



A Novel Channel-Spatial Deep Residual Attention Network for the Classification of Neurodegenerative Diseases from MRI Scans

Wardah Ibrar¹ · Muhammad Attique Khan² · Syeda Aimal Naqvi³ · Zain Hussain⁴ · Latifah Almuqren⁵ · Amina Hussain⁶ · Mohammad Alhefdi⁷ · Yunyoung Nam³

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Abstract

Personalized and precise classification of neurodegenerative diseases (Alzheimer's and brain tumors) is crucial for early diagnosis and patient care. Brain tumors and Alzheimer's disease are challenging to classify due to their varied shapes and features. In this work, we propose a novel four-block residual attention model for the classification of brain lesions and Alzheimer's disease in magnetic resonance imaging (MRI). The 4-block attention model integrates a channel attention module (CAMB) and a spatial attention module (SAMB) into each of its four blocks. We also implemented the Residual Attention Network (RAN) to improve overall disease information further and achieve better classification and generalization. An ablation study was conducted to determine the optimal number of blocks, testing RAN models with 2, 3, 4, and 5 blocks for training and validation. The proposed 4-block RAN model achieved an accuracy of 96.8% on the Alzheimer dataset and 98.5% on the Figshare Brain dataset. With only 115 layers and 6.3 million parameters, the proposed model is significantly more compact than state-of-the-art architectures while maintaining improved classification performance for brain lesions and Alzheimer's disease from MRI Scans.

Keywords Brain Tumor · Alzheimer disease · Attention Module · RAN Model · Classification · Generalizability

✉ Yunyoung Nam
ynam@sch.ac.kr

Wardah Ibrar
wardah.ibrar@ktu.edu

Muhammad Attique Khan
172649@korea.ac.kr

Syeda Aimal Naqvi
aimalnaqvi384@gmail.com

Zain Hussain
zain.hussain@glasgow.ac.uk

Latifah Almuqren
laAlmuqren@pnu.edu.sa

Amina Hussain
amina.hussain2@nhs.scot

Mohammad Alhefdi
Malhefdi@kku.edu.sa

¹ Department of Software Engineering, Kaunas University of Technology, Kaunas, Lithuania

² Center of Artificial Intelligence, Prince Mohammad bin Fahd University, Alkhobar, Saudi Arabia

³ Department of Computer Science and Engineering, Soonchunhyang University, Asan, South Korea

⁴ College of Medicine, University of Glasgow, Glasgow, UK

⁵ Department of Information Systems, College of Computer and Information Sciences, Princess Nourah bint Abdulrahman University, Riyadh 11671, Kingdom of Saudi Arabia

⁶ NHS Ayrshire & Arran, Ayr, UK

⁷ Computer Engineering Department, King Khalid University, Abha, Saudi Arabia

Introduction

Medical concerns are among the most pressing global challenges, driving continuous efforts by clinicians and researchers to improve diagnostic accuracy, treatment strategies, and patient outcomes [1]. The human nervous system is a highly complex and essential system that regulates cognitive, sensory, and physiological functions. Due to its structural and functional complexity, it is particularly vulnerable to a wide range of disorders that can severely impair quality of life. Among neurological disorders, neurodegenerative diseases and brain tumors represent two major and distinct categories with significant clinical and societal impact [2].

Neurodegenerative diseases affecting this system constitute a major global health challenge, among which Alzheimer's disease (AD) is the most prevalent. AD accounts for approximately 70% of all dementia cases [3]. AD is a neurodegenerative disorder characterized by β -amyloid-containing plaques and tau-containing neurofibrillary tangles. This disease causes cognitive impairment acquired in midlife and late life, but the presence of other neurodegenerative and cerebrovascular conditions influences its clinical impact. Despite remarkable advances in medicine, there is currently no treatment capable of stopping or slowing the progression of Alzheimer's disease [4]. Current research is focused on understanding how this disease alters the brain. The current diagnostic options remain limited to an expensive PET scan or an invasive lumbar puncture [5].

In parallel, brain tumors represent a critical oncological challenge with high morbidity and mortality rates. The World Health Organization (WHO) states that there are around 47 million dementia patients worldwide, and that figure is rising quickly each year; by 2030, there may be 82 million cases of dementia [6]. Around 29,000 instances of brain tumors are detected in the USA each year, and about 13,000 sufferers pass away, according to research from the National Brain Tumor (NBT) Foundation [7]. Furthermore, according to the latest Global Cancer Observatory (GLOBOCAN) 2022 estimates, brain and central nervous system (CNS) cancers continue to represent a significant global health burden. In 2022, brain and CNS cancers accounted for approximately 1.7% of all new cancer cases, making them the 19th most common malignancy and the 12th leading cause of cancer-related mortality worldwide.

Among primary brain tumors, gliomas, which arise from glial cells and include highly aggressive subtypes such as glioblastoma, are among the most common and clinically challenging, particularly due to their infiltrative nature and poor prognosis. Meningiomas, originating from the meninges, are often the most frequently diagnosed

benign brain tumors. In contrast, pituitary tumors (adenomas), though generally non-malignant, can cause significant endocrine dysfunction and mass effect symptoms [8]. Alzheimer's disease and brain tumors are two of the most important neurological diseases in the world, with a growing incidence. The World Health Organization estimates that there were around 57 million people with dementia globally in 2021, and that almost 10 million new cases are diagnosed annually. The most prevalent type of dementia is Alzheimer's disease, which is responsible for about 60–70% of dementia cases [9].

Therefore, early and accurate tumor identification is crucial for treatment planning and prognosis, yet it remains a complex task due to tumor heterogeneity and overlapping radiological characteristics. With so many patients worldwide, a variety of medical imaging methods are employed for diagnosis, including computed tomography (CT), PET (positron emission tomography), MRI (magnetic resonance imaging), and X-rays. MRI is a widely used neuroimaging technique that allows noninvasive visualization of the inside of the body [10, 11]. Researchers typically use MRI methods to identify and examine the brain [12]. This manual procedure is error-prone, laborious, and time-consuming. Moreover, delays could occur because radiologists are not always available. The limitations mentioned have driven the creation of computer-aided diagnosis (CAD) systems, designed to help clinicians enhance diagnostic accuracy, consistency, and efficiency [13, 14].

Early detection of diseases is now possible through machine learning (ML) and deep learning (DL) techniques, driven by advancements in computer technology and the availability of open-access neuro-related datasets [15, 16]. Deep neural networks have demonstrated high accuracy in detecting subtle and complex alterations in brain structure, tracking injury progression, and providing reliable results for determining the underlying cause of a condition [17]. Research has also shown that deep learning models can be effectively applied to medical imaging for the diagnosis of both viral and non-viral diseases, such as brain tumors, Alzheimer's, and others [18–20]. In this work, we addressed the above challenges and proposed a novel deep learning framework for classifying Alzheimer's disease and other brain-related diseases from MRI scans. The key contribution of the proposed model is as follows:

- An integrated classification system for multiple neurodegenerative diseases, such as brain tumors and Alzheimer's. Most previous studies focused either on tumors or on degenerative disease. Our research developed a comprehensive classification system for both brain tumors and Alzheimer's disease using MRI data.

- We present an innovative four-block attention model for accurate classification of brain lesions and tumors. The 4-block attention model combines the CAMB and SAMB layering structure used in each of its four blocks.
- The proposed four-block model provides an equivalent or superior level of accuracy with fewer layers (115), fewer parameters (6.3 M), and a total model size smaller than any other model at 22.17 MB.
- Our hybrid deep feature extraction and Neural Network-Based Classification strategy achieves the highest combined clinical accuracy on a large dataset of brain MRIs compared to previous studies.

Related Work

Deep learning has been widely used to develop automatic, semiautomatic, and hybrid models capable of accurately detecting and classifying tumors [21–23]. Inspired by the neural networks of the human brain, such models are typically represented as a sequence of layers, each of which is generated by a weighted sum of information from the previous layer. The first layer represents the input data, while the final layer represents the output. Multilayer architectures allow these models to tackle extremely complex problems while often requiring less human intervention than conventional machine learning techniques [24, 25].

Arumaitthurai et al. [26] introduced two methods for classifying brain tumors using deep learning and machine learning techniques. The first uses decision trees and SVM, while the second uses CNNs such as VGG19 and ResNet152. The Figshare brain tumor dataset was used to assess their effectiveness. The CNN-based method achieved an accuracy of 94.67%. Therefore, only 80.54% was achieved using the method based on statistical characteristics and an SVM classifier. Compared to other methods, the CNN-based approach performs better in classification. Abhilasha et al. [27] presented an AlexNet-based architecture that can be trained in less than an hour and produces results comparable to those for classifying pituitary tumors, gliomas, and meningiomas. They achieved 96.38% accuracy on the test dataset after training their model on the publicly accessible “Figshare” dataset. Singh et al. [28] demonstrated that brain tumor diagnosis was challenging due to the variability and overlap in MRI images. They designed a hybrid CNN model that employs CNNs, Support Vector Machines, Random Forests, and Multinomial Logistic Regression. The ensemble learning method achieves 96.08% accuracy and shows promising results on the Figshare dataset.

Recently, Aluri et al. [29] developed a new approach that combines SegNet and GTLO-LeNet to accurately classify

brain tumors into Gliomas, Meningiomas, and Pituitary tumors. The non-local means (NLM) filter was used to preprocess the input MRI image, denoising it. The SegNet model segmented the tumor area from the MRI image to achieve effective classification. In contrast, the LeNet model performed brain tumor classification (BTC) by optimizing its weights using the Golden Teacher Learning Optimization Algorithm (GTLO). The experimental results show that the GTLO-LeNet obtained an accuracy of 89.6%. Similarly, Mulla et al. [30] used a VGG-16 CNN architecture to classify three brain tumor classes: meningioma, glioma, and pituitary, and achieved 97.15% accuracy on the test dataset. Balasubramanian et al. [31] introduced a hybrid model for brain tumor detection using MRI. The model combines deep residual networks and Shepherd convolutional neural networks. An accuracy of 94% was achieved by incorporating Adaptive Wiener filtering and Conditional Random Fields–Recurrent Neural Networks (CRF-RNN). Another study by Ajagbe et al. [32] aimed to improve the classification of Alzheimer’s disease (AD) images using deep convolutional neural networks (DCNNs) and transfer learning techniques, while also expanding the evaluation metrics, as the limitations and capabilities of algorithms cannot be adequately captured by a small number of metrics.

The outcomes of their study were evaluated using six metrics, including accuracy, precision, recall, F1-score, computational time, and area under the curve. The CNN achieved the best in two categories, VGG-19 in three, and VGG-16 in one. Overall, the models reached accuracy values between 71.02% and 77.64%.

Yildirim et al. [33] employed a modified ResNet50 model to determine whether a subject had Alzheimer’s disease and the disease stage. Based on disease progression, cases were categorized into four stages. The proposed ResNet50-based model achieved an accuracy of 90%. Chaithra et al. [34] demonstrated that Alzheimer’s disease (AD) can be identified from MRI data and that disease stage can be classified using deep learning algorithms. The authors developed CNN architectures based on transfer learning for AD classification and prediction. The Kaggle AD dataset was used to train DenseNet121, MobileNet, InceptionV3, and Xception models. To ensure a fair comparison, all models were trained on the same dataset. Among them, DenseNet121 achieved the highest performance, with an accuracy of 91% on the test set. Khasanah et al. [35] used an Alzheimer’s MRI dataset to analyze the effect of class imbalance on the accuracy of the k-nearest neighbors (K-NN) method. The dataset, categorized into four groups, was used for training and testing classifications. Cross-validation analysis revealed modest performance, with accuracy values ranging from 45.86% to 50.47%. Priyatama et al. [36] focused on

applying machine learning to diagnose Alzheimer's disease using MRI data. Their approach aimed to support clinical decision-making and streamline the diagnostic process. The authors employed convolutional neural networks (CNNs) with transfer learning (VGG16 and VGG19) for Alzheimer's disease image classification. The algorithm accuracies were 75.01% for the CNN, 80.10% for VGG16, and 80.28% for VGG19. The mentioned techniques focused on either brain tumors or Alzheimer's disease. However, it is important to design a model that works for both diseases, with improved accuracy and precision. In addition, the mentioned techniques focused on pre-trained models, traditional machine learning, and transfer learning. In this work, we proposed a novel attention-based deep learning architecture for classifying brain tumors and Alzheimer's disease from MRI scans.

Materials and methods

This section describes the proposed architecture for classifying brain tumors and Alzheimer's disease from MRI scans. Two datasets, such as the Figshare Brain and Alzheimer's MRI datasets, are selected for evaluating the proposed model. The datasets are split at a 70:30 ratio for evaluation, and augmentation is performed afterward. The purpose of augmentation was to increase diversity and balance the number of classes for better learning by the designed model.

After that, the training set was passed to the proposed 4-block RAN architecture and trained using optimized hyperparameters. The trained model is used in the testing phase to obtain classification results and predicted labels. Figure 1 illustrates the framework of the proposed 4-block RAN model for neurodegenerative disease classification.

Dataset Description

Figshare Brain Dataset Figshare Brain Dataset: a publicly available dataset. The database includes 3064 T1-CE MR images from 233 people, representing three common types of brain tumors: pituitary (930 images), meningioma (708 images), and glioma (1426 images). These images were taken between 2005 and 2010 at Nanfang Hospital in Guangzhou, China, and Tianjin Medical University Hospital in China. Each image was obtained in three different planes: coronal (1045 images), axial (994 images), and sagittal (1025 images). The original images were gathered at 512×512 pixels and subsequently downsized to 224×224 pixels, the size supported by the transfer neural network. 70% of the available data was utilized for training and 30% for testing [37] Fig. 2.

Alzheimer's Disease MRI Dataset A collection of 6400 MR images representing four classes—mildly demented (MID), moderately demented (MOD), non-demented (ND), and

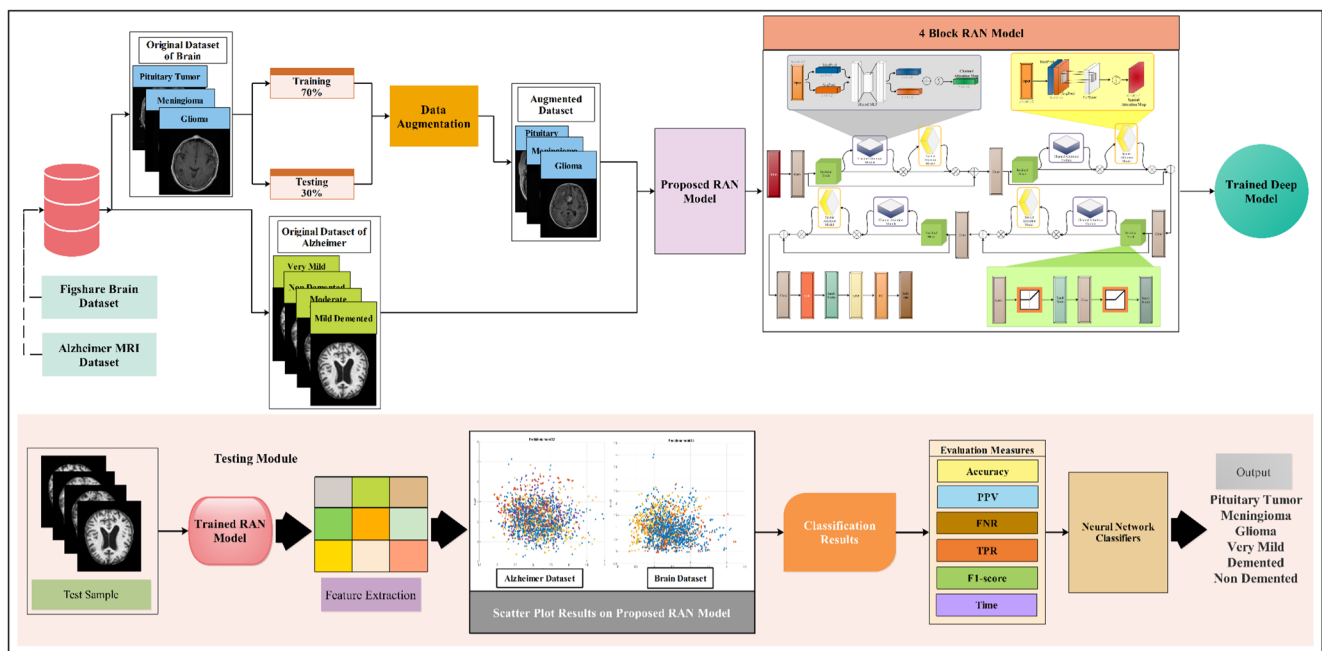
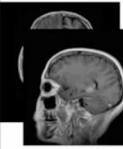
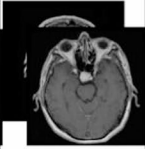
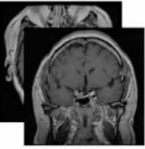
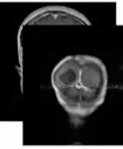
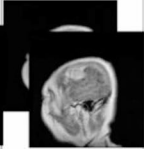
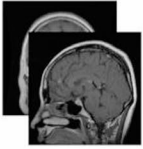
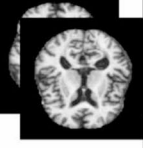
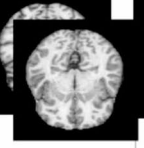
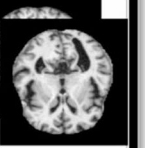


Fig. 1 Proposed 4-block RAN deep architecture for neurodegenerative disease recognition

Fig. 2 Sample images of the Figshare brain tumor dataset

Figshare Brain Tumor Dataset					
Training Part			Testing Part		
Glioma	Meningioma	Pituitary Tumor	Glioma	Meningioma	Pituitary Tumor
					
998 images	496 images	651 images	428 images	212 images	279 images

Alzheimer MRI Dataset			
Training Part			
Mild Demented	Moderate Demented	Non Demented	Very Mild Demented
			
2560 images	2560 images	2560 images	2560 images

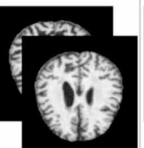
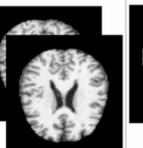
Alzheimer MRI Dataset			
Testing Part			
Mild Demented	Moderate Demented	Non Demented	Very Mild Demented
			
640 images	640 images	640 images	640 images

Fig. 3 Sample images of the Alzheimer MRI Dataset

very mildly demented (VMD)—was gathered from the open-source website Kaggle. The images in the collection are 176×208 . The images are now 176 by 176 in size [38]. Figure 3 displayed representative images from each of the four classes of this dataset. Figures 2 and 3 show the overall training and test images for both datasets.

Data Preprocessing

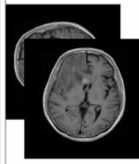
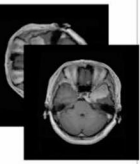
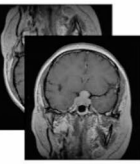
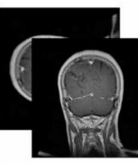
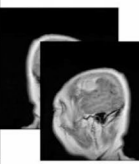
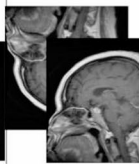
To train DL models efficiently, large quantities of high-quality data are required. The restricted availability of necessary data is a significant challenge for medical data analysis. The dataset used in this research is insufficient to achieve the required level of accuracy due to the problem's highly

imbalanced nature. Therefore, data augmentation is applied only to training samples to increase diversity and reduce class imbalance by generating additional samples for minority classes. Using this process, the original image is rotated, flipped, zoomed in, cropped, and translated to create a new image that is an identical image from multiple viewpoints [39]. After data augmentation, the images of both datasets were resized to 227×227 pixels. The distribution of data per class is shown in Fig. 4.

The Proposed RAN Model

The model starts by taking input images of size 227×227 , followed by a convolution layer with a depth of 32, a filter

Fig. 4 Data augmentation on a Figshare dataset

Figshare Brain Tumor Dataset					
Training Part			Testing Part		
Glioma	Meningioma	Pituitary Tumor	Glioma	Meningioma	Pituitary Tumor
					
2000 images	2000 images	2000 images	856 images	424 images	558 images

size of 3×3 , and a stride of 2. After this, we have created a residual block consisting of a convolutional layer with depth size 64, filter size 3×3 , and stride 1, followed by a RELU activation and a batch normalization layer. This pattern is repeated in the residual block, with a depth of 32, a stride of 1, and a filter size of 3×3 . After that, an additional layer is added, which ends the residual block and acts as the start of the channel attention module block (CAMB) [40]. CAM improves a network's learning capability with a small increase in computational power and decreases the number of parameters. The focus of the CAM module in this network is on extracting average and salient features of MRI scans along the channel dimension. Mathematically, the CAM block is defined as follows:

Consider the input convolutional layer feature map $F \in \mathbb{R}^{H \times W \times C}$, where $H \times W$ denotes the spatial dimensions of features from the convolutional layer, and C denotes the number of channels. Equations (1–2) represent the formulation of this module.

$$\phi_C(F) = \sigma(MLP(AP(F)) + MLP(MP(F))) \quad (1)$$

$$\psi' = \phi_C(F) \otimes F \quad (2)$$

Where $\phi_C(F)$ denotes the feature vector after the attention operation in the channel dimension, AP denotes the global average pool operation, MP denotes the global max pool operation, MLP denotes the multilayer perceptron that contains two fully connected layers, and $\psi' \in \mathbb{R}^{N \times C}$ represents the output of this module.

The CAMB starts with the global average and global max pooling layers added in parallel. Fully connected layers with

64 filters follow both of these layers. After that, a RELU activation layer is added, followed by another fully connected layer with 32 filters. Both these parallel layers are then concatenated using an addition layer. This combination of GAP and GMP, along with the fully connected layer, is also known as a shared MLP. Followed by the addition are the sigmoid function and resize-scale, with the scale set to 114×114 . After that, a multiplication concatenation is used to combine the addition layer at the start of CAMB with the output of the resize-scale layer.

The concatenation of an avgpool layer and a maxpool layer initiates a Spatial Attention Module Block (SAMB) [40]. The SAM module is focused on 'where' in the MRI scans, an informative part complementary to channel attention. The convolutional layer is applied on the concatenated feature map of the previous layer (CAM) to generate SAM $M_S(F) \in \mathbb{R}^{N \times C}$. Equations (3–4) represent the formulation of this module.

$$M_S(F) = \sigma(h^{7 \times 7}([AP(F); MP(F)])) \quad (3)$$

$$M_S(F) = \sigma(M_S(F) \otimes F) \quad (4)$$

Where the sigmoid function is represented by σ , and $h^{7 \times 7}$ is a convolutional operation of filter size 7×7 . In the proposed architecture, the SAM is followed by a convolutional layer with a filter size of 7×7 and a depth value of 32. A sigmoid function follows as an activation function. The multiplication concatenation is used to combine the CAMB output with the sigmoid output in SAMB. After that, an additional layer is inserted that concatenates the output of SAMB with the output of the convolution layer preceding the start of the residual block.

The next RAN block starts with a convolution layer with 128 depth, a 3×3 filter, and a stride of 2. After the convolution layer, a residual block is added in the same fashion as in the previous RAN block, changing the convolutional block depth to 96 and 128, respectively, while keeping the filter size 3×3 and the stride value 1. CAMB is inserted after the residual block, following the same pattern as in the previous RAN block, with fully connected layers of 96 and 128 filters, respectively. The CAMB ends after the insertion of the sigmoid function and resize-scale, with the scale set to 57×57 . After that, a multiplication concatenation layer is used to combine the addition layer at the start of CAMB with the resize-scale layer's output. The output of these layers serves as the starting point for SAMB. An additional layer concatenates the AvgPool and MaxPool layers. It is followed by a convolutional layer with a filter size of 7×7 and a depth of 128, followed by a sigmoid function. The multiplication concatenation is used to combine the CAMB output with the sigmoid output in SAMB. After that, an additional layer is added that concatenates the output of SAMB with the output of the convolution layer preceding the start of the residual block.

The third RAN block follows the same pattern as the previous RAN block. It starts with a 256-depth convolutional layer with a 3×3 filter and a stride of 2. The residual block is added in the same fashion as in the previous RAN block: after the initial convolution layer, as the start of the third RAN block, with the depth of the convolution layer set to 128 and 256, respectively, while keeping the same filter size and stride. CAMB is placed after the residual block in the same fashion, with the fully connected layers set to 128 and 256, respectively. The CAMB ends after the insertion of the sigmoid function and resize-scale, with the scale set to 29×29 . After that, a multiplication concatenation layer is used to combine the addition layer at the start of CAMB with the resize-scale layer's output. The output of these layers serves as the starting point for SAMB. The avgpool and maxpool layers are concatenated, followed by an addition layer, a 256-depth convolution layer with a 7×7 filter size, and a sigmoid function. The multiplication concatenation is used to combine the CAMB output with the sigmoid output in SAMB. After that, an additional layer is added that concatenates the output of SAMB with the output of the convolution layer preceding the start of the residual block.

The last RAN block is designed using a method similar to that of the previous RAN blocks. The Last RAN block is initialized with a 512-depth convolutional layer with

a 3×3 filter. A stride value of 2, followed by a residual block which consists of two pairs of convolution layers, RELU activation layer, and a batch normalization layer added sequentially, where the depth of the convolution layer is set to 256 and 512, respectively, while keeping the filter size 3×3 and the stride value is one. CAMB is placed after the residual block in the same fashion, with the fully connected layers set to 256 and 512, respectively. The CAMB ends after the insertion of the sigmoid function and the resize-scale, with the scale set to 15×15 . After that, a multiplication concatenation layer is used to combine the addition layer at the start of CAMB with the resize-scale layer's output. The output of these layers serves as the starting point for SAMB. Avgpool and maxpool layers are concatenated by an addition layer followed by the 512-depth convolution layer with a 7×7 filter size, and a sigmoid function. The multiplication concatenation is used to combine the CAMB output with the sigmoid output in SAMB. After that, an additional layer is added that concatenates the output of SAMB with the output of the convolution layer preceding the start of the residual block.

A convolution layer is added after the fourth RAN block, with a depth of 1024, followed by a GELU activation layer, GAP, a fully connected layer, and a softmax layer. The FC layer used the softmax activation function for the final classification. The mathematical formulation of this layer is defined by Eq. (5).

$$\Psi_{softmax} = \frac{\exp(H_{l_i}^T Y_i + \beta_{l_i})}{\sum_{j=1}^C \exp(H_{l_i}^T Y_i + \beta_j)} \quad (5)$$

Where $\Psi_{softmax}$ denotes the softmax activation function. The proposed model is trained using the categorical cross-entropy loss function. The mathematical formulation is:

$$\mathcal{L}_{CE}(\theta) = -\frac{1}{N} \sum_{i=1}^N \sum_{k=1}^K 1(y_i = k) \log(p_{i,k}) \quad (6)$$

$$\theta^* = \underset{\theta}{\operatorname{argmin}} \mathcal{L}_{CE}(\theta) \quad (7)$$

Where N denotes the overall training samples. K denotes the number of classes present in the selected datasets, y_i is the actual labels of the i^{th} sample, $p_{i,k}$ denotes the probability of I_i belonging to the class k , and θ denotes the learnable parameters of the proposed model. The detailed architecture of the proposed RAN model is illustrated in Fig. 5.

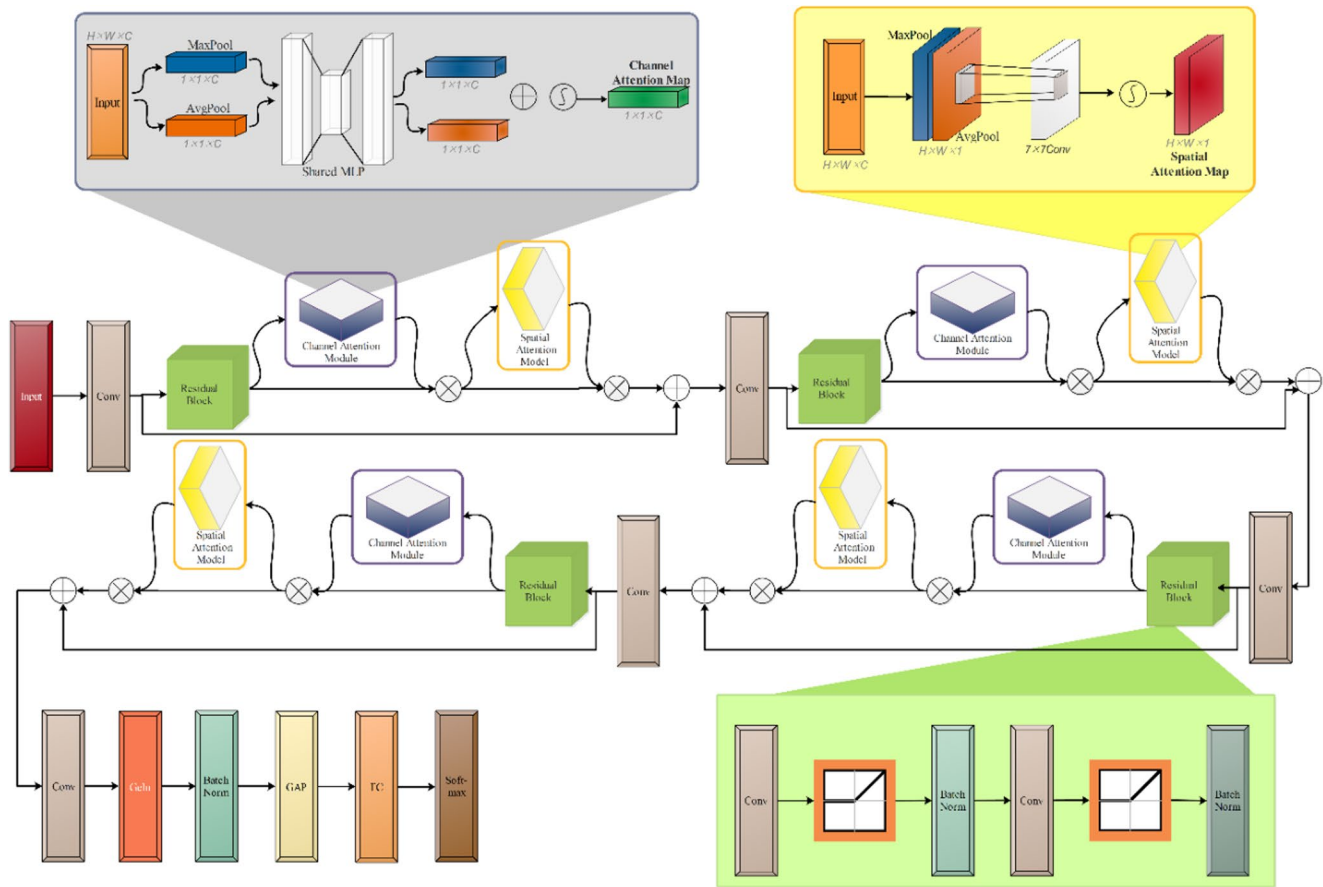


Fig. 5 Proposed RAN architecture for brain tumor and Alzheimer's disease classification

Hyperparameters Selection

After that, the training of the proposed model on the selected datasets is an important step. During training, several hyperparameters are selected, such as the initial learning rate, momentum, optimizer, epochs, and batch size. In the past, researchers employed manual hyperparameter selection, but this is not a good idea and is always discouraged; it is better to select these using an optimization technique. In this work, we used Bayesian Optimization (BO) [41] to select hyperparameters. Hyperparameter optimization aims to find the global optimal value u^* of an unknown blackbox model Δ , whose function $f(u)$ can be evaluated for any arbitrary $u \in \tilde{U}$. Hence,

$$u^* = \underset{u \in \tilde{U}}{\operatorname{argmax}} f(u) \quad (6)$$

The BO is employed to solve this problem using the objective function, a Gaussian process, and an acquisition

function. The Gaussian Process (GP) is based on the mean and standard deviation and defined as follows:

$$f(u) \sim GP(\mu(u), k(u, u')) \quad (7)$$

The expected improvement (EI) is employed as an acquisition function in this work, supported by strong theoretical guarantees and empirical effectiveness. EI is defined as follows:

$$EI(u, PD) = E[(\max(0, f(u) - f^*))] \quad (8)$$

Where PD denotes the posterior distribution for the GP, E denotes the expectation value, and $\mu(u)$ is a mean function. Based on the BO, the best hyperparameters are as follows: initial learning rate of 0.000206, momentum of 0.710, epochs of 30, batch size of 128, and optimizer of ADAM. The trained model is finally employed in the testing phase for the final classification results. The algorithm of the proposed framework is as follows:

Algorithm 1 Proposed RAN Network

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1: procedure RAN-Classification( $D, S$ )
2: Input: MRI dataset  $D = \{(I_i, y_i)_{i=1}^N\}$ , hyperparameter search space  $S$ 
3: Output: Trained model  $F_{\theta^*}$ , predicted labels  $\hat{Y}$ , and metrics  $M$ 
4:  $D_{Tr}, D_{TT} \leftarrow \text{Split}(D, 70:30)$ 
5: for each image  $I_i$  in  $D_{Tr} \cup D_{TT}$  do
6:  $\hat{I}_i \leftarrow P(I_i)$  resize to  $227 \times 227 \times 3$  and normalize
7: if  $I_i$  is grayscale then
8:  $I_{-i} \leftarrow \text{ReplicateChannels}(I_i)$ 
9: end if
10: end for
11:  $D_{Tr-Aug} \leftarrow \mathcal{A}(D_{Tr})$ 
12:  $U \leftarrow \{\eta, \mu, E, B, O\}$  for learning rate, momentum, epochs, batch size, and optimizer
13:  $s^* \leftarrow \arg \max_{s \in S} f(s)$ 
14:  $F_{\theta} \leftarrow \text{RAN}_{4B}(\cdot)$ 
15: for block  $b = 1$  to 4 do
16:  $Z_b \leftarrow \text{Conv}_b(H_{[b-1]})$ 
17:  $R_b \leftarrow \text{Res}_b(Z_b)$ 
18:  $C_b \leftarrow \text{CAMB}_{b(R_b)}$ 
19:  $S_b \leftarrow \text{SAMB}_{b(C_b)}$ 
20:  $H_b \leftarrow S_b \oplus Z_b$ 
21: end for
22:  $\theta^* \leftarrow \arg \min_{\theta} L(\theta; D_{train_{aug}}, s^*)$ 
23: for each test image  $\hat{I}_i$  in  $D_{TT}$  do
24:  $p_i \leftarrow \text{Softmax}(F_{\{\theta^*\}}(\hat{I}_i))$ 
25:  $\hat{y}_i \leftarrow \arg \max_k p_{\{i,k\}}$ 
26:  $\varphi_i \leftarrow \text{GAP}(H_4)$  and  $y_{i=1}^{NN} \leftarrow C_{NN}(\varphi_i)$ 
27: end for
28:  $M \leftarrow \{\text{Accuracy}, \text{Recall}, \text{Precision}, F1 - \text{score}, \text{AUC}, \text{FNR}, \text{FPR}\}$ 
29: return  $F_{\{\theta^*\}}, \hat{Y}, M$ 
30: end procedure

```

Proposed Testing Framework

In this section, the proposed model testing has been discussed. The testing of the proposed 4-block RAN architecture is divided into two phases. In the first phase, Softmax-based classification is performed, and the results are computed. Also, the model interpretability is analyzed through GradCAM visualization. In the second phase, the proposed model is tested on test samples, and deep features are extracted. The extracted features are evaluated using several neural network classifiers. Figure 6 describes the proposed model testing framework. 30% of the initial dataset, set aside for data augmentation testing, was used in this process.

Results and Discussion**Experimental Setup and Evaluation Metrics**

Neuroimaging investigations were conducted using the Brain Figshare and Alzheimer datasets. As mentioned

above, 70% of the images in each class were used for training, and the remaining 30% for testing, resulting in a 70:30 split of the dataset. A 10-fold cross-validation strategy was used during training and testing. Furthermore, the four-block RAN Network was trained by optimizing various hyperparameters, including the learning rate, number of epochs, momentum, mini-batch size, and optimizer. The hyperparameter settings were selected via Bayesian Optimization, as discussed in the proposed section. The entire experimental process was conducted in MATLAB 2025 b on a personal workstation with a 32GB Graphics card and 128GB of RAM. The performance of the proposed model is tested in the following experiments:

- A Softmax classifier is applied to evaluate classification performance on the selected datasets.
- Features classification using neural network classifiers, including narrow, wide, bi-layered, and tri-layered.
- These classifiers are applied to both datasets separately, and confusion matrices are generated for validation.

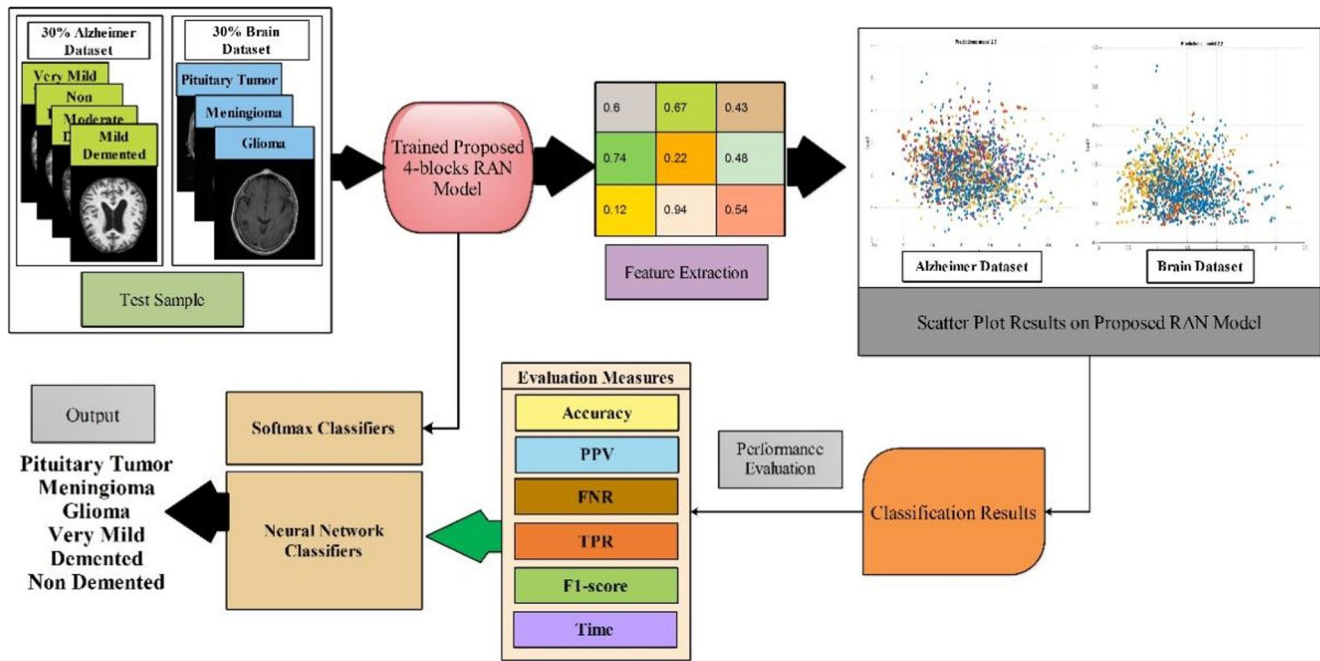


Fig. 6 Testing phase of the proposed 4-block RAN architecture

- Detailed ablation studies and comparisons were also conducted with several blocks and state-of-the-art techniques.

Proposed Model Brain Tumor Classification Results

Table 1 presents the classification performance of the proposed model using the augmented brain dataset. The Softmax is the top-performing classifier, with an outstanding 98.5% accuracy. Additionally, this classifier has a 98.5% sensitivity, a 98.36% precision, an AUC of 0.9954, an FPR of 0.007367, an F1 score of 98.432%, and an equivalent FNR of 1.5%. This table shows each classifier's computing time; the Softmax takes noticeably less time than the others. The other listed classifiers in this table, such as NNN, WNN, BNN, and TNN, achieved accuracies of 97.2%, 98.4%, 97.3%, and 97.4%, respectively. These classifiers also show improved performance on this dataset. According to the test results, the tri-layered neural network has the longest execution time of 13.06 s. Figure 7 depicts the confusion matrix of the Softmax classifier, which can be used to verify the performance of the proposed accuracy, precision,

and recall rates. In this figure, part (A) shows the recall rate verification, and part (B) shows the precision for each class. Overall, the proposed model shows improved performance across precision, recall, and accuracy.

Proposed Model Alzheimer's Disease Classification Results

Table 2 presents the results of the proposed 4-block RAN architecture for the Alzheimer's disease dataset. This table shows that the Softmax classifier achieved the highest accuracy of 96.8%. The other measures computed for this classifier are recall rate (96.75), precision (96.77), area under the curve (0.9973), FNR (3.25), and F1 score (96.76). The second-best accuracy was achieved by a Wide neural network (WNN) of 94.9%. The remaining classifiers had the best accuracy scores of 92.7%, 93%, and 93.4%, respectively. The confusion matrix of a Softmax classifier, illustrated in Fig. 8, can be used to verify the recall and precision rates obtained. Also, these figures show which class has the highest correct prediction rate, such as Moderate Demented

Table 1 Classification performance of the proposed 4-block RAN model using the Figshare Brain dataset for the suggested

Classifier	Accuracy (%)	Recall (%)	Precision (%)	FNR	Time (sec)	AUC	FPR	F1-Score (%)
NNN	97.2	96.9	97.2	3.1	9.8232	0.9887	0.014911	97.049
Softmax	98.5	98.5	98.36	1.5	8.1891	0.9954	0.007367	98.432
WNN	98.4	98.4	98.16	1.6	12.076	0.9976	0.007917	98.279
BNN	97.3	97.2	97.1	2.8	11.046	0.9889	0.013793	97.149
TNN	97.4	97.4	97.13	2.6	13.06	0.9894	0.013428	97.26

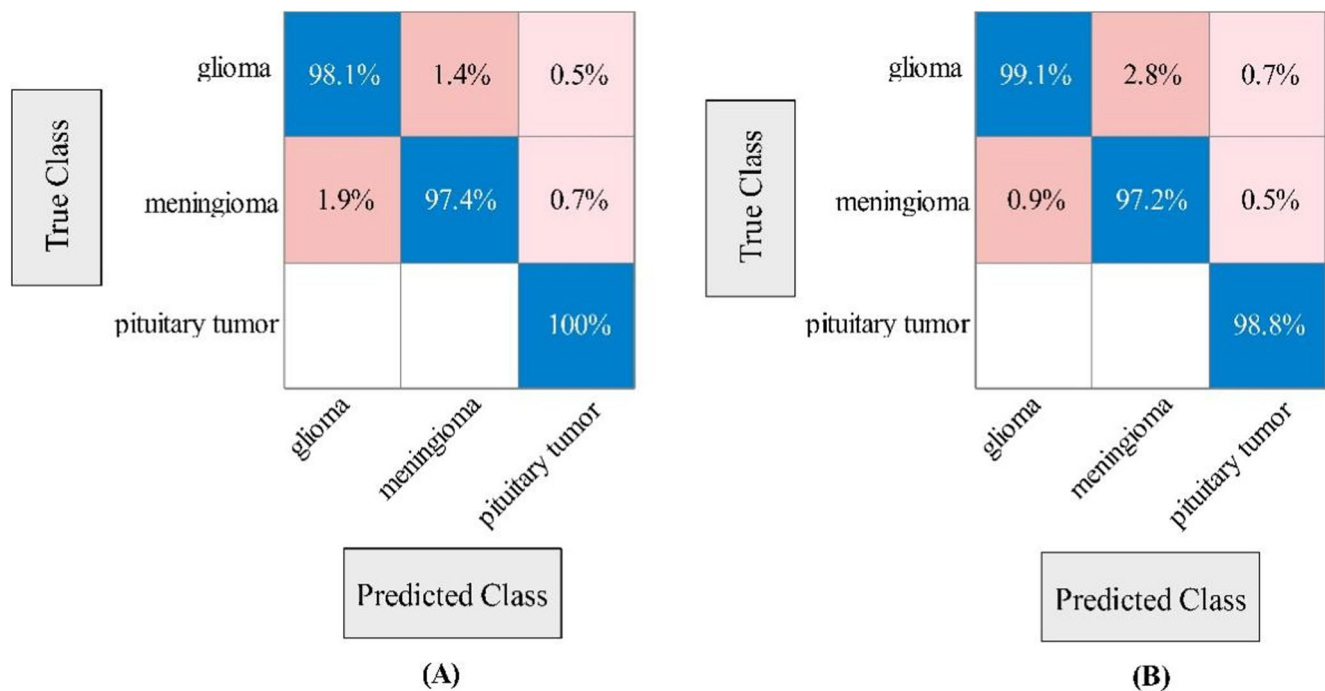


Fig. 7 Confusion matrix of Softmax classifier using Figshare brain dataset: Recall (A) and Precision rate (B)

Table 2 Classification outcomes of the suggested RAN model on an Alzheimer's MRI dataset

Classifier	Accuracy (%)	Recall (%)	Precision (%)	FNR	Time (sec)	AUC	FPR	F1-Score (%)
NNN	92.7	92.7	92.75	7.3	8.992	0.96972	0.02434	92.724
Softmax	96.8	96.75	96.77	3.25	5.3611	0.99737	0.010807	96.762
WNN	94.9	94.92	94.92	5.075	4.1968	0.99415	0.016927	94.925
BNN	93.0	92.95	93	7.05	33.673	0.96962	0.02343	92.974
TNN	93.4	93.4	93.47	6.6	18.618	0.98355	0.022005	93.437

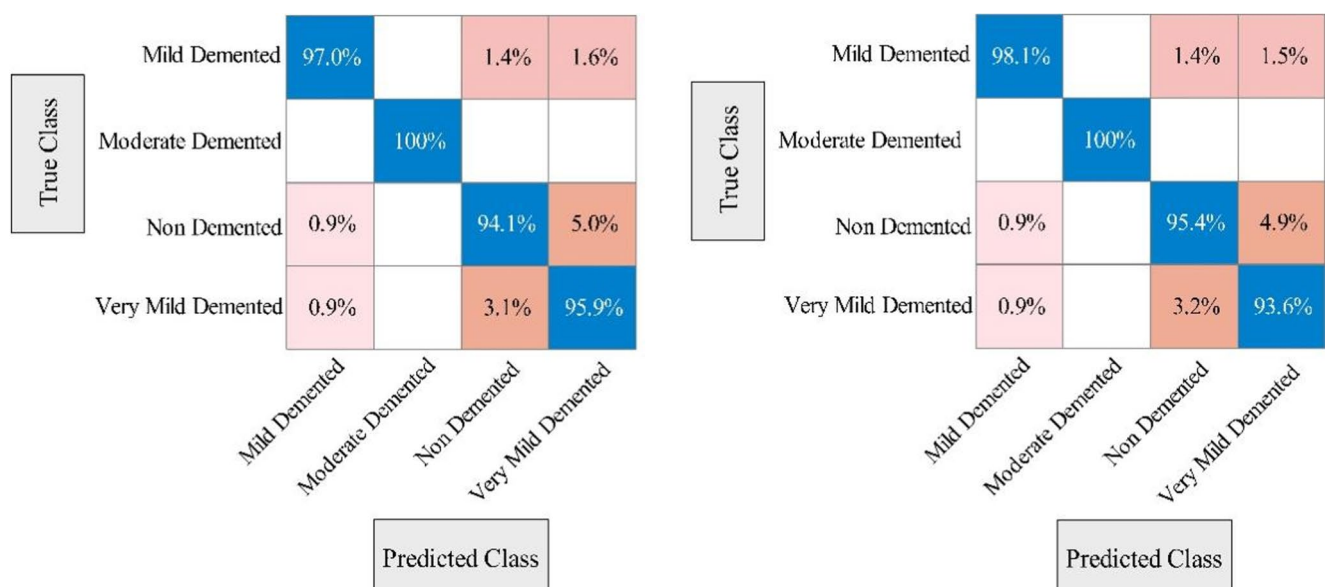


Fig. 8 Confusion matrix of Softmax classifier. (A) Recall rate; (B) Precision rate

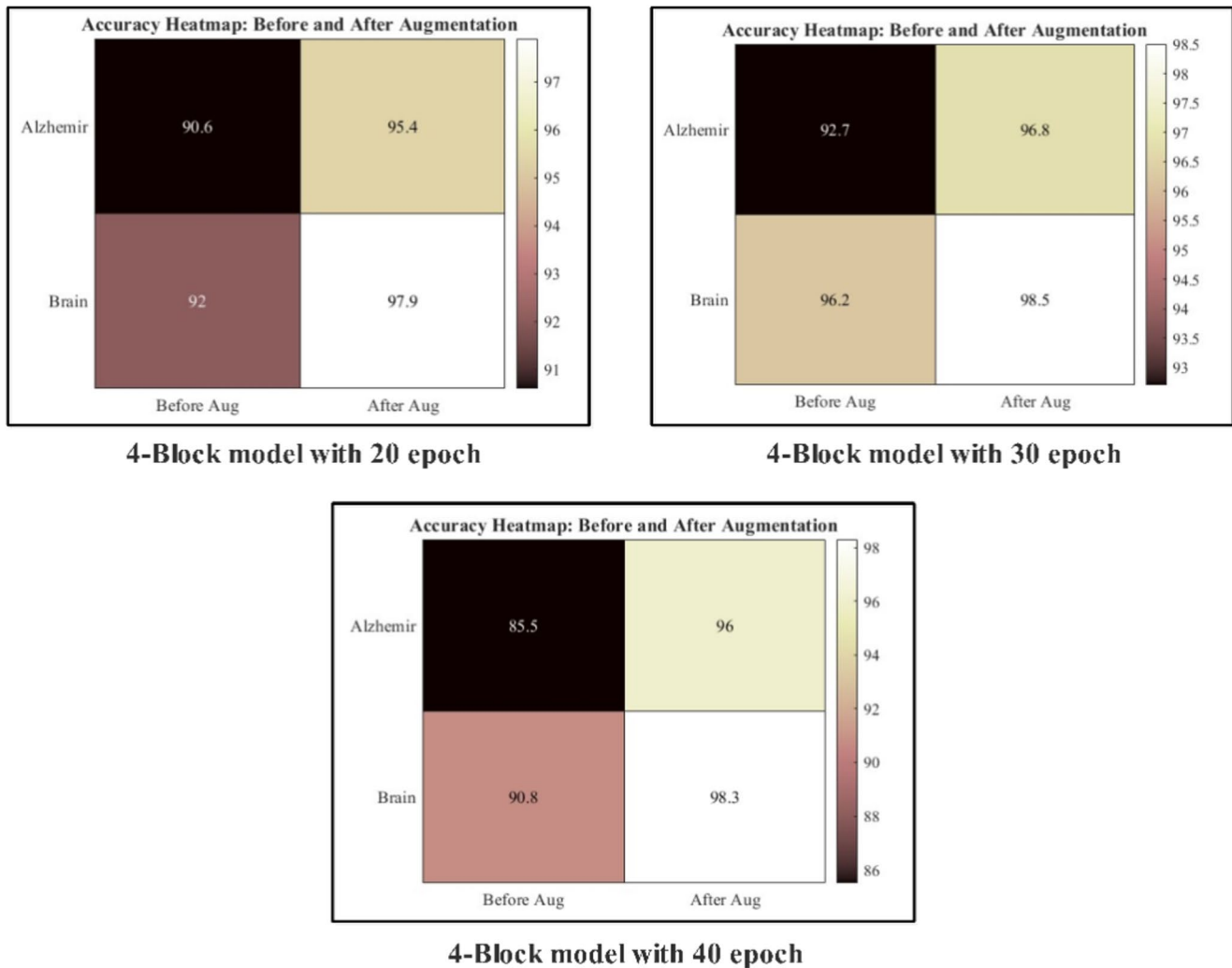


Fig. 9 Heat Map of the proposed 4-block RAN model with different epochs

Ablation Study 3- A detailed comparison was made based on the accuracy of the listed models in Fig. 11. The accuracy for the proposed 4-block RAN network was 96.8% on the Alzheimer MRI dataset and 98.5% on the Figshare Brain dataset, indicating strong performance on both datasets. To compare, a few existing deep learning models: GoogleNet achieved 83.0% and 88.9% on Alzheimer MRI and Figshare Brain datasets, respectively, while ResNet101 scored 86.0% and 89.0%, DenseNet201 scored 89.9% and 91.6%, and NasNetLarge scored 92.0% and 93.0%. AE ViT [46] achieved a competitive performance of 94.2%, while the Hybrid Network [47], IRBwSA [16], MultiScale MoE [48], Customized CNN [49], and CNN-SVM [50] achieved performance of 96.01%, 96.1%, 96.92%, 97.84%, and 84.77%, respectively. Overall, the proposed 4-block RAN architecture performed best on the Figshare Brain dataset and showed strong performance on the Alzheimer dataset, demonstrating its efficiency compared with advanced deep learning models.

Ablation study 4- An ablation study was conducted to compare the ablating effects of the Channel Attention Module Block (CAMB) and Spatial Attention Module Block (SAMB) under four different combinations of the proposed RAN architecture, as shown in Table 5. The baseline model without CAMB and SAMB had 94.21% accuracy on the Figshare Brain and Alzheimer datasets, respectively. The accuracy of the baseline model improved to 95.95% and 93.94% with the addition of CAMB to the Figshare and Alzheimer datasets, respectively, with increases of 1.74% and 0.78% on each. This suggests that the MRI feature representation is discriminative for channel-wise feature recalibration. Likewise, SAMB, when used individually, attained accuracies of 96.15% and 94.65% in the Figshare and Alzheimer datasets, respectively. This is an improvement of 1.94% and 1.49% for the two models, respectively, when compared to the baseline model. These findings show that spatial attention outperforms channel attention alone,

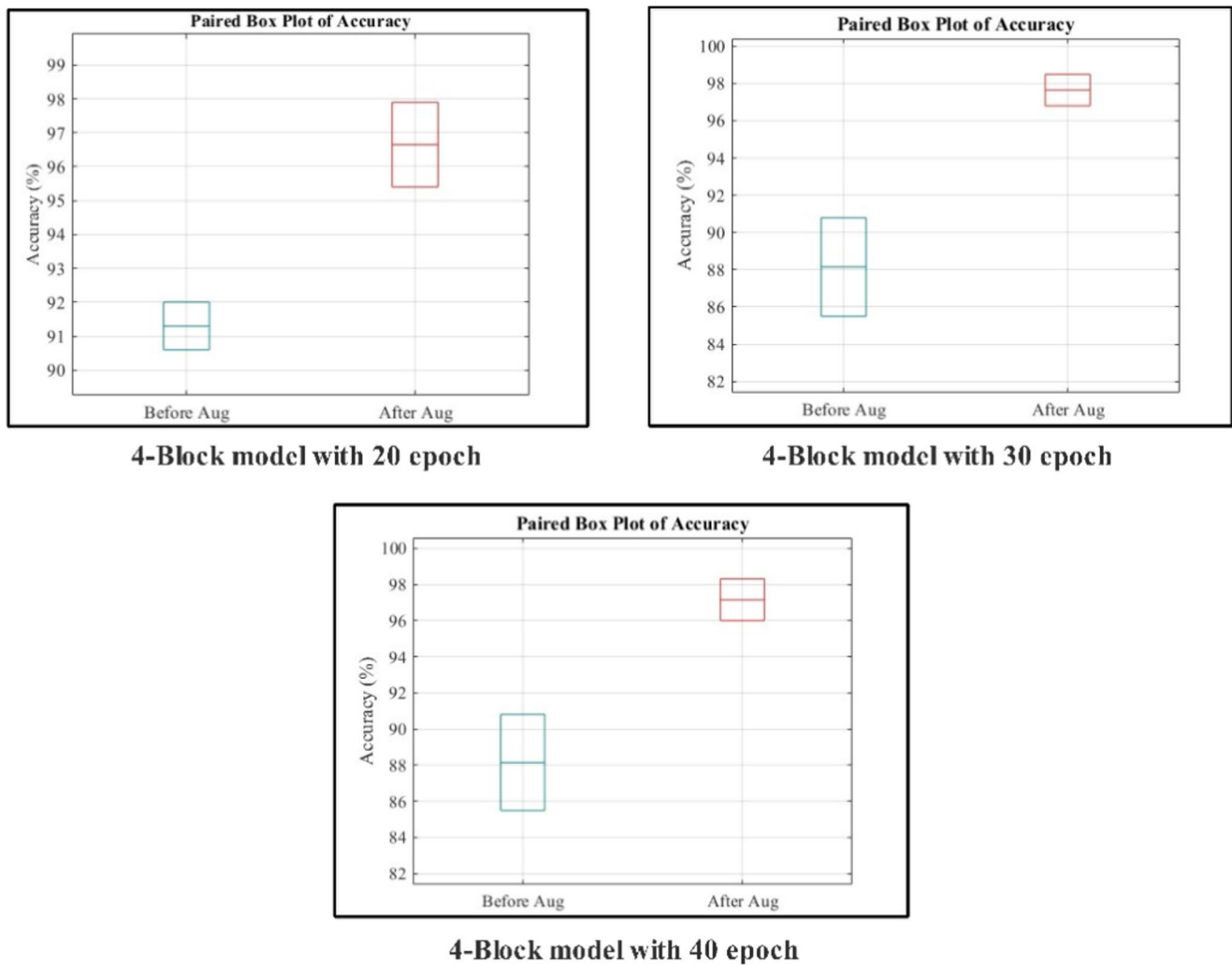


Fig. 10 Box plot of the 4-block RAN model with different epochs

Table 4 Comparison of the proposed model with state-of-the-art models based on learning parameters

Models	No. of Layers	No. of parameters	Size in MB
DenseNet201 [42]	708	20 M	77 MB
ResNet101 [43]	347	44.6 M	167 MB
NasNetLarge [44]	1243	88.9 M	332 MB
GoogleNet [45]	144	6.9 M	27 MB
Proposed 4-Block RAN	115	6.3 M	22.17 MB

helping the model focus on MRI regions associated with disease. The proposed complete model, which included both CAMB and SAMB, achieved the best accuracies of 98.53% and 96.80% when tested on the Figshare Brain and Alzheimer datasets, respectively. The complete model achieved 4.32% higher accuracy than the baseline model on the Figshare dataset and 3.64% higher accuracy on the Alzheimer dataset. In the Figshare and Alzheimer datasets,

the performance of the complete model was improved by 2.58% and 2.86%, respectively, compared to the CAMB-only model. These gains of 2.38% and 2.15% were obtained when the complete model was compared to the SAMB-only model. The present results validate the complementarity between CAMB and SAMB. CAMB optimizes feature selection in the channel, and SAMB optimizes the spatial localization of the discriminative regions. Combined

Fig. 11 Comparison of the proposed model with advanced deep networks

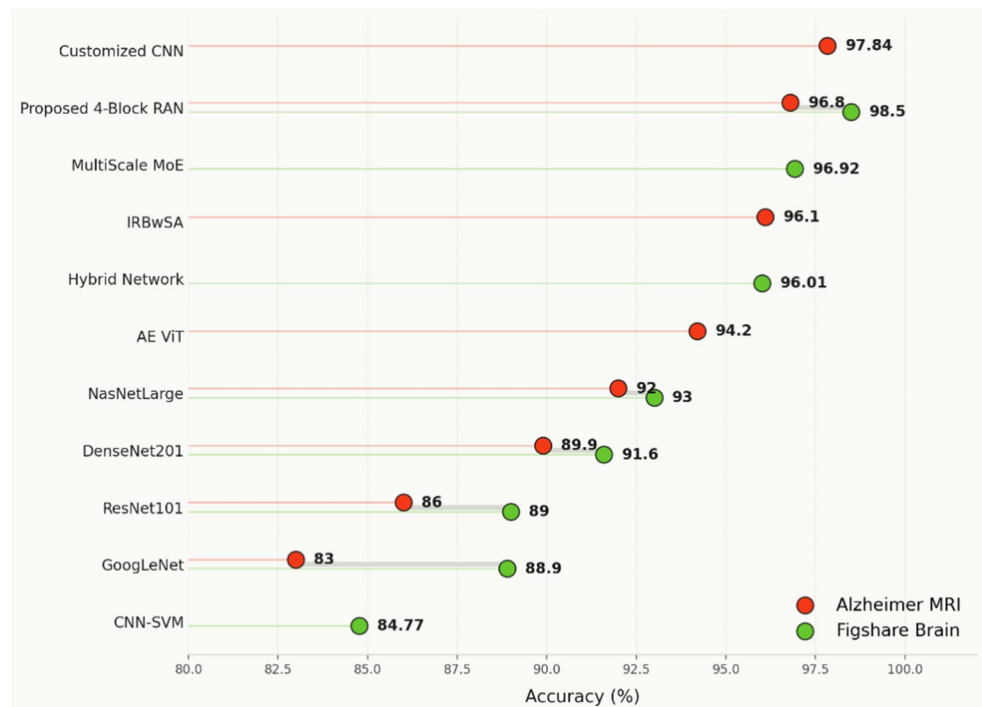


Table 5 Ablation study using the different configurations of modules in the proposed RAN model

Model variant	CAMB	SAMB	Figshare (%)	Alzheimer (%)
Baseline	✗	✗	94.21	93.16
Baseline+CAMB	✓	✗	95.95	93.94
Baseline+SAMB	✗	✓	96.15	94.65
Proposed Model	✓	✓	98.53	96.85

usage of them gives the best configuration of the proposed RAN architecture for the classification of brain tumors and Alzheimer's disease.

Proposed Model Interpretability

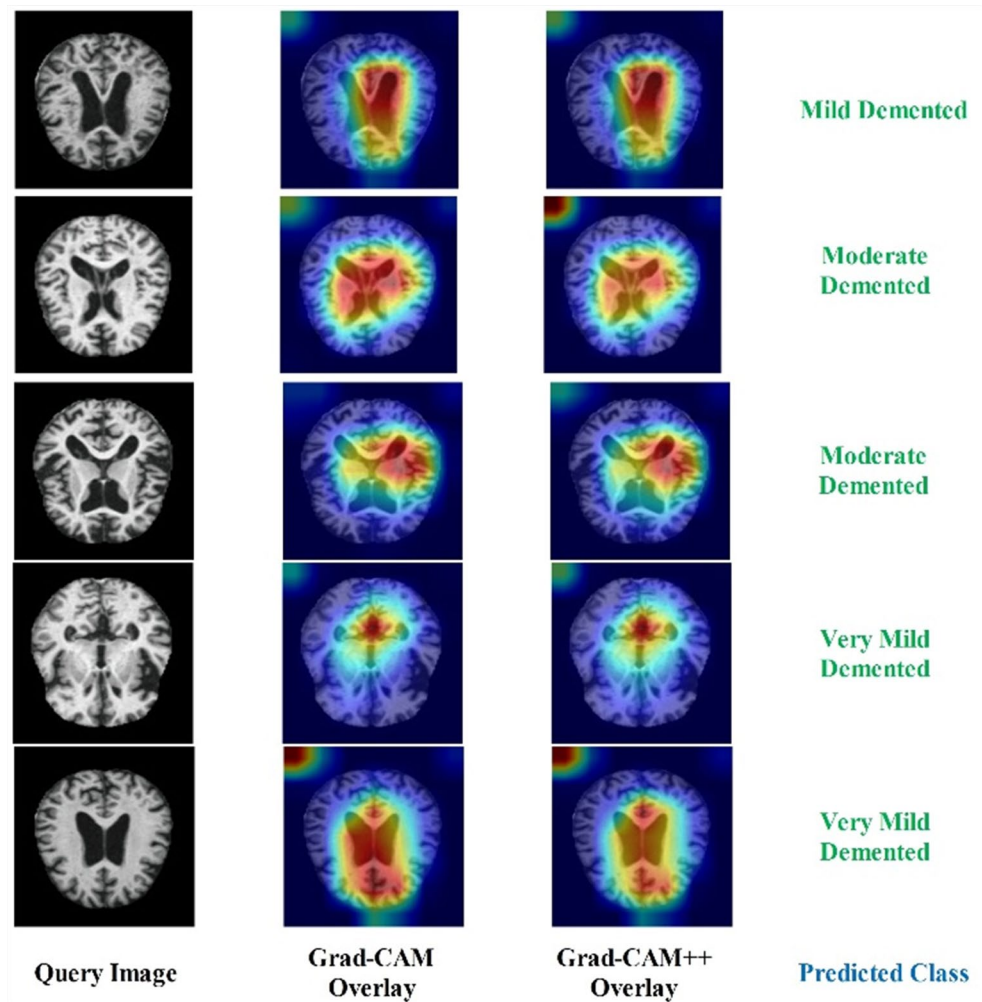
Lastly, we used visualization techniques such as Grad-CAM and Grad-CAM++ to interpret the proposed 4-block RAN architecture on selected datasets during testing. Figures 12 and 13 show the visual interpretation of the proposed model on a few test images. From these images, it is observed that the proposed model correctly classifies each image into a relevant class and then identifies the important region of interest using the visualization technique. In addition, the Grad-CAM++ technique provides better visualizations than simple Grad-CAM. Overall, the proposed model shows improved precision and interpretability in classifying brain tumors and Alzheimer's disease from MRI scans.

Overall Findings

After the experimentations on the selected datasets, ablation studies, and model interpretability, we observe the following key findings of this work:

- Softmax classifier obtained improved performance on the selected datasets using the proposed model for the brain and Alzheimer's datasets. The other neural network classifiers also performed better, achieving high precision.
- Several epochs are selected to observe the proposed model's behavior during training, and we find that epoch 30 yields the best performance.
- The trainable parameters of the proposed model are fewer than those of the other listed pre-trained models. Although we did not include many pre-trained models, we used the best-performing models for comparison.

Fig. 12 Proposed 4-block RAN architecture interpretability visual results for Alzheimer MRI Scans



- Clinically, the proposed model is well-suited due to its improved interpretability and low computational requirements.

Real-Time Implication

To illustrate the applicability of the framework, a clinical case study exploring MRI-based decision support is presented, along with a prototype clinical case study. In a real clinical workflow, patients' MRI scans might be resized, normalized, and converted to channels if they are suspected of having a brain tumor or Alzheimer's disease. The trained 4-block RAN model can thus recognize the MRI image as a specific disease class. The model makes predictions for glioma, meningioma, or pituitary tumor for brain tumor and for non-demented, very mild demented, mild demented, or moderate demented classes on the Alzheimer MRI. The proposed system could serve as a second opinion tool to assist radiologists. In addition to the

predicted class and confidence score, Grad-CAM and Grad-CAM++ visualizations can identify the image regions that most influenced the prediction. If the model output matches the radiologist's interpretation, it could enhance diagnostic confidence. Disagreements may be referred to another expert for review. The model is suitable for prototype integration into a lightweight clinical decision-support system, as it contains 6.3 million parameters and occupies 22.17 MB.

Conclusion

In this paper, a novel deep learning residual attention architecture is proposed for the classification of neurodegenerative diseases from MRI scans. The proposed architecture is called a 4-block RAN model that integrates CAMB and SAMB layering structures within a single framework. In the proposed model, the overall RAN architecture improved the model interpretability and generalizability. The proposed

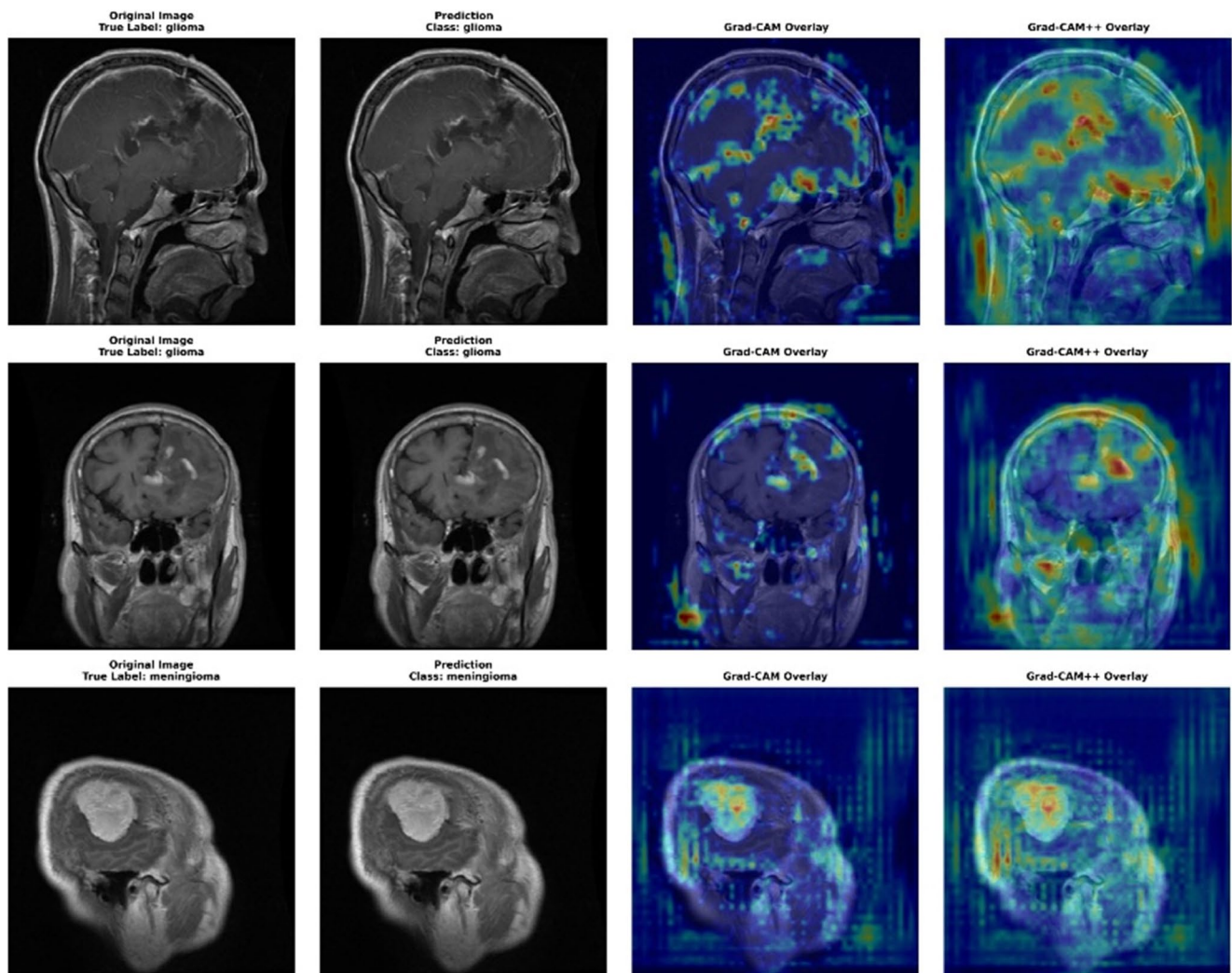


Fig. 13 Proposed 4-block RAN architecture interpretability visual results for Brain MRI Scans

architecture is trained with hyperparameters optimized using Bayesian Optimization (BO), rather than manual selection. The experimental process was conducted on two MRI datasets, such as brain tumor MRI Scans and Alzheimer's disease. On these datasets, the proposed model obtained improved performance of 96.8% and 98.5%, respectively. Based on detailed ablation studies, comparative analysis, and interpretation of results, we conclude that the proposed 4-block RAN architecture shows improved performance in terms of precision rate and accuracy. In addition, the proposed model contains fewer learning parameters, such as 6.3 million, which are better than the other listed pre-trained models. Due to fewer learning parameters, improved precision, and better interpretability, the proposed model is more suitable for clinical practice in analyzing brain tumors and Alzheimer's disease from MRI Scans. In the future, the attention blocks will be replaced with a state-space module, and the model will be evaluated on additional MRI datasets.

Author Contributions Wardah Ibrar, Muhammad Attique Khan, Syeda Aimal Naqvi, Zain Hussain, Latifah Almuqren, Amina Hussain, Mohammad Alhefdi, Yunyoung Nam. All authors contributed equally in this work.

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Data Availability The datasets used in this work are publically available for research purposes and properly cited in the main manuscript.

Declarations

Human Consent Not Applicable.

Competing interests The authors declare no competing interests.

Conflict of interest All authors declared no conflict of interest in this work.

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