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A HYBRID ENSEMBLE APPROACH COMBINING BAGGING AND SVM FOR ALZHEIMER'S DISEASE STAGE CLASSIFICATION

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ABSTRACT

Neurodegenerative illnesses, such as Alzheimer's disease, cause brain cell damage, resulting in structural loss and neuron death, with Alzheimer's being a common form of irreversible dementia in its advanced stages. Researchers are looking into biomarkers, neuroimaging, and machine learning to improve early diagnosis and care of Alzheimer's patients. Effective treatment of Alzheimer's disease (AD) depends on a precise medical diagnosis, and typical protocols involve constructing a single classifier by extracting features from longitudinal MRI data. When tested on the ADNI dataset for older persons, the ensemble bagging SVM model performs better than other approaches, demonstrating greater performance in important evaluation measures like accuracy, sensitivity, precision and recall.

Keywords: *Alzheimer's disease, SVM, Ensemble, Bagging, MRI.*

1. INTRODUCTION

The neurodegenerative disease known as Alzheimer's disease (AD) primarily affects the older population. It is characterized by a gradual decline in episodic memory, which is a hallmark symptom of the disease. Alzheimer's disease is the most prevalent cause of dementia, affecting between 50% to 75% of people with dementia.The global prevalence of dementia is estimated to be around 44 million, and it is expected to increase significantly by 2030 and 2050, with projections of 76 million and 135 million cases, respectively[1,2].

Numerous sophisticated classification systems use structural MRI brain images to distinguish AD from healthy people. A recent high-dimensional classification approach for detecting Alzheimer's disease and moderate cognitive impairment is based on historical data and clinical observations [3]. Despite difficulties in getting consistent diagnoses due to low agreement among memory clinic specialists, seeking other opinions from primary care providers can improve treatment methods in places without AD specialists worldwide 4]. It is critical to improve medical diagnosis precision by more effectively utilizing experts' knowledge. This paradigm is intended to assist healthcare practitioners, even those with less AD knowledge, in doing appropriate clinical assessments [5,6].

The CAD system illustrates the feasibility of employing neuroimaging MRI 2D slices to classify AD patients, providing a promising method for early detection and therapy.The major goal is to create a CAD system for AD classification utilizing MRI 2D slices. Based on MRI images from the Alzheimer's Disease Neuroimaging Initiative (ADNI) dataset, the system classifies patients using a hybrid model that combines CNNs and support vector machines (SVMs)[7].

Alzheimer's disease (AD) is generally diagnosed by the analysis of structural magnetic resonance imaging (MRI) data, which provides critical insights into brain shape and function. Specifically, grey matter densities, group comparisons of cortical thickness, morphometry, and texture measurements can all be obtained from structural MRI of the complete brain, offering a comprehensive understanding of the brain's structure and its alterations in AD[8].

Our objective is to analyze and compare various machine learning classifiers that use MRI scan analysis to identify Alzheimer's disease (AD). Specifically, we want to find the best classifier for discriminating between different phases of Alzheimer's disease by using the Alzheimer's Disease Neuroimaging Initiative (ADNI) dataset, which contains MRI scans and other data from older persons.

The present research presents a new classification strategy for accurately identifying individuals in many stages of Alzheimer's disease (AD) by combining structural MRI parameters such as grey matter densities, cortical thickness, morphometry, and texture measures. By incorporating these elements, the system hopes to increase diagnostic accuracy while reducing false positives and negatives, which can cause patients excessive concern and stress or postpone treatment. Bagging SVM is critical for avoiding overfitting in machine learning models because it provides variety among basic SVM models, each focused on different data elements, reducing overfitting risks and increasing classifier robustness for greater performance on unknown data. Evaluation criteria including accuracy, sensitivity, precision, and recall are used to evaluate the performance of classifiers.

The remaining portions of the paper are arranged as follows:Section 2 examines the research on AD diagnosis. Methodology is given below. Experiments and ML models are described in Section 4. In Section 5, the experiment results are examined. Some suggestions for more research in this area are included in the section 6 conclusion.

2. RELATED WORKS

A favourable diagnosis gives patients and their families more time to learn about the illness, make educated financial and lifestyle decisions, and prepare for future care needs. On the other hand, a negative diagnosis can support early action for reversible illnesses with comparable symptoms and allay worries about age-related memory deterioration. Since the present generation of symptom-delaying medications has a limited period of action, prompt administration via early identification is crucial. Early diagnosis and treatment of mental health conditions such as psychosis or depression prevent the expenses of Alzheimer's disease from accruing to both individuals and society. The possibility of creating preventive treatments becomes apparent as research continues. When an illness is detected early, there is a greater possibility that it can be treated before the patient experiences irreversible brain damage.Finally, early diagnosis further reduces the societal cost of AD by protecting patients' freedom longer and preparing families for the demands of AD patients. This is because institutionalization accounts for a significant portion of health care costs associated with AD [9,10,11,12].

M. Bachute et al. use machine learning techniques to improve the early detection of Alzheimer's disease. The main goals are to create and assess models that can reliably identify and categorize Alzheimer's using medical information. The study makes use of a number of machine learning methods, such as neural networks, random forests, decision trees, and support vector machines (SVM). This entails gathering medical datasets containing relevant biomarkers and cognitive test results, choosing significant features for model training, and then training and testing the models on various data subsets to determine their performance[13]. The OASIS dataset is utilized by Uddin & Co. (2023) to develop a voting classifier system for Alzheimer's disease diagnosis. The interpretability and ability of the machine learning model to handle uneven data may provide challenges [14]. Siddhartha Kumar Arjaria et al.'s paper uses the OASIS dataset to assess multiple machine learning algorithms for Alzheimer's diagnosis; with a few features, the methods achieve over 90% accuracy. The report also highlights key problems, such as the difficulty of comprehending sophisticated models and properly managing unbalanced datasets [15].

The literature evaluated shows considerable advances in machine learning for Alzheimer's disease diagnosis, but it also emphasizes crucial obstacles. Uddin & Co. (2023) highlight model interpretability difficulties while demonstrating the potential of ensemble learning with their vote classifier system. Similarly, Siddhartha Kumar Arjaria et al. find great accuracy using multiple approaches but encounter issues managing unbalanced datasets. These findings highlight the necessity of conducting more research to create interpretable, accurate, and dataset-handling models. The inclusion of recent studies, a variety of approaches, well-established datasets, and an acknowledgment of current issues have all contributed to the representative, current, and appropriate literature sample that supports the research problem. The identified research gaps

provide a clear path forward for advancing Alzheimer's disease diagnosis and treatment.

Using an ensemble learning strategy that combines many SVM classifiers to improve accuracy and robustness, our suggested model uses a complex bagging SVM (Support Vector Machine) approach. This approach takes advantage of SVMs' innate advantages when managing high-dimensional data and their capacity to identify the best hyperplanes for classification tasks. The feature set recovered from brain MR images is greatly enhanced by our model, which incorporates sophisticated texture analysis techniques including the Gray-Level Co-occurrence Matrix (GLCM), Gray-Level Dependence Matrix (GLDM), and Gray-Level Run-Length Matrix (GLRM). These texture analysis techniques are essential for detecting minute structural alterations linked to Alzheimer's disease because they extract complex patterns, spatial correlations and dependencies from the images.

The GLCM measures textural characteristics like contrast, correlation, energy, and homogeneity and offers useful information about the spatial distribution of pixel intensities. These characteristics aid in identifying variations in tissue textures, which are frequently symptomatic of neurodegenerative alterations. The gray level dependency within an image is measured by the GLDM, which provides information about tissue texture and homogeneity. Meanwhile, the GLRM measures the length of successive lines of pixels with the same intensity, which is very beneficial for detecting linear patterns and textures in brain pictures. When combined, these techniques offer a thorough and diverse understanding of the texture characteristics of brain tissues.

In addition to these sophisticated texture features, our model includes other significant features extracted from brain MR images. These could include shape descriptors, volumetric measurements, intensity-based characteristics, and higher-order statistical features. The model's ability to incorporate a broad range of neural structure and function enhances its overall classification performance by capturing a large variety of brain properties.
The bagging ensemble technique improves model reliability by lowering variance and reducing the danger of overfitting. As a result of training each SVM in the ensemble on a distinct subset of the data, the model is guaranteed to be robust to dataset variability and to generalize well to new data. This holds special significance in the field of medical imaging, as the variability of the data might present noteworthy obstacles to precise categorization.

Our objective is to improve the accuracy and dependability of Alzheimer's disease predictions, which will further the development of early detection and intervention techniques for neurodegenerative diseases. The management of Alzheimer's disease depends on early and correct diagnosis since it enables prompt intervention and the application of therapeutic options that can halt the illness's progression and enhance patient outcomes. Our model has the potential to improve diagnosis by giving doctors a useful tool for early Alzheimer's disease detection by giving a more nuanced and precise characterisation of brain structures.

3. METHODOLOGY

In Alzheimer's Disease (AD), the most common degenerative disorder, brain cells are gradually destroyed.
. AD is a major cause of dementia that gradually reduces a patient's ability to function independently in social, behavioural, and cognitive domains. Advanced machine learning models have shown better results in recognizing AD than standard machine learning techniques. These models perform exceptionally well because the diagnostic process is streamlined as they do not require manually crafted feature extraction. Furthermore, in order to improve their capacity to identify minute patterns suggestive of the illness, contemporary machine learning techniques can be tailored to large and intricate datasets. This capacity provides insights into disease development and possible therapy targets in addition to enhancing early identification.

With an emphasis on the application of SVM for AD diagnosis, this article covers the most recent breakthroughs and new trends in machine learning algorithms for identifying AD.The following figure in Figure 1 displays the general architecture of a computer-aided system meant to diagnose Alzheimer's disease at various stages utilizing brain imaging data. This approach combines complex machine learning algorithms with cutting-edge neuroimaging technology to improve the precision and dependability of early AD identification. The system may detect tiny biomarkers and patterns linked to various stages of Alzheimer's disease by

utilizing SVM to dynamically evolve and optimize neural network topologies. This method advances our knowledge of the disease's course and possible intervention techniques in addition to making diagnosis more accurate.

3.1.Image Preprocessing

Pre-processing the images involved performing the appropriate morphological operations. Pre-processing structural MR images consists of three basic steps: correcting non-uniformity, filtering noise, and controlling intensity. These actions result in the removal of the skull. This procedure involves removing objects like the eyes and skull that aren't related to the brain from MR brain pictures. This led to the development of an automated skull-stripping method based on mathematical morphology. A two-stage adaptive denoising technique is presented in this paper. An adaptive approach is used to detect noise in the first step. The input image is then denoised by applying the Hampel filter and the noise discovered.

3.2.Image Segmentation

The degree of accuracy of the entire study depends critically on segmentation. With the segmentation procedure, non-brain tissues are isolated after spatial leveling. In this study, the core slice of the brain in MRI is segmented utilizing a unique segmentation technique and proposed morphological operations for skull stripping. In order to improve diagnostic accuracy and efficiency in medical applications, skull stripping is crucial to the processing of brain images. Enhancing segmentation accuracy and decreasing misclassification of brain tissues are achieved by removing non-brain tissues. This technique makes a major contribution to the accurate detection of diseases like mild cognitive impairment and Alzheimer's disease.

The new method was evaluated with T1-weighted MRI brain images from the Alzheimer's disease dataset. The striking impression of the exposed brain is proof that the suggested approach works. Automated MR image segmentation helps clinicians make qualitative diagnoses. This is due to the fact that accurate anatomical region segmentation is necessary for a number of processing steps, including feature extraction and AD stage classification. A TDWT fuzzy set theory-based segmentation technique for AD-MR pictures was created in this work. One can apply the recommended segmentation result right away for an alternative feature extraction procedure.

3.3.Feature Extraction:

Feature extraction is evaluating image texture to acquire a better grasp of the characteristics that define the shape and texture of things. The hippocampus is one of the first brain regions to be impaired by Alzheimer's disease (AD). The hippocampus, which is responsible for memory and spatial navigation, is divided into two parts: the head and the body. Due to its connections to higher-order brain functions such as speech, memory, emotions, self-regulation, decision-making, motor control, and sensory perception, the grey matter of the cortex is essential. AD also has an influence on the white matter, which affects motor function by altering communication routes inside the brain. The study shows increased accuracy in identifying Alzheimer's disease using these extracted features by using Support Vector Machines (SVMs) for classification. The incorporation of sophisticated feature extraction and classification techniques improves our capacity to identify and comprehend AD, which in turn leads to improved patient outcomes and focused treatment approaches[16].

In this study, a new approach is used to improve the characterization of brain pictures for Alzheimer's disease categorization. Three different texture feature extraction methods are combined in this method: Gray-Level Dependence Matrix (GLDM), Gray-Level Run Length Matrix (GLRLM), and Gray-Level Co-occurrence Matrix (GLCM). A different perspective on the textures in the images can be gained from each technique.

GLCM uses the spatial correlations between pixel intensities to compute statistical characteristics that reveal structures and patterns in textures. To obtain information on texture consistency, GLRLM extracts features that measure the length of successive pixels with the same intensity. GLDM measures the distances between successive pixels that have the same intensity, providing information about texture continuity. By integrating these several methodologies, the study hopes to gain complementary information from brain pictures, capturing distinct texture and pattern abnormalities linked with Alzheimer's disease.
A full representation of visual information is made possible by this multi-feature combination strategy, which may enhance the accuracy of Alzheimer's disease classification and increase the identification of disease-related patterns in brain images. The goal

of this research is to improve diagnosis and understanding by utilizing these techniques in enhanced texture analysis, which will lead to more efficient medical imaging approaches for the evaluation of Alzheimer's disease.

3.4.Classification:

The research methodology was chosen to achieve the improvement of Alzheimer's disease (AD) diagnostic accuracy by analyzing and comparing several machine learning (ML) algorithms on MRI data from the ADNI dataset. The research approach was chosen to improve Alzheimer's disease (AD) diagnostic accuracy by comparing various machine learning (ML) algorithms to MRI data from the ADNI dataset. It analyzes algorithms including J48, KNN, SVM, and a hybrid model that combines bagging with SVM. It uses a classification framework with samples of AD, mild cognitive impairment (MCI), and normal controls. A thorough evaluation is guaranteed by the strong ADNI dataset and the use of MATLAB R2021b for implementation. Using performance indicators such as accuracy, recall, precision, and F1-score along with a performance analysis table, the design is appropriate for the research goals to effectively address the research objectives

3.4.1. Dataset splitting using k-fold cross-validation

A commonly used machine learning technique, 5-fold cross-validation, is used to assess the classifier's performance. This method divides the dataset into five equal pieces, utilizing each segment once as a validation set and the remaining four as training data in each iteration. Five iterations of this approach guarantee that each subset is utilized for validation precisely once. 5. Folder cross-validation, as opposed to a single train-test split, reduces bias and produces more reliable estimates of model performance by allowing the classifier's generalization ability to be evaluated robustly through the rotation of various subsets for validation. It is a common procedure in machine learning to assess classifiers, providing a dependable way to determine their predicted accuracy and applicability for actual use cases [17].

3.4.2 Techniques used:

The field of machine learning in medical imaging mostly used basic models and approaches prior to the introduction of our framework. Conventional methods frequently depended on first-order statistical features, which are merely measures of pixel intensity like mean, variance, skewness, and kurtosis. These qualities hindered our ability to understand the intricate patterns found in brain MR images, which in turn limited our ability to diagnose diseases like Alzheimer's disease with accuracy. k-nearest neighbors (KNN), decision trees, and logistic regression were popular machine learning techniques. While helpful, these models typically lacked the complexity and resilience required to manage the complex, high-dimensional data typical of brain imaging.

In our system, Support Vector Machines (SVMs) act as metaclassifiers within an ensemble learning structure, considerably improving categorization. SVMs are highly valued for their capacity to efficiently handle high-dimensional data and distinguish between classes by identifying the best hyperplane with the largest margin. By using SVMs as metaclassifiers, our method takes use of their strength in binary classification to increase overall accuracy. Furthermore, we use bootstrap aggregating, also known as bagging, as a crucial sampling method. In order to ensure variation across the subsets, bagging entails generating several training datasets using random sampling with replacement from the original dataset. A distinct SVM is trained on each subgroup to produce an ensemble of classifiers. This method improves the stability and robustness of the final model by combining the predictions from several models, which lowers variance and mitigates overfitting. Our approach is able to more accurately identify Alzheimer's disease by combining SVMs with bagging to better capture the complex patterns found in brain MR images.

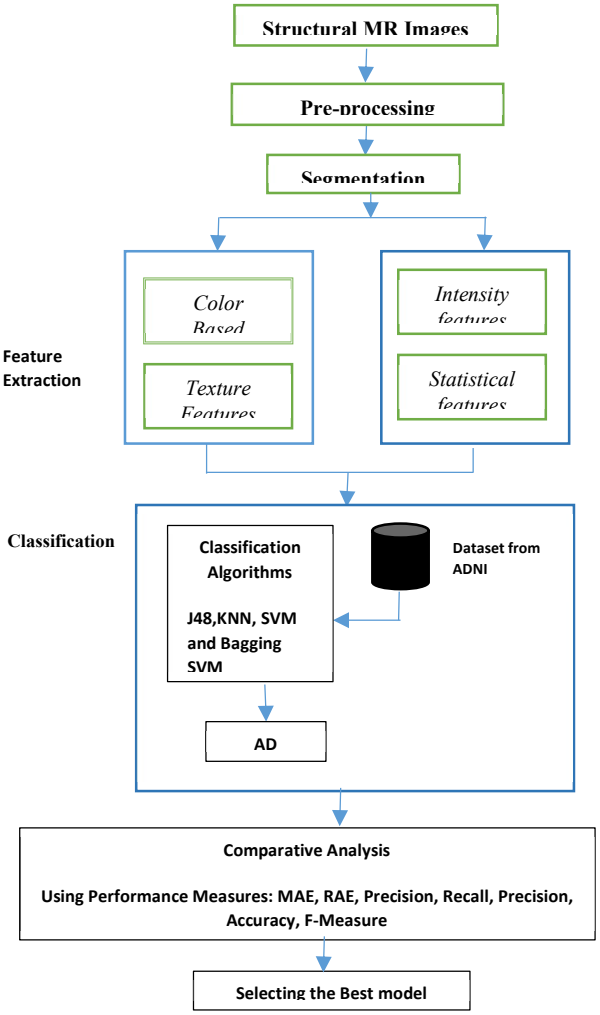

Figure 1. Proposed Methodology

3.4.2.1.KNN:

This method consistently produces similar outcomes when applied to similar training datasets. The majority class among a particular input's closest neighbors is used to determine the input's class. Objects are grouped by the k-Nearest Neighbours (K-NN) classification algorithm according to the dominant classes of their K nearest neighbours. In this case, K stands for a given positive integer that indicates how many neighbours were taken into account when making the categorization decision [18].

We must first compute a distance in parameter in order to quantitatively identify who our closest neighbours are.

$$D_j = \sqrt{\sum_{i=1}^{\text{ndim}} (x_i - y_i)^2} \quad (1)$$

The L2-normalized (Euclidean) distance is used to calculate the distances between points in parameter space. Here, d is the total distance from the jth observed datum to the point being predicted, and x_i and y_i represent the predictor values at the observed and unknown locations, respectively. The choice between L1-normalized and Euclidean distances is made in machine learning techniques such as k-Nearest Neighbours (kNN). L1-normalized distances are resistant to outliers, while Euclidean distances offer a direct analytical solution but are susceptible to outliers. We use Euclidean distance as our metric because our dataset has been cleared of anomalies. The mean and variance of the predictor values are set to zero. Following the computation of distances to every observed data point, the k closest neighbours are determined by utilizing the least distance. The predicted value at any point is the average of its nearest neighbors, weighted by the inverse of their scaled distances.

3.4.2.2.J48:

The J48 method builds its initial tree using a divide-and-conquer strategy, starting with the attribute having the highest gain ratio as the root node. Pessimistic pruning, which involves methodically eliminating unnecessary branches from the tree structure, is a technique used by the algorithm to increase accuracy. The algorithm splits data into two different categories for handling continuous properties. In order to retain the decision tree model's resilience and generalizability across various datasets and situations, pruning is an essential step in preventing overfitting [19].

$$E(S) = \sum_{i=1} - P\log_2 P_i \quad (2)$$

where c is the number of classes, Pi is the proportion of S belonging to class 'i'.

$$\text{Gain}(S, A) = \text{E(S) - value} \sum(A) \frac{S_v}{S} E(S_v) \quad (3)$$

Here, A represents the set of all possible values, S_v denotes the subset of S where function A has the value v. S corresponds to the entropy of the original collection, while predicting the entropy value.

3.4.2.3.Support Vector Machine:

This algorithm is well known for their remarkable performance in binary classification problems in a variety of engineering applications. Considering a

labeled training set $T = \{(x_i, y_i) | y_{i=1 \text{ or } -1}$,A basic method for creating a classifier is to define a hyperplane in the input feature space, or a transformed version of it, that best divides the two classes. $i = 1,\ldots,N\ \}$ T={$(x_i, y_i) | y_{i=1-or-1}$,i=1,…,N}. By maximizing the margin between the several classes, this approach seeks to improve the classifier's capacity for generalization, as per statistical learning theory[20]. Support Vector Machine (SVM) is recognized as a robust adaptation of the perceptron learning model due to its ability to maximize the margin between classes for better generalization and its use of kernel functions to handle non-linear separability. Additionally, SVM incorporates regularization to balance the margin and classification error, and is grounded in strong theoretical foundations from statistical learning theory, enhancing its overall performance and adaptability[21].

The soft-margin relaxation and the feature transformation ϕ are two crucial methods that provide SVM its strength in identifying intricate decision boundaries and preventing overfitting by permitting certain samples to deviate from the support hyperplanes.The SVM is represented as a quadratic programming problem as below:

$$\min_{W>R} \frac{1}{2} W^T \cdot I_n \cdot W + C(1_N^T \cdot \zeta)$$
$$s.t \qquad A\begin{pmatrix} W \\ \xi \\ b \end{pmatrix} \geq 1_{N^p} \qquad (4)$$

where A is the corresponding matrix

$$A = \begin{pmatrix} y_1\phi(x_1)^T, e_1, 1 \\ y_2\phi(x_2)^T, e_2, 1 \\ \vdots \\ y_N\phi(x_N)^T, e_N, 1 \end{pmatrix} \qquad (5)$$

N-dimension unit vector ϵ_k with kth coordinate equals 1.

The degree to which samples deviate from the support hyperplanes is measured by the slack vector of variables$\zeta = (\zeta_1, \zeta_2, \ldots, \zeta_N)^T$. Through the solution of the Karush-Kuhn-Tucker (KKT) optimality requirements, which are obtained from the Lagrangian function, the primal problem can be transformed into the dual problem [22].

Finally, the discriminative function is formulated as follows,

$$f(x) = \text{sign}\left(\sum_{\alpha'_n>0} y_n \alpha^*_n \phi(x_n)^T * \phi(x) + b\right), \quad (6)$$

The Lagrange multiplier for the i-th sample that meets the Karush-Kuhn-Tucker (KKT) optimality requirements is denoted by α. When the inner product of converted feature vectors is computed utilizing kernel methods, the computation process becomes more efficient.

$$\phi(x_n)^T + \phi(x_n) = K(x_n, x_n). \quad (7)$$

Furthermore, the classifier's representation is relatively sparse because only a tiny subset of the training data, known as support vectors, has positive Lagrange multipliers and influences the final decision. The remaining training data has no discernible impact on the classifier's performance; instead, these support vectors are essential in establishing the decision border.

3.4.2.4. Ensemble methods: a review

When a single classifier fails owing to limitations in the training dataset or biases in the presumed model, ensemble techniques address these concerns by merging numerous models. The ensemble's capacity for generalization is improved by this method, which guarantees a more balanced representation of the underlying distribution. Additionally, less complex criteria—like decision stumps—may provide weaker classifiers, which, when skillfully coupled, can help produce a strong and effective classifier[23].

In our framework, we used the bagging technique to create a range of models.By utilizing the bootstrapping technique, bagging, also known as bootstrap aggregation, and generates a variety of classifiers. To guarantee that every training example has an equal chance of being chosen, this method samples each one with a replacement.

Bootstrapping aggregation, often known as bagging, is an effective technique for building various classifiers. Through a method known as bootstrapping, which involves repeatedly sampling the training dataset with replacement, it generates several models. Every classifier undergoes training on a subset of the data, wherein samples are taken at random from the original distribution with an equal probability. This method minimizes overfitting and increases the robustness of the ensemble by ensuring that each model captures a distinct component of the variability in the dataset. Bagging boosts generalization ability greatly when compared to a single model trained on the full dataset.

Algorithm 1: Bagging algorithm.

(1) Input the whole training dataset with |D| = N

(2) For i from 1 to m:

(3) Sample from D by Bootstrapping trick to obtain D_i with $|D_i| = N\sim$

(4) Derive the model fi(x) by fitting Di

(5) Ensemble of the models $\{f_i(x) \mid i = 1,2, \ldots, m\}$ and obtain the final model F(x). In binary

classification cases $F(x) = \text{sign}(\sum_{i=1,2,\ldots,m} f_i(x))$

Bagging inspired the random forest model, which is well-known for its robustness and predictive power. Each decision tree in a random forest is trained using bootstrapping, which involves sampling subsets with replacement. Random forests are further distinguished by the randomization of features that they incorporate into the training process. Random forests opt to randomly choose a subset of features for consideration at each split, instead than taking into account all features. A more dependable and generalized prediction performance across a variety of datasets and applications is thus encouraged by this stochastic feature selection, which also increases the diversity among the trees [24].

3.4.2.4.Bagging SVM:

The ensemble techniques of bagging Support Vector Machine (SVM) have been applied in several domains to demonstrate its effectiveness in improving classification accuracy, preventing overfitting, and strengthening the stability of SVM models. Bagging, or Bootstrap Aggregating, is the process of training several SVM models on various subsets of training data and merging their predictions to improve overall performance. Bagging SVM has produced encouraging results in a variety of fields, including healthcare, finance, and image recognition, where precise categorization is critical. Bagging SVM minimizes variance and generalization error by aggregating predictions from many SVM models trained on distinct subsets of data, resulting in increased classification accuracy. This group method aids in obtaining many facets of the information. Additionally, by adding variety to the original SVM models, bagging SVM is essential in lowering overfitting, a major problem in machine learning models. The risk of overfitting to particular patterns in the training data is decreased because each SVM model in the ensemble focuses on a different feature of the data. This variability in model predictions aids in the development of a more resilient and stable classifier that works well on fresh, previously unknown data. Bagging SVM emerges as the most effective model with higher recall and lower miss rate, making it suitable for classifying spinal patients using key features [25,26].

Ensemble Bagging Algorithm

Select:
- X: Features of training data
- y: Labels or targets for training data in classification (for regression)
- B: Bootstrap sample count - SVM parameters (e.g., regularization parameter C, kernel type)

SVM_models = [] to initialize the ensemble of SVM models.

Regarding b = 1 to B: # Step 1: Samples using bootstrap
Establish a bootstrap example: bootstrap_sample(X, y) = X_b, y_b

Train an SVM model in step two.
Train an SVM model on X_b and Y_b with provided parameters.
SVM_model_b = Train_SVM(SVM_parameters, X_b, y_b)

#Step 3: Keep the ensemble's trained SVM model stored.
Add SVM_model_b to the SVM_models list.

Step 4: Aggregating Predictions (majority voting for categorization, averaging for regression)
For every new instance of x_new:
assemble all SVM_models' predictions for x_new

if Classification: By majority vote, aggregate projections
majority_vote(predictions) = predicted_label Store Expected_label

If Regression is used, average the predictions to create an aggregate.
Predicted_value = average(predictions)
Store Predicted_value rewrite this in another word

3.5.Performance Assessment Criteria

Model evaluation is critical in research to assure correctness and reduce errors. Relative Absolute Error (RAE), Mean Absolute Error (MAE), accuracy, precision, recall, and F-measure[27,28,29,20,31] important measures for evaluation. While accuracy evaluates correct predictions, precision evaluates exactness in positive predictions, recall quantifies properly identified positives, and F-measure strikes a balance between precision and recall, MAE measures average error size, and RAE normalizes MAE in relation to data scale. These measurements serve as critical benchmarks for assessing algorithm performance and improving research model refinement.

a. MAE

Mean Absolute Error (MAE) quantifies the average difference between continuous variables, such as predicted and observed values over a specified period.

$$\text{Mean Absolute Error} = \frac{1}{n}\sum_{j=1}^{n}|y_i - y| \quad (8)$$

b. The Relative Absolute Error (RAE

The Relative Absolute Error (RAE) is calculated using two variables: tentative or estimated values and experimental values. The absolute error to the experimental value is the ratio that is used to determine RAE. Due to its dimension lessness, it is commonly stated as a percentage or fraction.

$$\text{Relative Absolute Error} = \frac{\sum_{j=1}^{n}|P_{ij}|}{\sum_{j=1}^{n}|T_j - \bar{T}|} \quad (9)$$

where P_{ij} is the value forecast by the specific model I for record j (out of n records), T_j is the goal value for record j_i and $\bar{T}$ is as follow.

$$\bar{T} = \frac{1}{n}\sum_{j=1} T_j \quad (10)$$

The numerator is equivalent to 0 for a good suit, and $\text{Ei} = 0$.

c. Accuracy

Accuracy is an important parameter for evaluating classification models. It denotes the fraction of accurately predicted observations compared to all predictions produced by the model.

$$\text{Accuracy} = \frac{\text{TP+TN}}{\text{TP+TN+FP+F}} \quad (11)$$

d. Precision

It is the proportion of optimistically expected, correctly predicted observations to positively anticipated all observations

$$\text{Precision} = \frac{\text{TP}}{\text{TP+FP}} \quad (12)$$

e. Recall

The percentage of accurately detected positive cases (true positives) among all real positive instances is referred to as recall, sensitivity, or true positive rate.

$$\text{Recall} = \frac{\text{TP}}{\text{TP+FN}} \quad (13)$$

f. F-Measure.

g. It is a weighted average of Precision and Recall that accounts for all erroneous positives and, in certain cases, false negatives. F1-Measure is typically more useful than accuracy, especially if you have an uneven class distribution, even though it is intuitively not as simple as precision.

$$\text{FM} = \frac{2*\text{Precision}*\text{Recall}}{\text{Precision+Rec}} \quad (14)$$

4. RESULT AND DISCUSSION:

The datasets for this investigation were obtained from the ADNI database, which may be accessed at adni.loni.ucla.edu. The National Institute on Aging (NIA), the National Institute of Biomedical Imaging and Bioengineering (NIBIB), the Food and Drug Administration (FDA), commercial pharmaceutical companies, and nonprofit organizations worked together to create ADNI in 2003. There are 100 samples in the dataset: 20 samples with Alzheimer's disease (AD), 40 samples with mild cognitive impairment (MCI), and 40 samples of normal controls. T1-weighted MR images in the sagittal plane serve as representations for these samples. The dataset contains 49 male and 51 female subjects aged 57 to 95 years with an average of 95.

MATLAB provides powerful tools for putting machine learning methods into practice. These tools include libraries for statistical analysis, data preprocessing, and training and evaluating models. In this study, MATLAB R2021b was used to construct machine learning methods, specifically for Alzheimer's disease (AD) stage identification. Our method makes use of machine learning, statistical analysis, and image processing methods. To improve the precision and robustness of AD diagnosis, we specifically integrated bagging with Support Vector Machines (SVM). The efficacy of this approach was proven through extensive trials, which addressed the inherent limitations of individual classifiers and outperformed them. Based on current data, bagging, and SVM integration are beneficial for Alzheimer's disease stage and early diagnosis.

The proposed design uses machine learning (ML) methodologies to improve Alzheimer's disease categorization accuracy. A total of 3038 examination records out of 3798 images, or 80% of the dataset, are designated for training, while 760 records out of 3798 images, or 20% of the dataset, are designated for testing. The suggested framework's effectiveness is evaluated using metrics such as accuracy, recall, precision, and the F1-score. These metrics offer thorough assessments of the model's performance in relation to numerous categorization accuracy and reliability metrics.

Table 1: Stage Wise Prediction Of Alzheimer's Disease Using Various ML Algorithms

Algorithm Details	***Stage wise Alzheimer disease Prediction***			
	Normal	*Stage1*	*Stage2*	*Stage3*
J48	1252	408	32	691
KNN	1273	404	0	723
SVM	1489	767	43	980
Proposed	1544	794	44	1068

Table 2: Performance Analysis of ML Algorithms

Algorithm Details	***Performance Metrics***			
	Accuracy	*Recall*	*Precision*	*F1-Score*
J48	61.7	61.5	71.4	57.6
KNN	63.2	58.3	75	63.2
SVM	86.3	85.4	88.1	85.5
Proposed	90.8	90.3	93.6	89.8

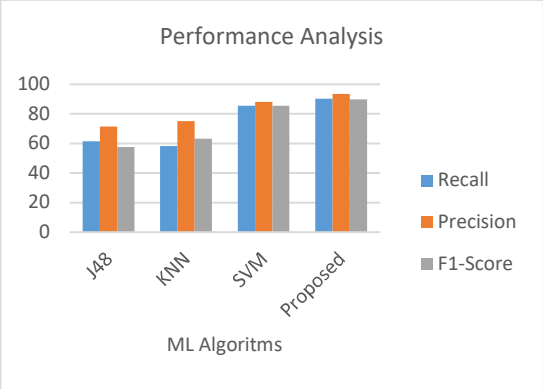

Fig 2: Precision, Recall,F1-Score Analysis On ADNI Dataset

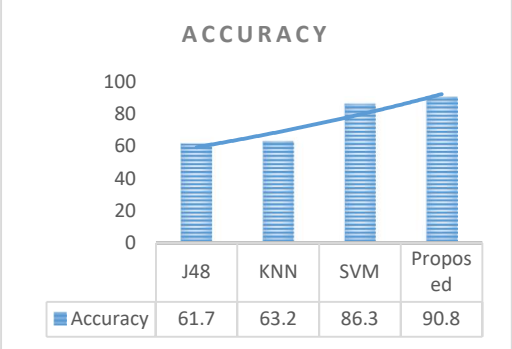

Fig 3 : Accuracy Achieved Through Each Classifier

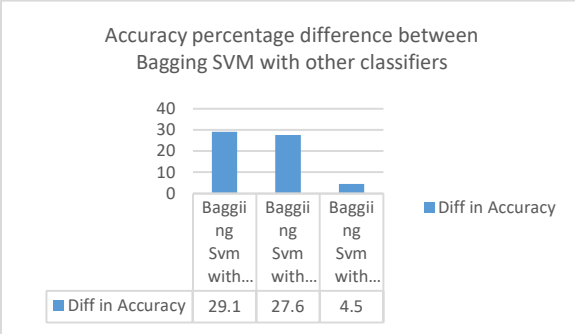

Fig 4. : Accuracy Percentage Difference Between Bagging SVM And Other Classifiers

Table.3. Performance Analysis With Error Rate

Algorithms	***MAE (%)***	***RAE(%)***
J48	37.2	36.7
KNN	36.8	34.5
SVM	13.7	14.8
Proposed	7.2	8.6

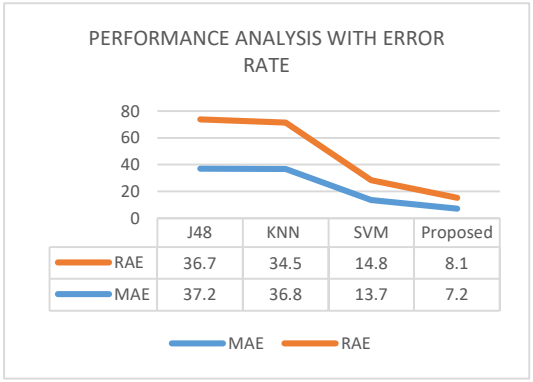

Fig 5 : Performance Analysis With Error Rate

Table 2 shows a comparison of the proposed algorithm's performance to existing algorithms. Table 2 displays the results of the suggested technique, which shows that it can classify Alzheimer's disease with an accuracy of 90.8%, sensitivity (recall) of 90.3%, precision of 93.6%, and F1-score of 89.8%. When taken as a whole, these measures show how well the suggested method diagnoses Alzheimer's disease.

It is evident from the table and accompanying figure that the suggested bagging SVM technique performs noticeably better than the other algorithms that are currently in use. The proposed method's greater performance is demonstrated by its higher accuracy, sensitivity, precision, and F1-score values. Furthermore, Figure 5 validates these findings by demonstrating that the bagging SVM method has the lowest error rate among the assessed strategies.

These findings demonstrate the suggested method's robustness and dependability in categorizing Alzheimer's disease, highlighting its potential as a better substitute for current classification algorithms. An extremely useful method for Alzheimer's disease early identification and staging is the combination of bagging with SVM, which not only increases classification accuracy but also strengthens the durability of the model.

5. CONCLUSION AND FUTURE DIRECTION

In order to classify Alzheimer's Disease (AD) using MRI scans, this study compares four distinct classifiers using information from the ADNI database to investigate different machine learning methodologies. The most successful approach among those examined was the suggested bagging-SVM classifier, which demonstrated the best performance in identifying AD phases. In addition to its superior performance in AD diagnosis, the SVM-based method merits more research since it may be used to improve patient outcomes and other medical activities. Enhancing data gathering procedures to improve model training and evaluation should be the main emphasis of future research. The accuracy of the model may also be improved by incorporating cutting-edge methods like deep learning. Diagnostic performance can be greatly enhanced by deep learning models, which can extract and learn complicated patterns from big datasets. The proposed technique could potentially be used to diagnose other neurodegenerative conditions, such as Parkinson's and Huntington's disease, allowing for earlier detection and treatments. Overall, the ensemble SVM classifier has performed well in AD diagnosis, making it an important tool for reliable disease detection and diagnosis.

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