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Non-Invasive Methods to Predict the Chances of Alzheimer's Disease

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ABSTRACT

Biomarker integration is an important and imperative process in the research of Alzheimer's condition, where non-invasive information gathered from various sources are integrated for more precise and earlier diagnosis. This paper investigates non-invasive biomarkers, such as MRI imaging, by using CNN and SVM machine learning models for the prediction of development of AD. For Neuroimaging the ADNI dataset is one of the most common datasets used in machine learning applications for Alzheimer's prediction. This work also evaluates the feasibility of other datasets, including the OASIS dataset, given the great value of imaging and clinical data it has. One promising direction in this domain is wearable data, where data collection could be non-invasive. This has enormous potential to enhance the diagnosis reliability and efficiency of non-invasive diagnosis of Alzheimer's. ADNI will have a significant part in the prediction of Alzheimer's due to the comprehensive longitudinal data it offers, the facilitation of biomarker identification, and large-scale data sharing to enable the development of precise early detection models. OASIS also offers complete longitudinal and cross-sectional neuroimaging data, and demographic information to facilitate collaborative research and validation of predictive models. These are indeed important data that will enable us to train powerful algorithms to permit early detection and prognosis for Alzheimer's disease. This study will contribute to extending current predictive methods by integrating these multimodal biomarkers and datasets and providing tools for non-invasive diagnosis in Alzheimer's disease.

Keywords: *Alzheimer's Disease (AD), Convolutional Neural Network (CNN), Mild Cognitive Impairment (MCI), Magnetic Resonance Imaging (MRI), Convolutional Neural Network (CNN), Support Vector Machine (SVM), Open Access Series of Imaging Studies (OASIS) and Alzheimer's Disease Neuroimaging Initiative (ADNI) Datasets.*

1. INTRODUCTION

Among neurodegenerative diseases, AD is a progressive condition and significantly influences cognitive function, especially memory. Indeed, Alzheimer's condition represents 50-70% cases of cognitive impairment, and its progression is silent for many years due to underlying mechanisms at play, such as amyloid accumulation, synapse failure, and neuronal death which take time before manifestations of clinical symptoms appear. The established diagnostic criteria, such as those from the DSM-5 and NINCDS-ADRDA, usually diagnose AD when extensive deterioration of the brain has already impaired daily functioning. [1] In 50% to 60% of cases, moderate cognitive impairment is considered an important preclinical stage before the transition to dementia.

It is found to affect 7.6% in the 55-59-year-old category, 9.5% among those aged 60 to 69, 14.6% in the age range of 70–79 category, as well 23.6% in the persons aged more than 80 years of age. However, early diagnosis has been hampered as there is a lack of dependable biomarkers, non-invasive and affordable that could predict the development of MCI to AD with more than 95% accuracy. Although there is the promise of success with the various methods being devised that incorporate genomics, structural and functional neuroimaging, and neurophysiological assessments, small sample sizes and short follow-up times are but a few concerns that point to high variability and a need for further thorough research to enhance early detection and intervention strategies in AD.

AD destroys parts of the brain that are engaged in language, reasoning, and social behaviour. The initial manifestations of AD arise in the [2] entorhinal cortex and hippocampal regions, which are related to memory. Symptoms of AD include behavioural abnormalities, linguistic difficulty, and memory loss, all of which can vary among individuals. These symptoms of AD will be usually preceeded by a preclinical stage of MCI, when individuals have memory problems but are still able to function. In general, deep learning approaches, namely GAN, LSTM networks, RNN, and CNN can be widely used in machine learning to analyze patterns through data. CNNs classify images well, RNNs handle sequential data, LSTM networks handle problems that RNNs have with vanishing gradients and GANs generate new data comparable to the training set.

AD is the leading cause of dementia, estimated by a worldwide context to be responsible for 50–75% of the cases. Other variants of dementia include frontotemporal dementia, estimated at 10–15%, Lewy Body disease at 10–25%, and vascular dementia at 20–30%. It is estimated that in 2019, Dementia was diagnosed in 50 million people, and by 2050, that figure will rise to 131.5 million. It is estimated that the global economic cost of AD will reach US$2 trillion by 2030 [3]. The pathophysiology of AD begins years before the onset of clinical symptoms, such as memory loss and difficulty finding words, with structural and chemical changes in the brain AD diagnostic technique follows several steps,[4] such as feature extraction, segmentation, pre-processing, data gathering, and classification.

Studies have found that women who have polycystic ovary syndrome (PCOS) may be at an increased risk for Alzheimer's disease, and the possible connection might be its association with hormonal imbalances and metabolic abnormalities. PCOS is a hormonal condition that results in [5] polycystic ovaries and irregular menstrual cycles, which raises the risk of diabetes, insulin resistance, infertility, and Alzheimer’s disease. Insulin resistance is a common problem that affects a sizable percentage of women with PCOS. This may result in compensatory hyperinsulinemia, which is elevated insulin levels. Excessive insulin might exacerbate the hormonal imbalance by increasing the synthesis of androgens.

Elevated levels of luteinizing hormone (LH) associated with PCOS are linked to decreased functional connectivity in the right frontal lobe, as shown in MRI. The psycho-social condition of PCOS might otherwise negatively affect women regarding their health as the physical symptoms and reproductive outcomes might influence their mental health. Integrating AI in the analysis of health complex data would support healthcare providers in identifying PCOS symptoms through hormonal imbalances and develop specific prevention strategies tailored to individual lifestyle, diet, and health profiles. [6] The risk of PCOS using linear regression, multi-model stacking, and gradient boosting can be well predicted. However, in terms of performance, multi-model stacking with logistic regression was significantly better than other models.

Despite all these promises, research regarding the diagnosis of AD using DL has remained low, particularly concerning the exploration of cutting-edge deep-learning architectures for diagnostic applications. Among others, this systematic literature review outlines the future direction for research on AD early detection, and it underlines the importance of neuroimaging data for the diagnosis of AD using both DL and classic ML techniques.

1.1 PROBLEM STATEMENT

The current detection of AD is through finding out biomarkers linked to the brain's tau and amyloid beta proteins by study of cerebrospinal fluid (CSF); PET imaging, which depicts abnormalities within the brain through radioactive tracers; traditional neuroimaging modalities, like MRI and CT, used to identify structural changes of the brain. These methods have their utility but are often beset with huge costs and a time requirement and are dependent on infrastructural facilities that limit accessibility and scalability. Addressing the problems mentioned above, our research proposal put forward a new approach using large datasets of brain images and non-invasive biomarkers for the analysis of MRI brain images using machine learning models.

1.2 EXISTING SYSTEM

In the traditional method of Alzheimer's prediction, invasive methods and costly imaging modalities are typically used. Cerebrospinal Fluid (CSF) test is a prevalent technique that takes a sample of CSF during a lumbar puncture (spinal tap). This can measure Alzheimer's biomarkers like amyloid beta and tau protein levels, which are the crucial markers of Alzheimer's pathology. Although this technique is good for the detection of Alzheimer's-related changes, it is invasive, uncomfortable for the patient, and may have risks like infections or headaches. Positron Emission Tomography (PET) scanning is a second method of detecting Alzheimer's disease through detailed brain imaging following the intravenous injection of a radioactive tracer. PET scans identify brain abnormalities seen in Alzheimer's disease. PET scans, however,

are not only expensive but also involve the use of radioactive material, specialized equipment, and facilities and are therefore less available for use on a routine basis.

Other imaging methods, including CT and MRI yield structural images of the brain that can display atrophy or abnormalities associated with Alzheimer's. While less intrusive than CSF examination, these methods are also very costly, time-consuming during examinations, and require specialized settings.

1.3 DRAWBACKS OF EXISTING SYSTEM

Although accurate, these techniques have a number of important limitations in common. They are costly, time-consuming, and need highly specialized equipment, which limits their availability and scalability. Routine screening and early detection for large groups are therefore difficult. Moreover, problems may only be identified after extensive brain alterations have already taken place, which reduces the scope for early intervention.

The reliance on such high-cost or invasive means is such that Alzheimer's disease can pass unnoticed until late, when it bypasses the possibility of taking preventive action in time. Delayed detection is not only problematic from a patient outcomes perspective but is also heavily loaded in financial costs for the health system. Due to these challenges, the demand for non-invasive, inexpensive, and scalable means to anticipate the likelihood of Alzheimer's disease prior to notable symptom development is an immediate requirement.

1.4 PROPOSED SYSTEM

In our solution, we created a multimodal model architecture capable of working with diverse complex datasets while supporting high accuracy. This architecture utilizes a CNN model for efficient feature extraction, taking advantage of its ability to learn spatial hierarchies in the data. We then use a SVM model for classification after feature extraction, which enhances the robustness of the system to categorize the features accurately.This fusion of CNN and SVM enables us to design a strong framework that can overcome the issues raised by varied datasets without sacrificing performance.

1.5 ADVANTAGES OF PROPOSED SYSTEM

- The CNN-SVM model synergizes the benefits of

deep learning and SVM classification. CNN is superior at automatically deriving intricate features from neuroimaging data, detecting fine patterns in

brain structures, which are a sign of early-stage

Alzheimer's disease.

- SVM effectively utilizes these derived features to

separate healthy subjects and those with Alzheimer's. The accuracy of SVM classification enhances the overall accuracy of the system.

- Combination of CNN and SVM forms a strong and stable system that can process high-dimensional, complex data such as MRI scans, supporting consistent performance even with massive datasets.
- Early detection of minute changes in the brain, supported by this system, facilitates initial diagnosis of Alzheimer's disease at initial stages, leading to improved prognosis and treatment planning.
- Hybrid CNN-SVM model ensures reductions in overfitting problems that are usually encountered in deep learning models, by merging CNN's feature extraction with SVM's regularization strength. This provides improved generalization to novel data.
- The system is very scalable and adaptable to various forms of neuroimaging data, and hence is also appropriate for clinical use across various stages of AD diagnosis.

2. RELATED WORK

C. Kavitha et al. have given a paper on predictive ML models for the detection of early-stage Alzheimer's disease. [7] The paper explores algorithms such as Decision Trees, SVM, Random Forest (RF), and XGBoost, with emphasis on data preprocessing, feature selection, and training on MRI datasets. Gender, education, brain volume, and age are the key predictors, and Random Forest and XGBoost are found to perform the best. The research points to the promise of these models to augment early detection and intervention approaches to Alzheimer's.

Juan Felipe Beltrán et al. proposed a method for employing machine learning methods based on ADNI data to forecast the progression of AD from MCI. This study highlights that low-cost, [8] non-invasive blood biomarkers can be as effective as neuroimaging, like MRI, for early detection when combined with cognitive testing in a multi-modal approach.

Laura M. Winchester et al. reviewed the applications of AI and machine learning in Alzheimer's biomarker discovery. While

promising plasma biomarkers like [9] Aβ42 and p-tau217 are under investigation, the review calls for more diverse data collection, AI refinement, and validation of non-invasive biomarkers to improve clinical applicability.

Minseok Song et al. applied the Random Forest algorithm using brain MRI data from the ADNI dataset to identify Alzheimer's disease, highlighting its strength in handling high-dimensional and noisy data. [10] The study demonstrated high classification accuracy with RF, MLP, and CNN, identifying key biomarkers such as the inferior lateral ventricle, hippocampal, and amygdala, and emphasized the potential of RF for prior detection and longitudinal studies in Alzheimer's diagnosis.

Jose M. Alonso et al. presented a multi-modal, double-layered model for identifying AD and its prediction, utilizing info from 1,048 ADNI participants. [11] The model achieved 93.95% accuracy in classifying AD and MCI patients and 87.08% accuracy in predicting MCI progression to AD, incorporating the SHAP framework for enhanced explainability and proposing future studies to integrate longitudinal data and network science for improved clinical application.

Aristidis G. Vrahatis et al. [12] emphasized the need for early Alzheimer's diagnosis using non-invasive methods like blood tests, imaging, wearable sensors, and digital biomarkers, which are less risky and more comfortable than traditional invasive techniques. They emphasise the importance of DL and AI in managing the computational burden of these approaches.

Morshedul Bari Antor et al. conducted multivariate study using the OASIS dataset to predict Alzheimer's diagnosis with ML models, comprising SVM, random forests, logistic regression, and decision trees. After fine-tuning, [13] SVM achieved the highest accuracy at 92%, with the study emphasizing the need for early diagnosis.

Lin Liu et al. propose the diagnosis of Alzheimer's using ML to analyze speech characteritstics from the [14] VBSD dataset, which includes recordings from elderly speakers with and without AD. Their model, using Logistic Regression CV, proved more accurate and cost-effective compared to conventional diagnostic methods, demonstrating AI's capacity for prior detection and improved outcomes in neurodegenerative disease management.

Sergio Grueso et al. reviewed the use of ML methods in forecasting the advancement of AD from MCI, analyzing [15] 116 out of 452 studies focused on neuroimaging data like MRI and PET. They discovered that CNN model attained a greater mean accuracy of 78.5% than Support Vector Machines, which had an average accuracy of 75.4%, with accuracy improving when integrating MRI and PET data.

Farman Ali et al. defined a double-layered DL model using ADNI data to predict Alzheimer's progression, integrating neuroimaging, cognitive scores, cerebrospinal fluid biomarkers, and demographic features. [16] Their model achieved 93.87% accuracy in multiclass categorization with mean absolute error of 0.1375 in regression, outperforming traditional models and highlighting the need for improved model explainability and integration of additional modalities.

Rashmi Kumari et al. proposed a state-of-the-art DL model for AD diagnosis based on 3D MRI scans, integrating Graph Attention Networks (GAT) with Dynamic Convolutional Graph Neural Networks (DCGNN) to improve classification rates. [17] Their model classified with 93.34% accuracy in the case of AD vs. CN, 83.67% accuracy for CN vs. MCI, and 79.1% accuracy for AD vs. MCI when validated with the ADNI dataset.

Bazarbekov et al. reviewed the usage of ML and AI techniques in diagnosis of Alzheimer's, highlighting the influence on cognitive functions and the significance of early and accurate detection. [18] The review analyzes various data sources, including PET, MRI, EEG, sensor data, and MEG.

Xinxing Zhao et al. studied the use of structural MRI scans with artificial intelligence in the Alzheimer's diagnosis [19] demonstrating the efficiency of ML and DL in early and accurate detection. They discuss the workflow of CAD systems, emphasizing the importance of standardizing data and addressing imaging variability.

Taliah Tajammal et al. proposed an advanced DL-based approach for AD diagnosis utilizing efficient MRI data from ADNI , [20] achieving 99.6% accuracy in binary classification and 98.8% in multi-class classification of AD stages. Their approach, which combines a Custom Convolutional Neural Network with an ensemble of models.

Niyamat M. A. Chimthanawala et al. emphasized the significance of Alzheimer's disease prior detection, reviewing promising non-invasive biomarkers such as plasma [21] Aβ42/Aβ40 ratio, phosphorylated tau proteins, neurofilament light chain, miRNAs, inflammatory markers like GFAP and YKL-40, and ophthalmic biomarkers detected by OCT.

Jhansi Rani Kaka et al. introduced the DE-MSVM method by combining AlexNet-based feature extraction, image normalization, and multiobjective [22] optimization to enhance Alzheimer's classification in their proposed method, showing that the technique is more accurate and robust than some recently proposed techniques, including DE-SVRPSO and GA-SVRPSO, and many others, with a classification accuracy of 98.13%.

Elham S. Amini et al. explored the interaction between sex hormones, reproductive history, and genetic risk in women's brain aging related to Alzheimer's, analyzing data from [23] 16,854 women. The study reveals that cumulative hormone exposure accelerated brain aging, while multiple pregnancies had protective effects, and emphasizes the importance of personalized approaches to women's cognitive health, especially in relation to APOE e4 genotype and hormone replacement

therapy timing.

3. MATERIALS AND METHODOLOGY

3.1 Patients MRI Images

This study explores T1-weighted cross-sectional MR brain scans obtained from publicly available datasets. The data for this research was provided by the OASIS database, specifically the OASIS-3 dataset. OASIS-3, the most recent version, is designed to openly share neuroimaging data with the scientific community. The dataset is categorized into different classes based on the severity of Alzheimer's disease, and images were utilized for training and testing purposes.

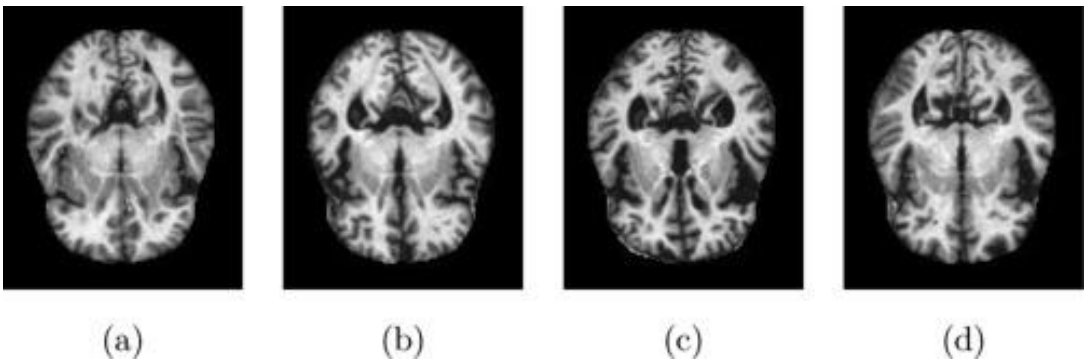

Fig. 1. MR images illustrating examples for various dementia stages: (a) No Dementia (ND), (b) Moderate Dementia (MoD), (c) Mildly Demented (MD), and (d) Very Mild Dementia (VMD), from left to right, respectively.

To develop a consistent CNN-SVM model, a huge quantity of training data needs to be used to avoid overfitting and ensure the system's generalizability. In medical studies, though, access to large datasets is frequently difficult due to privacy issues. This is particularly the case in Alzheimer's disease (AD) research, where having access to large numbers of neuroimaging scans has been a long-standing issue. In addition, small and imbalanced datasets usually cause overfitting, negatively affecting the model's performance and accuracy. Data augmentation methods are generally used to counteract these issues in order to reduce data sparsity and class imbalance and enhance the CNN-SVM model's robustness and efficiency.

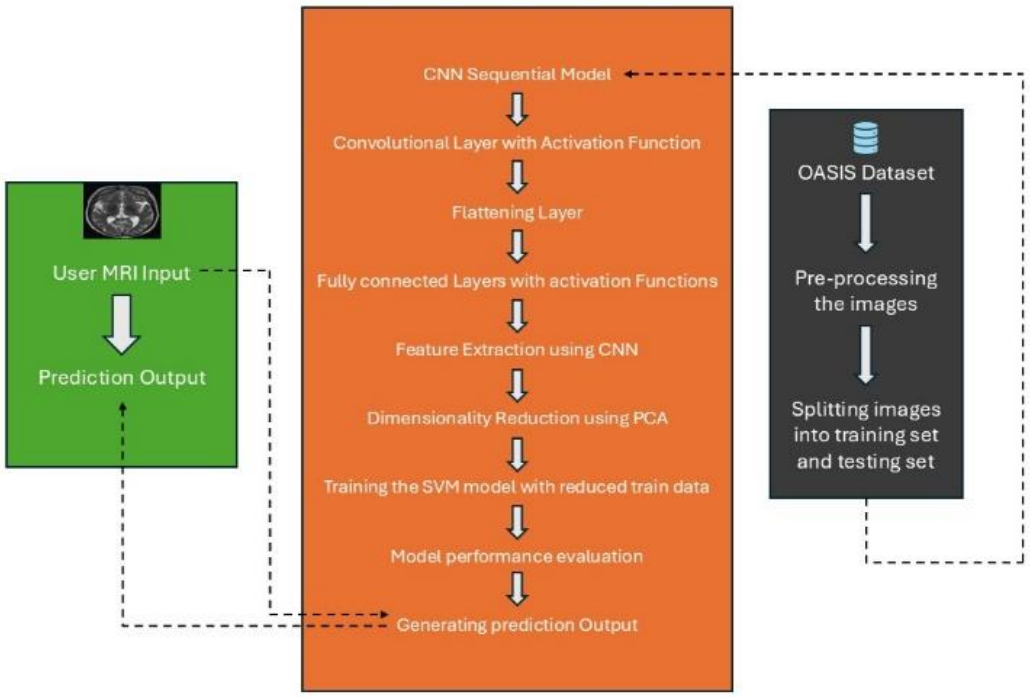

Fig. 2. Three-tier Architecture of the system

3.2 Proposed Framework

This paper pivots on the CNN-SVM multimodal for Alzheimer's disease prediction. A CNN-SVM hybrid is a model that utilizes the feature extraction capability of CNN and the classification capability of SVM. It combines the benefits it offers from using CNN for images with the strength of SVM in classification tasks. CNNs are usually applied for image-based tasks because the convolutional filters take spatial hierarchies of the input for pattern detection. Although CNNs more commonly use Softmax functions for classification, SVMs offer better alternatives mainly when there are small datasets or when a clear separation margin between classes is a priority. Replacing the Softmax with SVM helps focus the model on maximizing the margin between points, therefore helping improve classification and generalization in several tasks.

Three-Tier Architecture of the CNN-SVM Model

The proposed system architecture for predicting Alzheimer's disease using non-invasive methods is organized into three distinct tiers: data preprocessing, feature extraction and dimensionality reduction, and classification. Each tier is designed to optimize the accuracy and efficiency of the model. Below is a detailed breakdown of each tier:

3.2.1 Data Preprocessing Tier

This stage prepares the input data for subsequent processing and modeling. The OASIS dataset, consisting of MRI images, undergoes a series of preprocessing steps to enhance the quality and standardize the data.

3.2.1.1 Preprocessing Steps:

- **Resizing and Normalization:** MRI images are resized to uniform dimensions, ($X \in (R)^{H*W*C}$) where H, W, and C represent height, width, and channels, respectively. Normalization scales pixel intensities to the range [0,1], ensuring consistent numerical representation.

$$X_{normalized} = \frac{(\min(X) - X)}{(\min(X) - \max(X))}$$

- **Splitting Dataset:** The pre-processed data is then divided into testing and training sets in a 20:80 ratio to validate the model effectively.
- **Data Augmentation:** certain techniques are applied to artificially the dataset size, thereby reducing overfitting and improving generalization.

3.2.2 Feature Extraction and Dimensionality Reduction Tier:

This tier employs a CNN for extracting high-dimensional, hierarchical features from MRI images.

3.2.2.1 Feature Extraction Using CNN:

The CNN sequential model comprises several layers:

- **Convolutional Layer:** Extracts spatial features by convolving the input image X with a series of kernels or filters W. Each filter produces a feature map:

$$Z_{ij} = \sum_{m,n} W_{mn} X_{i+m,j+n} + b)$$

where 'b' is the bias term.

- Non-linear transformations, such as ReLU (max(0,x)), are applied to introduce non-linearity.
- **Pooling Layer:** Reduces the spatial size of feature maps while retaining essential features. In the case of max pooling:

$$P_{ij} = \max(Z_{ij})$$

- **Flattening Layer:** Transforms the multi-dimensional feature maps into a 1D vector appropriate for classification.

3.2.2.2 Dimensionality Reduction Using CNN:

The high-dimensional feature vectors extracted by CNN are further reduced using PCA to retain only the most significant features. PCA re-projects the data onto a reduced-dimensional space:

$$Y = X W_{PCA}$$

Where W_{PCA} is the matrix of eigenvectors corresponding to the top k eigenvalues, and k is chosen such that 95%–99% of variance is retained.

3.2.3 Classification Tier

3.2.3.1 SVM Classifier:

SVM determines the optimal hyperplane with maximum margin between two classes to separate them distinctly.

3.2.3.2 Kernel Trick:

To address non-linearly separable data, the kernel trick is used for feature mapping to a higher dimension. The Radial Basis Function (RBF) is:

$$K(y_i,y_j)=\exp(-\gamma||y_i - y_j ||\text{^}2)$$

where γ is a hyperparameter that controls the extent to which a single training sample influences the model.

Components of CNN- SVM unit:

1. Input Layer: This consists of medical imaging data in the form of MRI or PET scans that act as inputs to the model. Such images are highly dimensional and contain basic spatial information regarding the detection of Alzheimer's disease.

2. Convolutional Layers: These layers include modifying the source image with filters for feature extraction like edges, textures and patterns. Convolutional layers enable learning spatial hierarchies of features relevant to the early identification of brain atrophy and other indicators of Alzheimer's.

3. Pooling Layers: These layers decrease computations and dimensionality by reducing the resolution of feature maps generated by the convolutional layers to avoid overfitting. average pooling and max pooling are typically used while preserving crucial features.

4. Flattening layer: In the flattening layer, after a series of pooling and convolutional layers, the last feature map is converted into a one-dimensional vector by flattening it. This vector contains high-level features that represent the image. Then, it proceeds to feed into the dense layer.

5. Fully Connected (Dense) Layer: The collected features are flattened after multiple convolutions and pooling layers before moving on to one or more dense layers, which helps in learning non-linear combinations of features presenting higher-level abstractions relevant to Alzheimer's diagnosis.

6. Feature extraction using CNN: The flattened feature vector produced by the CNN, which encodes the image's most important characteristics, is now ready for classification. Instead of using a softmax layer (as is typical in CNNs), this feature vector is passed to an SVM for classification.

7. Dimensionality reduction using PCA: Before fitting the SVM, PCA (Principal Component Analysis) is applied to reduce dimensionality, retaining components that explain upto 99% of the variance. This improves classification accuracy and computational efficiency by focussing on significant patterns and eliminating noise. PCA reduces the dimensions while retaining most of the information which in turn helps in reduced storage & computational requirements

8. SVM Classifier: SVM determines whether the input is of Alzheimer's disease or not, based on features learned, by finding a maximum-margin hyper-plane that classifies the classes.SVM for classification is performed using LinearSVC. To achieve this, we want to find a hyperplane that can separate data classes well, i.e., (1).

$$f(x) = w^T x + b \qquad (1)$$

Here, *w* denotes weight vector, *b* denotes bias, and *x* denotes input vector. The optimization objective is to maximize the margin and minimize the classification errors given by (2) with the parameter C controlling the trade-off.

$$min_{w,b}\frac{1}{2}||\ w\ ||^2 + C\sum_{i=1}^{N}\max(0, 1 - y_i(w^T x_i + b)) \qquad (2)$$

x - Input feature vectors from training & testing i.e *x_train_reduced* and *x_test_reduced.*

b - Bias term learned by SVM during training.

w - Weight vector learned by SVM during training.

F(x): Decision function calculated (1) used for classification.

9. Performance evaluation and output predictions: Overall performance is calculated with the help of various metrics such as Accuracy Precision recall F1 Score and CV Accuracy using (5), (6), (7), (8), (9) which are discussed in later sections of this paper.

10. Output Layer: The SVM final output gives a binary output**,** say, Alzheimer's vs. non-Alzheimer's or multi-class classification, say, healthy, mild cognitive impairment, and Alzheimer's. The SVM decision boundary is used in making the prediction based on features which might have been extracted by the CNN.

3.3 PROPOSED MODEL DESCRIPTION

Instead of using a single algorithm, we developed a multimodal model architecture catering to various complex datasets without compromising on accuracy. In this architecture, we employed a SVM for classification after using a convolutional neural network CNN for feature extraction.

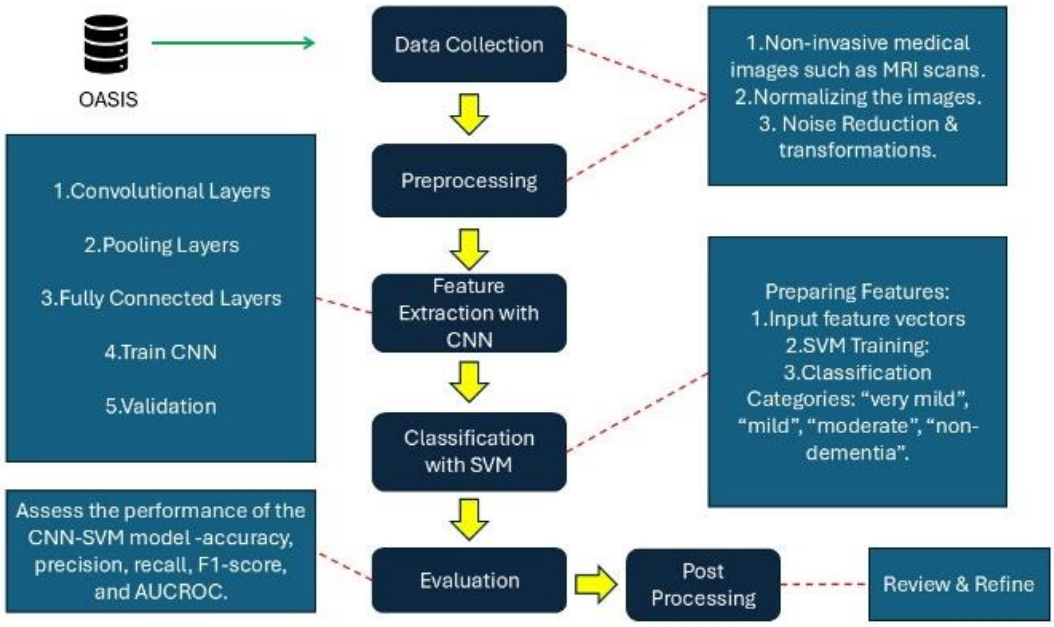

Fig. 3. CNN-SVM Multimodal Workflow

3.3.1 Data Collection

MRI images have been retrieved from OASIS corpus where there are several scans of a patient which are further processed to decrease skewing and overfitting issues.

3.3.2 Preprocessing

We have normalized the images collected into a fixed size and format along with the application of some transformations that resulted in making the data set rich in diversity and have strong models and decreased the problem of overfitting.

3.3.3 Feature Extraction with CNN

Design CNN Architecture:

Number of Layers: Prepare a multiple-layer CNN with many Convolutional, Activation functions (e.g. ReLU), Pooling, and dropout layers. The ReLU (Rectified Linear Unit) activation function which is depicted in (3) introduces nonlinearity into the model and keeps positive values unchanged while setting negative values to zero.

$$ReLU(x) = \max(0, x) \qquad (3)$$

Convolutional Layers: Feature Extraction using convolutional operations on the input images. After Convolutional Layers we apply Batch Normalisation to stabilize training, accelerate convergence, and reduce sensitivity to initialization.

Pooling Layers: Use MaxPooling or AveragePooling layers. These reduce the dimension but do leave most of the important features behind. Fully Connected Layers: Add fully connected layers to further process the features before passing them on to classification

We use dropout, where we randomly zero a portion of the input units at training time, post Pooling and Dense layers, to avoid overfitting.

$$y_i = \begin{cases} 0, & with\ probability\ p \\ \frac{x_i}{1-p}, & with\ probability\ 1-p \end{cases} \qquad (4)$$

Train CNN:

This uses pre-process image inputs to train the CNN. Suitably choose a loss function for updating model weights.

Feature Extraction:

After training, apply CNN to obtain feature vectors from images. These vectors would have been representations of the learned high-level features of the CNN.

3.3.4 Classification with SVM

Preparing Features:

Input: Feed the feature vectors extracted from CNN into SVM classifier Train SVM

SVM Training: Feed the feature vectors to SVM classifier for training. Choose an appropriate kernel, such as radial basis, and fine-tune SVM hyperparameters, like C and gamma, using grid search and cross-validation.

Classification: Classification with trained SVM: Classify the feature vectors into the different classes - "very mild", "mild", "moderate", and "non-dementia".

3.3.5 Evaluation & Post processing

The effectiveness of the CNN-SVM model can be measured using different performance metrics by applying it on a test dataset that is not used during training.

Analysing the Results: Overview of Classification Apart from measuring its overall performance, gain insight into how the model classifies cases and potential regions for improvement.

Refine: Improve the model based on how good or bad the model is performing.

4. RESULTS

This model uses CNNs for salient feature extraction from magnetic resonance imaging (MRI) with a reduction in the dimensionality of features via PCA.

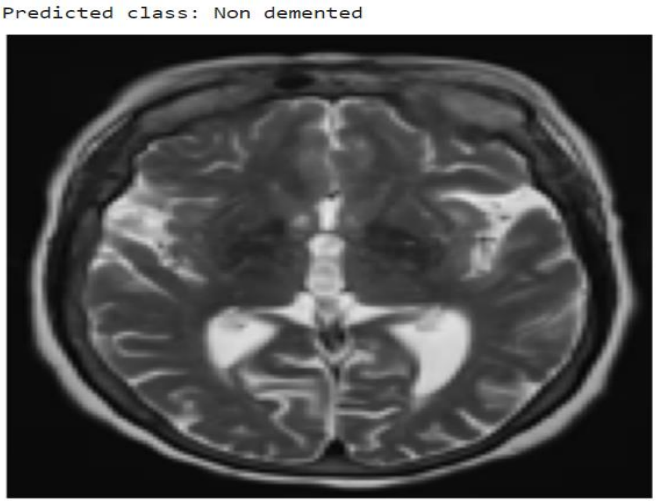

Fig. 4. Sample Brain MRI predicted as non-demented

Classification based on the reduced features. Accuracy and cross-validation score: the model reached a level of 92.30% and 88.36%, respectively. Sample output is shown in Fig.4.

4.1 Confusion Matrix

A class represents a specific stage of cognitive impairment. The confusion matrix shows how accurately the model predicts each Alzheimer's stage, indicating classification errors and model performance.

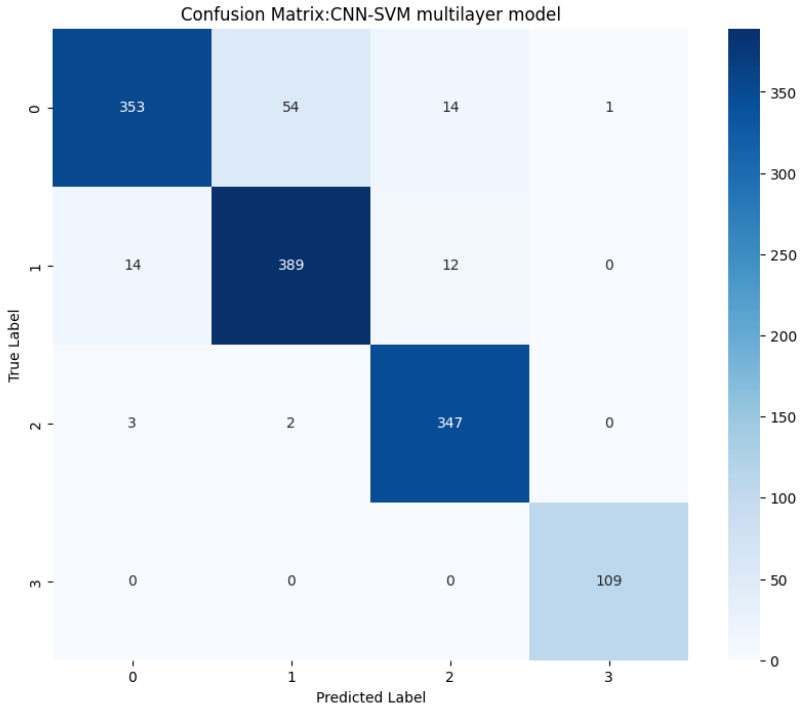

Fig. 5. Confusion matrix of CNN-SVM multilayer model

Class 0

TP = 353(Predicted as 0, Actual 0)

FN = 54 + 14 + 1 = 69(Predicted as 1, 2, or 3, Actual 0)

FP = 14 + 3 + 0 = 17 (Predicted as 0, Actual 1 or 2 or 3)

TN = 389 + 12 + 0 +2 + 347 + 0 + 109 = 859

Class 1:

TP = 389 (Predicted as 1, Actual 1)

FN = 14 + 12 = 26 (Predicted as 0 or 2, Actual 1)

FP = 54 + 2 + 0 = 56 (Predicted as 1, Actual 0, 2 or 3)

TN = 353 + 14 + 1+ 2 + 347 + 0 + 109 = 826

Class 2:

TP = 347 (Predicted as 2, Actual 2)

FN = 12 + 2 = 14 (Predicted as 0 or 1, Actual 2)

FP = 14 + 54 + 0 = 68 (Predicted as 2, Actual 0 or 1 or 3)

TN = 353 + 389 + 1 + 0 + 109 = 852

Class 3:

TP = 109 (Predicted as 3, Actual 3)

FN = 0 (Predicted as 1, Actual 3)

FP = 1 + 0 + 0 = 1 (Predicted as 3, Actual 0 or 1 or 2)

TN = 353 + 54 + 14 + 14 + 389 + 12 + 2 + 347 = 1185

4.2 Classification Report

The below classification report gives a detailed overview of the performance of a predictive model over four classes labelled 0, 1, 2, and 3. The different metrics precision, recall, as well as the F1-score, are calculated using (5), (6), (7) in addition to the model's overall accuracy and class averages.

$$Precision = \frac{TP}{TP+FP} \quad (5)$$

Calculates the number of correct positive results out of the total cases.

$$Recall = \frac{TP}{TP+FN} \quad (6)$$

Calculates the ratio of actually recognized true positives to all existing actual positives.

$$F1 = 2 \times \frac{(Precision \times Recall)}{(Precision + Recall)} \quad (7)$$

It gives one measure that is equally balanced between recall and precision by computing the hormonic mean of the two.

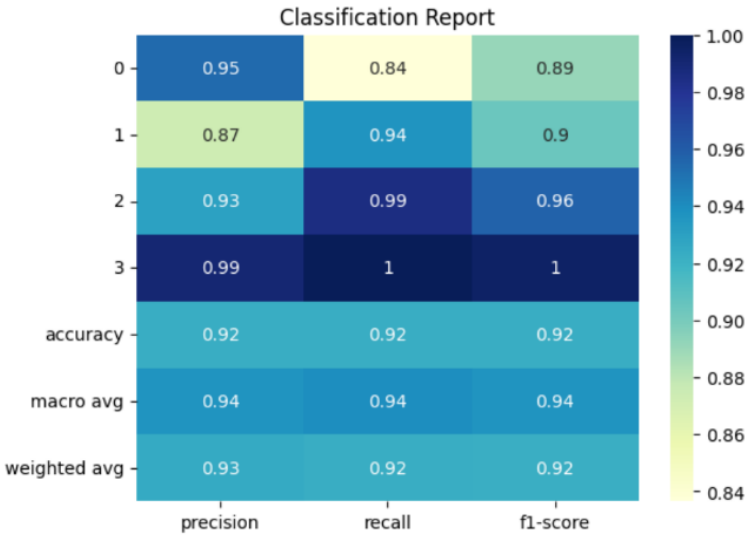

Fig. 6. Classification report determining the performance

of the model.

-**Class 0**, being the first category with an F1-score of 0.89, a 0.84 recall, and a precision of 0.95

-**Class 1**, which has a lower metric with an F1-score of 0.82, precision of 0.87, and recall value of 0.79

-**Class 2**, which has good performance with a recall of 0.99, a precision of 0.93 and an F1-score value of 0.96.

-**Class 3** is almost a perfect classifier, with F1-score = 1.00 and flawless precision and recall at 1.00.

Overall, the accuracy of the model stands at 0.92 calculated using (8), which means that 92% of the predictions performed by the system are accurate.

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

Average performance of every class is calculated by macro average, but it does not pay much heed to class imbalance. Whereas number of occurrences in each class is considered by the Weighted average and shows a relatively more balanced perspective of performance.

This classification report thus underlines the fact that the model is very robust in the accurate classification of instances, especially in Class 3, but points to areas where performance may be improved in Classes 0 and 1.

4.3 Cross-Validation Accuracy:

The graph below represents the cross-validation of a predictive model accuracy variation in relation to five folds. On the graph, the fold number is plotted versus the x-axis on the y-axis vs. accuracy. In this respect, it gives a picture about the stability of the model's performance, as well as its generalization concerning the different data subsets.

$$CV\ Accuracy = \frac{1}{k}\sum_{j=1}^{n} Accuracy_j \quad (9)$$

where *k* is the number of folds, and $Accuracy_j$ represents the accuracy obtained from each fold *j*.

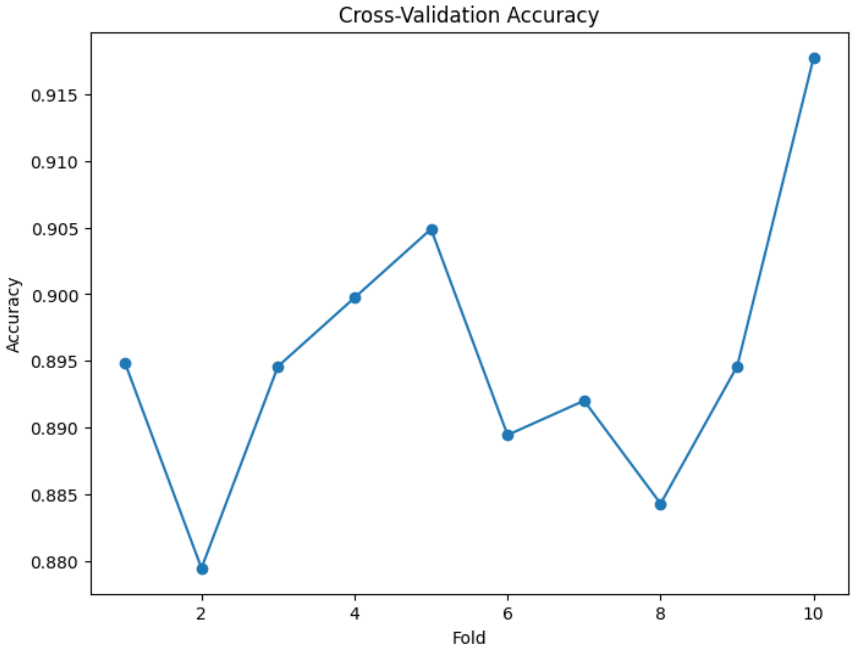

Fig. 7. Cross-validation accuracy of the model

Ten subsets (folds) are created from the dataset in the case of 10-fold cross-validation (as shown in the graph). Iteratively, the model is tested on four subsets after being trained on the others, using each fold once for testing. The individual accuracies from these 10 folds are then averaged using the formula above to get the overall CV accuracy.

The 10 Folds in the above graph Fig.6 represent:

- **Fold 1**: Accuracy starts relatively high at around **0.89**, showing a good initial performance.
- **Fold 2**: The accuracy experiences a drop to approximately **0.88**, indicating some variability in performance.
- **Fold 3**: There is another dip in accuracy, reaching the lowest point at around **0.88**.
- **Fold 4**: The accuracy significantly improves, surging to approximately **0.90**, marking a positive recovery.
- **Fold 5**: The accuracy rises further, peaking at around **0.91**, the highest accuracy observed in this cross-validation process.
- **Fold 6**: A moderate decline is observed, with accuracy dropping back to approximately **0.89**.
- **Fold 7**: Accuracy stabilizes at a similar level, remaining around **0.89**, showing consistency.
- **Fold 8**: A slight decline occurs again, bringing the accuracy to around **0.885**.
- **Fold 9**: A modest upward trend is seen, with accuracy climbing back to approximately **0.89**.
- **Fold 10**: Accuracy ends on a high note, reaching the maximum at **0.915**, the highest value across all folds.

These fluctuations in accuracy across the folds indicate variability in the model performance perhaps caused by differences in the data subsets used in the different folds or perhaps by model sensitivity to specific data features. Accuracies at the bottom and the top are vastly different, making a case for studying model stability and data consistency. Accuracy recovery in Fold 4 from the drop in Fold 3 gives rise to the possibility of overfitting issues or that there might be outlier data affecting the predictions of the model.

-**Mean Accuracy:** The average of the accuracies of each fold. For this case, it outputs roughly 0.902. -**Range of Accuracy:** The difference between its highest accuracy value and the smallest accuracy value obtained. For this data, the difference is calculated to be 0.035, meaning that there was a spread of model performance over different datasplits. The graph of cross-validation performance given here is a very essential tool for diagnostics, where areas are indicated that need tuning in the model, balancing in data, or additional feature engineering needs to be adjusted to optimize robustness and accuracy of prediction models.

4.4 Receiver Operating Characteristic (ROC) Curve:

The ROC curve plots the sensitivity and false alarm rate for every class in a classification model against each other, indicating the trade-off between the two. The Area Under the Curve (AUC) values, ranging from 0.97 to 1.0, demonstrate the model's high discriminatory power. AUC close to 1 indicates excellent performance, while curves above the diagonal random-guessing line confirm the algorithm's reliability in differentiating between classes. This visualization validates the effectiveness of the CNN-SVM hybrid model for multi-class classification.

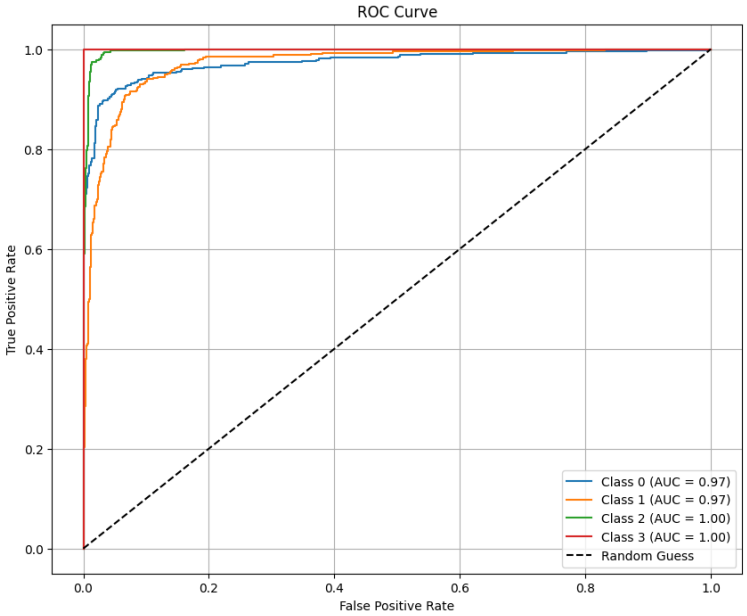

Fig. 8. ROC Curve of CNN-SVM multilayer model

ROC Curve Calculations:

The ROC curve is produced by varying the classification decision threshold and recording the following values at each point.

1. **False Alarm Rate:**

This informs us how frequently negative cases are wrongly labeled as positive.

$$Falsealarmrate = \frac{False\ Positives}{False\ Positives + False\ Negatives}$$

2. **Sensitivity :**

This quantifies how many true positive instances are correctly classified by the model.

$$sensitivity = \frac{True\ Positives}{True\ Positives + False\ Negatives}$$

The ROC curve plots TPR against FPR at various thresholds.

AUC Metric:

The Area Under the Curve (AUC) provides one value that estimates how well the classifier works.

- An AUC of 1.00 indicates perfect classification with no errors.
- An AUC of 0.50 represents random guessing.

The AUC values for the four classes are shown in Figure 7. The key observations are as follows:

- **Class 0:** AUC = 0.97, indicating excellent classification performance.
- **Class 1:** AUC = 0.97, indicating excellent classification performance.
- **Class 2:** AUC = 1.00, indicating perfect classification without false positives or false negatives.
- **Class 3:** AUC = 1.00, also indicating perfect classification.

The high AUC values for all classes suggest the classifier performs exceptionally well across all categories. Classes 2 and 3 achieved perfect AUC scores, implying the classifier made no errors in predicting these classes. The slightly lower AUC values for Classes 0 and 1 (0.97) indicate a minimal rate of misclassification, which is still highly commendable

4.5 Precision – Recall Curve:

Precision - Recall (PR) curve gives a detailed analysis of the effectiveness of the CNN-SVM system by demonstrating the precision vs. recall trade-off for every class. High precision in the curves suggests the model's capability at minimum false positives for precise detection of positive instances. and high recall suggests its capability to include most of the true positive instances. The curves, near the top-right corner for all classes, illustrate the strength of the CNN-SVM system in finding the trade-off between recall and precision. These findings confirm the model's effectiveness in performing multi-class classification tasks. Slight decreases in precision at lower recall values for some classes indicate possible areas for further optimization to enhance the model's overall effectiveness

PR Curve Calculations:

The PR curve indicates the relation between precision and recall for varying classification thresholds., offering insights into the tradeoff between these two metrics.

1. **Recall :**

Recall measures the proportion of actual positive cases which are correctly classified.

$$TPR = \frac{True\ Positives}{True\ Positives + False\ Negatives}$$

2. **Precision**:

Precision computes the proportion of those cases correctly classified as positive over all the positive cases predicted.

$$TPR = \frac{True\ Positives}{True\ Positives + False\ Positives}$$

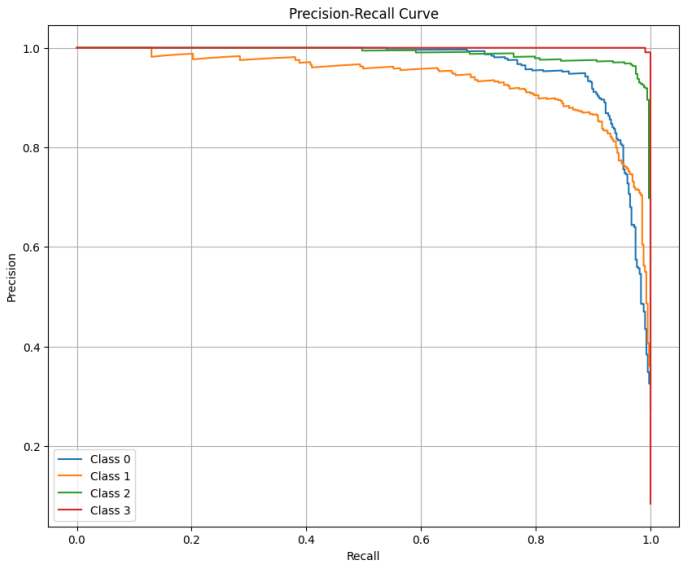

Fig. 9. PR Curve of CNN-SVM multilayer model

The PR curves for the four classes are shown in Figure 2. Key observations include:

- **Class 0:** Precision and Recall are high but show a slight tradeoff at higher recall values.
- **Class 1:** Similar to Class 0, with a good trade-off between recall and precision.
- **Class 2:** Nearly perfect precision across all recall levels, indicating exceptional classification performance.
- **Class 3:** Also demonstrates near-perfect precision and recall, with minimal tradeoff observed.

Observations:

- **Class 2 and Class 3:** classes exhibit near-perfect PR curves, reflecting the ability of the classifier to correctly identify and distinguish positive instances with a minimum of false positives and false negatives.
- **Class 0 and Class 1**: Minor decreases in accuracy at higher recall levels indicate the performance of the classifier might be optimized for these classes.

The PR curve analysis shows the good performance of the classifier on all classes with almost perfect precision and recall for Classes 2 and 3. Although Classes 0 and 1 also show good performance, slight improvements can be achieved in balancing precision and recall at higher thresholds. This analysis shows how good the classifier is, especially in imbalanced datasets, and gives a good understanding of how it acts in separating positive instances.

4.6 Accuracy Vs PCA Retention Rate:

The following bar plot illustrates the interaction between PCA retention rates and model accuracy. With an increase in PCA retention rate, model accuracy increases, showing that keeping more components results in the model's ability to capture more variance, thus improving performance. The accuracy percentages, from 84.9% to 92.3%, are labeled above every bar to give exact measures of the model's performance at various PCA retention levels. This chart illustrates the significance of PCA in reducing dimensions and optimizing the model.

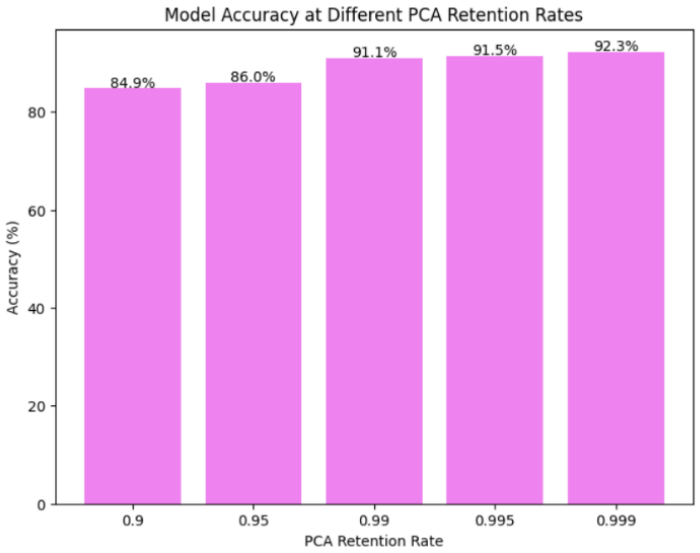

Fig. 10. Accuracy Vs Retention Rate bar plot of CNN-SVM multilayer model

Principal Component Analysis (PCA) is a dimension reduction technique for lower-dimensional projection of high-dimensional data such that the projection retains as much information(variance) as possible.

Step-by-Step Process:

1. **Standardize the Data:**

Center the data by subtracting the mean and, optionally, scale it to unit variance.

$$Z = \frac{X - \mu}{\sigma}$$

2. **Compute Covariance Matrix:**

Calculate the covariance matrix to measure the relationships between features.

$$\Sigma = \frac{1}{n-1} Z^T Z$$

3. Perform Eigen Analysis:

Determine the eigenvalues and eigenvectors of the covariance matrix..

a. Eigenvectors represent the directions of the principal components

b. Eigenvalues (λ) are the amount of variance explained by each principal component.

4. Select Principal Components:

Retain a subset of principal components based on the desired variance retention rate. If k is the number of selected components, the cumulative variance is:

$$Cumulative\ Variance\ Retained = \frac{\sum_{i=1}^{k} \lambda_i}{\sum_{i=1}^{m} \lambda_i}$$

5. Transform Data:

Project the original data onto the selected principal components:

$$Z_{PCA} = Z.W_k$$

Where W_k contains the eigenvectors corresponding to the top k eigenvalues.

Model Accuracy Analysis:

- **PCA Retention vs. Accuracy**: As PCA retention rate increases, more information is preserved, allowing the model to better classify the data, resulting in higher accuracy.
- **Tradeoff**:
  - Lower retention rates (e.g., 0.90, 0.95) reduce dimensionality more aggressively, leading to information loss and decreased accuracy.
  - Higher retention rates (e.g., 0.99, 0.999) retain nearly all information, enabling the model to maintain or improve accuracy.

5. DISCUSSIONS

5.1 Algorithm Performance:

The CNN-SVM multimodal model demonstrates outstanding performance in AD detection from MRI images with a 92.3% accuracy, proving the system's capability to cope with the intricacies of medical image classification. The integration of CNN and SVM enables the model to take advantage of the strengths of both methods. CNNs are particularly effective at extracting spatial and hierarchical features from MRI scans, detecting slight patterns that point to Alzheimer's development. The features which are extracted are then fed to SVM, which is specifically good at detecting accurate decision boundaries in high-dimensional feature spaces and improving classification performance. This synergy guarantees that feature extraction and classification are both tuned for the application.

The robustness of the CNN-SVM model is further strengthened by attentive preprocessing methods and design decisions. Preprocessing methods include normalization, resizing, and scaling to cope with variability in MRI images. Not only does this enhance the system's capability to generalize to novel data, but it also limits overfitting. The architecture of CNN is set up in order to obtain finer features with stacks of convolutional layers using ReLU activation succeeded by max-pooling to ensure the conservation of the most important features. The flattened feature vector is given as an input to the SVM, and thanks to the kernel trick, which allows for the non-linear transformation, it becomes capable of segregating Alzheimer's and non-Alzheimer's types efficiently. Such a two-step approach makes it both computationally light and accurate.

The performance of the algorithm is a testament to the combination of DL and classical ML approaches. Through the integration of CNNs' capacity to process unstructured image data with SVMs' power of accurate classification, the model delivers outstanding accuracy despite the scarcity of labeled data. The application of hinge loss in SVM guarantees the fine-tuning of decision boundaries to reduce misclassifications. Also, the hybrid model surpasses individual CNNs and other classifiers, and therefore it is a good and efficient solution for the prior detection of Alzheimer's. The 92.3% accuracy, coupled with the efficacy of the model, indicates its viability for practical use, especially in enhancing early diagnosis, supporting clinicians, and enabling timely medical interventions.

6. CONCLUSION

In summary, this paper uses the novel integration of a CNN-SVM multi-layer model with MRI data and other non-invasive diagnostic modalities, such as speech analysis, saliva testing, and retinal imaging, to promote initial stage diagnosis and identification of AD. This combined approach intends to overcome limitations imposed by conventional diagnostic methods such as cerebrospinal fluid testing and PET scans. Through the high-end feature extraction properties of CNNs and the accuracy of SVMs in classification, , this method is able to effectively detect early Alzheimer's through minor brain structure patterns, thus distinguishing between diseased patients and normal subjects. The model provides an end-to-end, non-invasive diagnosis tool that considerably boosts the diagnostic field.

For making it precisely relevant, ADNI and OASIS datasets are utilized for calibration and validation of the system's capability on a large scale to large datasets. This will finally enhance the efficiency of the model in actual clinical settings. Looking to the future, this study plans on integrating information from wearable devices, which would make it possible for continuous, non-invasive monitoring thus enhancing the rates of early diagnosis This study is a tremendous improvement over Alzheimer's diagnostics, as it offers a more accurate, cost-effective, and accessible option compared to conventional methods.By inc-reasing the diagnostic accuracy and expandability of this model,this paper establishes a good foundation for more personalized treatment strategies and better handling of AD, being a breakthrough in the combat against this debilitating condition

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