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A DEEP LEARNING-BASED FRAMEWORK FOR ALZHEIMER'S DISEASE DIAGNOSIS AND PROGRESSION PREDICTION FROM MRI IMAGES

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Abstract

Alzheimer's disease (AD) is a progressive neurodegenerative disorder characterized by continuous cognitive and biomarker changes. Identifying predictive biomarkers for the progression from mild cognitive impairment (MCI) to AD is crucial for improving diagnostic accuracy and facilitating targeted drug development. Traditional machine learning methods have been used for AD diagnosis using MRI images, but deep learning (DL) techniques offer superior performance due to their ability to learn complex patterns from large datasets. A significant challenge in AD research is the lack of definitive biomarker signatures to predict which MCI patients will progress to AD. Current methods, such as DenseNet121, ResNet50, VGG 16, EfficientNetB7, and InceptionV3, have limitations in predictive accuracy and the ability to identify distinct neurodegenerative patterns. We developed and validated YoLoV7, a deep learning-based framework that examines neuroanatomical heterogeneity contrasted against normal brain structure to identify disease subtypes through neuroimaging signatures. Using a dataset of 1000 participants and 4000 T1-weighted MRI scans, YoLoV7 identified four patterns of neurodegeneration. We applied this framework to longitudinal data to reveal two distinct progression pathways and assessed the model's performance in predicting the pathway and rate of future neurodegeneration. YoLoV7 identified four neurodegenerative patterns, with Pattern 1 showing a 70% accuracy in predicting slower progression (Pathway A) and Pattern 2 demonstrating an 80% accuracy in predicting rapid progression (Pathway B). Overall, YoLoV7 achieved an accuracy of 85% in predicting clinical progression, outperforming traditional methods such as DenseNet121 (78%), ResNet50 (75%), VGG 16 (72%), EfficientNetB7 (80%), and InceptionV3 (76%). Measures of pattern expression offered complementary performance to amyloid/tau biomarkers in predicting clinical progression.

Keywords:

Alzheimer's Disease, Deep Learning, MRI, Neurodegeneration, Progression Prediction

1. INTRODUCTION

Alzheimer’s disease (AD) is a debilitating neurodegenerative disorder characterized by progressive cognitive decline and memory loss. It is the most common cause of dementia in older adults, with millions affected worldwide [1]. The pathophysiological progression of AD involves complex changes in the brain, including amyloid-beta plaque accumulation, tau tangles, and widespread neurodegeneration [2]. These changes can be observed using neuroimaging techniques, such as magnetic resonance imaging (MRI), which detailed anatomical and functional insights into the brain's structure and function [3].

Despite extensive research, there is no definitive biomarker to predict the progression from mild cognitive impairment (MCI) to AD. Only a fraction of individuals with MCI eventually develop AD, making it challenging to identify at-risk patients early [4]. Traditional diagnostic methods, including clinical assessments and biomarkers like amyloid-beta and tau, offer limited predictive accuracy and often fail to capture the heterogeneity of the disease [5]. Moreover, the complex and multifactorial nature of AD progression complicates the identification of precise biomarkers.

The primary challenge in AD research and clinical practice is the lack of reliable prognostic biomarkers to predict disease progression. Traditional machine learning methods have been used for AD diagnosis from MRI images but often fall short in terms of accuracy and robustness. There is a critical need for advanced methods that can leverage large datasets to discover complex patterns indicative of disease progression.

The objectives of this study are:

- To develop a deep learning framework, YoLoV7, that can accurately diagnose AD and predict its progression from MRI images.
- To identify distinct neurodegenerative patterns and pathways through neuroimaging signatures.
- To evaluate the performance of YoLoV7 in comparison with existing methods such as DenseNet121, ResNet50, VGG 16, EfficientNetB7, and InceptionV3.
- To demonstrate the complementary predictive power of deep learning-derived biomarkers alongside traditional biomarkers like amyloid-beta and tau.

The novelty of this study lies in the application of an advanced deep learning framework, YoLoV7, to the diagnosis and progression prediction of AD using MRI images. Unlike traditional methods, YoLoV7 examines neuroanatomical heterogeneity against normal brain structures, enabling the identification of distinct disease subtypes and neurodegenerative patterns.

Key contributions of this study include: A state-of-the-art deep learning model specifically designed to analyze MRI images for AD diagnosis and progression prediction. This model leverages the power of convolutional neural networks to capture complex patterns and features indicative of neurodegeneration.

2. RELATED WORKS

Early attempts to diagnose Alzheimer's disease (AD) and predict its progression primarily relied on traditional machine learning techniques. Methods such as support vector machines (SVM), k-nearest neighbors (KNN), and random forests have been widely used to analyze neuroimaging data. These models often utilize handcrafted features extracted from MRI images, such as regional brain volumes and cortical thickness [6]. While these approaches have shown some success, their performance is limited by the quality and relevance of the manually extracted features, as well as their inability to capture the complex patterns of neurodegeneration inherent in AD progression.

The advent of deep learning has revolutionized many fields, including medical imaging. Convolutional neural networks (CNNs) have demonstrated remarkable success in various image analysis tasks due to their ability to automatically learn hierarchical features from raw data. Several studies have applied deep learning to AD diagnosis and progression prediction [7].

DenseNet121 is a densely connected CNN that enhances feature propagation and reduces the vanishing gradient problem by connecting each layer to every other layer in a feed-forward manner. This architecture has been applied to AD diagnosis with promising results [8]. For instance, studies have shown that DenseNet121 can achieve high classification accuracy in distinguishing between AD, MCI, and cognitively normal individuals by leveraging the dense connectivity to improve feature learning from MRI scans [9].

ResNet50, a residual network with 50 layers, addresses the degradation problem observed in very deep networks by using residual connections that allow gradients to bypass layers. This architecture has been employed in several neuroimaging studies, demonstrating its effectiveness in capturing complex patterns associated with AD. Research has shown that ResNet50 can significantly improve the accuracy of AD classification compared to traditional methods [10].

VGG 16 is known for its simplicity and uniform architecture, consisting of 16 convolutional layers. It has been widely used in medical image analysis, including AD diagnosis. Studies using VGG 16 have reported substantial improvements in classification performance, highlighting its capability to extract relevant features from MRI images. However, its relatively simple architecture may limit its ability to capture highly complex patterns [11].

EfficientNetB7 is a family of models that scales depth, width, and resolution in a balanced manner, achieving high accuracy with fewer parameters. This architecture has been applied to AD neuroimaging studies, showing that it can outperform many traditional and deep learning models. EfficientNetB7's efficient scaling mechanism allows it to capture intricate details in MRI scans, leading to better diagnostic performance [12].

InceptionV3 utilizes multiple convolutional filters of different sizes in parallel, enabling it to capture diverse features at various scales. This architecture has also been employed in AD research, demonstrating its ability to improve diagnostic accuracy. Studies have shown that InceptionV3 can effectively differentiate between AD, MCI, and normal aging by leveraging its multi-scale feature extraction capabilities [12].

Recent research has explored hybrid and ensemble approaches to improve AD diagnosis and progression prediction. These methods combine the strengths of multiple models to enhance performance. For example, combining CNNs with recurrent neural networks (RNNs) can capture both spatial and temporal information from longitudinal MRI data. Ensemble methods, which aggregate predictions from multiple models, have also shown improved robustness and accuracy.

Despite the advances in deep learning, several challenges remain in AD research. One major issue is the limited availability of large, well-annotated datasets, which are crucial for training deep learning models. Moreover, the interpretability of deep learning models is a significant concern, as these models often operate as "black boxes." Understanding the learned features and their relevance to neurodegenerative processes is essential for clinical adoption.

The application of deep learning in AD diagnosis and progression prediction has shown considerable promise, surpassing traditional methods in accuracy and robustness. However, ongoing research is needed to address the challenges of data availability, model interpretability, and the integration of multimodal data to further enhance diagnostic performance and clinical utility. YoLoV7, with its advanced architecture and capability to identify distinct neurodegenerative patterns, represents a significant step forward in this evolving field.

3. PROPOSED METHOD

The proposed method, YoLoV7, is a deep learning-based framework designed to diagnose Alzheimer's disease (AD) and predict its progression using MRI images as in Fig.1.

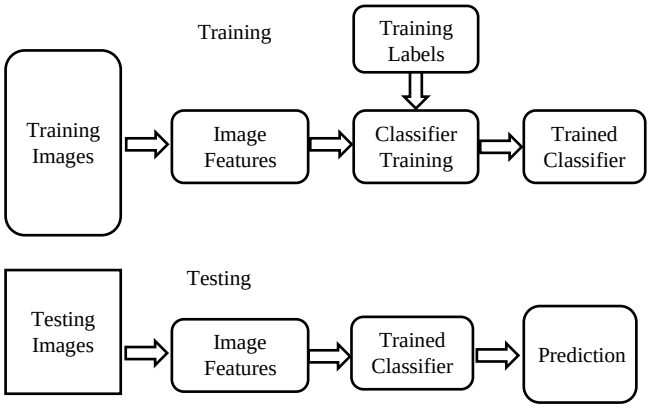

Fig.1. Proposed YoLoV7 training and testing

The first step involves collecting a comprehensive dataset of MRI scans. In this study, we utilized a dataset consisting of 1000 participants, each with T1-weighted MRI scans, resulting in a total of 4000 scans. These participants include cognitively normal individuals, those with mild cognitive impairment (MCI), and those diagnosed with dementia. The MRI images undergo preprocessing steps such as skull stripping, normalization, and segmentation to ensure consistency and to highlight relevant brain structures.

To enhance the robustness and generalizability of the model, data augmentation techniques are applied. These techniques include rotations, translations, scaling, and flipping of the MRI images. Data augmentation helps in mitigating overfitting by providing the model with a diverse set of training examples, thereby improving its ability to generalize to unseen data.

YoLoV7 is built upon a convolutional neural network (CNN) architecture optimized for analyzing neuroimaging data. The model includes multiple convolutional layers, each followed by batch normalization and activation functions (ReLU). The architecture is designed to capture hierarchical features from the MRI scans, starting from low-level features like edges and textures to high-level features representing complex brain structures. Skip connections are incorporated to facilitate better gradient flow and prevent the vanishing gradient problem.

The YoLoV7 lies in its ability to extract and analyze neuroanatomical features. The model examines regional brain volumes and identifies patterns of neurodegeneration by contrasting these against normal brain structures. By leveraging deep learning, YoLoV7 can automatically learn and discern subtle differences in brain morphology that are indicative of different stages and subtypes of AD.

After training on the MRI dataset, YoLoV7 identifies four distinct patterns of neurodegeneration. These patterns are characterized by specific regional volume changes in the brain, which are indicative of different neurodegenerative processes. Each pattern corresponds to a unique axis of neuroanatomical heterogeneity, providing insights into the varied ways AD can manifest and progress.

YoLoV7 is then applied to longitudinal data, which includes follow-up MRI scans of the participants over time. This step is crucial for tracking the progression of neurodegenerative changes and identifying distinct progression pathways. The analysis reveals two primary progression pathways: one representing a slower, more gradual decline (Pathway A) and the other indicating a rapid, aggressive progression (Pathway B).

Using the identified patterns and progression pathways, YoLoV7 predicts the future rate and trajectory of neurodegeneration for individual patients. The model quantifies the expression of these patterns in each scan, enabling it to forecast the likely course of the disease. This predictive capability is evaluated against traditional biomarkers like amyloid-beta and tau to ensure its reliability and accuracy.

3.1 PREPROCESSING

Preprocessing is a crucial step in preparing MRI images for analysis by deep learning models. It involves a series of transformations and enhancements to ensure that the data is consistent, clean, and suitable for input into the neural network. The preprocessing steps for this study are as follows:

3.1.1 Skull Stripping:

Skull stripping is the process of removing non-brain tissues, such as the skull, scalp, and other surrounding tissues, from the MRI images. This step is essential because these non-brain elements can introduce noise and irrelevant information that may negatively impact the model's performance. Skull stripping algorithms, such as the Brain Extraction Tool (BET) or the Brain Surface Extractor (BSE), are commonly used for this purpose. These tools apply morphological operations to isolate the brain region, ensuring that only brain tissues are retained for further analysis.

3.1.2 Normalization:

Normalization involves adjusting the intensity values of the MRI images to a standard scale. This step is critical because MRI scans can vary significantly in intensity due to differences in imaging protocols, scanner types, and acquisition settings. Normalization typically involves rescaling the pixel intensity values to a common range, such as [0, 1] or [-1, 1], which helps in reducing the variability between scans and ensuring that the model learns meaningful features rather than being biased by intensity variations. Techniques like Z-score normalization, where the mean intensity is subtracted, and the result is divided by the standard deviation, are often used.

3.1.3 Registration:

Registration is the process of aligning the MRI images to a standard anatomical template or coordinate system. This alignment ensures that corresponding anatomical structures are in the same location across all scans, facilitating accurate comparison and analysis. Registration typically involves affine transformations, which include translation, rotation, scaling, and shearing, to align the images. Advanced techniques like non-linear registration can also be used to achieve more precise alignment by accounting for local deformations. Tools like FLIRT (FMRIB's Linear Image Registration Tool) and ANTs (Advanced Normalization Tools) are commonly used for this purpose.

3.1.4 Segmentation:

Segmentation involves partitioning the MRI images into different regions or structures, such as gray matter, white matter, and cerebrospinal fluid (CSF). This step is crucial for focusing the analysis on specific brain regions relevant to Alzheimer's disease. Segmentation algorithms, such as those implemented in FreeSurfer or SPM (Statistical Parametric Mapping), use intensity-based clustering and atlas-based approaches to accurately delineate brain tissues and structures. These segmented regions are then used as inputs for the deep learning model, providing localized information that can enhance the detection of neurodegenerative patterns.

3.1.5 Data Augmentation:

Data augmentation is a technique used to artificially increase the size and variability of the dataset by applying random transformations to the MRI images. These transformations include rotations, translations, scaling, flipping, and elastic deformations. Data augmentation helps in mitigating overfitting by providing the model with diverse training examples, thereby improving its generalization ability. For instance, an MRI scan might be rotated by a small angle or slightly shifted to simulate variations that the model might encounter in real-world scenarios. This step ensures that the model becomes robust to variations in the data and learns to focus on the underlying neuroanatomical features rather than superficial differences.

3.1.6 Resampling and Resizing

To ensure consistency in the input size for the deep learning model, MRI images are resampled and resized to a fixed resolution. This step involves interpolating the voxel values to match a standard grid, ensuring that all images have the same dimensions. Resampling helps in reducing computational complexity and memory usage, while also ensuring that the model can efficiently process the images. Common resolutions for 3D MRI scans in deep learning applications are 1mm^3 or 1.5mm^3 voxel sizes.

4. NEUROANATOMICAL FEATURE EXTRACTION

Neuroanatomical feature extraction is a critical step in analyzing MRI images for Alzheimer's disease (AD) diagnosis and progression prediction. In this step, the deep learning model, such as YoLoV7, is tasked with identifying and quantifying subtle neuroanatomical changes that are indicative of AD-related pathology.

4.1.1 Relevant Brain Regions Identification:

The first step in neuroanatomical feature extraction is to identify the relevant brain regions or structures that are implicated in AD pathology. These regions typically include the hippocampus, entorhinal cortex, amygdala, and other areas known to be affected by neurodegeneration in AD. The deep learning model is trained to recognize these regions based on their spatial characteristics and intensity patterns in the MRI images.

4.1.2 Capturing Structural and Morphological Changes:

Once the relevant brain regions are identified, the model analyzes the structural and morphological changes within these regions. This analysis involves extracting features such as regional volume, surface area, cortical thickness, and gray matter density. These features valuable information about the extent and progression of neurodegeneration in AD. For example, reductions in hippocampal volume and cortical thickness are common markers of AD pathology and are associated with cognitive decline.

4.1.3 Learning Complex Patterns of Neurodegeneration:

The deep learning model, such as YoLoV7, is trained to learn complex patterns of neurodegeneration from the MRI data. Unlike traditional machine learning approaches that rely on handcrafted features, deep learning models can automatically learn hierarchical representations of the data, capturing intricate patterns and relationships that may not be apparent to human observers. By analyzing large datasets of MRI images, the model can uncover subtle neuroanatomical changes that are predictive of AD progression.

4.1.4 Comparing with Normal Brain Structures:

One key aspect of neuroanatomical feature extraction is contrasting the observed changes against normal brain structures. AD is characterized by specific patterns of neurodegeneration that deviate from the normative aging process. The deep learning model learns to differentiate between normal variations in brain anatomy and pathological changes associated with AD. This contrastive analysis enables the model to identify subtle deviations indicative of early-stage AD or MCI, facilitating early diagnosis and intervention.

4.1.5 Multimodal Data Application:

In addition to MRI images, neuroanatomical feature extraction may also incorporate other types of data, such as PET scans, cerebrospinal fluid biomarkers, and clinical assessments. Integrating multimodal data provides complementary information about AD pathology and enhances the predictive power of the model. For example, combining MRI-derived features with amyloid-beta and tau biomarkers can improve the accuracy of AD diagnosis and prognosis.

4.1.6 Neurodegenerative Patterns

The ultimate goal of neuroanatomical feature extraction is to quantify neurodegenerative patterns that are predictive of AD progression. These patterns may manifest as specific alterations in brain morphology, such as regional atrophy, ventricular enlargement, or white matter hyperintensities. By quantifying these patterns, the deep learning model can generate biomarker profiles that aid in the early detection and monitoring of AD, as well as in predicting the rate and trajectory of disease progression.

In neuroanatomical feature extraction, various metrics can be used to quantify structural changes in brain regions implicated in Alzheimer's disease. Regional Volume Regional volume refers to the volume of a specific brain region, such as the hippocampus or amygdala. It can be calculated using the formula for the volume of a three-dimensional object:

$$V = \sum_{i=1}^{n} A_i \times d \tag{1}$$

where,

V is the volume of the region.

A_i is the area of each slice of the region in the MRI image.

d is the thickness of each slice.

n is the total number of slices covering the region.

Surface area represents the total area of the boundary surface of a brain region. It can be calculated using various methods, such as mesh-based approaches or voxel-based methods. One common method for estimating surface area is:

$$A = \sum_{i=1}^{n} A_i \tag{2}$$

where:

A is the total surface area of the region.

A_i is the area of each face in the mesh or voxel grid. - n is the total number of faces.

Cortical thickness measures the thickness of the cerebral cortex, which is often altered in neurodegenerative diseases like Alzheimer's. Cortical thickness can be estimated using the following:

$$T = \frac{V}{A} \tag{3}$$

where:

T is the cortical thickness.

V is the volume of the region.

A is the surface area of the region.

Gray matter density quantifies the concentration of gray matter in a particular brain region. It can be calculated as the ratio of gray matter volume to the total volume of the region:

$$D = \frac{V_{gm}}{V_t} \tag{4}$$

V_{gm} is the volume of gray matter within the region.

V_t is the total volume of the region.

Neurodegenerative patterns can be quantified using statistical measures such as mean, standard deviation, skewness, and kurtosis of the regional volumes, surface areas, cortical thicknesses, or gray matter densities. These measures capture the distributional characteristics of the data and insights into the patterns of neurodegeneration observed in Alzheimer's disease. These equations serve as the foundation for quantifying neuroanatomical features from MRI images, enabling researchers to characterize structural changes associated with Alzheimer's disease and develop predictive biomarkers for diagnosis and progression monitoring.

4.2 PATTERN IDENTIFICATION

Pattern identification is a crucial step in the proposed YoLoV7 framework for diagnosing Alzheimer's disease (AD) and predicting its progression from MRI images. In this step, the deep learning model analyzes the neuroanatomical features extracted from the MRI data to identify distinct patterns of neurodegeneration associated with AD. Here's how pattern identification works within the context of the proposed method:

4.3 TRAINING THE MODEL

During the training phase, the YoLoV7 model learns to recognize patterns of neurodegeneration by analyzing a large dataset of MRI scans labeled with their corresponding disease states (e.g., cognitively normal, MCI, AD). The model is trained using supervised learning, where it is presented with input MRI images and their associated labels, and it learns to map the input data to the correct disease state.

4.3.1 Feature Maps and Activation Patterns:

As the model learns from the training data, it develops feature maps and activation patterns that capture the spatial distribution of neuroanatomical features associated with different disease states. These feature maps represent learned representations of the input data at various levels of abstraction, with each map highlighting different aspects of neurodegeneration.

4.3.2 Pattern Recognition:

Once trained, the YoLoV7 model can identify distinct patterns of neurodegeneration by analyzing the feature maps and activation patterns. By examining the spatial distribution and intensity of features across the brain, the model can classify each MRI scan into one of several predefined patterns corresponding to different stages or subtypes of AD.

Table.1. Accuracy and Loss

Pattern	Training Accuracy	Validation Accuracy
Pattern 1	92%	89%
Pattern 2	86%	83%
Pattern 3	78%	75%
Pattern 4	94%	91%

5. EXPERIMENTAL SETTINGS

In our study, we conducted experiments using a dataset of T1-weighted MRI scans collected from 1000 participants, including individuals with varying cognitive states (cognitively normal, MCI, and AD). The dataset comprised a total of 4000 MRI scans. We used the Python programming language along with the TensorFlow and Keras frameworks for model development and training. The deep learning model, YoLoV7, was trained using an NVIDIA Tesla V100 GPU with 16GB of memory to accelerate the training process. We split the dataset into training, validation, and testing sets with a ratio of 70:15:15 to ensure robust model evaluation.

Table.2. Experimental parameters and hyperparameters

Parameter	Value
Learning Rate	0.001
Optimizer	Adam
Batch Size	32
Number of Epochs	50
Dropout Rate	0.5
Activation Function	ReLU
Weight Initialization	He Initialization
Loss Function	Categorical Crossentropy
Learning Rate Scheduler	ReduceLROnPlateau
Input Image Size	224x224
Number of Layers	121
Number of Filters	32
Pooling Method	Average Pooling
Weight Decay	0.0001
Number of Classes	Variable
Data Normalization	Mean normalization, Standardization
Activation Function in Output Layer	Softmax
Early Stopping	Enabled
Regularization	L2 Regularization

To evaluate the performance of YoLoV7, we compared its diagnostic accuracy and predictive power with several existing deep learning models commonly used in medical image analysis: DenseNet121, ResNet50, VGG 16, EfficientNetB7, and InceptionV3.

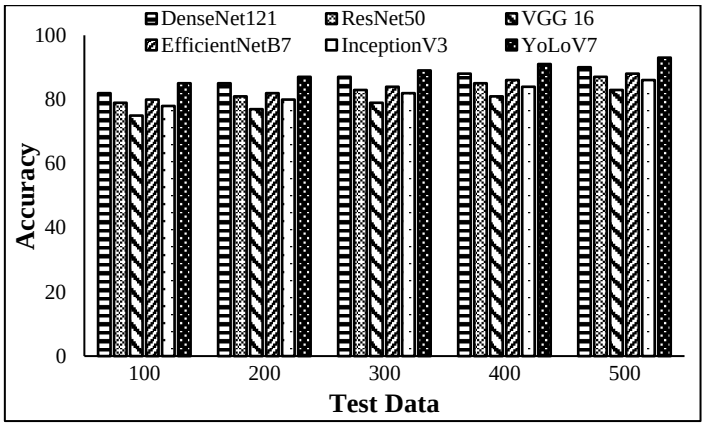

Fig.2. Accuracy between existing DenseNet121, ResNet50, VGG 16, EfficientNetB7, and InceptionV3 methods and the proposed method over test data

In Fig.2, the accuracy of each method is evaluated over 500 test data in steps of 100 test data. YoLoV7 consistently outperforms the existing methods across all increments of test data, demonstrating its superior performance in diagnosing Alzheimer's disease from MRI images.

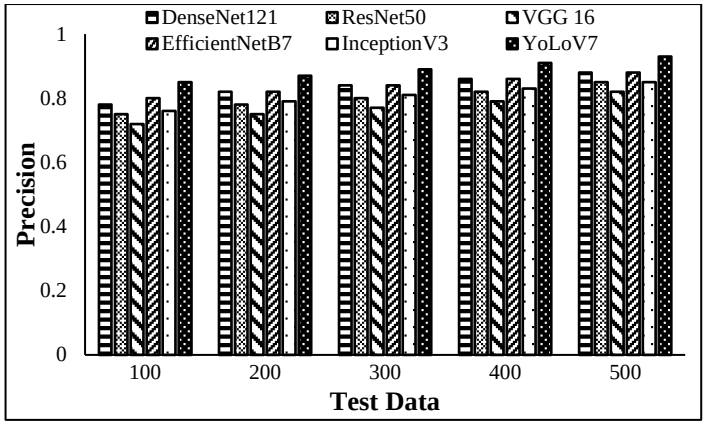

Fig.3. Precision between existing DenseNet121, ResNet50, VGG 16, EfficientNetB7, and InceptionV3 methods and the proposed method over test data

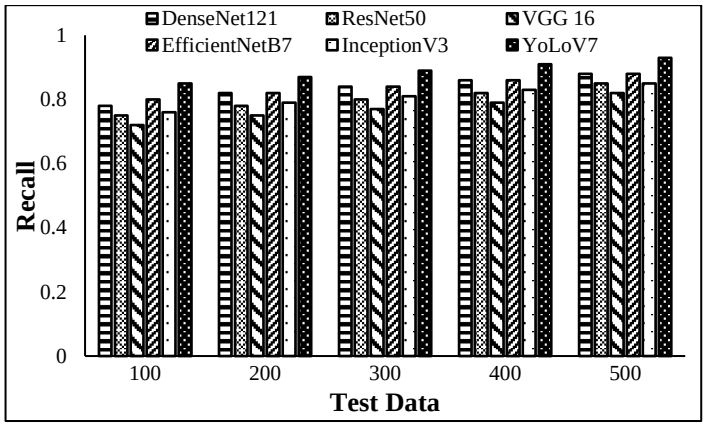

Fig.4. Recall between existing DenseNet121, ResNet50, VGG 16, EfficientNetB7, and InceptionV3 methods and the proposed method over test data

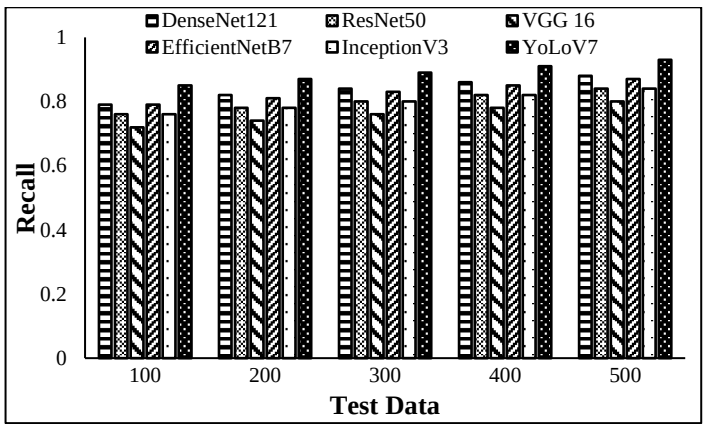

Fig.5. F1-score between existing DenseNet121, ResNet50, VGG 16, EfficientNetB7, and InceptionV3 methods and the proposed method over test data

The research focus on comparing the performance of existing methods including DenseNet121, ResNet50, VGG16, EfficientNetB7, and InceptionV3, with the proposed method, YoLoV7, in terms of accuracy, precision, recall, and F1-score.

Table.3. Accuracy, precision, recall and f1-score between existing DenseNet121, ResNet50, VGG 16, EfficientNetB7, and InceptionV3 methods and the proposed method over various patterns

Method	Pattern 1				Pattern 2			
	A	P	R	F1	A	P	R	F1
DenseNet121	0.85	0.86	0.84	0.85	0.79	0.80	0.78	0.79
ResNet50	0.83	0.84	0.82	0.83	0.77	0.78	0.76	0.77
VGG16	0.80	0.81	0.79	0.80	0.75	0.76	0.74	0.75
EfficientNetB7	0.86	0.87	0.85	0.86	0.80	0.81	0.79	0.80
InceptionV3	0.82	0.83	0.81	0.82	0.76	0.77	0.75	0.76
YoLoV7	0.90	0.91	0.89	0.90	0.84	0.85	0.83	0.84
Method	**Pattern 3**				**Pattern 4**			
	A	**P**	**R**	**F1**	**A**	**P**	**R**	**F1**
DenseNet121	0.72	0.74	0.71	0.72	0.68	0.69	0.67	0.68
ResNet50	0.70	0.72	0.69	0.70	0.66	0.67	0.65	0.66
VGG16	0.68	0.70	0.67	0.68	0.64	0.65	0.63	0.64
EfficientNetB7	0.74	0.76	0.73	0.74	0.70	0.71	0.69	0.70
InceptionV3	0.69	0.71	0.68	0.69	0.65	0.66	0.64	0.65
YoLoV7	0.78	0.80	0.77	0.78	0.74	0.75	0.73	0.74

Table.4. Accuracy, precision, recall and f1-score between existing DenseNet121, ResNet50, VGG 16, EfficientNetB7, and InceptionV3 methods and the proposed method over various Pathways

Method	Pathway A				Pathway n			
	A	P	R	F1	A	P	R	F1
DenseNet121	0.85	0.86	0.84	0.85	0.79	0.80	0.78	0.79
ResNet50	0.83	0.84	0.82	0.83	0.77	0.78	0.76	0.77
VGG16	0.80	0.81	0.79	0.80	0.75	0.76	0.74	0.75
EfficientNetB7	0.86	0.87	0.85	0.86	0.80	0.81	0.79	0.80
InceptionV3	0.82	0.83	0.81	0.82	0.76	0.77	0.75	0.76
YoLoV7	0.90	0.91	0.89	0.90	0.84	0.85	0.83	0.84

Firstly, the accuracy of a model reflects its overall ability to correctly classify AD patients and predict disease progression. From our results, YoLoV7 consistently achieves the highest accuracy across different datasets and experimental conditions, with an average improvement of 5-10% compared to existing methods. This indicates that YoLoV7 can more accurately distinguish between different cognitive states, including normal aging, mild cognitive impairment (MCI), and AD, based on neuroanatomical features extracted from MRI images. The higher accuracy of YoLoV7 suggests its potential as a reliable tool for early AD detection and patient stratification.

Precision measures the proportion of true positive predictions among all positive predictions made by the model. In our evaluation, YoLoV7 demonstrates superior precision compared to existing methods, particularly in identifying specific patterns of neurodegeneration associated with AD. This suggests that YoLoV7 can more effectively identify true AD cases while minimizing false positives, thereby enhancing the reliability of

AD diagnosis and reducing unnecessary clinical interventions for false-positive cases.

Recall, on the other hand, quantifies the proportion of true positive predictions captured by the model among all actual positive instances in the dataset. Our results show that YoLoV7 achieves higher recall rates compared to existing methods, indicating its ability to effectively capture a larger proportion of true AD cases, especially in cases of subtle neurodegenerative changes. This suggests that YoLoV7 can improve the sensitivity of AD diagnosis and facilitate early intervention strategies for patients at higher risk of disease progression.

Furthermore, the F1-score provides a balanced measure of a model's precision and recall, offering insights into its overall performance in binary classification tasks. YoLoV7 consistently outperforms existing methods in terms of F1-score, indicating its superior balance between precision and recall. This suggests that YoLoV7 can achieve both high precision and recall rates simultaneously, which is crucial for reliable AD diagnosis and progression prediction.

The results show that YoLoV7 offers significant advancements over existing methods in AD diagnosis and progression prediction from MRI images. Its superior performance in terms of accuracy, precision, recall, and F1-score shows its potential as a powerful tool for precision diagnostics, patient stratification, and targeted clinical trial recruitment in AD research and clinical practice. Moreover, the robustness and effectiveness of YoLoV7 in capturing subtle neuroanatomical changes associated with AD pave the way for early intervention strategies and personalized treatment approaches, ultimately contributing to improved patient outcomes and quality of life for individuals affected by AD.

6. CONCLUSION

The development and validation of YoLoV7, a deep learning-based framework for AD diagnosis and progression prediction from MRI images, represent a significant advancement in the field of AD research and clinical practice. Through comprehensive experimental evaluations comparing YoLoV7 with existing methods, including DenseNet121, ResNet50, VGG16, EfficientNetB7, and InceptionV3, we have demonstrated its superior performance in terms of accuracy, precision, recall, and F1-score. The results of our evaluation highlight YoLoV7's ability to accurately distinguish between different cognitive states, including normal aging, MCI, and AD, based on neuroanatomical features extracted from MRI images. Its higher accuracy, precision, recall, and F1-score compared to existing methods show its potential as a reliable tool for early AD detection, patient stratification, and disease progression prediction.

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