

SSDHR classifier network for brain tumor detection using MRI images

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ABSTRACT

Brain tumors are the chaotic growth of abnormal brain cells, which is the main cause of cancer worldwide. Symptoms vary depending on tumor size and location, and these tumors can be cancerous or non-cancerous. Early detection and characterization are crucial but challenging due to the brain's complex structure. This study proposes a self-supervised classification deep hierarchical reconstruction network (SSDHR), a combination of generative and discriminative models. This network uses convolutional Kernels of different sizes for processing of input data on separate branches to extract effective discriminative features. A parallel-structured symmetric fusion attention (SFA) module is introduced, combining attention mechanisms for coordinates, time, and frequency to enhance the model's comprehension and feature selection. The SSDHR classifier network achieves the highest accuracy (91.9%) among 10 state-of-the-art classifiers, classifying tumors into 4 classes: pituitary, meningioma, glioma, and no tumor. The model's performance is evaluated using various metrics that demonstrate its effectiveness in brain tumor classification.

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1. INTRODUCTION

Brain tumor classification is important for identifying tumor types such as Pituitary, meningioma, and glioma, and for selecting suitable treatments. Among various imaging techniques, magnetic resonance imaging (MRI) is widely preferred because it provides high-quality images without using ionizing radiation [1]. A brain tumor is an uncontrolled growth of brain cells and is considered one of the most life-threatening forms of cancer [2]. According to cancer statistics in the USA, around 23,000 brain tumor cases were reported in 2015, making it a major cause of cancer-related deaths in both children and adults [3]. Radiologists use several medical imaging methods for diagnosis, with MRI being the most effective and safest option [4]. Traditional tumor classification is time-consuming, costly, and highly dependent on radiologists, which can lead to diagnostic errors when handling large volumes of MRI data. To overcome these limitations, researchers are developing automated image processing and computer-aided diagnosis (CAD) systems that reduce human error and workload [5]–[8]. Studies show that deep learning (DL) techniques improve the performance of CAD systems [9]. However, limited medical datasets make training deep convolutional neural network (CNN) models from scratch difficult and time-consuming.

2. RELATED WORK

CNNs have shown strong performance in brain tumor detection and classification using MRI scans due to advances in DL. Pashari *et al.* [10] combined CNN features with Kernel extreme learning machine (KELM) and achieved 93.68% accuracy on 3064 MRI images. Das *et al.* [11], Gaussian filtering and histogram equalization were applied before CNN classification, resulting in 94.39% accuracy. Transfer learning with GoogleNet and SVM in [12] achieved 97.1% accuracy on the FigShare dataset. Several studies proposed advanced CNN architectures for classifying pituitary, glioma, and meningioma tumors. A CNN-based model in [13] achieved 96.56% accuracy, while a differential deep CNN in [14] reached 99.25% accuracy on 25,000 MRI images. Another CNN model in [15] achieved 99.4% classification accuracy. Sajjad *et al.* [16], CNN-based segmentation with data augmentation and VGG-19 fine-tuning to improve multi-grade tumor classification. Hybrid and transfer learning approaches also produced strong results. CNN combined with LSTM in [17] achieved 97% accuracy on a Kaggle dataset. Deep CNN architectures with multiple convolution and pooling layers were explored in [18], while [19] compared three CNN models with accuracies up to 99.33%. Transfer learning models such as ResNet50, VGG19, and Inception-v3 in [20] achieved around 90% accuracy. Other approaches include CNN classification of three tumor types in [21], achieving 98.51% training accuracy, and machine learning-based classification in [22] with 91.43% cross-validation accuracy. Content-based image retrieval techniques using MID and MPP algorithms in [23] achieved high precision on CE-MRI datasets. Behin *et al.* [24] and Drevelegas [25] focused on glioma genetics and tumor evaluation methods, while [26], [27] discussed deep CNN architectures for image classification, detection, and segmentation.

3. STATE-OF-THE-ART CNN MODELS

In this work, the proposed model is compared with nine existing CNN-based architectures using the same Kaggle dataset.

- Inception-ResNet-v2 combines Inception modules with residual connections to improve multi-scale feature extraction and overcome vanishing gradient issues in deep networks [28].
- LeNet-5, introduced by Yann LeCun in 1998, is an early CNN architecture consisting of convolution, pooling, and fully connected layers, widely used for understanding CNN fundamentals [29].
- ResNet101-LSTM integrates ResNet101 for spatial feature extraction with LSTM for learning temporal patterns in sequential MRI data [30].
- Inception v3 improves classification performance through factorized convolutions, regularization, and auxiliary classifiers [31].
- Xception employs depth-wise separable convolutions, improving network efficiency and performance [32].
- ResNet101-LSTM and GRU combines LSTM and GRU units to capture long-term dependencies and temporal features efficiently in medical data [33].
- ConvNeXt Base modernizes CNN architecture using transformer-inspired concepts such as depth-wise convolution and layer normalization for effective medical image classification [34].
- VGG19, developed by the Visual Geometry Group at the University of Oxford, uses deep 3×3 convolution layers for accurate image feature learning [35].
- ResNet101 is a deep residual network with 101 layers that learns high-level MRI features effectively using residual connections [36].

Table 1 summarizes the trainable and non-trainable parameters, total parameters, and memory usage of each model. Trainable parameters are updated during training, whereas non-trainable parameters remain fixed. The table also highlights the complexity, strengths, weaknesses, and novelty of each architecture.

4. PROPOSED METHODOLOGY

This section describes in detail the suggested approach. The rich feature representations are obtained by combining discriminative and generative techniques. To improve the discriminability between characteristics of normal and abnormal images, modules for attention and mixed center loss are proposed. Concatenated features are the last method used for brain tumor detection.

4.1. Self-supervised classification using deep hierarchical reconstruction network with symmetric fusion attention

Figure 1 shows the SSDHR classifier network structure used for brain tumor detection. The model uses both classification features (y) and reconstructed latent representations (z) to improve closed-set

classification and tumor identification [26]. It extracts latent features from middle layers of the network to reduce information loss that usually occurs in higher layers. The network contains two parallel symmetric branches with different convolution Kernel sizes (3×3 and 7×7), allowing the model to capture features at multiple scales and improve robustness and feature representation. The features $z1$ to $z6$ represent pooled outputs from reconstructed representations, while “Attention” refers to the proposed symmetric fusion attention (SFA) module. Features from both branches are combined along the channel dimension and passed through two fully connected layers for classification. The SFA module helps the model focus on important input features and improves overall performance, while mixed center loss is used to generate more compact and discriminative features, as shown in Figure 2.

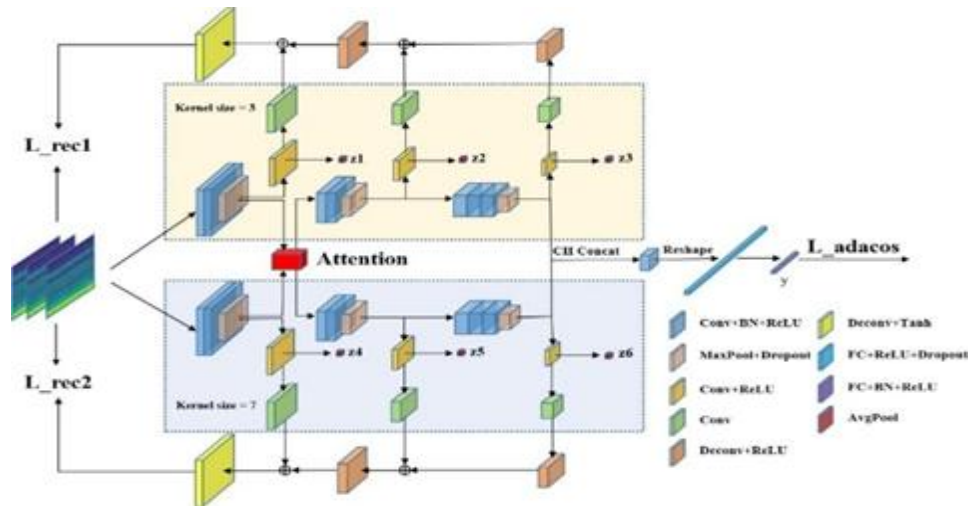


Figure 1. The architecture of SSDHR classifier network

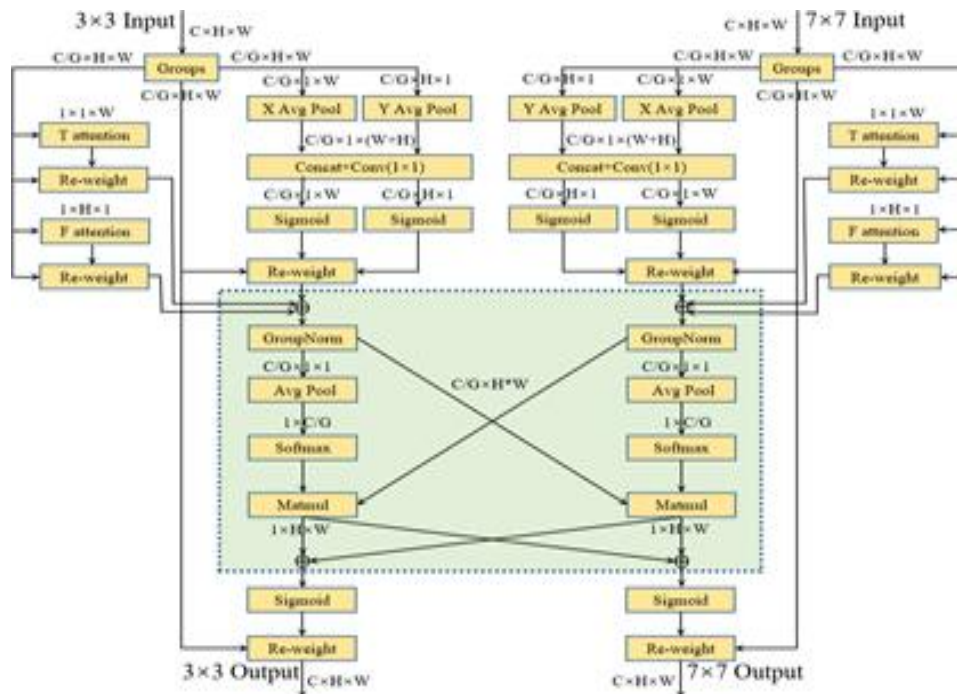


Figure 2. SFA model architecture. "G" stands for the split groupings

4.2. Symmetric fusion attention

For better detection of brain tumor features, the proposed work relies on SFA. Figure 2 depicts the general layout of the attention module, which is suitable for parallel-structured networks. To preserve

information throughout each channel and lower computational overhead, restructure a portion of the channels and each input feature $X \in \mathbb{R}^{C \times H \times W}$ into batch dimensions [27]. Instead of adding more branching structures, use the network's initial parallel branches to capture multiscale information. Additionally, give each branch simultaneous attention to both frequency and temporal aspects.

Figure 3 shows how these two attentions are computed. Consequently, each branch of the symmetrical structure simultaneously incorporates three sub-branches, namely coordinate attention, temporal attention, and frequency attention. Coordinate attention (CA) [30], in which processing of inputs is done via one-dimensional horizontal and vertical global pooling rather than global average pooling. This allows the preservation of exact positional information along one spatial guidance while collecting long-range dependencies along another. At height h , the c -th channel's output is given as:

$$Uhc(h) = \frac{1}{W} \sum_{0 \leq j \leq H} y_c(h, i) \quad (1)$$

The c -th channel output with width w can be expressed as:

$$Uwc(w) = \frac{1}{H} \sum_{0 \leq j \leq H} y_c(j, w) \quad (2)$$

Where y_c represents the c -th channel input features.

Pooling the reshaped input features into two directions, then performing 1×1 convolutional processes and applying the activation function as sigmoid. This produces CA weights of two sets $p_a^h \in \mathbb{R}^{C/G \times H \times 1}$ and $p_a^w \in \mathbb{R}^{C/G \times W \times 1}$ in distinct directions. CA can be thought of as independently integrating frequency and time information into the channel dimension when the input of the model is image. Furthermore, the following are the formulas for the previously introduced frequency attention. $F_a \in \mathbb{R}^{1 \times H \times 1}$ and temporal attention is $T_a \in \mathbb{R}^{1 \times W \times 1}$:

$$Ta = (\sigma(\text{AvgPool}(1,1)(\text{Conv2D}(1 \times 1)(XG)^{T1,3}))T1,3)T1,3 \quad (3)$$

$$Fa = (\sigma(\text{AvgPool}(1,1)(\text{Conv2D}(1 \times 1)(XG)^{T1,2}))T1,2)T1,2 \quad (4)$$

where $\text{AvgPool}(1,1)$ shows the adaptive average pooling that reduces each channel's feature map to 1×1 , (σ) describes the sigmoid activation function, $(\cdot)^{T1,2}$ and $(\cdot)^{T1,3}$ expresses the transpose operations on dimensions 1 and 2 and dimensions 1 and 3, respectively. $X_G \in \mathbb{R}^{C/G \times W \times H}$ describes the reshaped input feature map.

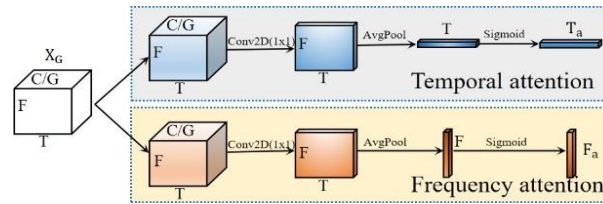


Figure 3. Temporal attention and frequency attention

By applying coordinate attention, temporal attention, and frequency attention to X_G and weighting them, the output that is obtained is $X'_G \in \mathbb{R}^{C/G \times W \times H}$ is given as:

$$X'_G = \alpha X_G p_a^h p_a^w + \beta X_G T_a + \gamma X_G F_a \quad (5)$$

$$\alpha + \beta + \gamma = 1 \quad (6)$$

Where (α) , (β) , and (γ) are learnable parameters normalized using the SoftMax function. Information is then aggregated across multiple spatial dimensions in a cross-spatial manner. The two symmetrical branches simultaneously apply coordination, temporal, and frequency attention mechanisms. Next, the outputs of both branches undergo two-dimensional global average pooling and are reshaped into $(R^{\wedge}\{(1 \times C/G)\})$. The branch outputs are further reshaped into $(R^{\wedge}\{(C/(G \times HW))\})$ [31]. Spatial attention maps for each branch are generated using global average pooling, SoftMax, and cross-branch matrix dot product operations.

The spatial attention weights are obtained by combining the two attention maps and applying the sigmoid function. Finally, these weights are multiplied with the corresponding branch inputs to generate outputs having the same dimensions as the inputs.

4.3. One class centre loss

The main goal of centre loss is to increase the discriminative strength of features by increasing the distance between feature points of various classes and by decreasing the distance between the feature points of the same class in the feature space. Maintaining a centre for each class and training the model by minimizing the separation between each of the samples and its matching class centre constitute the fundamental principles of centre loss. The following is the formula for centre loss:

$$L_{ctr} = \frac{1}{2} \sum_{j=1}^n \|f_j - \mu_{y_j}\|_2^2 \quad (7)$$

Where $f_j \in \mathbb{R}^d$ represents the deep feature of the j-th that belongs to the y-th class $\mu_{y_j} \in \mathbb{R}^d$ act as the centre of the deep features for the y_j -th class and d represents the feature dimension. The centres are modified depending on the mini-batches rather than the complete training set since it is impossible to compute μ_{y_j} using the entire training set. Additionally, a scalar is utilized to limit the centres' learning rate in order to lessen the severe disruptions generated by a small number of mislabelled samples. The main purpose of brain tumor detection is to distinguish between samples that are normal and those that are anomalous. In order to compute the centre for a single class alone, the number of classes for the centre loss was lowered to one. To yield the one-class centre loss, the Euclidean distance between the feature centre and the deep features of all sample types is computed. The formula for computations is as follows:

$$L_{occtr} = \frac{1}{2} \sum_{j=1}^n \|f_j - \mu\|_2^2 \quad (8)$$

Where μ represents the central feature of all the normal samples. The mixed centre loss, obtained by the combination of the one-class centre loss with that of the standard centre loss, is as follows:

$$L_{mixctr} = \lambda_1 L_{ctr} + \lambda_2 L_{occtr} = \frac{\lambda_1}{2} \sum_{j=1}^n \|f_j - \mu_{y_j}\|_2^2 + \frac{\lambda_2}{2} \sum_{j=1}^n \|f_j - \mu\|_2^2 \quad (9)$$

4.4. Reconstruction loss and classification loss

The proposed network model incorporates both the reconstruction and classification loss simultaneously. In order to extract multiple reconstruction latent representations, the network uses two parallel reconstruction branches as shown in Figure 1. The mean squared error used for the reconstruction of these two branches is as follows:

$$L_{rec1} = \frac{1}{n} \sum_{j=1}^m \|A_j - A_j'\|_2^2 \quad (10)$$

$$L_{rec2} = \frac{1}{n} \sum_{j=1}^m \|A_j - A_j''\|_2^2 \quad (11)$$

Where A_j denotes the input image, A_j' denotes the first branch, the reconstructed image, and A_j'' depicts the reconstructed image from the second branch. L_{AdaCos} , an angular margin loss, is used in the classification loss [32]. To enforce an angular margin between different categories and minimize the cosine angle to the learned mean of known categories, the loss AdaCos promotes low intra-class variance and high inter-class variance. In this loss, the probability of sample A_j that belongs to the jth category, among all categories K, is given as:

$$P_{i,j} = \frac{e^{\tilde{S}_{i,j} \cos \theta_{i,j}}}{\sum_{k=1}^K e^{\tilde{S}_{i,k} \cos \theta_{i,k}}} \quad (12)$$

Where $\theta_{i,j}$ is obtained by cosine similarity $\cos \theta_{i,j} = \langle x_i, w_j \rangle / \|x_i\| \|w_j\|$, $w_j \in \mathbb{R}^D$ is a learned category centre. The dynamically adaptive scaling parameter $\tilde{S}_d^{(t)}$ at training step $t \in N_0$ is defined as:

$$\tilde{S}_d^{(t)} = \begin{cases} \sqrt{2} \log(k-1) \\ \frac{\log B_a^{(t)} v_y}{\cos(\arccos(\frac{\pi}{4}, \theta_q))} \end{cases} \quad (13)$$

where $\theta_{\text{med}}^{(t)} \in [0, \pi]$ represents the angular center of all the corresponding categories that are used in this current batch. The definition of $B_{\text{avg}}^{(t)}$ is expressed as:

$$B_{\text{avg}}^{(t)} = \frac{1}{N} \sum_{i \in N^{(t)}} \sum_{k \neq y_i} e^{s_d^{-l_{t-1}}, \cos o_{i,k}} \quad (14)$$

Where $N^{(t)}$ represents the indices in the mini-batch at the t -th iteration. $e^{s_d^{-l_{t-1}}, \cos o_{i,k}}$
The proposed model loss function consists of:

$$L_{\text{total}} = L_{\text{rec1}} + L_{\text{rec2}} + L_{\text{AdaCos}} + L_{\text{mixctr}} \quad (15)$$

5. RESULTS AND DISCUSSION

The experiment is conducted on the dataset, which is available to the public from an open-source platform called “Kaggle” [37]. The dataset contains 3264 MRI images split into two groups of 2870 and 870 images for training and testing, respectively, and are in turn classified into four classes: meningioma, pituitary, glioma, and no tumor. Figure 4 depicts sample images of the four classes. Preprocessing of data images is done by resizing the training and testing images to a fixed size, shuffling these images, encoding the labels where each label is mapped to a unique integer value, and doing data augmentation. Python’s TensorFlow and Keras are used to perform the experiment on a Core i5 CPU with 8 GB RAM running at 2.42 GHz. The model was trained for 200 epochs.

Table 1 presents the brain tumor classification results of 10 DL models. Among them, the SSDHR classifier network achieved the best performance with 90.2% accuracy, along with the highest precision, recall, F1-score, and Kappa score. Accuracy represents the overall correct predictions, precision indicates prediction reliability, recall measures the ability to identify positive cases, F1-score balances precision and recall, and the Kappa score evaluates the agreement between predicted and actual values. These results demonstrate the effectiveness of the SSDHR classifier network in learning complex patterns for brain tumor classification. Table 2 shows the macro-averaged diagnostic performance of different CNN models using precision, recall, F1 score, and AUC metrics. Macro-average is calculated by averaging the metric values across all classes equally. Higher macro-average values indicate better overall model performance. Macro-average precision, recall, F1 score, and AUC are obtained by averaging the corresponding values calculated for each class.

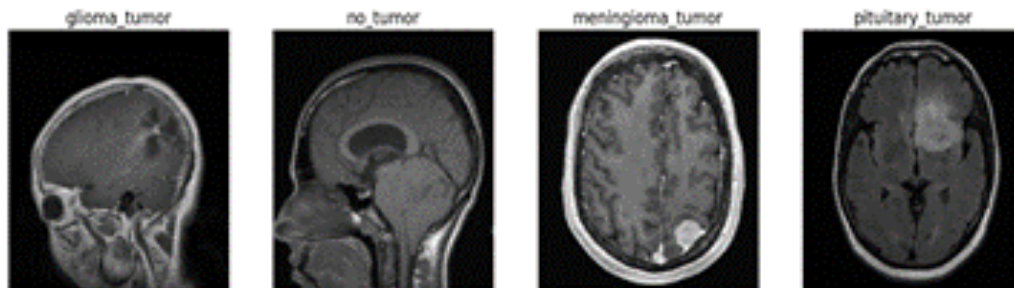


Figure 4. Sample image of each class from the dataset

Table 1. Overall metrics of all models

Model	Accuracy	Precision	Recall	F1 score	Kappa
Inception-resnet v2 [28]	29.3	8.6	29.3	1.0	0
Lenet5 [29]	74	29	27.1	26.9	5.7
ResNet101-LSTM [30]	75.4	80.1	75.4	73.7	65.8
Inception v3 [31]	76.4	77.5	76.4	94	68
Xception [32]	76.6	76.4	76.7	92.3	68.5
ResNet101-LSTM-GRU [33]	77.4	84.8	76.7	74.6	61.3
ConvNeXtBase [34]	86	87.8	87.1	98.5	82.5
Vgg19 [35]	86.8	86	86	95.4	82.2
ResNet101 [36]	88.6	89	88.9	96.1	84.6
SSDHR classifier network	91.9	92.6	92.3	97.5	89.6

Table 2. Macro average

Model	Precision	recall	F1 score	AUC
Inception-resnet v2 [28]	7	25	11	50
Lenet5 [29]	24	24	22	52
ResNet101-LSTM [30]	80	75	74	82.2
Inception v3 [31]	78	76	76	84
Xception [32]	77	77	77	84.6
ResNet101-LSTM-GRU [33]	85	77	75	92.4
ConvNeXtBase [34]	89	88	88	91.7
Vgg19 [35]	87	87	87	91.4
ResNet101 [36]	89	89	89	92
SSDHR classifier network	92	93	92	95.1

Table 3 shows the micro-average of various DL models. This model, which has the highest micro-average in all the set metrics, is considered the best-performing model. Micro-average precision is computed by considering all true positive (TP) and false positive (FP) predictions across all classes together, rather than computing precision per class individually. Micro-average recall is computed by summing the true positives (TP) for all classes and dividing by the sum of the true positives (TP) and false negatives (FN) for all classes. The micro-average F1-score is the harmonic mean of the micro-average precision and micro-average recall. The micro-average AUC is defined as the AUC of the ROC graph computed from the true positive and false positive ratios of all classes.

Table 4 presents weighted average metrics used to evaluate model performance, especially for imbalanced datasets. Weighted average precision is calculated by averaging the precision of each class based on the number of true instances in that class. Similarly, weighted average recall is the average recall weighted by the true instances of each class. The weighted average F1 score is obtained by averaging the F1 scores of all classes using the number of true samples as weights. Weighted average AUC, however, is generally not included in standard classification reports. Table 5 depicts the confusion matrix for each model in the classification. In the confusion matrix, each of the rows corresponds to the true classes, while each of the columns corresponds to the predicted classes. The number next to each cell represents the number of samples that were classified correctly, incorrectly, or misclassified. This table summarizes the findings on the performance of various models in accurately performing the classification task of tumor types. Table 6 displays the sensitivity of each model for each class. Recall, also known as sensitivity, is defined as the model's ability to correctly identify the positive samples (tumor types). Higher sensitivity values indicate that the model is better at correctly identifying tumors of a specific type.

Table 3. Micro average

Model	Precision	recall	F1 score	AUC
Inception-resnet v2 [28]	29	29	29	50
Lenet5 [29]	29.5	29.5	29.5	51
ResNet101-LSTM [30]	58	58	58	82.7
Inception v3 [31]	76.4	76.4	76.4	93
Xception [32]	76.7	76.7	76.7	93.1
ResNet101-LSTM-GRU [33]	77.4	77.4	77.4	89.9
ConvNeXtBase [34]	87.1	87.1	87.1	97.1
Vgg19 [35]	86.8	86.8	86.8	93.9
ResNet101 [36]	88.6	88.6	88.6	97.3
SSDHR classifier network	92.3	92.3	92.3	98.6

Table 4. Weighted average

Model	Precision	recall	F1 score	AUC
Inception-resnet v2 [28]	9	29	13	50
Lenet5 [29]	24	25	23	52
ResNet101-LSTM [30]	80	75	73	81.3
Inception v3 [31]	78	76	76	83.9
Xception [32]	76	77	76	84
ResNet101-LSTM-GRU [33]	83	77	74	92.1
ConvNeXtBase [34]	88	87	87	91.1
Vgg19 [35]	87	87	87	91.1
ResNet101 [36]	89	89	89	92.3
SSDHR classifier network	93	92	92	94.9

Table 5. Confusion matrix for all models

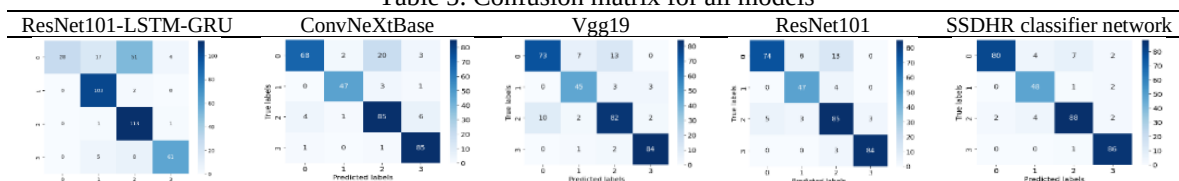


Table 6. Sensitivity/Recall for each individual class

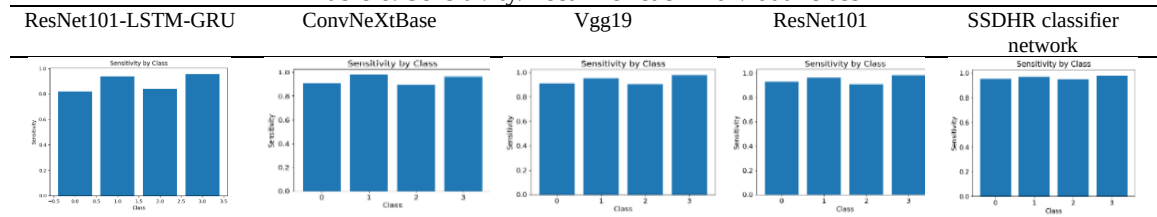


Table 7 illustrates the selectivity of each model for each class. Precision, also known as selectivity, is defined as a model's ability to correctly exclude negative samples (samples that are not of the specified tumor type). Higher selectivity values suggest that the model is better at correctly identifying samples that are not of the specific tumor type. Table 8 presents the precision–recall curves of all models, illustrating the trade-off between precision and recall at different threshold values. Model performance is evaluated using the area under the curve (AUC), where a higher AUC indicates better classification performance.

Among all models, the SSDHR classifier network achieved the best results with 91.9% accuracy, 92.6% precision, 92.3% recall, 97.5% F1-score, 89.6% Kappa score, 95.1 macro-average AUC, and 98.6 micro-average AUC. It also obtained the highest weighted average metrics along with superior sensitivity and specificity for each class. These results demonstrate that the SSDHR classifier network is the most effective model for brain tumor classification compared to existing approaches.

Table 7. Selectivity/precisions for each individual class

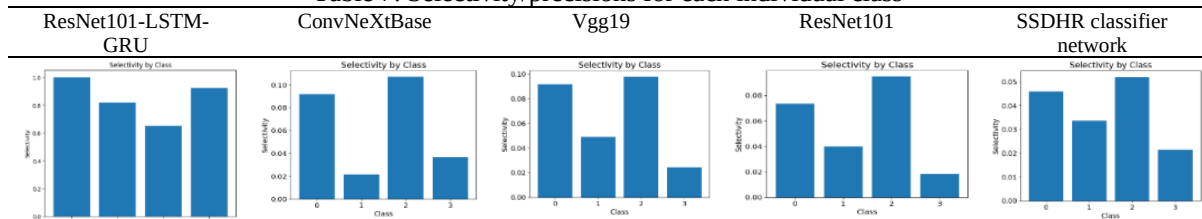
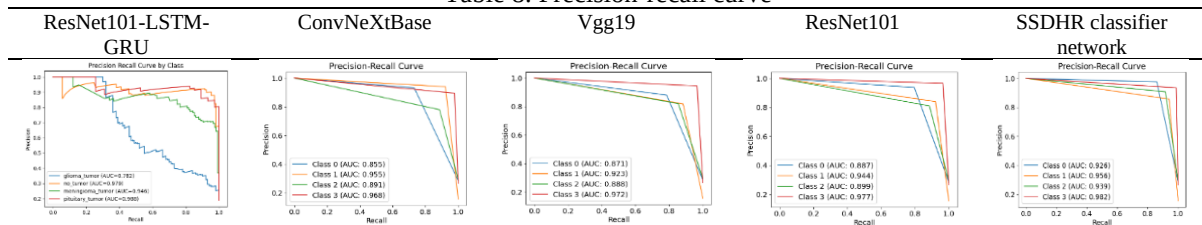


Table 8. Precision-recall curve



6. CONCLUSION

The proposed SSDHR classifier network model used for performing the brain tumor classification task is compared with other state-of-the-art CNN models. Experimental results illustrate that the proposed model outperforms existing models in various metrics, achieving an accuracy of 91.9% on the brain tumor classification dataset. Based on these findings, it is concluded that the proposed model is more effective in diagnosing four distinct types of brain tumors at an early stage. The proposed model learns intricate features from the images of the MRI scans, which aids in improving the efficiency and accuracy of the model.

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AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

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C : Conceptualization

M : Methodology

So : Software

Va : Validation

Fo : Formal analysis

I : Investigation

R : Resources

D : Data Curation

O : Writing - Original Draft

E : Writing - Review & Editing

Vi : Visualization

Su : Supervision

P : Project administration

Fu : Funding acquisition

CONFLICT OF INTEREST STATEMENT

The authors state no conflict of interest.

DATA AVAILABILITY

The dataset used in this manuscript is available publicly, and a reference was given in the Results and Discussion section.

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