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RESEARCH ARTICLE

Improving the detection of Alzheimer's Disease by Class Activation Mapping and Deep Neural Network Analysis of Cerebrospinal Fluid Biomarkers

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Abstract: Alzheimer disease (AD) is a neurodegenerative disorder in which beta-amyloid plaques and tau tangles accumulate in the brain. This complicates communication among brain cells, leading to shrinkage of the brain and worsening cognitive decline. It is a significant global health concern that must be investigated immediately. Molecular indicators of the development of Alzheimer disease have been detected in various physiological tissues. The improvement of epigenetic markers is a new angle in the pathophysiology of Alzheimer disease. However, their role in the initial diagnosis and prognosis of Alzheimer disease remains unclear. This study integrates Class Activation Mapping (CAM), Deep Neural Networks (DNNs), and Cerebrospinal Fluid (CSF) analysis to develop a robust diagnosing and categorizing Alzheimer disease system. CAM has also been shown to improve interpretability by showing how different biomarkers, such as amyloid-beta, total tau, and phosphorylated tau, influence model outputs. The suggested CAM-DNN framework begins with preprocessing of CSF biomarkers and feature extraction. Next, it trains a DNN to classify individuals into three categories: cognitively normal, mild cognitive impairment (MCI), or Alzheimer disease (AD). The trained network then uses CAM to identify and learn relevant features that are associated with each classification. This assisted us in determining how the biomarkers relate to the disease. When comparing the method with publicly available datasets, it has been proven accurate, precise, and good at recalling things during classification. Biologically significant patterns are also observed in CAM visualizations and demonstrate the importance of CSF biomarkers in AD progression. This study shows that DNNs can be combined with CAM to provide accurate, understandable diagnoses of Alzheimer's disease, although also indicates the importance of CSF biomarkers in explaining the major etiological contributors to the condition. The results provide groundwork to develop therapeutically useful, interpretable, and non-invasive diagnostic tools concerning Alzheimer disease.

Keywords: Alzheimer's Disease, Cerebrospinal Fluid (CSF) Analysis, Deep Neural Networks (DNN), Neurodegenerative Disorders Tau Proteins.

INTRODUCTION

Dementia is a type of cognitive impairment that makes it hard for people to think, remember things, and reason. It also affects their behavior, making it hard for them to do routine tasks and live on their own. The condition occurs in multiple stages, starting with minimal functional impairment during an initial phase through to a late stage when the person becomes fully dependent on others to carry out everyday functions. It may take ten years after Alzheimer disease (AD) symptoms appear before neurological problems become apparent. [1]. In this initial phase, the brain experiences numerous harmful developments, among them being abnormal protein folding that causes the development of tau tangles and amyloid plaques. Healthy neurons deteriorate, malfunction slowly, and lose connectivity with other neurons. A broad spectrum of other intricate alterations in the brain is considered to contribute to the pathogenesis of AD [2].

AD is the most common form of dementia. It is a progressive disease that starts with mild memory impairment and ends with the loss of the ability to take action in response to stimuli or participate in a conversation. Nevertheless, the timely and precise diagnosis container has a great influence on patient outcome and postpone memory loss [3]. Enhanced attention to risk minimization has resulted in new findings and outcomes. Evidence suggests that people with healthy lifestyles are less likely to improve dementia. Besides, behaviors that have proven effective in the prevention of diabetes and cancer potentially alleviate cognitive decline [4]. Machine learning (ML) is a subdivision of AI that enables AI to learn by processing data and algorithms in a way that resembles how people learn. The increased application of ML in medical care has facilitated the identification and treatment of illnesses in greater numbers [5]. Applying machine learning to examine patient data in electronic health records can reveal significant details and trends. ML methods have significantly contributed to addressing hard, highly nonlinear classification and prediction tasks [68]. Additional studies are urgently needed to understand the causes of Alzheimer Disease to improve early diagnosis and treatment of the disease. The focus of our analysis lies in the application of machine learning to quantify the efficacy of various scheme to enhance the early detection of Alzheimer disease. The increasing incidence of Alzheimer's

Disease necessitates immediate enhancement of early detection methodology [9].

This paper examines the application of modern machine learning techniques to enhance the detection of Alzheimer's Disease, focusing on Class Activation Mapping and Deep Neural Network Analysis of Cerebrospinal Fluid Biomarkers. The research aims to classify subtle trends associated with Alzheimer pathology through the application of deep artificial neural networks to cerebrospinal fluid biomarkers. Class Activation Mapping (CAM) is an approach that visualizes and highlights the key component of biomarkers that aid unhealthiness identification. The method can help us examine better and gain further insight into the relationship between CSF indicators and the progression of Alzheimer disease. It means that we can know when people are wrong earlier and more confidently. The project was inspired by increasing need to rapidly and precisely identify the presence of Alzheimer disease, a progressive neurological disorder afflicting millions of people globally. Contemporary diagnostic methods can depend on subjective evaluation and imaging systems, potentially delaying the process of identifying issues. The current study aims to enhance the diagnosis of Alzheimer disease through the use of Class Activation Mapping (CAM) alongside deep neural network (DNN) analysis of cerebrospinal fluid (CSF) biomarkers.

By integrating these high-quality computational algorithms, we desire to discover small patterns in biomarker data. Through these trends, a more objective, sensitive, and accurate detection tool might emerge that can enable patients to get care earlier and with improved outcomes.

The main contributions of this study:

- To improve Class Activation Mapping (CAM), Deep Neural Networks (DNNs), and Cerebrospinal Fluid (CSF) analysis in order to create a strong system for diagnosing and classifying Alzheimer's disease.
- The suggested method, CAM-DNN, works by pre-processing CSF biomarkers and extracting features, and then training a DNN to sort people into groups based on whether they are cognitively normal, have MCI, or have AD.
- Lastly, the CAM visualizations show physiologically important patterns, which show how important CSF biomarkers are in the development of AD.

The Outlines of our research work is section 2 speaks about background of study, section 3 proposed system, section 4 Results and discussion and 5 conclusion
Table 1 talks about the main points of our investigation.

1. Background for Literature survey

AD is a serious neurological disorder that has a big influence on memory, thinking, and behavior. Because of this, it is important to find it early so that therapy can work. This survey seeks to investigate progress, obstacles, and novel approaches in the detection of Alzheimer's disease. We want to know how far we've come and what we can do to improve early diagnosis by looking at current diagnostic methods, new technology, and biomarkers. In [10] conducted a study with 125 subjects, categorized into five groups of 25: AD, MCI, EMCI, LMCI, and NC. Utilizing two pretrained methods, ResNet-18 and DenseNet-121, at the corresponding time, the investigator took features from MRI images. By combining these qualities, they were able to better sort AD.

To correct the differences among the two networks' final feature maps, they suggested adopting a weight randomization method, like Xavier or Kaiming, to make the fully connected layer more even. The weighting techniques goal is to gather the most meaningful information from both models.

In [11] introduced a CNN architecture for the effective diagnosis of brain malignancies utilizing MR images, aiming to illustrate the advantages of MRI in tumor diagnosis. They had 500 pictures of persons without tumors, 926 pictures of glioma tumors, 937 pictures of meningioma tumors, and 900 pictures of pituitary tumors. The investigation examined the CNN approach with various widely used approaches, including as ResNet-50, VGG16 and Inception V3. They used 80% of the information to develop the algorithm and separated the remaining into testing and validation sets to test it. In [12], a deep learning model called s2MRI-ADNet was introduced. It classifies Alzheimer disease (AD) by a combination of Euclidean and graph structures using structural MRI images. This article highlights the significance and explication of learning structural connectivity patterns related to Alzheimer disease. The BrainBagNet had a position-based gate (PG) established in [13]. This gate uses 3D coordinates to combine location data from brain images.

This technique utilized both positional and MR scan data to integrate patch-level class evidence for image-level predictions. To confirm its effectiveness, they conducted comprehensive research on two publicly available datasets: the Alzheimer's Disease Neuroimaging Initiative (ADNI) dataset and the Australian Imaging, Biomarkers and Lifestyle (AIBL) dataset.A rapid, economical, and portable diagnostic method employing brain magnetic resonance imaging was established in [14]. They used the very expensive DenseNet121 model, which had an 87% accuracy rate in diagnosing the disease. On the other hand, the authors created and combined two models, LeNet and AlexNet, after making a few modifications. Their method used three parallel filters to extract features. The article demonstrated that their method achieved a 93% accuracy rate in detecting the condition.

In [15] presented a multi-class organization strategy for AD that attained an accuracy of 96.66% utilizing a Multilayer Perceptron classifier with 3D-CNN features. The authors introduced a patch-based methodology, a multilayer neural network for organization, and a 3D-CNN for feature extraction. The heat map showed atrophic brain areas linked to AD, NC, and MCI, which helped doctors tell the difference between dementia caused by AD and cognitive decline that comes with age. However, the researchers agreed that the application of multimodal scans like fMRI, PET, and cerebrospinal fluid analysis could further improve the detection abilities of the technique. In [16] utilized T1-weighted MRI images to investigate the ability of a CNN process to distinguish between patients with Alzheimer disease (AD) and those with temporal lobe epilepsy (TLE) and healthy controls. The authors utilized a feature visualization method to detect the areas used by the CNN to distinguish between types of illnesses. In [17] hypothesized that white matter abnormalities within the brain were an early sign of moderate cognitive impairment (MCI). The current study attained 96% source localization accuracy in differentiating between Mild Cognitive Impairment (MCI) and Normal Controls (NC) through EEG-based source localization method. The study, however, was constrained by its limited dataset and the method of source location that used only 29 electrodes.

1.1 Research Gap

Although the findings are a milestone in Alzheimer disease research, early and precise diagnosis is a pressing issue. Existing diagnostic procedures, such as neuroimaging and cerebrospinal fluid analysis, are sometimes not sensitive enough, costly, and intrusive in the initial phases of the disease. Reliable biomarkers that can be used to establish whether an individual has AD before it manifests are scarce. This highlights the urgency of cost-effective, non-invasive, and highly sensitive diagnostic instruments that can detect Alzheimer's Disease during its initial phases. Also, modern studies are largely based on the discovery of biomarkers in specific populations, which creates a deficit of knowledge on the variability of these biomarkers in other populations and contexts.

1.2 Problem identification of existing system

The majority of contemporary diagnostic techniques are based on the late manifestation of the disease symptoms, which can complicate treatment and worsen the situation. It is important to find things early so that they can be dealt with and taken care of. Two frequent methods are cognitive testing and imaging, which can sometimes provide significant false negatives and false positives. This may result in misdiagnosis or unnecessary treatments. Most methods are centered around a single type of modality, such as PET or MRI scans, and do not incorporate the other helpful information, such as genetic factors, biomarkers, and cognitive tests.

2. Proposed System

In this section, we discuss Class Activation Mapping (CAM), Deep Neural Networks (DNNs), and Cerebrospinal Fluid (CSF) analysis to provide a robust framework to locate and categorize Alzheimer's disease. The predictions of the model are simplified by making the predictions of the model easier to comprehend by displaying how various biomarkers, including amyloid-beta, total tau, and phosphorylated tau, influence these predictions. The methodology, CAM-DNN, entails preprocessing CSF biomarkers and derivation of features, followed by the training of a DNN to categorize individuals as cognitively normal, MCI, or AD. We use CAM on the trained network to find and study essential features that are linked to each category. This gives us information about how biomarkers are related to diseases. The block diagram of CAM-DNN is shown in Figure 1.

RESULTS AND OBSERVATIONS:

diagram of CAM-DNN is shown in Figure 1.

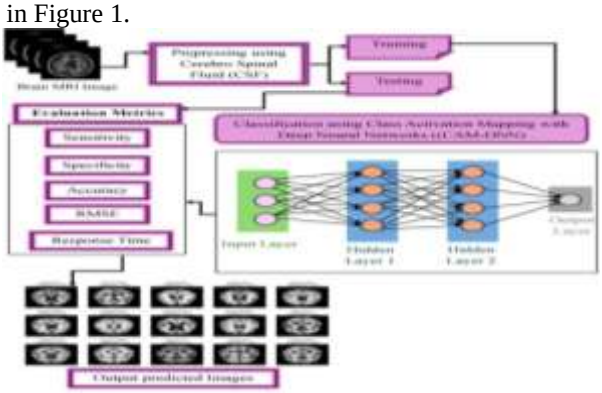

Figure 1: Block diagram of the CAM-DNN model

2.1 Dataset

There are a number of ways to find out if someone has Alzheimer's disease, such as brain MRIs, PET scans, neurological exams, and others. We employ two separate datasets of brain MRI images in this study: ADNI and OASIS. Also, these datasets have other subsets, like merged sets, enhanced sets, and others.

2.1.1 ADNI Dataset

Alzheimer's data is provided by ADNI in 3D volumetric Nifti or DICOM format. The dataset is meant to make it easier to build algorithms for image processing because working with 3D data directly can be hard. The ADNI baseline dataset, which includes Nifti pictures, is where the 2D axial images in the collection were taken from. The dataset is divided into three classes: CN (Cognitively Normal, comprising 1,440 images), MCI (Mild Cognitive Impairment, comprising 2,590 images), and AD (Alzheimer's Disease, comprising 1,124 images). The entire dataset contains 5,154 images [18]. Figure 2 shows the ADNI dataset images, while Figure 3 and Table 1 illustrate the dataset distribution by class for the ADNI dataset.

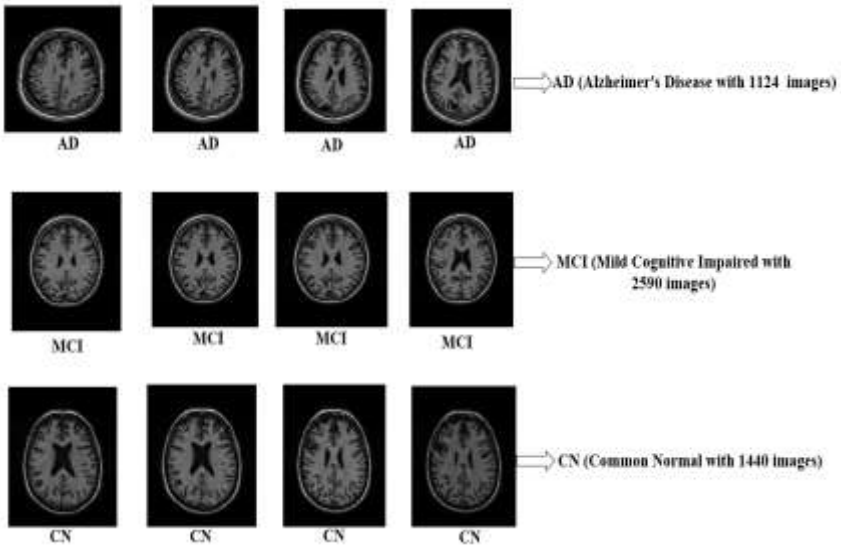

Figure 2: ADNI dataset images in kaggle

Table 1: Dataset Distribution by Class for ADNI Dataset

Class	Number of Images
MCI	2590
CN	1440
AD	1124

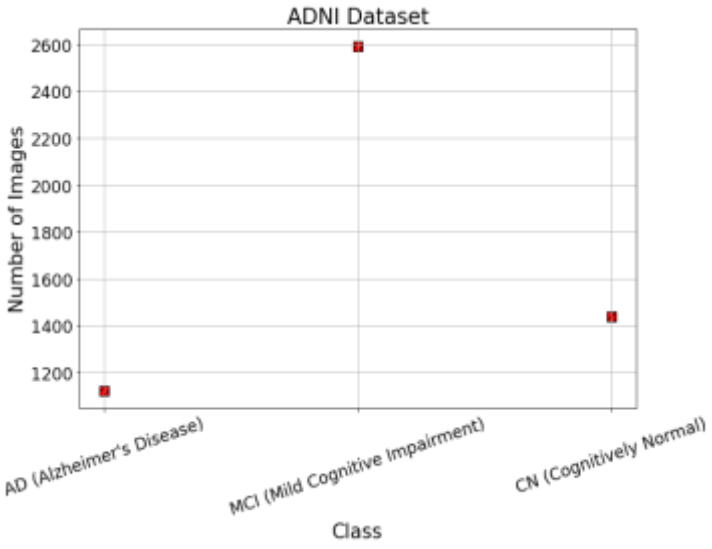

Figure 3: Dataset Distribution by Class for ADNI Dataset

2.1.2 OASIS Dataset

The zip file contains the OASIS MRI dataset, which contains of 9,488 brain MRI images divided into four classes: 488 images for moderate dementia (MOD), 3,000 images for non-demented (ND), 3,000 images for very mild dementia (VMD), and 3,000 images for mild dementia (MLD) [19]. The main purpose of this dataset is to give people a useful tool for finding and evaluating early signs of AD. The photos from the OASIS dataset are shown in Figure 4. The OASIS dataset's class distribution is shown in Table 2 and Figure 5.

Table 2: Dataset Distribution by Class for OASIS Dataset

Class	Number of Images
VMD	3000
MLD	3000
MOD	488
ND	3000

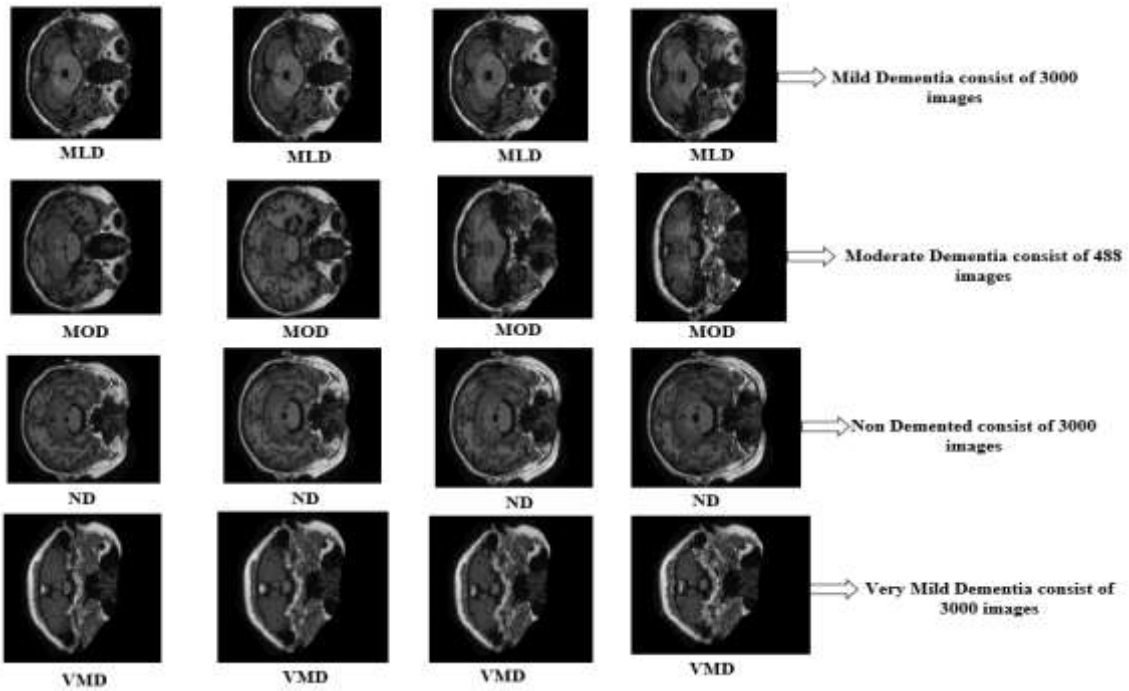

Figure 4: OASIS Dataset images in Kaggle

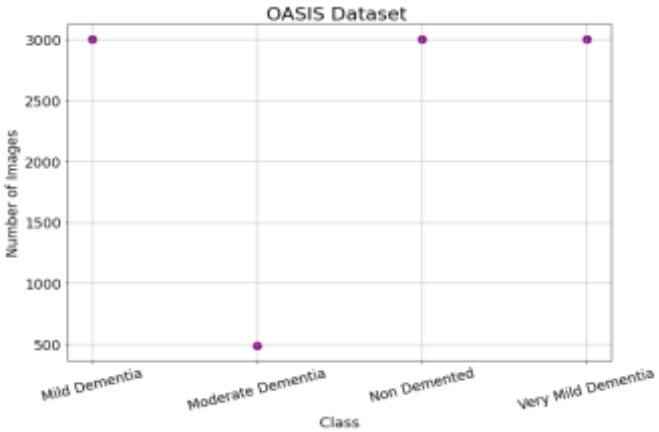

Figure 5: Dataset Distribution by Class for OASIS Dataset

2.2 Preprocessing

Cerebrospinal fluid (CSF) is a clear, colorless fluid that surrounds the brain and spinal cord. It acts as a cushion and a way for waste to leave the body and nutrients to enter. Cerebrospinal fluid (CSF) has appear as a important technique for predicting Alzheimer's disease

(AD), as it can show atypical brain irregularities, regard the accumulation of amyloid-beta plaques, neuronal damage and tau tangles [20]. There are many signs in CSF that can help us figure out what AD is and how to treat it. The most important biological indications are:

1. Amyloid-beta $(A\beta)$: The quantity of amyloid-beta peptide in the cerebrospinal fluid (CSF) is an essential biomarker. In Alzheimer's illness, amyloid-beta plaques develop up in the brain. However, the levels of these plaques in the CSF tend to go down as the peptide builds up in the brain.

2. Total Tau (t-tau): Tau is a protein that helps neurons maintain their microtubules stable.

In Alzheimer's disease (AD), tau experiences abnormal phosphorylation, leading to neurofibrillary tangles that disrupt neuronal function. A substantial amount of entire tau (t-tau) in CSF indicates that neurons are dead or injured.

3. Phosphorylated Tau (p-tau)**:**Phosphorylated tau is a specific form of tau that is thought to be more actively involved in the disease process by forming complexes in the brain. More severe AD is connected to higher levels of p-tau in CSF, which may imply that neurodegeneration is still going on.

CSF Biomarkers in AD Diagnosis:

Amyloid-beta (Aβ): Lower CSF $A\beta42$ Levels show that amyloid plaques are building up in the brain.

Total Tau (t-tau): Higher CSF t-tau Levels show how much damage has been done to neurons and are a sign of neuronal injury.

Phosphorylated Tau (p-tau): Elevated levels of p-tau in cerebrospinal fluid (CSF) aid in differentiating Alzheimer's disease from other forms of dementia, particularly due to their association with tau tangles.

1. Amyloid-beta $(A\beta)$ as a function of AD severity:

A decrement in CSF $A\beta42$ levels is associated with AD progression. Equation 1 shows how the two things are related:

$$A\beta_{42}=\frac{C_{A\beta42}}{1+e^{\left(-\alpha\cdot(t-T_{threshold})\right)}} \quad (1)$$

where$A\beta_{42}$ is the concentration of amyloid-beta 42 in CSF, $C_{A\beta42}$ is the baseline concentration of amyloid-beta 42,α is the rate of change of $A\beta$ levels over time,t is time,$T_{threshold}$ is the time threshold where $A\beta$ levels begin to significantly drop.

2. Tau (t-tau) levels and neuronal injury:

Tau levels in CSF increase, serving as a marker for neuronal injury. This relationship can be modeled as follows in equation 2:

$$T_{tau}=\gamma\cdot\left(1-e^{-\beta.(t-T_{start})}\right) \quad (2)$$

Where T_{tau} is the concentration of total tau in CSF, γ represents the maximum concentration of tau observed in the later stages of AD, β is the rate at which tau accumulates in the CSF, $t$is time,T_{start} is the start time of noticeable tau increase.

3. Phosphorylated Tau (p-tau) as an AD marker:

The change in phosphorylated tau (p-tau) concentration can be expressed in equation 3:

$$P_{tau}=\delta\cdot\left(1+e^{-\lambda\cdot(t-T_{initial})}\right) \quad (3)$$

Where P_{tau} is the phosphorylated tau concentration in CSF,δ is the amplitude of p-tau response,λ is the rate of p-tau change, t is time, $T_{initial}$ is the time when significant increases in p-tauare first observed.

2.3 Alzheimer's Disease Detection through Class Activation Mapping (CAM) and Deep Neural Network (DNN) Analysis

DNNs are a class of ML models designed to recognize patterns in complex data by learning since large datasets. For Alzheimer's disease (AD), deep neural networks (DNNs) can be trained using characteristics derived from cerebrospinal fluid (CSF) biomarkers, including amyloid-beta and phosphorylated tau. The DNN model learns to classify patients into different phases: CN, MCI, or AD. Some people still think of DNNs as "black-box" structures, resulting in it hard to figure out how the system produces its forecasts. CAM is employed to render the process simpler to comprehend so that this problem may be fixed.

Class Activation Mapping (CAM)

CAM is a technique that displays the parts of the input data have the biggest impact on the forecast made by the approach. In the framework of Alzheimer's disease (AD) diagnosis, CAM aids in pinpointing the biomarkers or traits that are particularly crucial for distinguishing among various phases of cognitive normalcy (CN), Alzheimer's disease (AD) and mild cognitive impairment (MCI) [21]. Heatmaps made by CAM demonstrate which elements of the input data have the most effect on the model's judgment. When you combine CAM with DNNs, you get not just a classification result but also a clear picture of the features that caused the model to make its decisions. This makes it easier to realize the method predictions and form them many dependable for medical application.

1. DNN Prediction Function: A typical DNN used for the classification of AD can be signified by the function in equation 4:

$$\hat{y}=f(X;\theta) \quad (4)$$

Where $\hat{y}$ is the predicted class (e.g., CN, MCI, AD), X is the input feature vector (e.g., biomarker levels of amyloid-beta, tau, etc.), θ shows the neural network's parameters (weights).

2. Loss Function for DNN Training: To train the DNN, a loss function is used to decrease the prediction error. For an organizational task involving categorical

classification, the loss function utilized is cross-entropy with softmax activation.

$$L(\hat{y},y) = -\sum_i y_i \log(\hat{y}_i)$$

(5)

In equation 5, where y_i is the true class label, $\hat{y}_i$ is the predictive likelihood of class i (output of the softmax function).

3. Class Activation Mapping (CAM): CAM is applied to visualize the features in the input data that contributed to the method's decision. The general method for generating a CAM is as follows:

- First, the DNN produces a prediction, and the output of the final convolutional layer is utilize to generate the map.
- The contribution of each feature can be visualized as a weighted sum of the convolutional feature maps, computed in equation (6):

$$CAM(x) = \sum_k \alpha_k \cdot f_k(x)$$

(6)

Where $CAM(x)$ the class activation map for input x, $f_k(x)$ represents the activation of the k-th feature map from the last convolutional layer, α_k is the weight for the k-th feature map, which is learned during the training of the DNN (often by averaging the gradients of the output with respect to the feature map).

4. Gradient-Based CAM (Grad-CAM) for Improved Visualization:Grad-CAM is an improved version of CAM that employs gradients to more effectively discover and present the most important parts that lead to the choice. Equation (7) shows how the Grad-CAM method works:

$$\text{Grad-CAM}(x) = \text{ReLU}\left(\sum_k \text{grad}_k \cdot A_k(x)\right)$$

(7)

Where $\sum_k \text{grad}_k$ is the gradient of the output class score with respect to the k-th feature map, $A_k(x)$ is the activation of the k-th feature map for the input x, ReLU is used to keep only positive gradients, which helps focus on the features that make the classification better.

2.4 Strengths of proposed method

The combination of Class Activation Mapping (CAM) and Deep Neural Networks (DNNs) makes it possible to accurately find AD by looking at cerebrospinal fluid biomarkers, which leads to high organization accuracy. • CAM makes the model easier to understand by pointing out important areas in the biomarkers, which gives us useful information about how the disease works. • The suggested method works well to deal with the difficulties of AD detection, giving reliable results at all stages of the disease.

3. Result and discussion

3.1 Experimental setup

We used the Google Colab environment in this study to train our models with Python 3.7, TensorFlow, and the Scikit-learn package. Google Colab gives us access to computing power and lets us change the hardware and use limits. Additionally, we used various Python packages, including NumPy, Pandas, Matplotlib, and Keras. We also worked with DICOM files using Pydicom, a Python library. Versions 2.0.0 of TensorFlow and TensorFlow-GPU were utilized. Figure 6 shows the confusion matrix for the ADNI and OASIS datasets. Figure 7 depicts the result of predicted images for dataset.

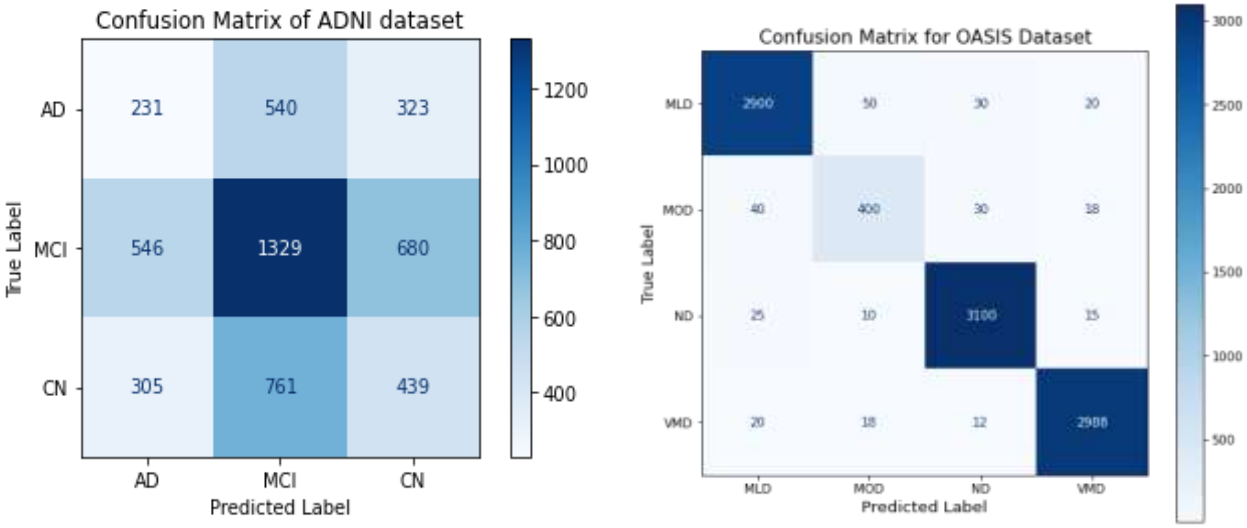

Figure 6: Confusion matrix for ADNI Dataset and OASIS Dataset

3.2 Performance Metrics

Sensitivity, sometimes mention to as the True Positive Rate or SNV, is the percentage of actual positive cases that a framework accurately detects. It shows that the model can find positive cases.. Sensitivity can be given in equation (8)

$$\text{Sensitivity} = \frac{\text{TruePositives}}{\text{TruePositives} + \text{FalseNegatives}} \quad (8)$$

Specificity, also known as SPV, refers to a detection test's ability to accurately classify true negatives individuals who do not have the condition—among all those who are genuinely negative. Specificity is defined in equation (9)

$$\text{Specificity}=\frac{TN}{TN+FP} \quad (9)$$

The accuracy metric (ACC) divides the overall number of predictions by the number of right predictions to determine how accurate a model is overall. It is given in equation (10)

$$\text{Accuracy}=\frac{\text{TruePositives}+\text{TrueNegatives}}{\text{Total Predictions}} \quad (10)$$

People often use the RMSE measure to figure out how well a model can predict things. To classify something, you have to find the square root of the average of the squared disparities between the actual and expected outcomes. Lower RMSE values mean that the model is more accurate. . RMSE can be calculated by equation (11)

$$RMSE=\sqrt{\frac{1}{N}\sum_{i=1}^{N}\left(y_i-\hat{y}_i\right)^2} \quad (11)$$

The time it takes for a model or procedure to respond to a question or input after it has been received is called the response time. In the context of AD detection models, response time measures how quickly the system provides a diagnosis or classification after receiving patient data. It is defined by equation (12)

$$\text{ResponseTime}=T_{response}-T_{input} \quad (12)$$

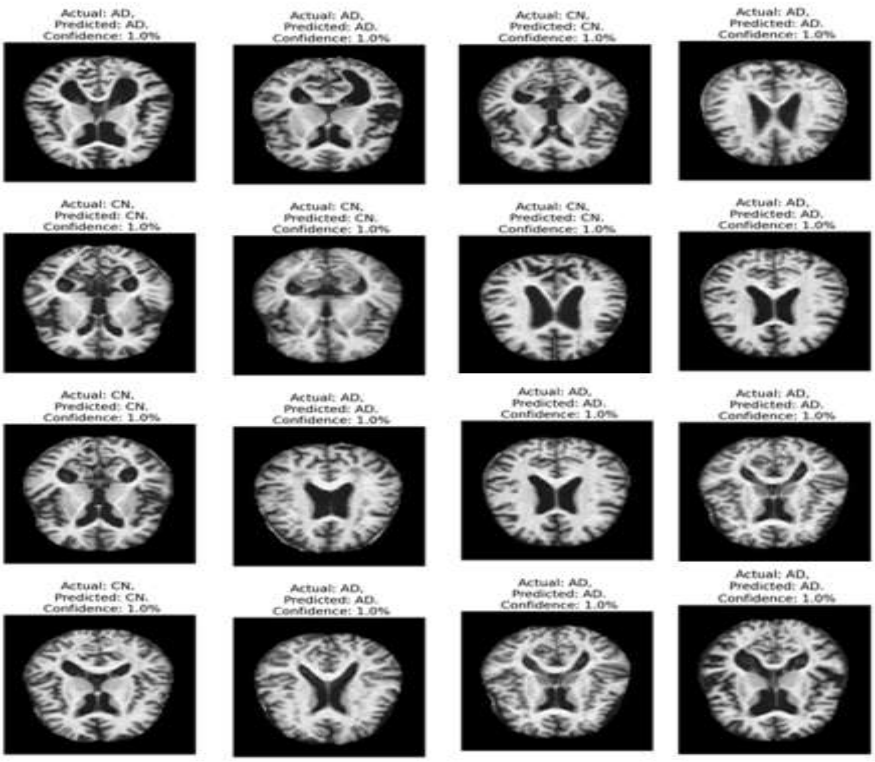

Figure 7: Output predicted images for dataset

3.3 Comparative Methods

CNN (Convolutional Neural Network) [22]: A CNN-based DL technique was developed for predicting Alzheimer's disease (AD) from MRI images. The output of the CNN method was associated with the experimental accuracy of the RNN method.

EDRNN ((Enhanced Deep Recurrent Neural Network) [23]: There were also a DRNN, a CNN, and a Recurrent Neural Network (RNN) employed and looked at in addition to an EDRNN.

Table 3: Comparison of Model Performance on ADNI and OASIS Datasets

Models	ADNI Dataset			OASIS Dataset			
	AD/MCI	AD/CN	MCI/CN	ND/MLD	ND/MOD	ND/VMD	MLD/MOD /VMD
	SNV/SPV/ ACC	SNV/SPV/ ACC	SNV/SPV/ ACC	SNV/SPV/A CC	SNV/SPV/A CC	SNV/SPV/A CC	SNV/SPV/ ACC
CNN	76.34/81.2 6/68.34	61.56/73.1 9/69.91	87.34/66.2 1/79.31	67.45/80.44/ 60.34	67.34/71.19/ 89.23	77.35/76.34/ 63.23	66.45/73.98 /84.45
EDRNN	89.45/78.1 2/88.45	77.23/87.2 3/87.28	72.91/89.4 5/89.81	81.23/72.18/ 81.23	78.37/88.55/ 77.32	89.12/62.91/ 79.43	79.23/89.55 /88.14
Proposed	92.22/93.7 6/95.56	90.34/94.1 7/96.38	93.65/92.3 4/96.91	90.88/93.37/ 95.22	92.98/90.91/ 96.66	92.19/93.54/ 95.71	90.33/94.87 /98.87

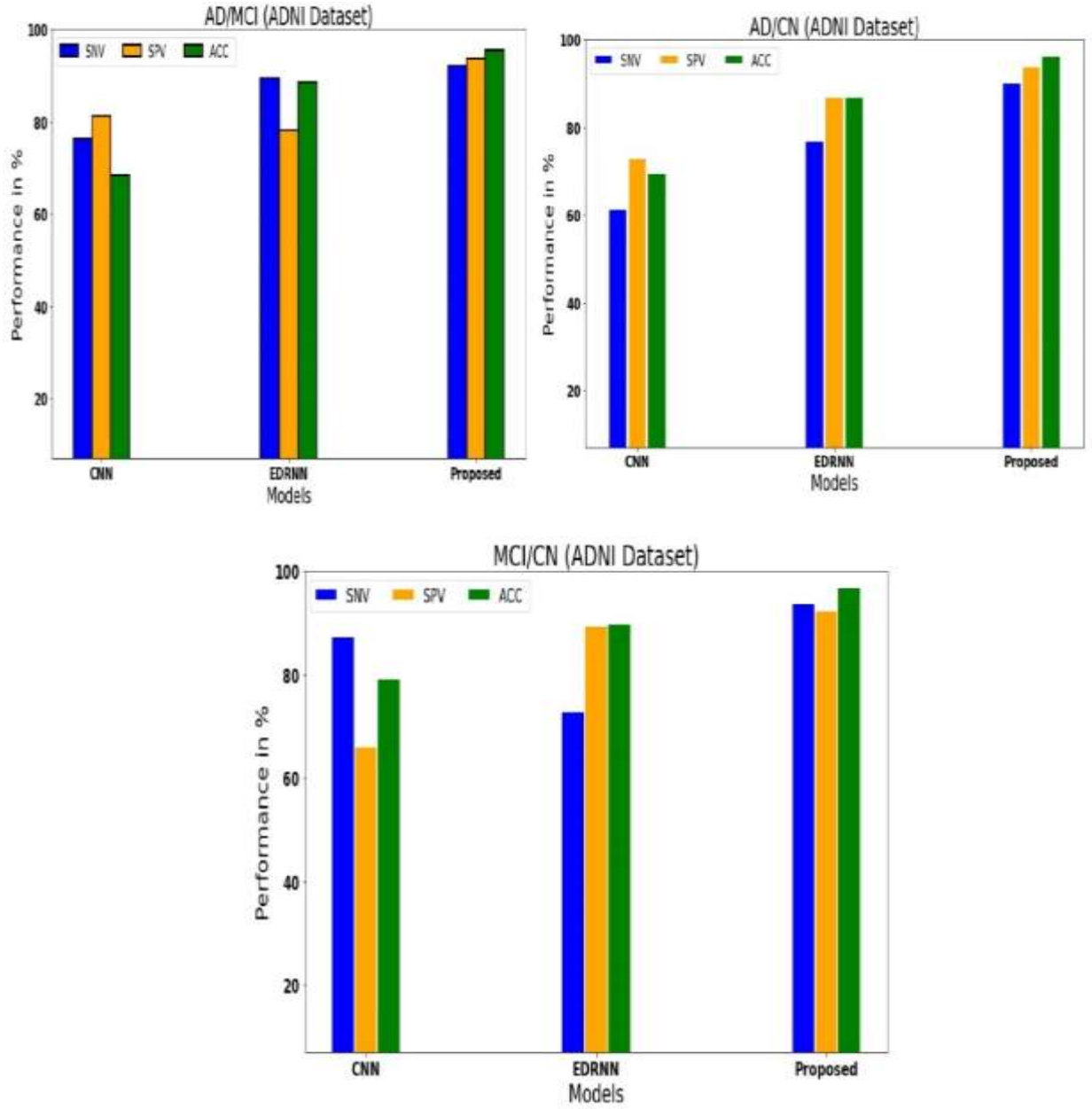

Figure 8: Comparison of Model Performance on ADNI Datasets

Figure 8 and 9, along with Table 4, analyze the performance of CNN, EDRNN, and the present models on the OASIS and ADNI datasets using SNV, SPV, and ACC measures.The suggested method always works better than both CNN and EDRNN on the ADNI dataset. It performs best for AD/MCI (92.22%/93.76%/95.56%) and MCI/CN

(93.65%/92.34%/96.91%) groups. In each category, the proposed methodology outperforms the prior estimating methods applied to the OASIS dataset. The results for ND/MLD (90.88%/93.37%/95.22%) and ND/VMD (92.19%/93.54%/95.71%) are quite good. The same is true for SNV, SPV, and ACC. The suggested model is very accurate and reliable overall, and it does better than CNN and EDRNN on the two data sets.

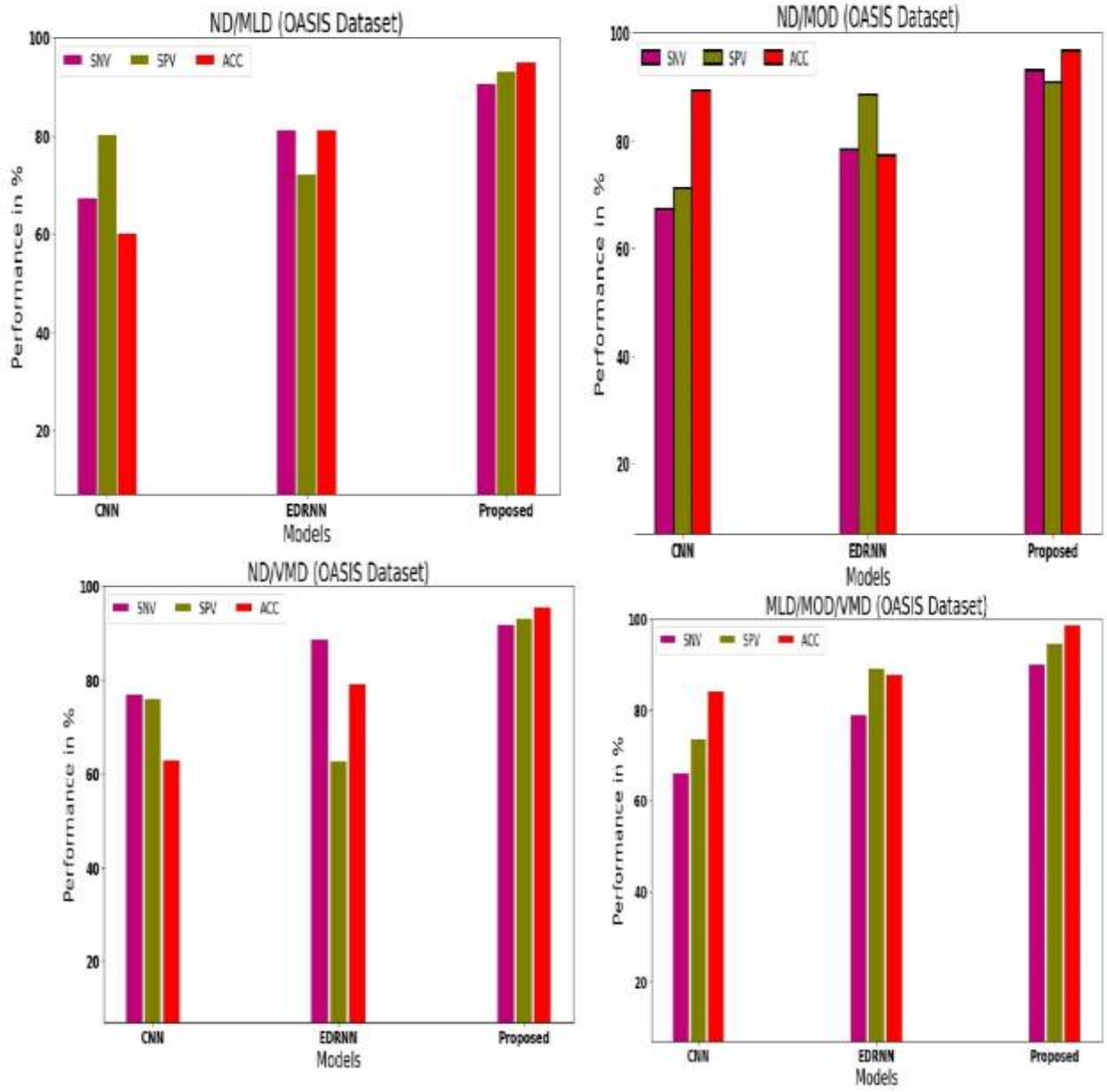

Figure 9: Comparing how well models work on OASIS datasets

Table 4: RMSE Execution Examination of Models on ADNI and OASIS Datasets

Models	**ADNI Dataset**			**OASIS Dataset**			
	AD/MCI	AD/CN	MCI/CN	ND/MLD	ND/MOD	ND/VMD	MLD/MOD/ VMD
	RMSE			RMSE			
CNN	41.87	32.18	30.65	24.98	35.78	34.45	25.55
EDRNN	23.18	28.55	22.76	14.65	16.87	21.87	19.23
Proposed	13.76	15.67	12.76	10.43	12.65	17.76	11.87

The examination of the models depicts in Figure 10 and Table 4 for the ADNI and OASIS datasets display that the projected scheme works improved. The RMSE values for the ADNI dataset are notably higher for the CNN model (41.87% for AD/MCI and 30.65% for MCI/CN) and much lower for the EDRNN model (23.18% for AD/MCI and 22.76% for MCI/CN). The present method , on the another hand, has well lower RMSE values (13.76% for AD/MCI and 12.76% for MCI/CN). The technique also works well with the OASIS dataset, depicting constant dominance with the lowest RMSE values, such as 10.43% for ND/MLD and 11.87% for MLD/MOD/VMD. It is better than either CNN and EDRNN. The results show that the proposed framework is strong and precise in finding differences across phases of AD progression. This renders it more effective to plan your work.

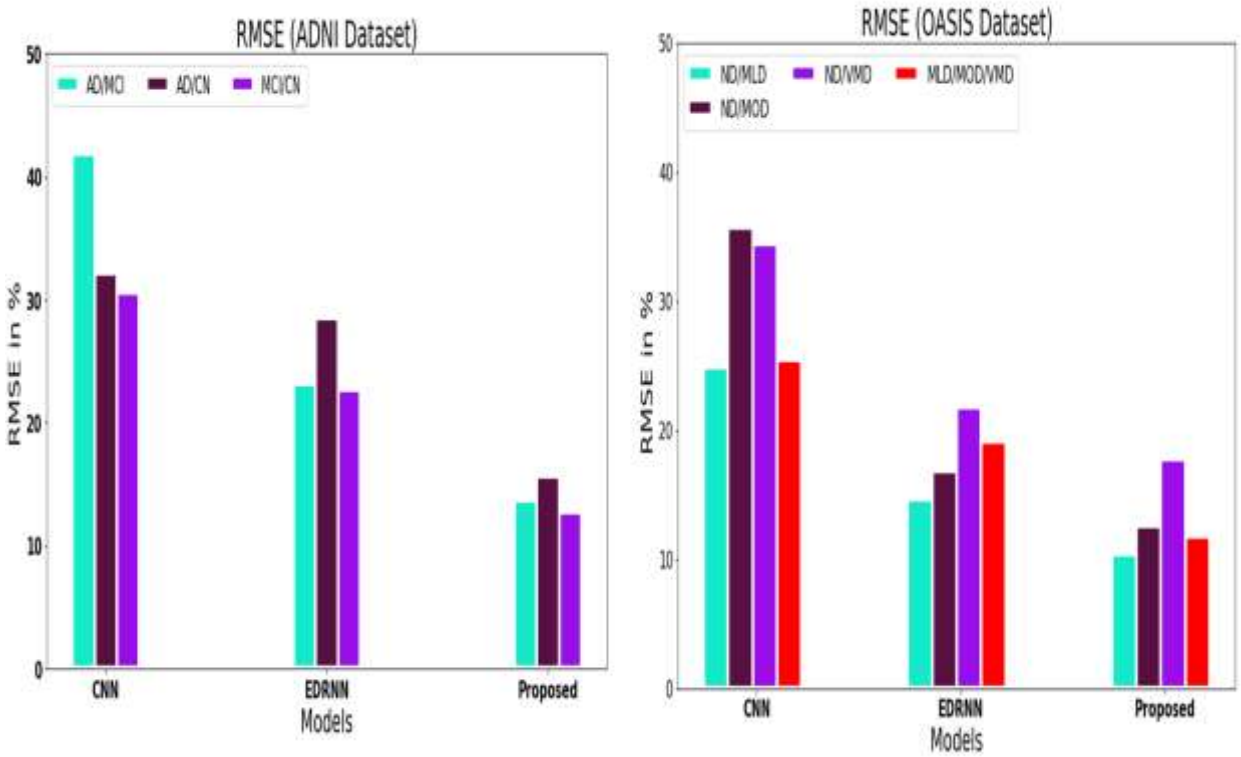

Figure 10: RMSE Execution of Models on ADNI and OASIS Datasets

Table 5: Response Time Performance Examination of Methods on ADNI and OASIS Datasets

Models	ADNI Dataset			OASIS Dataset			
	AD/MCI	AD/CN	MCI/CN	ND/MLD	ND/MOD	ND/VMD	MLD/MOD/ VMD
	Response Time			Response Time			
CNN	7.876	12.116	10.965	15.765	14.654	11.532	8.113
EDRNN	9.234	10.765	13.876	13.116	9.876	7.876	6.656
Proposed	1.654	5.176	3.654	5.953	3.654	2.876	1.876

Table 5 and Figure 11 indicate the extent to which the recommended approach performs by displaying how long it takes to respond to requests in the ADNI and OASIS datasets. When applied to the ADNI dataset, the proposed technique yields the quickest response times: 1.654 ms for AD/MCI and 3.654 ms for MCI/CN. This is a lot faster than CNN (7.876 ms and 10.965 ms, respectively) and EDRNN (9.234 ms and 13.87 ms, respectively). The recommended approach also often leads to rapid reaction times on the OASIS dataset, with 5.953 seconds for ND/MLD and 1.876 ms for MLD/MOD/VMD. These are better than CNN and EDRNN. The fact that it works this well means that the suggested method is good for detecting and categorizing AD in real time.

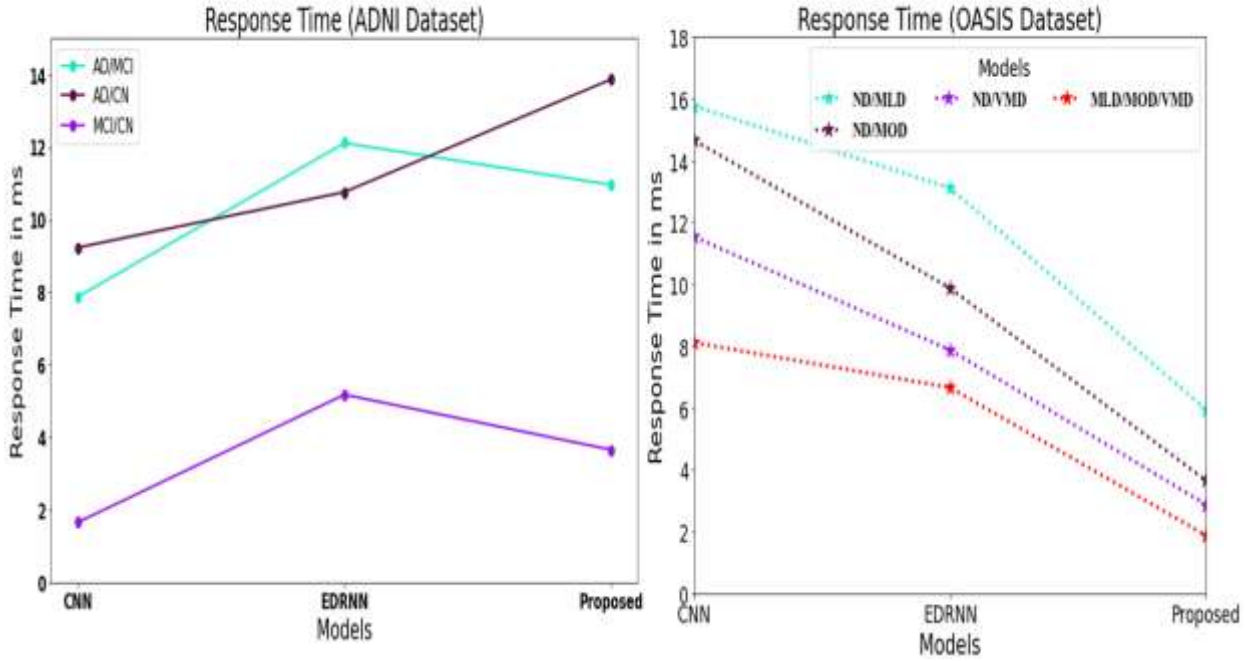

Figure 11: Comparison of Model Response Time Performance on ADNI and OASIS Datasets

3.4 Training and Testing validation Loss and Accuracy

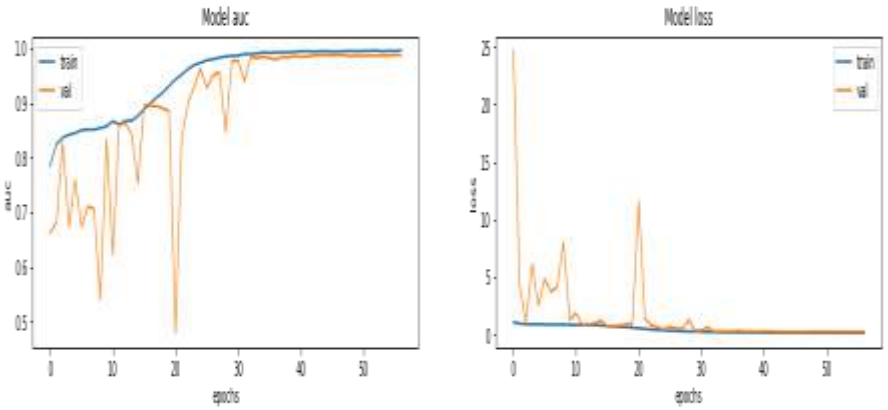

Figure 12: Training and Testing validation Loss and Accuracy

Using training-validation loss and accuracy, Figure 12 depicts the way the AD recognition method works. This shows the extent to which the framework acquires knowledge along with how efficiently it can use what it develops in new scenarios. The training-validation loss is falling down all the time, which means the model is learning key patterns. The training-validation accuracy is good and steady, which means that the model can correctly identify illustrations. By keeping an eye on these measures, you can be confident that the model isn't either underfitting or overfitting. This makes it reliable for discovering AD in an extensive variety of datasets.

3.5 ROC Curve

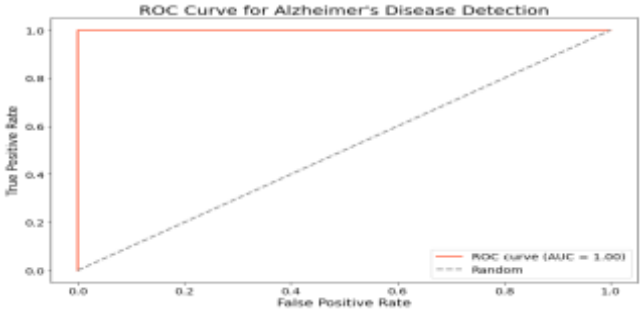

Figure 13: ROC Curve for Alzheimer disease detection

The ROC curve, that illustrates the balance between the true positive rate (sensitivity) and the false positive rate (1-specificity), gives a clear picture of how well the model can discover AD (Figure 13). The area under the curve (AUC) is a highly essential number that shows how effectively the model can discern the difference between examples that are good and cases that are bad. The better AUC value for this study suggests that the model is strong enough to employ CAM-DNN to look at cerebrospinal fluid biomarkers and detect them correctly.

3.6 Ablation study Analysis

The suggested method requires all modules. In this part, we conduct a series of ablation experiments on the ADNI and OASIS datasets to evaluate the justification for the proposed CAM-DNN and to compare it with established models, including CNN and EDRNN. The goal of these tests is to show why we propose CAM-DNN and to look at how its design has changed.

Table 6: Ablation Study on Alzheimer's Disease Detection Model

Method	Accuracy
Full CAM-DNN	96.49
Without CAM	87.81
Without DNN	80.23
Without CSF Analysis	76.24

Table 6 and Figure 14 demonstrate the ablation study that was done to see how each of the adjusted sections of the proposed CAM-DNN model helped. The whole CAM-DNN had an accuracy of 96.49%, which illustrates the way all of its elements worked in concert. When the CAM element was removed, the precision dropped to 87.81%. This shows how important it is for feature localization. When the DNN was removed, the model only achieved 80.23% correct. This demonstrates the extent of deep neural networks required to do any decent job sorting. Without the inclusion of CSF analysis, the accuracy dropped to 76.24%. This shows how important it is to study cerebrospinal fluid to enhance the model's diagnostic presentation. The CAM-DNN structure's all-around design is the greatest way to get the most accurate results, as these data indicate.

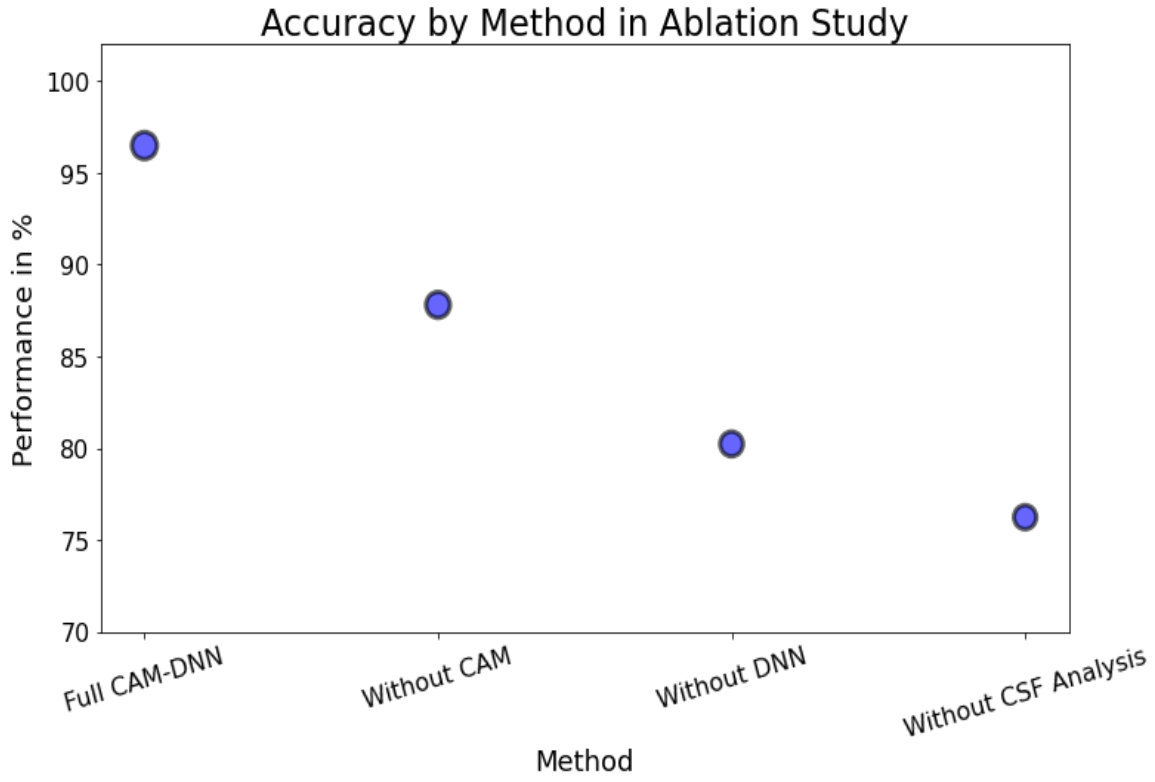

Figure 14: Ablation Study on Alzheimer's Disease Detection Model

3.6.1 Influence of DNN

DNNs have improved AI and data-based decision-making in several areas. DNNs have advantages at finding patterns and relationships in big datasets that are hard to see. This has helped a lot with systems that can interpret normal language, recognize sounds and visuals, and work on their own. They can apply what they learn to suit a wide range of needs,

which has changed several fields, including healthcare diagnostics, financial projections, and tailored recommendations. Even if they have worked, there are still problems to solve, such as explainability, robustness, and moral difficulties. This is why research is still going on to make them better and stronger.

3.6.2 The K-fold cross validation

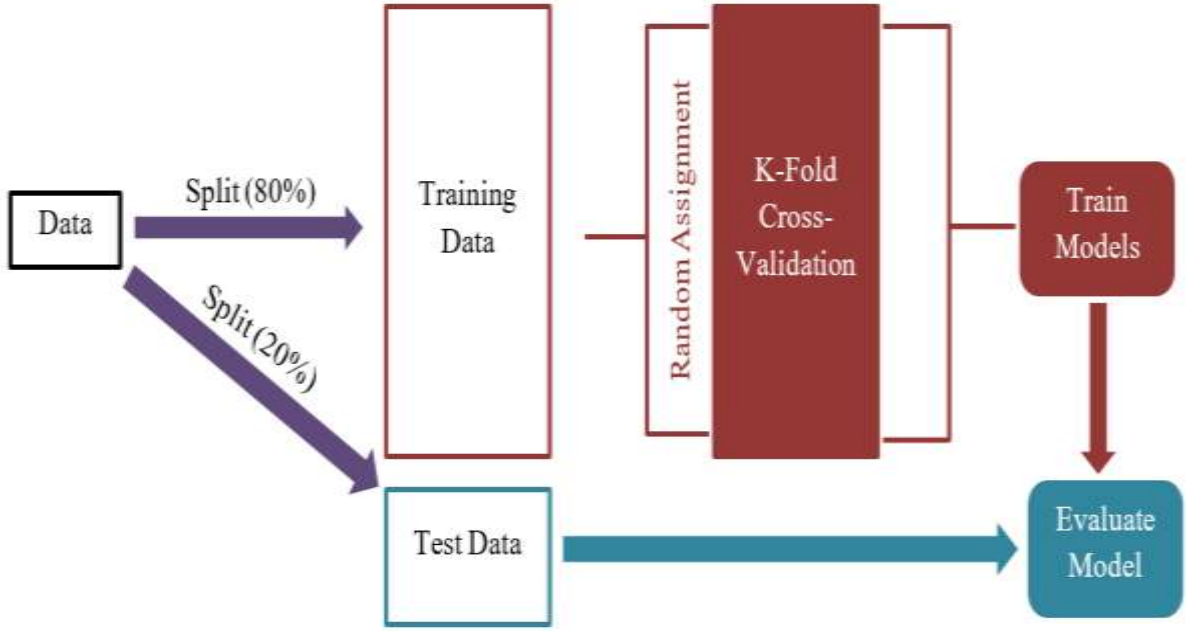

Figure 15: Architecture diagram of K-Fold Matrix

Figure 15 shows how to train and estimate an ML model. First, 20% of the dataset is utilized for testing, while the other 80% is used for training. The training data is separated into K random groups, or "folds," using a process called K-Fold Cross-Validation. The model is trained on the other folds, and each fold is a test set. This method makes the model more dependable by reducing the effects of data changes. After cross-validation, the model is trained on the entire training set. Finally, the model's output is compared to the test data that was set aside to gain an unbiased perspective of how well the model can generalize.

Table 6 Comparative accuracy examination of the suggested approach against alternative models.

Table 8: Comparison of accuracy analysis

Author's	Model	Dataset	Accuracy
Hazarika, R.A. [27]	DEMNET	Multiclass	95.23%
Yildirim, M. et al. [24]	Multi-deep CNN	Multiclass	88.9%
Hilal, A.M. et al. [25]	3D CNN model	Multiclass	89.47%
Han, D.H. et al. [26]	AlexNet	Multiclass	92.85%
Our Work	**CAM-DNN**	**ADNI and OASIS**	**96.49%**

The accuracy of the proposed CAM-DNN strategy is compared to the best multiclass organization methods in Table 6 and Figure 16. Yildirim et al. [24] attained an accuracy of 88.9% using a Multi-deep CNN, whereas Hilal et al. [25] marginally enhanced the accuracy to 89.47% with a 3D CNN model. Han et al. [26] significantly improved the accuracy to 92.85% with AlexNet, and Hazarika et al. [27] improved it even more to 95.23% with their DEMNET model. The CAM-DNN method, on the another hand, does a developed job of presenting with an accuracy of 96.49% on the ADNI and OASIS datasets. It shows that it executes much effectively and is more reliable than some other new ways.

Limitations & Challenges

The application of CAM-DNNs intend a notable progression in the determination of Alzheimer's disease by cerebrospinal fluid biomarkers; yet, many constraints and obstacles persist. The essential for large, high-quality datasets may extent their utilization to smaller or much diverse groups of people. Also, DNNs are hard to precede because they aren't clear, so clinical validation and reliability are rather critical. If biomarker data are collected and prepared in the same way each time, even the model implementation can be inconsistent. We need to arrange the data better, find methods to make it clearer, and perform strong validation on as huge an array of data as possible to ensure that medical functions are useful and precise.

Figure 16: Comparison of accuracy analysis

CONCLUSION

This paper discusses the effectiveness of combining CAM and DNN with CSF biomarkers to enable the physician to provide a precise diagnosis of AD. By combining the predictive power of DNN and the interpretability of CAM, the proposed method leads to a greater accuracy but also offers valuable information on the biomarker regions that are essential in the diagnosis process. The findings illustrate the approach is effective using data across different sources and may be an effective instrument to identify and categorize early indicators of AD. The research makes it a bit easier to use AI techniques that already exist in clinical diagnostics. This will result in improved, more understandable and easier methods to identify neurodegenerative diseases. Future research can focus on developing the model to include other biomarkers and medical imaging data to further improve its utility and generalizability.

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