A Review of Recent Advances in Alzheimer's Disease Machine Learning Algorithms for Early Mild Cognitive Impairment Prediction

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ABSTRACT:
Research into early Alzheimer's disease (AD) is the main focus of clinical investigations. Clinical progression predictions from normal to moderate cognitive impairment (MCI), MCI to dementia, AD, or non-progression are not very accurate. Medication utilization is decreased and trial efficiency is increased with accurate symptomatic progressor identification. Preparing for Alzheimer's therapy would thus be easier with an early diagnosis. As a result, the disease could develop more slowly. Alzheimer's may be recognized using machine learning algorithms. The performance categorization of patients with Alzheimer's disease may be improved using advanced machine learning. As a result, this research builds upon previous diagnostic studies of Alzheimer's disease conducted since 2016. Participant nation, data modalities and characteristics, feature extraction techniques, number of follow-up data points, anticipated time from mild cognitive impairment to Alzheimer's disease, and machine learning models are all taken into account in this overview of studies on Alzheimer's detection. The characteristics and machine learning models used in earlier Alzheimer's research may be explained to novice researchers by this review. Because it is structured to adhere to the many elements of the Machine Learning technique, this study aids researchers in objectively assessing the literature on Alzheimer's detection. learning models used in earlier Alzheimer's research may be explained to novice researchers by this review. Because it is structured to adhere to the many elements of the Machine Learning technique, this study aids researchers in objectively assessing the literature on Alzheimer's detection.

1. Introduction

The gradual breakdown of brain cell protein components, leading to the accumulation of plaques and tangles, is the hallmark of Alzheimer's disease (AD), a neurodegenerative disorder [1]. Cognitive function deteriorates dramatically because these abnormal proteins block their components from interacting with one another. There is a 10% probability that mild cognitive impairment (MCI) may progress to Alzheimer's disease (AD) [2, 3]. Mild cognitive impairment (MCI) is a transitional condition between CN and dementia. With an estimated 55 million cases globally, Alzheimer's disease is the sixth biggest killer [4]. According to the most current worldwide Alzheimer's Report, this data was gathered.

It might take a long time to diagnose Alzheimer's disease. Biomarkers for Alzheimer's disease may now be efficiently collected with the use of diagnostic technologies including positron emission tomography (PET) scans, computed tomography (CT), and magnetic resonance imaging (MRI) [5]. Artificial intelligence (AI) combined with biomarker data could pave the way for earlier disease detection. Anomaly detection, signal analysis, assessment and classification of neurodevelopmental disorders (specifically autism), detection and management of neurological disorders, monitoring and care for the elderly, cybersecurity and trust management, analysis of ultrasound images, detection and management of various diseases, delivery of smart healthcare services, text and social media mining, understanding student engagement, and many more

complex research endeavors have been drawn to artificial intelligence (AI) in recent years, especially deep learning (DL) and machine learning (ML).

The ability of ML and DL algorithms to analyze large datasets and identify trends that humans would miss has led to their extensive usage in AD prediction [6–8]. Timely diagnosis and treatment are made possible by machine learning and deep learning models' capacity to discover patterns and signals that indicate the early stages of illnesses. A growing number of studies are pointing to the remarkable success that deep learning algorithms have had so far in predicting the onset of Alzheimer's disease [9–11].

The lack of transparency in machine learning and deep learning models has greatly hindered their mainstream usage, even if they have shown promising results in predicting Alzheimer's disease [12]. Medical practitioners may be reluctant to use these models in real-world scenarios because of their opaqueness and lack of interpretability [13]. To make educated decisions about a patient's treatment, doctors must comprehend the logic behind models that indicate a high risk for Alzheimer's disease. To that end, XAI, which stands for AI models that exhibit greater transparency and interpretability, has grown in significance over the last several years. Some examples of XAI methods include saliency maps and feature significance analysis. Famous explainable AI methods in the field of Alzheimer's disease prediction using deep learning and machine learning include SHAP and LIME [14].

Deep learning (DL) has great potential for clinical decision support in a variety of diseases, including Alzheimer's disease (for imaging analysis) [15-17], diabetes mellitus [18, 19], and cancer [20, 21]. The primary advantage of deep learning over other shallow learning techniques is its ability to extract the best predictive characteristics straight from raw data given a set of labeled examples. Regarding single data modalities, such as images [22, 23], EHRs [24], and SNPs [25], DL performs better than shallow learning. DL techniques facilitate training and prediction even in the case of insufficient data [26]. Here, we develop a novel deep learning architecture for clinical decision support that can predict the stage of Alzheimer's disease (AD) based on clinical data, images, and genetic information.

Despite extensive financial investment in clinical trials and decades of study, no anti-Alzheimer's medicine is now available. Clinical studies for innovative, possibly efficacious approaches to producing anti-Alzheimer medications have not yet shown favorable outcomes [26, 27]. Researchers and campaigners continue to ascertain the precise etiology of the illness. The prevailing hypothesis for Alzheimer's Disease (AD) is that it is a multifactorial condition in which both genetic and environmental factors accelerate the aging process.

More than 600 genes, environmental influences, and epigenetic modifications contribute to the etiology of Alzheimer's disease [28, 29]. Genetic anomalies associated with Alzheimer's disease include germline mutations, mitochondrial DNA mutations, and single nucleotide polymorphisms. The objective of therapeutic clinical therapy for Alzheimer's Disease is the enhancement of behavioral, cognitive, and non-cognitive symptoms. In the last twenty years, no new drugs aimed at Alzheimer's disease have received FDA clearance. The current aim in the development of novel anti-AD drugs is to use disease-modifying agents that postpone the beginning of an existing condition or impede its progression. Cellular oxidation, tau protein, and A are now the most potential targets for altering the pathological condition of Alzheimer's disease [30].

This study aims to provide a thorough summary of the current knowledge of Alzheimer's disease pathogenesis, including its classifications, diagnostic biomarkers, and authorized pharmaceutical and non-pharmacological therapy approaches. We examine the burgeoning significance of epigenetics and the microbiome in the development of Alzheimer's disease, along with the prospective uses of genetic and epigenetic therapies. This article reviews pharmaceuticals currently in development or clinical trials, analyzes their advantages and disadvantages, examines

recent targeted approaches, and outlines critical factors for the successful conduct of future clinical trials. Furthermore, we explore innovative methodologies for Alzheimer's disease detection and pharmacological development using network biology, artificial intelligence, and machine learning. The development of Alzheimer's disease (AD) is a possibility for certain people with mild cognitive impairment (MCI), especially those with MCI. On the other hand, severe Alzheimer's disease (AD) may occur in some people who still have moderate cognitive impairment (MCI), often called stable mild cognitive impairment (sMCI). Clinicians must identify individuals who may have sMCI and pMCI. If a clinician can identify prospective Alzheimer's patients early on, they will have a better chance of providing appropriate diagnostic and treatment choices. This might help halt the hazardous progression of Alzheimer's disease, which can be very challenging for both the patient and their loved ones to cope with. This is analogous to how sMCI aids in medicine prescription by determining the severity of cognitive impairment. This has the potential to alleviate some of the extra expenses that persons with MCI may incur [31-33].

1.1. Mechanisms of Alzheimer's disease

The accumulation of oligomers, or hydrophobic A aggregates, that are not properly eliminated leads to an increase in the amount of extracellular A plaques, a hallmark of Alzheimer's disease. Another feature is the formation of neurofibrillary tangles (NFTs). These tangles are made up of tau, an intracellular protein that is insoluble and related to microtubules. Presented in Figure 1 is the MetaCore [34] pathway map, which provides a concise overview of the key genes, proteins, and processes, associated with the pathophysiology of AD. To further demonstrate their druggability, we marked on the map which network objects are recognized AD biomarkers according to the MetaCoreTM and which ones are drug targets for existing treatments shown in Figure 1.

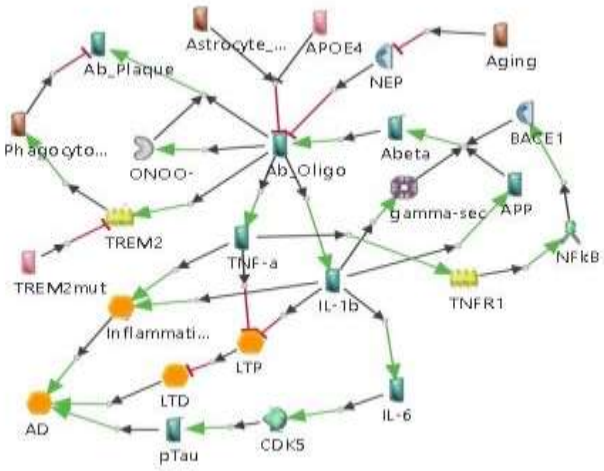

Figure 1: Mechanisms of Alzheimer's Disease

1.2. Contribution

- The research uses a systematic review approach that complies with the guidelines set out by OASIS and ADNL dataset to ensure a complete and in-depth examination.
- Several characteristics are shared by patients with pMCI and sMCI. For example, atrophy of certain brain regions is seen in both pMCI and sMCI individuals.
- The inability of the characteristics obtained from various multi-modal data sets to be generalized is another major barrier.
- One-way transportation ML is more efficient than ML models for multi-modal data processing.
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2. Related Works

Alzheimer's disease (AD) ranks sixth among US causes of mortality and is the most prevalent neurodegenerative illness [35, 36]. The global illness burden of AD is projected to surpass $2 trillion by 2030 [37], making early identification of the disease critical. Clinical symptoms alone are insufficient to identify the pathology and development of Alzheimer's disease (AD) in fewer than half of AD patients, despite substantial research and improvements in clinical practice. The most definitive histological evidence of Alzheimer's disease is the presence of amyloid plaques and neurofibrillary tangles. In the early stages of Alzheimer's disease, synapses and neurons are lost, but plaque is not [38]. Investigations on the causes of Alzheimer's disease are an ongoing part of the AD project's data and data mining efforts [39-41]. Imaging, genetic, and protein biomarkers have recently been added to the list of AD biomarkers, which already include neurological tests and scores (e.g., MMSE scores), clinical symptoms (e.g., dementia, memory loss), and clinical symptoms [42]. The lack of a holistic view of AD progression is because the majority of this research only used data from a single modality to find biomarkers. Functional magnetic resonance imaging (fMRI), imaging genetics [43–48], positron emission tomography (PET) [49, 50], structural magnetic resonance imaging (T1 weighted, T2 weighted), and a plethora of other imaging modalities have all been used in several AD multi-modal investigations. Phenotypes and data labeling have both been enhanced by integrating genetics with clinical data. Merging PET and MRI data has improved prediction using DL models like auto-encoders and deep-belief networks [51], in addition to shallow learners.

Alzheimer's disease is one of the deadliest types of dementia due to its rapid progression. There is a chance it will kill someone. Alzheimer's disease has the potential to seriously impair a person's cognitive abilities [52]. You should see a professional if your cognitive abilities are a problem. Many types of dementia may arise from a patient's cognitive deterioration. Physicians find it challenging to identify individuals who may acquire Alzheimer's disease since dementia comes in a variety of ways [53].

Finding biomarkers for Alzheimer's disease and other types of dementia is one of the most important study topics for scientists [54-56]. They used a rat model to perform studies to detect Alzheimer's patients.

Determining whether the medication is effective in delaying the onset of Alzheimer's disease is the main objective of the rat experiments. Because of this, much of the research being done now focuses on examining the consequences of Alzheimer's disease and its therapies in rats. These studies are being carried out by doctors who believe that the risk factors for AD that they have found in rats may also be present in people. Consequently, researchers are examining how the same neuroimaging changes seen in rats affect human bodies [57–59].

Finding people with Alzheimer's at a baseline or screening visit may help doctors make better health-related decisions. In this manner, the doctor may use more potent medications to delay the progression of the illness. Additionally, early Alzheimer's detection improves the patient's health outcomes. Furthermore, treatment approaches are more effective when used early in the course of the illness.

Likewise, the early phases of a disease are when the effects of medications are most noticeable [60]. Researchers have generally used longitudinal (visit) data from patients to generate early predictions. Longitudinal data collected from several follow-up periods, including first, second, third visits, and so on, comprise the relevant information and features that would evolve with time [61, 62].

By combining temporal brain shrinkage with neuroimaging and cerebrospinal fluid testing for neurofibrillary tangles, beta-amyloid, and tau proteins, Alzheimer's disease may be confirmed in its late stages, when dementia symptoms are already apparent. It is still difficult for clinicians to

use the signs that are available from positron emission tomography (PET) and magnetic resonance imaging (MRI) data to diagnose mild cognitive impairment (MCI) patients early on in their development of Alzheimer's disease (AD) dementia. Public databases such as the Alzheimer Disease Neuroimaging Initiative (ADNI) (http://adni.loni.usc.edu) have made available to the scientific community a large amount of longitudinal neuroimaging datasets including individuals with healthy brains, mild cognitive impairment (MCI), and Alzheimer's disease (AD), as well as other variables like demographics, genetics, and cognitive assessments. This should help with this challenge. To classify and automatically identify the development of moderate cognitive impairment (MCI) and Alzheimer's disease (AD), these datasets may be evaluated and analyzed using machine learning (ML) algorithms and other modern computational approaches [63, 64]. These cutting-edge devices may find their way into clinical settings where they might aid in early diagnosis and prognosis.

The goal of the machine learning paradigm is to classify people according to a variable of interest by training an algorithm on a dataset that contains neuroimaging findings and other clinical parameters. The goal is to find common patterns in the dataset. In the case of early detection and differentiation of Alzheimer's Disease (AD) from stable Mild Cognitive Impairment (MCI), for instance, the algorithm learns to categorize data based on the diagnosis and determines the most important characteristics for group differentiation. One possible application of the learned algorithm in treatment planning is to identify patients for whom a diagnosis is still pending [64, 65, 66]. Any ailment marked by distinct patterns in the brain or abnormalities in anatomy may be treated using this method. To read about the same goals and methods discussed concerning ADD/ADHD, schizophrenia, and autism, see Arbabshirani, Plis, Sui, & Calhoun [67].

Machine learning algorithms have recently shown promise in picture classification, according to research [68-70], whether the people are healthy, have mild cognitive impairment (MCI), or have Alzheimer's disease (AD). Although this categorization provides important information about AD biomarkers, it is still necessary to determine and predict whether a patient with mild cognitive impairment (MCI) will progress to Alzheimer's disease (AD) dementia or remain stable so that this technology can have a greater impact on clinical practice by enabling doctors to develop individualized treatment plans. To forecast the development of Alzheimer's disease dementia from Mild Cognitive Impairment, this comprehensive research aims to evaluate current classification approaches that use machine learning algorithms applied to neuroimaging data together with other characteristics.

3. Methods

In conducting this study, we followed the guidelines laid forth by PRISMA [71, 72]. We scoured the literature for studies that used neuroimaging data and machine learning (ML) algorithms to predict when dementia would progress from mild cognitive impairment (MCI) to Alzheimer's disease (AD). A patient initially diagnosed with mild cognitive impairment (MCI) may later be diagnosed with Alzheimer's disease (AD) based on clinical criteria, such as the MMSE and CDR scales, and NINCDS/ADRDA criteria for probable AD dementia, during a three-year follow-up period for ADNI databases and a one-year follow-up period for AddNeuroMed databases [73, 74]. This condition is known as "progressive MCI" or pMCI. If a patient's initial diagnosis of moderate cognitive impairment does not change over the follow-up period, we classify them as having "stable MCI" (sMCI).

It must have been published in English between 2010 and 2021 to be eligible for inclusion. We did not include works published before 2010 since there were major differences in approach (such as the creation of deep learning algorithms) and technology (such as computing power, and graphics processing units) compared to what is considered contemporary. Even when looking at articles published in the early and late 2010s, there are methodological problems. These

discrepancies are mostly explained by the improvements in methodology and the increase of the ADNI database, both of which made previously unattainable technological advances possible.

3.1. Dataset

3.1.1. ADNI Dataset

Alzheimer's Disease Neuro-Imaging Initiative (ADNI), The dataset consolidates researchers investigating the progression of Alzheimer's disease from moderate cognitive impairment (MCI). The ADNI project integrates data from many cognitive assessments, including MRI, PET, neuroimaging, genetic analyses, and others. The dataset consists of five years of participant data collected from hospitals around North America. The major objective of this research activity is to identify biomarkers for the early identification of Alzheimer's disease via Machine Learning techniques. Clinical trial metrics and biomarkers are optimized, verified, and standardized using ADNI datasets [75-77].

3.1.2. Open Access Series of Imaging Studies (OASIS) dataset

More than a thousand patients' multimodal data points collected across varying periods make up the OASIS dataset. Neuroimaging and cognitive test results collected over a certain period make up the dataset. There are more than 10,000 3D sliced MRI images included in the set.

The goal of the study is to use clinical, neuroimaging, genetic, and other markers to proactively identify individuals who may develop mild cognitive impairment or Alzheimer's disease. Data from 416 patients, ranging in age from 16 to 96 years, make up the OASIS dataset. Everyone included in the study is right-handed. Beyond half of the people included in the dataset are beyond the age of 50 [78, 79].

3.2. Data Preprocessing

3.2.1. Missing Values

Although the occurrence of missing values is very low (less than 7%), the majority of the dataset's characteristics do contain them. We start by adding a new tag to the feature set whenever a value is missing for that feature. Subsequently, new input values are generated using the residual characteristics and the original tags. What follows is an application of a random forest method to forecast values that will be missing from the new tag [80].

3.2.2. Data Augmentation

Our dataset contains three thousand cases of NC, however only 150 AD cases and 750 MCI samples are included. The data imbalance might potentially considerably hinder the effectiveness of the machine learning system. For example, overfitting may occur if the training data is not balanced. We use the adaptive synthetic sampling approach (ADASYN) to solve the issue [81]. ADASYN may generate samples for the minority class adaptively based on its distribution shown in Figure 2.

	image	label
0	/kaggle/input/fdata-adni-dataset/AugmentedAlzh...	Late mild cognitive impairment
1	/kaggle/input/fdata-adni-dataset/AugmentedAlzh...	Late mild cognitive impairment
2	/kaggle/input/fdata-adni-dataset/AugmentedAlzh...	Late mild cognitive impairment
3	/kaggle/input/fdata-adni-dataset/AugmentedAlzh...	Late mild cognitive impairment
4	/kaggle/input/fdata-adni-dataset/AugmentedAlzh...	Late mild cognitive impairment

	ID	M/F	Hand	Age	Educ	SES	MMSE	CDR	eTIV	nWBV	ASF
0	OAS1_0001_MR1	F	R	74	2.0	3.0	29.0	0.0	1344	0.743	1.306
1	OAS1_0002_MR1	F	R	55	4.0	1.0	29.0	0.0	1147	0.810	1.531
2	OAS1_0003_MR1	F	R	73	4.0	3.0	27.0	0.5	1454	0.708	1.207
3	OAS1_0004_MR1	M	R	28	NaN	NaN	NaN	NaN	1588	0.803	1.105
4	OAS1_0005_MR1	M	R	18	NaN	NaN	NaN	NaN	1737	0.848	1.010

Figure 2: Data Augmentation

3.2.3. Data Normalization

There is a specific range of values for each dataset attribute. As a consequence, the trained model may provide illogical results by favoring the characteristic with higher values. To mitigate this impact, data normalization is essential [82]. Each feature undergoes max-min normalization, which may be represented as equation 1.

$$X = \frac{X - min_x}{min_x - max_x}$$

3.3. Feature Selection

The dataset comprises 47 parameters, including demographics, daily lifestyle, medical history, and regular physical tests (Table 2). Dimensionality reduction is essential for achieving simplicity and evaluating the model's complexity. The curse of dimensionality may adversely impact the model's runtime and storage resource utilization, particularly for non-scalable classifiers. Consequently, feature selection methodologies are necessary. Before using the classifier, feature selection is a preprocessing operation that identifies representative features to reduce redundant and superfluous elements while retaining essential information from the original dataset shown in Figure 3.

	Age	Educ	SES	MMSE	CDR	eTIV	nWBV	ASF	M/F_F	M/F_M	CDR_
0	74	2.0	3.0	29.0	0.0	1344	0.743	1.306	1.0	0.0	SD
1	55	4.0	1.0	29.0	0.0	1147	0.810	1.531	1.0	0.0	SD
2	73	4.0	3.0	27.0	0.5	1454	0.708	1.207	1.0	0.0	DML
3	74	5.0	2.0	30.0	0.0	1636	0.689	1.073	0.0	1.0	SD
4	52	3.0	2.0	30.0	0.0	1321	0.827	1.329	1.0	0.0	SD

Figure 3: Feature Selection

3.4 Feature Extraction

Table 1 constraints for feature extraction techniques described.

Technique	Extracted features	Remarks	Ref.
NSCT	The features of a system are described using terminology like entropy, contrast, energy, variance, standard deviation, skewness, and kurtosis.	1. Multiscale, multi-direction, shift-invariance, and superior frequency selectivity and regularity than CT are notable aspects of NSCT. 2. Make certain that multiscale and directionality characteristics are present.	[83, 84]
GLCM	Contrast, Entropy Correlation, Inverse Difference Moment, Variance, Sum Average, Sum Entropy, Difference Entropy, Inertia, Cluster shadow, and Cluster	1. The pixels' spatial connection is taken into account. 2. Textural characteristics were extracted.	[85, 86]

	Prominence are all names that may be used to represent the same phenomena.	3. Applied to the feed-forward neural network's training.	
DWT	Entropy, homogeneity, dissimilarity, and contrast are all terms that may be used to describe energy.	1. Using consecutive high pass and low pass filtering on different scales, extract features from an MRI. 2. Explain a signal's function in terms of localized frequency information.	[87]
PCA	Remove the primary components that account for the most volatility in the data. Covariance is a metric for determining the connection between datasets' dimensions.	1. The eigenvectors and eigenvalues of the data covariance matrix may be used to identify principal components. 2. The key benefit is that data patterns may be compressed without losing information by lowering the number of dimensions.	[88, 89]
GABOR	When a function is convolved with the Gabor wavelet, the frequency information near the center of the Gaussian is recorded. Gabor wavelets occur in a variety of forms and are characterized by parameters that govern direction, frequency, phase, size, and aspect ratio.	1. Its primary function is to extract textural characteristics. 2. The high computational cost of the convolution calculation used in the feature extraction method is an issue with these Gabor texture measurements. 3. The identification process is aided by just a tiny portion of the filters.	[90-95]

3.5. Machine Learning Classification

The optimal classifier for AD/MCI prediction is found by comparing many ML models, such as 2 basic classifiers and 3 ensemble classifiers.

K-Nearest Neighbours (KNN), and Random Forest (RF) are the two basic classifiers. A coherent approach that combines several base learners to achieve improved performance is ensemble learning. RF, KNN, and other machine learning methods may be used to train the basic learners in this methodology. There are two ways to create foundational learners: the parallel approach and the sequential approach. After combining all of the basic learners, two common combination procedures are weighted average for classification and majority voting to produce an upgraded learner.

A comprehensive examination led to many modifications of inclusion and exclusion criteria. They were removed before inclusion in the findings. Subsequently, they were eliminated based on the information extracted from the abstracts of the publications. The study primarily focused on articles using longitudinal data from MCI to AD to delineate distinct outcomes for the categorization of individuals with pMCI and sMCI. This is due to the use of follow-up data analysis in these investigations. Research that depends only on cross-sectional data to Numerous rounds of inclusion and exclusion criteria were used after a comprehensive examination. Duplicate papers were removed before inclusion in the findings. Subsequently, they were eliminated based on the information included in the abstracts of the publications. The study primarily focused on articles using longitudinal data from MCI to AD to delineate distinct outcomes for the categorization of individuals with pMCI and sMCI. This is due to the use of follow-up data analysis in these investigations. Therefore, we excluded studies that relied only on cross-sectional data to categorize individuals with pMCI and sMCI. Papers must include a clear elucidation of performance

indicators to be eligible for evaluation. The investigations comprised comprehensive descriptions of many performance parameters, such as accuracy, sensitivity, specificity, area under the curve (AUC), and receiver operating characteristic (ROC). The selected research must adhere to the criteria for a coherent and reliable report and our systematic selection procedure guarantees.

3.6. Performance Evaluation

Despite their usefulness in solving regression and classification problems, decision trees and deep convolution neural networks a kind of supervised learning—are not always the best option. The decision-making process and dataset features are explained by internal nodes, while the classification conclusion is provided by leaf nodes.

3.6.1. Accuracy

The accuracy of a classifier measures how well it achieves its objective. The degree to which a predictor correctly forecasts the value of an attribute given new data in this case, the class label is known as its accuracy.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \qquad (2)$$

3.6.2. Precision

One way to define precision is as the proportion of genuine positives to the sum of all positive and negative outcomes respectively.

$$Precision = \frac{TP}{TP + FP} \qquad (3)$$

Were, TN: True Negative, FN: False Negative, TP: True Positive, FP: False Positive

3.6.3. Recall

Calculating recall is as simple as dividing the number of observed occurrences by the number of projected outcomes. In the context of binary classification, "recall" and "sensitivity" are often considered synonyms. You might say that the chance of the request succeeding is the same as the chance of the request returning the correct record.

3.6.4. ROC

Visualizing the clinical specificity and sensitivity of a test or set of tests at different cut-off points is possible using ROC curves. Analyzing the ROC (receiver operating characteristic) curve provides further evidence for the use of the tests stated before.

4. Results and Discussion

Two ensemble learning models are used in this work to forecast the severity of damage that occurs in Alzheimer's disease. This was made possible with the help of the free and open-source Python 3.10 programming language. Furthermore, the Scikit-learn package and the Python tools KNN and RF made the model training approach quite straightforward. To construct the models, we partitioned the dataset as follows: We separated the data into subsets for training and validation using 70% of it, and we reserved 30% for testing to see how well the model worked. Figures 2 and 3 show the accuracy results and evaluation of the models' performance throughout the hyperparameter tuning phase. The models were developed using the training dataset, but the validation dataset was used to verify these findings. The best values to use for the mathematical models' hyperparameters are provided in Table 2.

The below diagram illustrates Figure 4 and 5, we can see a confusion matrix that shows how well a classification model performed across four categories: Cognitively Normal, Early Mild Cognitive Impairment, Late Mild Cognitive Impairment, and Alzheimer's disease. The model's accuracy in forecasting the EMCI class is 1582, which is the highest of any class, according to the matrix; next on the list are CN (1169) and AD (1185). The LMCI class, on the other hand, seems to be the most difficult, with a comparatively large proportion of CN (131 cases) and EMCI (429

cases) misclassifications. The model's shortcomings are shown by the matrix, especially when comparing adjacent cognitive stages such as LMCI and EMCI, which may indicate that there is some overlap in the features that are represented.

Figure 4: Confusion Matrix

Table 2: Algorithms Accuracy, hyperparameter, and Range Values

Algorithms	Performance Metrics	Hyperparameter	Range
KNN	Accuracy = 90%	learning_rate m-depth	0.01-0.05 0.05
RF	Accuracy = 91.5%	learning_rate m-depth	0.08-0.09 0.05
Proposed Ensemble Methods	Accuracy = 95.8%	learning_rate m-depth	0.08-0.12 0.05

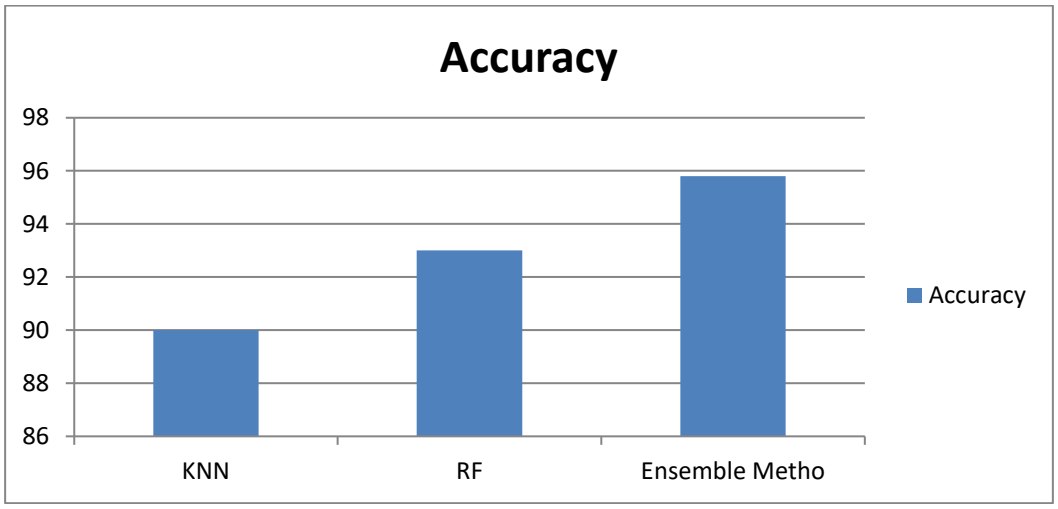

Figure 5: Accuracy Results

5. Conclusion

It is uncertain exactly what distinguishes MCI converters from AD converters. Thus, investing in high-quality feature selection algorithms that can search large datasets for optimal parameter values is vital. This research also highlights the lack of international hospital data studies. With big cooperative AD data, researchers may better experiment with different populations and construct an appropriate model, such as a single model for generalized people within a country or continent. This inquiry requires a wider model. We forecast using ensemble learning. Our model makes a forecast and explains each feature's contribution to prediction classifiers. Experimental evidence shows the model operates effectively, supporting prior investigations. Our technique

predicts the outcome and illuminates the relationship between physical sickness, lifestyle decisions, and cognitive function, which may help clinicians advise older patients. Our strategy may be beneficial in clinical settings and gives a new perspective on AD computer-aided diagnostics.

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