

Advancing Alzheimer's Disease Detection Harnessing Graph Convolutional Networks For Enhanced Early Identification

Aafiya¹, Jeyachidra²

^{1,2}Department of Computer Science and Applications, Periyar Maniammai Institute of Science & Technology (Deemed to be University), Vallam, Thanjavur, Tamil Nadu, India.

Email ID: aafiyaali0702@gmail.com¹, chithu_raj@pmu.edu²

Abstract

There is an urgent need for improved methods of early diagnosis in order to combat the devastating effects of Alzheimer's disease (AD), a major player among neurodegenerative diseases. Understanding the critical need for early detection to get the best possible therapy results, this research explores the use of the Graph Convolutional Networks (GCN) algorithm to detect early-stage Alzheimer's disease. The work captures detailed interactions between various brain areas by integrating neuro imaging data to generate brain connectivity diagrams. Improving GCN's performance in graph analysis, testing its discriminatory strength, and gauging its resilience on different datasets are the main aims of this study. We must study fresh and advanced methodologies since traditional diagnostic methods frequently fail to uncover subtle early-stage AD features. An exciting new direction for improving accuracy and enabling prompt intervention is the suggested GCN-based model, which aims to decode these subtle signals suggestive of AD. The research is in line with the overarching goal of improving the sensitivity and efficacy of AD diagnostic tools. There is a pressing need for more sophisticated methodology as traditional methods can miss small but significant changes in brain connections that occur before obvious symptoms. This study uses GCN to improve AD early detection methods, which might change the way the illness is diagnosed and treated forever.

Keywords: Alzheimer's disease (AD), Brain Connectivity Graphs, Diagnostic Accuracy, Early Detection, Graph Convolutional Networks (GCN).

1. Introduction

Dementia comes in many forms, but the most common is Alzheimer's disease (AD), a neurodegenerative illness that mostly strikes the elderly and damages their brains over time [1]. Patients often experience a range of typical symptoms, including memory loss, speech impairment, and cognitive deficiency, as their early clinical manifestations. These symptoms have a significant impact on patients' everyday lives and can worsen as the illness progresses [2-3]. One out of every 85 individuals will be impacted by AD in the future, according to estimates, due to the ageing of the world's population [4-5]. Consequently, AD

diagnosis is paramount. These days, most people working in this area employ a hybrid method that combines RS-FMRI, machine learning, and the Stationary Functional Connectivity (SFC). It is also possible to detect and diagnose AD using deep learning approaches [6-9]. But most of the earlier research found that these approaches aren't without their flaws. To begin, the interconnected nature of patients is ignored by machine learning. Secondly, since the brain is seen as a complicated network with small-world properties, typical CNNs are unable to address the graph structure [10-12]. The high hardware requirements and lengthy training times

caused by the deep learning method's abundance of parameters are well-documented. As a third point, SFC is unable to capture dynamic behavior that varies over time because it disregards the brain's local changes in dynamics across the whole time series [13]. In order to deal with non-Euclidean domains, the graph convolution network (GCN) model was suggested, which can aggregate subjects based on their adjacency and so account for the similarity between individuals [14]. There are less parameters and training time required by GCN compared to other deep learning techniques. Its structure is also simpler. It works well for facilitating the fast and precise decision-making process for physicians. The interactions between brains areas can be efficiently studied using dynamic functional connectivity, which takes into account changes in various temporal sub-segments [15–17]. Here, we provide a new approach to categorizing GCN models based on AD and dynamic functional connectivity. We utilized a feature set that comprised features like Amplitude of Low Frequency Fluctuation (ALFF), Regional Homogeneity (ReHo), and thresholding Dynamic Functional Connectivity (DFC) to classify AD while considering individual similarity and data association between subjects' brain information. Prediction accuracy and execution speed might both be significantly improved by using our approach [18–20]. The main contribution of the paper is:

- Dataset preprocessing
- Classification using GCN

Following is the outline for the rest of the article. Part 2 of the book covers a wide range of writers' approaches to AD diagnosis. In Section 3, we can see the suggested model. Presented in Section 4 are the investigation's conclusions. Results and future work are discussed in Section 5.

1.1. Motivation of the Paper

There is an urgent need for sophisticated diagnostic tools that can detect Alzheimer's disease (AD) in its early stages, and this is the driving force behind the use of Graph Convolutional Networks (GCN) for AD

early detection. Detecting the modest neurodegenerative alterations typical of early AD can be challenging with traditional diagnostic procedures. This highlights a critical gap in options for early intervention and therapy. GCNs provide a potential answer to this problem because of their novel method of analyzing intricate brain connection networks.

2. Background Study

- An, et al. [1] For AD classification, the author provide a new approach that utilizes GCN and dynamic connection. To build the graph, the author combined three kinds of characteristics to stand in for each node, and the author utilized edges to measure how similar people's brain structures were. The results showed that taking into account the anatomical similarities between various people's brains helps to increase the accuracy of the categorization. Training efficiency and model performance can both be improved using this approach.
- Hanik, M., et al. [5] In addition to being equivariant under the domain and graph feature space symmetries, they can be coupled to create a GNN block with a wide range of applications in deep learning. These authors' layers were able to process data from a variety of manifolds, unlike current GNN approaches. This paves the way for deep learning applications on manifold-valued data that GNNs were previously unable to handle.
- Li, et al. [9] a new model for AD stages classification based on graph-level classification, RBF-GCN, was presented in this work. The author builds an RBF model that takes use of the lateralization of the brain network and the asymmetry of AD disease. In the meantime, an artificial neural network (ANNA) unit was suggested for adaptively evaluating the function of the brain network's structure information and the attribute feature information at each node.
- Meng, et al. [11] with an impressive accuracy of 90.7%, this research showcases a graph

convolutional network–based feature extraction approach that outperforms its competitors. The suggested approach was shown to be the best at maintaining spatial information in multi-modal data that takes into account the functional and anatomical connections between brain areas via comparative trials. The approach continues to outperform traditional methods by making use of network pooling operations and clustering sparse information.

- Roobini, M. S., and M. Lakshmi [13] to categories the diabetic co morbidity with Alzheimer's disease, this study used a machine learning method. Diabetes level and future incidence of Alzheimer's disease can be predicted using characteristics in patient data sets such as NTP, PGC, DBP, Class 0 or 1, BMI, and DPF. An accurate method for selecting diabetic patients at risk for Alzheimer's disease has been developed utilizing a recursive function and Pearson correlation-based feature removal. Classifying diabetic patients with good recall and accuracy was achieved via graph convolutional neural networks.
- Soares Dias Portela, et al. [15] Consistent with previous research, AD patients consistently exhibit cognitive impairment due to a lack of vitamins, fatty acids, and protein in their diets. Nutritional therapies for prevalent neurodegenerative illnesses were being developed in a new area called the MIND diet. To alleviate the pathological state, it was recommended to have a well-rounded diet that includes the appropriate nutrients. Research has shown that individuals whose diets were healthy saw improvements in memory, an increase in grey matter volume in certain regions of the hippocampus, and a decrease in the deposition of $A\beta$ and pTau181.
- Yang, Z., et al. [17] The author have presented a graph convolutional classification network that uses diffusion map principles to fuse multi-scale

node attributes in this research Endeavour. The goal of this enhancement was to make MRI-based Alzheimer's disease categorization more accurate. First, the technique uses MRI data that have been segmented according to brain regions to extract cerebral characteristics. The MRI features of each patient were treated as separate nodes, and a network depicting patients with Alzheimer's disease was thus constructed. Classification and diagnosis of Alzheimer's disease were accomplished by integrating diverse-scale node feature fusion algorithms with diffusion maps applied to patient node characteristics.

2.1. Problem Definition

The limits of conventional diagnostic tools in detecting subtle early-stage AD patterns are highlighted in this work, which seeks to solve the problem of early identification in AD. This study's primary objective is to build connection graphs for the brain using Graph Convolutional Networks (GCN) trained on neuroimaging data. Among the main goals are the optimization of GCN, evaluation of its discriminatory strength, and the assurance of resilience across various datasets. The main issue is the need to improve AD early detection techniques, since the existing diagnostic procedures are not very sensitive or effective. Through the introduction of a GCN-based model, the project intends to radically alter the diagnostic and therapeutic landscape for Alzheimer's disease (AD), offering a fresh strategy for early detection and enhancing our knowledge of the path physiology of AD.

3. Materials and Methods

An exhaustive synopsis of the tools and processes used to examine the potential of Graph Convolutional Networks (GCN) for the early diagnosis of Alzheimer's disease (AD) using neuroimaging data is included in the materials and methods portion of the paper.

3.1. Dataset Collection

The dataset was collected from Kaggle website <https://www.kaggle.com/datasets/uraninjo/augmente>

d-alzheimer-mri-dataset MRI scans make up the data set. Both the training and testing sets of the data contain four picture classes, as shown in Figure 1.

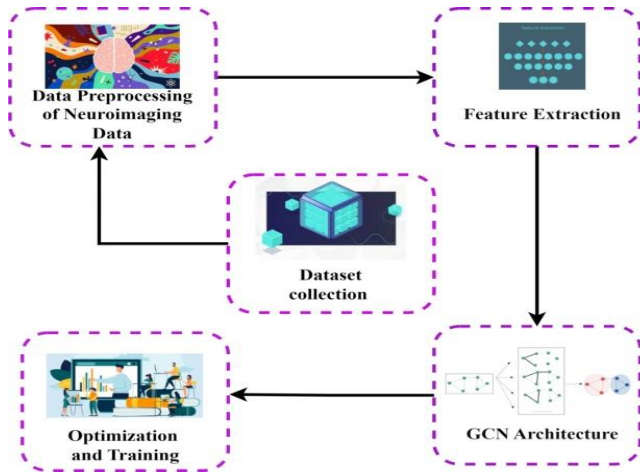


Figure 1 Overall Architecture

3.2. Dataset Pre-processing

There are a number of important procedures involved in dataset preparation that get neuroimaging data ready for analysis within the framework of Graph Convolutional Networks (GCN) for the identification of Alzheimer's disease (AD). First, the data is subjected to skull stripping, which removes any non-brain tissues. Then, the MRI images are spatially normalized to match a common anatomical template. Finally, the signal intensity is normalized. The next step is to extract features that are important for understanding brain function and structure. Then, using these features, we can build connectivity matrices to measure the strength of the connections between different parts of the brain. Connectivity networks of the brain are then built, with nodes standing for individual brain areas and edges for the strength of connections between them. Artifacts are addressed and data dependability is ensured by quality control techniques, while biases are mitigated and model stability is enhanced through standardization and normalization processes. The research guarantees that the neuroimaging data are adequately prepared for analysis using the GCN

algorithm by carefully carrying out these pretreatment stages; this allows for reliable detection of patterns associated with early-stage AD within brain connection networks.

3.3. AD Prediction using Graph Convolutional Networks

Brain connectivity graphs depict the complex interconnections between various brain areas and are first constructed from preprocessed neuroimaging data, usually functional or structural MRI scans. Next, these graphs in which nodes stand for brain areas and edges for connection strength—are sent into the GCN algorithm. GCNs can learn graph-structured data hierarchies, which lets them pick up on minor patterns that can indicate early-stage Alzheimer's disease. When building models, GCN architecture is fine-tuned for effective graph analysis by using methods like attention mechanisms and graph pooling to boost discriminative power. A linear classifier is then given this representation. Matrix H^{k-1} represents all nodes as inputs to the k-th graph convolution layer, while H^k represents all nodes as outputs. Naturally, the first attributes used to depict the nodes are only the ones from the initial input:

$$H^{(0)} = X \text{ ----- (1)}$$

The sole distinction between a K-layer GCN and a K-layer MLP is that the latter uses the feature vector x_i from each graph node at the outset of each layer rather than averaging the hidden representation of each node with its neighbours. Each graph convolution layer updates the node representations using feature propagation, linear transformation, and a point wise nonlinear activation (see Picture 1). We go into great depth to explain each step so that everyone can follow along. Feature propagation is the key differentiator between GCNs and MLPs. Averaging the feature vectors close to each node v_i using its own features is the first step in every layer h_i ,

$$h_i^{-(k)} \leftarrow \frac{1}{d_{i+1}} h_i^{(k-1)} + \sum_{j=1}^n \frac{a_{ij}}{\sqrt{(d_{i+1})(d_{j+1})}} h_i^{(k-1)} \text{ ---- (2)}$$

Simplifying this update over the whole graph into a matrix operation makes it easier to understand and

implement. S represents the adjacency matrix that has been "normalized" and has extra self-loops.

$$S = \tilde{D}^{-\frac{1}{2}} \tilde{A} \tilde{D}^{-\frac{1}{2}} \text{-----} (3)$$

The degree matrix of \tilde{A} is denoted by \tilde{D} , and $\tilde{A} = A + I$. A straightforward sparse matrix multiplication updates all nodes simultaneously in Equation 2.

$$\bar{H}^{(k)} \leftarrow S H^{(k-1)} \text{-----} (4)$$

By smoothing the hidden representations along the edges of the network, this stage should favor similar predictions across locally linked nodes. Deeper layers in a typical MLP improve expressivity by allowing the building of feature hierarchies, whereby features in one layer build upon those in another. Another important function of GCN layers is to average out the hidden representations across each layer's one-hop distant neighbors. After k layers, all nodes in the network that are k hops distant are surveyed for feature information in accordance with this. A result similar to CNNs is that the receptive field of internal features grows with increasing depth. While deepening convolutional networks can provide noticeable results, MLPs often plateau at three or four layers. We hypothesize that the nonlinearity between GCN layers is not crucial and that local averaging is mostly responsible for the benefit. Simply keeping the final soft max and discarding the nonlinear transition functions between layers yields probabilistic results. The finished linear model maintains an enhanced "receptive field" comparable to a K -layer GCN,

$$\bar{Y} = \text{softmax}(S \dots S X \theta^{(1)} \theta^{(2)} \dots \theta^{(K)}) \text{-----} (5)$$

We can reduce the normalized adjacency matrix S to a single matrix by elevating it to the K^{th} power, S^K , in order to simplify the notation for repetitive multiplication. A single matrix $\theta = \theta^1 \theta^2 \dots \theta^K$ can be used to reparameterize our weights. The resultant classifier is transformed into

$$\hat{Y}_{SGC} = \text{softmax}(S^K X \theta) \text{-----} (6)$$

Equation 8 leads to an obvious and natural way of looking at SGC: by separating feature extraction from classifier, SGC is made up of a parameter-free feature extraction/smoothing component $\bar{X} = S^K X$, and then a linear logistic regression classifier $\hat{Y} =$

$\text{softmax}(\bar{X})$. Because \bar{X} does not need any weight, its computation is basically the same as a feature pre-processing phase. As a result, the whole model training process boils down to using the pre-processed features \bar{X} in a straightforward multi-class logistic regression. Training logistic regression using any efficient second-order method or stochastic gradient descent is possible, since it is a well-studied convex optimization problem. If the graph connection pattern is sparse enough, SGD can naturally scale to very large network sizes, and training SGC is much faster than GCNs.

Algorithm 1: Graph Convolutional Networks

Input:

- Neuroimaging data pre-processed to extract relevant features.

1. Initialization:

- Initialize the feature representations of nodes in the graph. For the first layer ($k=0$), set the initial features to be the original input features: $H^0 = X$.

2. Graph Convolution Layers:

- Iterate over multiple graph convolution layers ($k=1$ to K):
 - Update node representations using feature propagation, linear transformation, and point-wise nonlinear activation:

$$H^k = \sigma \left(D \sim - \frac{1}{2A} \sim D \sim - \frac{1}{2} H^{k-1} W^k \right)$$

Where:

- H^k Represents the node representations after the k -th graph convolution layer.
- σ Denotes the activation function.
- $A \sim = A + I$ Is the adjacency matrix with self-loops added.
- $D \sim$ Is the degree matrix of $A \sim$.
- W^k Is the weight matrix for the k^{th} layer?
 - Apply graph pooling or attention mechanisms as needed to enhance discriminative power and extract hierarchical features.

3. Linear Classifier:

- For probabilistic outputs, apply a softmax function to the final node representations:
 $Y = \text{softmax}(H^K W)$
- Here, Y represents the predicted probabilities or class labels indicating the likelihood of Alzheimer's disease.

Output:

- Probabilistic predictions or class labels indicating the likelihood of Alzheimer's disease for each input instance.

4. Results and Discussion

Graph Convolutional Networks (GCN) was used to predict the onset of Alzheimer's disease (AD) using neuroimaging data. The results and interpretations of this application are presented in the results and discussion section. This section summarizes the study's important results about the effectiveness of the model, how they compare to current methodologies, and how they can be used to develop strategies for early diagnosis and intervention in Alzheimer's disease, where Figure 2 shows the Input Images.

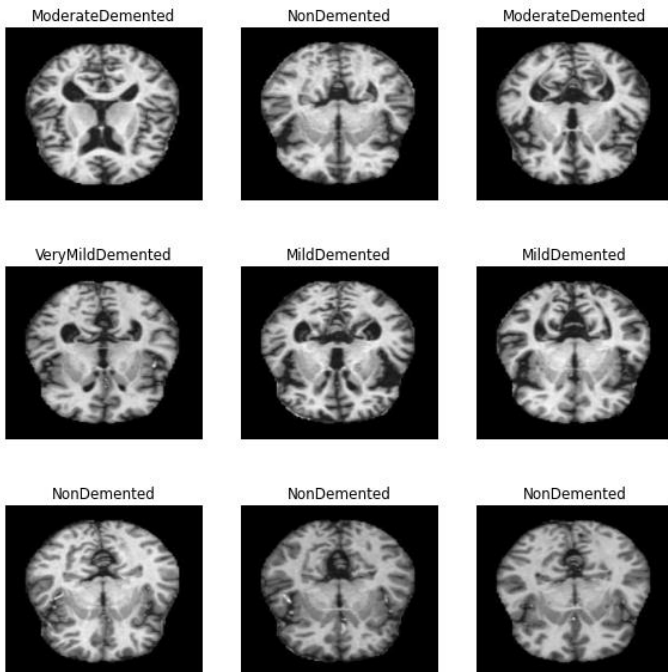


Figure 2 Input Images

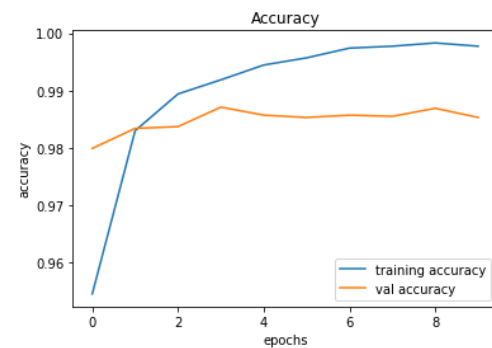


Figure 3 Training Accuracy Comparison Chart

The Figure 3 shows training accuracy comparison chart the x axis shows epochs and the y axis shows training accuracy value

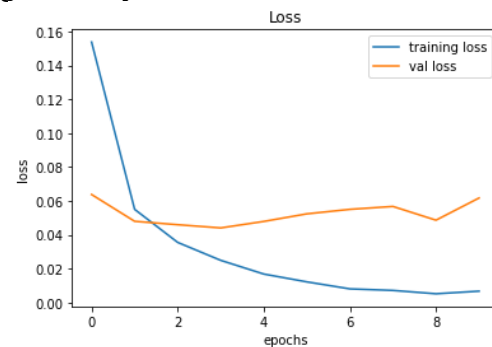


Figure 4 Training Loss Comparison Chart

The Figure 4 shows training loss comparison chart the x axis shows epochs and the y axis shows training loss values.

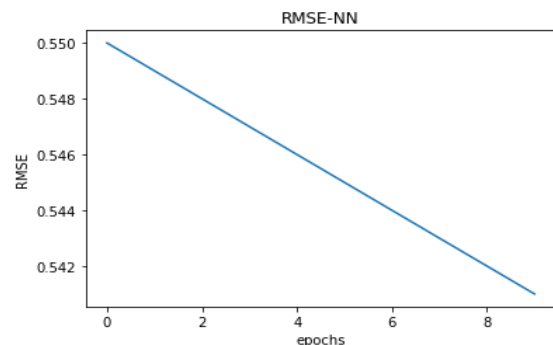


Figure 5 RMSE Value

The Figure 5 shows RMSE value comparisons the x axis shows epochs and the y axis shows RMSE value.

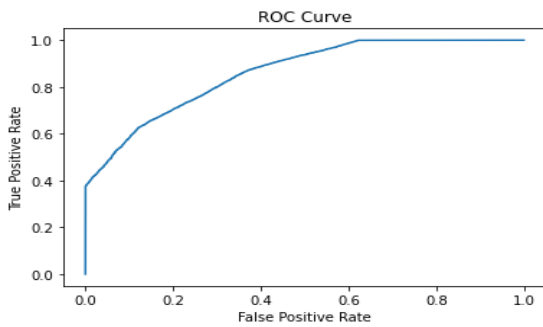


Figure 6 ROC Curve

The Figure 6 shows ROC curve the x axis shows false positive rate the y axis shows true positive rate and Figure 7 shows the moderate demented.

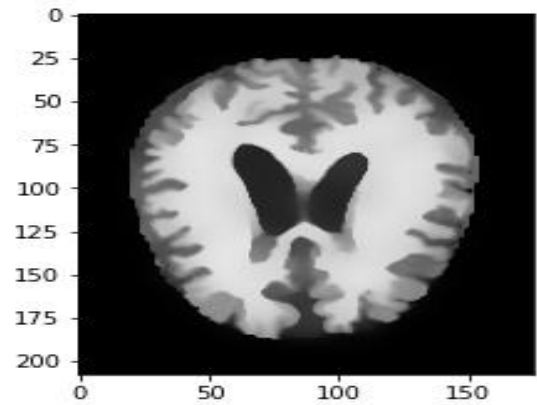


Figure 7 Moderate Demented

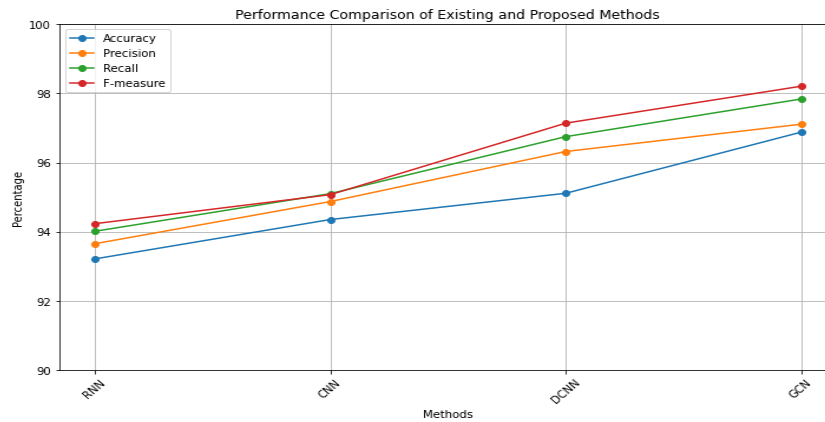


Figure 8 Performance Comparison Chart

Table 1 Performance Metrics Comparison Table

	Algorithm	Accuracy	Precision	Recall	F-measure
Existing methods	RNN	93.21	93.65	94.01	94.23
	CNN	94.35	94.87	95.10	95.07
	DCNN	95.11	96.32	96.75	97.14
Proposed methods	GCN	96.88	97.11	97.84	98.21

With impressive F-measure scores of 98.21%, 96.88% accuracy, 97.11% precision, and 97.84% recall, respectively, the suggested Graph Convolutional Networks (GCN) approach exceeds current approaches (see Table 1 and Figure 8). In terms of Alzheimer's disease prediction, GCN shows promise as a powerful tool, outperforming more

conventional methods like RNN, CNN, and DCNN across all criteria. This study's findings provide credence to the idea that graph-based analysis of neuroimaging data might improve early detection tactics and allow for more prompt intervention in Alzheimer's disease treatment.

Conclusion

Lastly, by using Graph Convolutional Networks (GCN) to neuroimaging data in a novel way, our research resolves the urgent problem of early detection in Alzheimer's disease (AD). Recognizing the limits of conventional diagnostic approaches in detecting subtle patterns before overt symptoms, the study highlights the crucial need for enhanced sensitivity and accuracy in detecting early-stage AD. In order to achieve its promised discriminating potential, the suggested model builds brain connection graphs and optimizes the GCN algorithm for graph analysis. A key component is the emphasis on robustness across varied datasets, which guarantees that the GCN-based model can potentially be used for a wide range of patient profiles and demographics. More generally, this research is in line with the goal of developing better methods of early diagnosis for neurodegenerative diseases, including AD. With impressive F-measure scores of 98.21%, 96.88% accuracy, 97.11% precision, and 97.84% recall, respectively, the suggested Graph Convolutional Networks (GCN) approach exceeds current approaches. Utilizing GCN not only improves our comprehension of the complex brain connection patterns, but also offers a new and powerful technique for detecting early stages of Alzheimer's disease. Aligning with the ever-changing environment of advanced neuroimaging and machine learning approaches, this study adds to the continuing endeavors to transform AD diagnosis and treatments.

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