negative outcome.

Negative result (FN): number of accurate negative predictions minus the number of actual negatives

Error rate

Error rate (ERR) is computed as the fraction of total number of imperfect predictions to the total number of test data. The finest possible error rate is 0.0, whereas the very worst is 1.0. Minimization of this error rate will be the prime objective for any classifier.

$$ERR = \frac{FP + FN}{TP + TN + FN + FP}$$

ALGORITHM	ERROR
	RATE
RANDOM FOREST	0.75
SUPPORT VECTOR MACHINE	0.5
CONVOLUTIONAL NEURAL	0.4
NETWORK	







According to the aforementioned graph, the proposed CNN method offers a lower failure rate than the current technique.

Accuracy

The percentage of overall flawless forecasts to the complete test data is known as accuracy (ACC). Additionally, it can be written as 1 - ERR. The maximum accuracy is 1.0, and the minimum accuracy is 0.0.

$$ACC = \frac{TP + TN}{TP + TN + FN + FP} \ge 100$$

ALGORITHM	ACCURACY
RANDOM FOREST	50%
SUPPORT VECTOR MACHINE	65%
CONVOLUTIONAL NEURAL	80%
NETWORK	





According to the graph above, the proposed CNN algorithm has a higher accuracy rate than the current approach.

V. CONCLUSION

Because of their delicacy, the difficulty of executing operations, and the high expenses, disorders affecting the brain are among the most challenging diseases to treat. Contrarily, since the surgery's outcomes are not certain to be successful, the operation itself need not be successful. Hypertension, which affects adults and is one of the most prevalent brain disorders, causes varied degrees of memory loss and knowledge forgetfulness. Depending on each patient's situation. For these reasons, it's critical to identify memory loss, assess the patient's state of deterioration, and confirm the diagnosis of Alzheimer's disease by brain MRI scans. In this study, we can apply deep learning classification algorithms to classify Alzheimer's disease. The suggested approach is utilized to enhance patient care, lower expenses, and enable quick and accurate analysis



in sizable investigations. The method, which was highly helpful for doctors in diagnosing the Hypertension, was implemented using the model, which was created using the Python programming language.

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