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A Novel Lightweight Explainable Deep Learning Framework for Automated Brain Tumor Segmentation and Classification

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ABSTRACT: This research work presents an explainable lightweight deep learning approach to automate brain tumor extraction and classification using MR images. This method incorporates lightweight feature extractor sharing, joint segmentation and classification branches, and explainability using Grad-CAM. The proposed approach will aim to identify the relevant features of the tumor in an accurate way with minimal computational cost. Explainable artificial intelligence (XAI) techniques will be incorporated to identify and highlight critical regions within the tumor, thereby enhancing the interpretability of the model's predictions. The performance of the method would be assessed in terms of the evaluation metrics used for segmentation and classification problems. The proposed framework achieved 98.34% classification accuracy, 98.02% precision, 97.72% recall, 98.55% specificity and 97.32 F1-score indicating improved classification performance on the BRISC 2025 dataset. This framework also achieves high precision and recall with 98.6% specificity, 95.3% DSC, and 91.0% IoU, demonstrating accurate tumor segmentation with effective identification of non-tumor regions. The contributions of each module to the research have been further verified via ablation studies. So, this framework is anticipated to yield an accurate, effective, and interpretable method for computer-based detection of brain tumors.

1. INTRODUCTION

Among all types of neurologic disorders, brain tumors are one of the most serious illnesses and correct diagnosis of such diseases is crucial for their subsequent treatment. MRI is widely used for diagnosing brain tumors since this technology allows us to obtain comprehensive information on brain structure and the tumor itself [1,4]. However, manual analysis and classification of tumor regions is laborious and depends on the qualifications of the radiologist. In recent years, there has been much success achieved using artificial intelligence and deep learning techniques in brain tumors analysis [6,7]. Deep learning algorithms can perform automatic feature extraction and produce accurate results of segmentation and classification. Nonetheless, current approaches require a lot of computing power and are often referred to as black boxes that cannot be easily interpreted in clinical practice [8].

In order to overcome these drawbacks, a lightweight explainable deep learning framework for automated brain tumor segmentation and classification is proposed in this work. This framework tries to reduce computational complexity while ensuring accurate detection and classification of the tumor at the same time. Also, XAI techniques have been used to find the areas responsible for making predictions from the model. The novelty and contributions of the research work are as follows:

- A unified framework for simultaneous brain tumor segmentation and classification is introduced using an end-to-end framework.
- A lightweight model is proposed which uses shared feature extractor and multi-scale attention mechanism for reducing the computational complexity of the model while preserving the prediction accuracy of 98.34%.

- Cross-task interaction between the segmentation and classification task is introduced where the features can interact and complement each other to enhance the performance of the multi-task learning framework.
- The explainable AI model is introduced for creating visual evidence of predictions made by the model.

The research paper is divided into the following: The relevant literature is presented in section 2. Research methodologies and its mathematical modelling are discussing in section 3. Datasets and implementation details are described in section 4. Experiment results and analysis is presented in section 5. Ablation study and computational complexity described in 6 and 7 respectively. Limitations and Clinical Implications is described in section 8. At last, section 9 summarises the conclusions followed by references.

2. LITERATURE REVIEW

Recently, the role of artificial intelligence and deep learning in automatic analysis of brain tumor from MR images is becoming more and more important. The traditional image processing techniques such as thresholding, watershed segmentation and morphological operations have been widely used to extract tumor. These techniques are computationally simple, but performance can be affected by noise, intensity variations and complex tumor boundaries. In particular, deep learning methods such as U-Net and its variants have greatly improved brain tumor segmentation by automatically learning discriminative features from MR images [9,12]. Residual, attention based, multi-modal architectures that captured both local and global tumor characteristics lead to further improvements in segmentation accuracy. However, many advanced networks contain large amounts of parameters, which increases the computational cost and memory

Deep learning for brain tumor classification has also been explored by several researchers, who have employed convolutional neural networks (CNNs) to distinguish between various types of tumors[13,14]. The results are promising in terms of accuracy, precision, recall and F1-score. But differences in MRI acquisition protocols and datasets may affect models' generalization. Recently, in the era of the demand of interpretable and trustworthy predictions in clinical applications, explainable artificial intelligence (XAI) has been paid much attention. We can use visualization methods such as Grad-CAM (Gradient-weighted Class Activation Mapping). to highlight the regions of the image that influence the decision of the model. Grad-CAM is an explainable AI technique used to visualize which parts of an image a convolutional neural network (CNN) focuses on to make a prediction [15,19]. However, very few research efforts have combined lightweight architecture, accurate segmentation, tumor classification and explainability in one framework [20,21]. Therefore, it is necessary to develop an efficient and interpretable deep learning model for reliable brain tumor segmentation and classification with reduced computational complexity [24,25]. The research aims to fill this gap by introducing a Lightweight Explainable Deep Learning Framework for Automated Brain Tumor Segmentation and Classification. Table 1 shows the gap analysis of the existing approaches over the proposed research direction.

Table 1. Research Gap of the Existing Approaches

References	Approach	Major Findings	Research Gap	Proposed Research Direction
[16,17]	Thresholding, watershed and morphological procedures	Computationally simple and efficient.	Noise sensitive and uneven tumor borders.	AI-based segmentation method
[2,3]	U-Net and its variants	Provide precise segmentation of brain tumors	Requirement of considerable computational resources	Develop a lightweight encoder-decoder architecture
[11,18]	CNN	High classification accuracy	Limited interpretability of model decisions	Integration of explainable AI techniques

[5,28]	Multimodal Deep Learning	Improves tumor feature representation	Requires multiple MRI sequences and higher computational cost	Efficient feature fusion with reduced complexity
[22,26]	Transformer and advanced hybrid networks	Effectively capture complicated and widespread tumor features	High computing demands and large number of parameters	Efficient feature extraction
[10,23]	Explainable AI-based models	Improve transparency using methods such as Grad-CAM	Explainability is not consistently integrated with segmentation and classification	Incorporate lightweight XAI for both tumor localization and classification

The key gap observed in the literature review is the absence of a framework which can offer all four aspects i.e., accurate tumor segmentation, robust classification, minimum computational complexity, and interpretation of prediction at the same time. Hence, the research problem to be solved by this study is the development of an explainable and lightweight deep learning framework.

3. PROPOSED METHODOLOGY

The suggested framework is for performing tumor localization, segmentation, classification, and visualization on brain MR images as show in the Fig.1. This design is aimed at achieving reduced computational costs without sacrificing the quality of segmentation and classification. The main innovation lies in the fact that both tasks segmentation and classification are done in one lightweight framework instead of being implemented via two separate deep learning models.

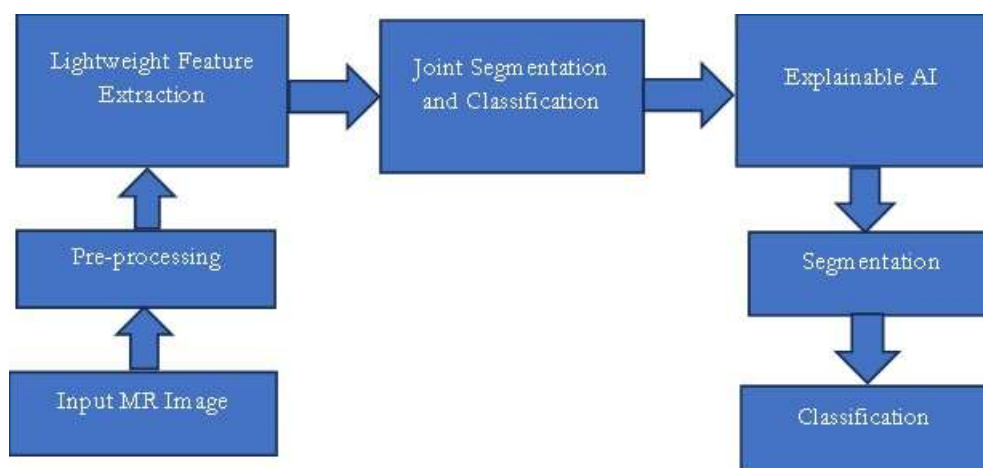


Fig. 1. Lightweight explainable deep learning framework

3.1 Input MR Image

The framework takes a brain magnetic resonance (MR) image as input. As input data, MR images with their usual features of low contrast, noise, and intensity inhomogeneity are used. Let's denote the input MR image as:

$$I_0 \in \mathbb{R}^{H \times W \times C} \quad (1)$$

where H , W and C denote image height and width, and C channels respectively.

3.2 Pre -processing

The pre-processing stage includes resizing, denoising, intensity normalization, and data augmentation as shown in Fig.2.

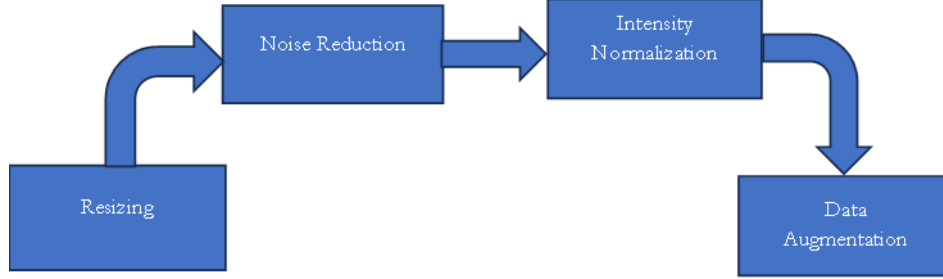


Fig.2. Pre-processing stage of segmentation and classification framework

Here, MR images are resized into a fixed spatial resolution of 256×256 as:

$$I_r = \mathcal{R}(I_0) \quad (2)$$

where $\mathcal{R}(\cdot)$ denotes the resizing operation.

This ensures that all input images have the same dimensions. MR images may contain acquisition noise. A Gaussian filtering operation is used to reduce the noise as:

$$I_n(x, y) = \sum_i \sum_j G_\sigma(i, j) I_r(x - iy - j) \quad (3)$$

where the Gaussian kernel is as:

$$G_\sigma(i, j) = \frac{1}{2\pi\sigma^2} \exp\left(-\frac{i^2 + j^2}{2\sigma^2}\right) \quad (4)$$

Here, σ controls the degree of smoothing.

The objective is to $I_r \rightarrow I_n$ while preserving important tumor boundaries.

MRI intensity values can vary considerably between patients and scanners. Min-max normalization can be performed as:

$$I_{norm} = \frac{I_n - I_{min}}{I_{max} - I_{min}} \quad (5)$$

which maps the intensity values approximately into $I_{norm} \in [0, 1]$

To improve generalization and reduce overfitting, transformations such as rotation, flipping, scaling and translation can be applied to the normalized image as:

$$I_a = \mathcal{T}(I_{norm}; \theta) \quad (6)$$

where $\mathcal{T}$ represents an augmentation transformation and θ represents its parameters.

Therefore, the complete preprocessing operation is as:

$$I_p = \mathcal{T} \left[\mathcal{N} \left(\mathcal{D}(\mathcal{R}(I_0)) \right) \right] \quad (7)$$

Where, $\mathcal{R}$ = resizing, $\mathcal{D}$ = denoising, $\mathcal{N}$ = intensity normalization, $\mathcal{T}$ = data augmentation.

3.3 Lightweight Feature Extraction

This lightweight feature extraction (LFE)/encoder module as shown in Fig. 3 uses Depthwise Separable Convolution (DSConv), which reduces the number of parameters and computational cost compared with standard convolution. This convolution is as:

$$Z_d(i, j, c) = \sum_{m=-k/2}^{k/2} \sum_{n=-k/2}^{k/2} K_d(m, n, c) I_p(i, +, mj + nc) \quad (8)$$

Where, K_d = depthwise convolution kernel, $k \times k$ = kernel size, c = input channel, Z_d = depthwise feature map.

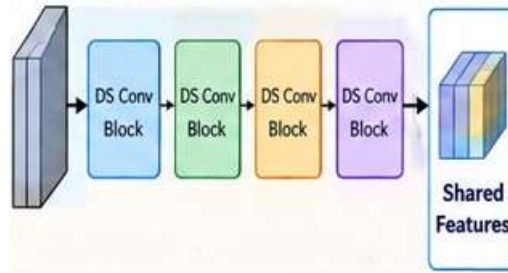


Fig.3. Lightweight Feature Extraction Architecture

A 1×1 convolution then combines information across channels as:

$$Z_p(i, j, o) = \sum_{c=1}^C K_p(c, o) Z_d(i, j, c) + b_o \quad (9)$$

where K_p is the pointwise convolution kernel and o denotes the output channel.

Thus, the depthwise separable convolution can be written compactly as:

$$Z = \phi \left(\text{PW} \left(\text{DW}(I_p) \right) \right) \quad (10)$$

where $\phi(\cdot)$ represents the ReLU activation function.

The final shared lightweight representation is therefore as:

$$F_s = \text{DSConv}_4 \left(\text{DSConv}_3 \left(\text{DSConv}_2 \left(\text{DSConv}_1(I_p) \right) \right) \right) \quad (11)$$

where F_s is the shared feature representation subsequently provided to the segmentation and classification heads.

Hence, the parameter reduction ratio for standard convolution to depthwise convolution is as:

$$R = \frac{k^2 C_{in} + C_{in} C_{out}}{k^2 C_{in} C_{out}} \quad (12)$$

The pre-processed MR image I_p is passed through a sequence of depthwise separable convolutional (DSConv) blocks to obtain computationally efficient deep features. Each DSConv block consists of a depthwise convolution followed by a 1×1 pointwise convolution, formulated as $F_l = \phi[PW_l(DW_l(F_{l-1}))]$, where $F_0 = I_p$. The final shared feature representation is $F_s = F_L$, which is simultaneously utilized by the segmentation and classification branches. Compared with conventional convolution, DSConv reduces the parameter requirement from $k^2 C_{in} C_{out}$ to $k^2 C_{in} + C_{in} C_{out}$, thereby improving computational efficiency while retaining discriminative spatial and channel-wise information.

3.4 Joint Segmentation and Classification

This joint segmentation and classification (JSC) module in Fig.4 show the central component of the framework. A lightweight feature extraction is learned from the pre-processed MR images and subsequently supplied to two task-segmentation and classification heads. This multi-task design allows segmentation and classification to benefit from common tumor-related features. The segmentation head uses a decoder with skip connections to reconstruct a pixel-level tumor mask.

Let the encoder generate feature maps: $F_1, F_2, \dots, F_L$

The decoder progressively up-samples the deepest representation:

$$D_{l-1} = \mathcal{D}_l(D_l) \quad (13)$$

and combines it with the corresponding encoder feature using a skip connection:

$$D'_l = \mathcal{C}(D_l, F_l) \quad (14)$$

Where, $\mathcal{D}_l$ = upsampling/decoder operation and $\mathcal{C}$ = feature concatenation.

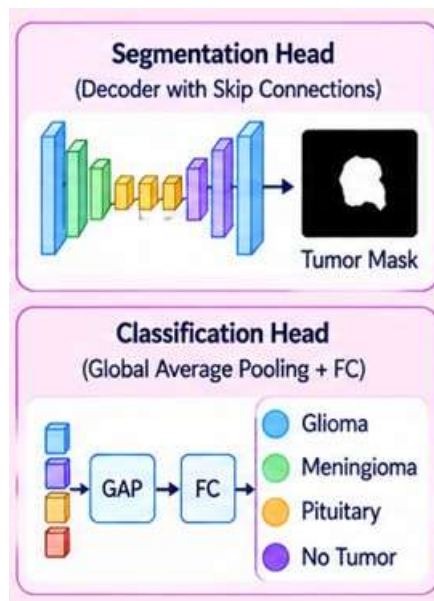


Fig.4. Joint segmentation and classification architecture

Thus, the segmentation pathway can be represented as:

$$F \rightarrow D_1 \rightarrow D_2 \rightarrow \dots \rightarrow D_L \rightarrow M \quad (15)$$

The final tumor probability map is as:

$$P_s(x, y) = \sigma(z_s(x, y)) \quad (16)$$

where σ is the sigmoid function as:

$$\sigma(z) = \frac{1}{1+e^{-z}} \quad (17)$$

The binary tumor mask is obtained by thresholding:

$$\hat{M}(x, y) = \begin{cases} 1, & P_s(x, y) \geq \tau \\ 0, & P_s(x, y) < \tau \end{cases} \quad (18)$$

Where τ is commonly selected as 0.5.

The segmentation loss function is the combination of Binary Cross-Entropy and Dice loss:

$$L_{seg} = \lambda_{bce} L_{BCE} + \lambda_{dice} L_{Dice} \quad (19)$$

Where

$$L_{BCE} = -\frac{1}{N} \sum_{i=1}^N [y_i \log p_i + (1 - y_i) \log(1 - p_i)] \quad (20)$$

And

$$L_{Dice} = 1 - \frac{2 \sum_i p_i y_i + \epsilon}{\sum_i p_i + \sum_i y_i + \epsilon} \quad (21)$$

The Dice coefficient itself is:

$$Dice = \frac{2|M \cap \hat{M}|}{|M| + |\hat{M}|} \quad (22)$$

The classification head receives the shared feature representation and converts it into a tumor-class prediction. In Fig.4, Global Average Pooling (GAP) is first applied. For a feature map F_k of size $H \times W$:

$$g_k = \frac{1}{HW} \sum_{i=1}^H \sum_{j=1}^W F_k(i, j) \quad (23)$$

Thus:

$$F \in \mathbb{R}^{H \times W \times K} \rightarrow g \in \mathbb{R}^K \quad (24)$$

GAP substantially reduces the number of parameters compared with a large fully connected layer, supporting the lightweight design. The pooled features are then passed to a fully connected layer:

$$z = Wg + b \quad (25)$$

where W and b are learnable parameters.

For four classes that is {Glioma, Meningioma, Pituitary, No Tumor} the Softmax probability for class c is:

$$P_c = \frac{e^{z_c}}{\sum_{k=1}^4 e^{z_k}} \quad (26)$$

The predicted class is:

$$\hat{y} = \arg \max_c P_c \quad (27)$$

The classification loss is categorical cross-entropy as:

$$L_{cls} = -\sum_{c=1}^C y_c \log(P_c) \quad (28)$$

where $C = 4$ in the illustrated framework.

Since segmentation and classification are performed simultaneously, the total training loss can combine both losses as:

$$L_{total} = \alpha L_{seg} + \beta L_{cls} \quad (29)$$

Where, L_{seg} = segmentation loss, L_{cls} = classification loss, α = segmentation-loss weight and β = classification-loss weight. The weights can be experimentally optimized by taking $\alpha = \beta = 0.5$.

3.5 Explainable AI

The XAI module explains why the network produced a particular prediction. The module uses Grad-CAM and feature-importance visualization. Suppose Y^c represents the output score for class c , and A^k is the k^{th} feature map of the selected convolutional layer. Grad-CAM first calculates the gradient as:

$$\frac{\partial Y^c}{\partial A_{ij}^k} \quad (30)$$

The importance weight of feature map k is calculated using global average pooling of the gradients as:

$$\alpha_k^c = \frac{1}{Z} \sum_i \sum_j \frac{\partial Y^c}{\partial A_{ij}^k} \quad (31)$$

where, $Z = H \times W$

The Grad-CAM map is then:

$$L_{Grad-CAM}^c = ReLU(\sum_k \alpha_k^c A^k) \quad (32)$$

The ReLU operation retains the regions contributing positively to the selected prediction. The resulting heatmap is superimposed on the original MR Image as:

$$I_{XAI} = I_p \oplus L_{Grad-CAM}^c \quad (33)$$

Where $\oplus$ represents visualization/overlay.

Regions with stronger activation indicate image areas that contributed more strongly to the predicted tumor class. The feature-importance component provides a visual interpretation of the learned features.

Let the learned representation be: $F = [f_1, f_2, \dots, f_K]$

The importance of each feature can conceptually be represented as:

$$w_k = \left| \frac{\partial Y^c}{\partial f_k} \right| \quad (34)$$

Higher w_k indicates greater influence on the prediction. A normalized feature-importance score can be expressed as:

$$\tilde{w}_k = \frac{w_k}{\sum_{j=1}^K w_j} \quad (35)$$

Thus, the XAI module provides prediction and important regions of the MR images. This makes the model more interpretable for medical-image analysis.

3.6 Output Module

The final resultant output produces segmentation, classification and explainability map from the MR images. The segmentation head produces $\hat{M}(x, y)$ that represents the predicted tumor mask. From the mask, tumor-related measurements can also be calculated. The classification head produces $\hat{y} = \arg \max_c P_c$ that provide the tumor may be glioma, meningioma, pituitary and no tumor. The Grad-CAM branch generates as:

$$L_{XAI} = L_{Grad-CAM} \quad (36)$$

which highlights the MRI regions responsible for the prediction. Therefore, the final framework generates:

$$\text{Output} = \{\text{Tumor Mask, Tumor Class, Explainability Map}\} \quad (37)$$

This proposed framework combines image preprocessing, feature learning, joint tumor segmentation and classification, and prediction explanation in a single framework. Preprocessing entails image input standardization by resizing, noise reduction, intensity normalization, and data augmentation. Feature learning involves a shared feature extractor for extracting discriminatory features in space and semantics, which are concurrently passed into the segmentation head and a GAP-FC classification head. The segmentation path produces the tumor mask at a pixel level, while the classification path makes predictions on the tumor type based on softmax probability scores. A weighted multi-task loss function is used to optimize the two paths simultaneously. Finally, Grad-CAM technique is applied to detect image areas that are important to the predicted class.

4. DATASET AND IMPLEMENTATION DETAILS

Evaluation of the suggested approach was done using the publicly available BRISC 2025 brain MRI dataset for segmentation and classification of brain tumors[28]. It includes 6,000 MRI brain images that belong to four classes of diagnoses: glioma, meningioma, pituitary tumor, and no tumor. Apart from image-level classes, this experiment includes 4,793 MRI brain images together with tumor segmentations at the pixel level. The existence of paired image-mask data allows for training and testing both classification and segmentation within the research work. The original classification consists of 5,000 training and 1,000 testing images, whereas the segmentation component contains 3,933 training and 860 testing image-mask pairs. For the present study, the training portion was further divided using an 80:20 stratified split to obtain 4,000 training and 1,000 validation images for classification and 3,146 training and 787 validation image-mask pairs for segmentation, while the test sets were retained exclusively for final evaluation. All images were resized to 256×256 pixels and intensity-normalized, while segmentation masks were resized using nearest-neighbour interpolation and converted into binary tumor masks. Training images were augmented using controlled geometric and intensity transformations, whereas validation and testing data underwent preprocessing without augmentation.

Test datasets were completely independent and used exclusively for final performance evaluation. All MRI images were scaled to 256×256 , filtered using Gaussian filters, and intensity-normalized using the min-max normalization prior to training. Data augmentation methods such as rotation, flipping, scaling, and translation were used only on the training dataset, but validation and test images were not augmented. For the segmentation problem, corresponding masks were resized using nearest-neighbour interpolation and binarized, where 1 is a tumor region and 0 is a non-tumor/background region. For the classification problem, an image was labeled as belonging to one of the four diagnosis classes, and the classifier produced a class probability using a Softmax output layer. The network architecture uses four consecutive DSConvs as a shared lightweight feature extractor, followed by two task-specific heads: a decoder with skip connection for tumor segmentation and fully connected classification head based on global average pooling for tumor classification. The proposed final architecture has a total of 7.81 million trainable parameters, having a computational complexity of 9.84 GFLOPs, a model size of 17.81 MB, and average inference time of 11.23 ms per image. The model has been trained for 100 epochs using the Adam optimizer, where the learning rate was set to 0.0001 and batch size is 16. The loss function in the case of the joint problem is defined as $L_{total} = 0.5L_{seg} + 0.5L_{cls}$. Grad-CAM was used for explainability purpose where the gradient of the selected class score with respect to the feature maps is calculated. Global average pooling was used for getting the gradient-based channel weights and a ReLU-activated weighted feature map is generated. The resulting activation map was resized and superimposed on the pre-processed MR image regions showing stronger activation were interpreted as image areas contributing more strongly to the predicted tumor class.

The optimal parameter values were selected based on experimental analysis in order to obtain the highest accuracy. This set of parameter values includes the learning rate, batch size, number of epochs, optimizer, and architectural settings of the neural network. Table 2 shows the optimal parameter during training for the implementation of the proposed framework [27]. Top of Form This framework was implemented in Python on Google Colab using TensorFlow/Keras with GPU support. This framework was optimized through the Adam optimizer, and was analysed on the basis of evaluation metrics. Explainable Artificial Intelligence methods have been incorporated in order to visualize parts of the images which contribute towards the prediction of the model.

Table 2. Optimal Parameter for the Proposed Framework

Parameter	Candidate selected
Optimizer	Adam
Learning rate	0.0001
Batch size	16
Epochs	100
Activation function	Relu
Output Activation	Softmax

5. EXPERIMENTAL RESULTS AND ANALYSIS

5.1 Qualitative Visualization

Performance of the suggested Framework was tested in terms of its classification, segmentation capacity and generalization ability on the BRISC 2025 brain MRI dataset [28]. The predicted output tumor mask and Explainability Grad-CAM Map of the proposed method is displayed in the Fig. 5. The explainability map highlighting the regions that contributed most strongly to the model's prediction. The close spatial correspondence between the ground-truth and predicted masks indicates effective localization and segmentation of the tumor region. The overlay and explainability visualization further demonstrate that the model focuses primarily on the tumor area, providing an interpretable representation of its decision-making process.

5.2 Quantitative Performance Analysis

The obtained experimental data were assessed based on the accuracy, precision, recall, Specificity, F1- Score, Dice Similarity Coefficient (DSC) and Intersection over Union (IoU) metrics [29]. This evaluation is conducted on the basis of a confusion matrix containing True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN). The equations (38-44) are the measures of evaluation:

$$\text{Accuracy} = \frac{TP+TN}{TP+TN+FP+FN} \quad (38)$$

$$\text{Precision} = \frac{TP}{TP+FP} \quad (39)$$

$$\text{Recall} = \frac{TP}{TP+FN} \quad (40)$$

$$\text{Specificity} = \frac{TN}{TN+FP} \quad (41)$$

$$\text{F1 Score} = \frac{2X \text{ Precision} X \text{ Recall}}{\text{Precision} + \text{Recall}} \quad (42)$$

$$\text{DSC} = \frac{2X \text{ Precision} X \text{ Recall}}{\text{Precision} + \text{Recall}} \quad (43)$$

$$\text{IoU} = \frac{Tp}{Tp+FP+Fn} \quad (44)$$

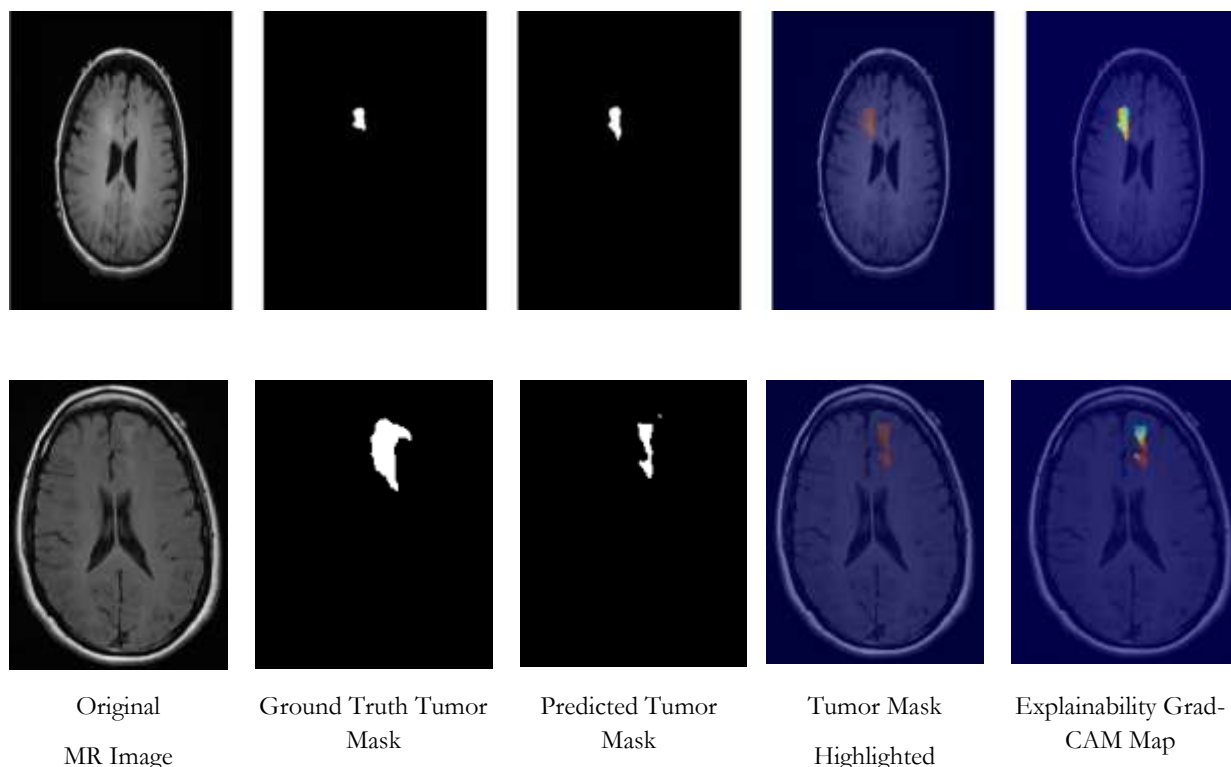


Fig. 5. Qualitative visualization of the proposed framework

Table 3. Quantitative Classification Performance

Class	Accuracy (%)	Precision (%)	Recall (%)	Specificity (%)	F1-Score (%)
Glioma	98.21	97.84	97.56	98.43	96.61
Meningioma	97.86	97.32	96.94	98.16	97.13
Pituitary	98.47	98.11	97.88	98.62	97.62
No Tumor	98.74	98.52	98.31	98.88	97.81
Micro Average	98.32	97.96	97.67	98.52	97.29
Weighted Average	98.34	98.02	97.72	98.55	97.32

The framework was able to distinguish tumor from non-tumor classes in the case of binary classification and also classify tumors based on their category in the case of multi-class classification. This shows that the lightweight approach may provide reliable classification results while keeping low computational complexity. Besides, the use of the explainable AI system allowed for providing visual explanations of the predictions made by the framework, namely for pointing out the image regions, which played a crucial role in the classification process. Class-wise classification performance of the proposed lightweight explainable deep learning framework is shown in the Table 3.

Table 4 presents a comparative evaluation of the proposed method against several existing deep-learning and convolutional neural network (CNN) approaches for brain tumor image classification. The comparison is based on four widely used performance metrics: Accuracy, Precision, Recall, and Specificity. Among the existing methods, DenseNet reported an accuracy of 91.58%, while the Designed CNN achieved 92.66%. PCANet obtained 94.02% accuracy, followed by R-CNN, which achieved 96.66% accuracy. In comparison, the proposed method achieved 98.34% accuracy, indicating improved classification

performance on the evaluated dataset. The proposed method also obtained 98.02% precision, 97.72% recall, and 98.55% specificity.

Overall, the results demonstrate that the proposed framework provides consistently high values across all four-evaluation metrics, indicating its ability to correctly classify tumor and non-tumor cases while reducing false-positive and false-negative predictions. The relatively high specificity further indicates effective identification of negative cases, whereas the high recall reflects strong detection of positive tumor cases.

Table 4. Quantitative classification performance comparison

Method/ Reference	Accuracy (%)	Precision (%)	Recall (%)	Specificity (%)	F1-Score (%)
DenseNet[13]	91.58	93.24	92.56	93.12	92.12
CNN[14]	92.66	94.12	94.94	93.96	93.34
PCANet[15]	94.02	94.52	95.071	96.08	94.56
R-CNN[16]	96.66	95.91	96.28	97.12	95.72
Proposed	98.34	98.02	97.72	98.55	97.32

Within this segmentation paradigm, Dice Similarity Coefficient (DSC) is a crucial evaluation criterion as it assesses directly the level of intersection between the segmented tumor region and the tumor region of the reference segment. The higher the Dice Similarity Coefficient value, the better the alignment between the predicted segmentation mask and the reference one. Likewise, Intersection over Union (IoU) calculates the degree of overlap between the segmented region and the reference region. Within medical image segmentation, IoU calculates how much the segmented tumor region overlaps with the tumor region in the MR image. The higher the IoU value, the more accurate the tumor segmentation. Table 5 indicate the segmentation performance of the proposed framework on the BRISC test set.

Table 5. Quantitative segmentation performance

Method	Precision (%)	Recall (%)	Specificity (%)	DSC (%)	IoU (%)
DenseNet	91.8	89.2	95.5	90.4	82.6
CNN	93.8	91.7	97.2	92.9	86.8
PCANet	94.9	92.8	97.7	94.1	89.0
R-CNN	95.8	93.5	98.1	94.8	90.1
Proposed	96.5	94.2	98.6	95.3	91.0

The performance of the proposed framework shows an increased precision and recall, implying its capability to classify tumor pixels with reduced rates of false positives and false negatives. The high 98.6% specificity implies a higher capability of identifying the non-tumor areas. Also, the 95.3% DSC and 91.0% IoU prove significant spatial correspondence between the tumor region prediction and reference segmentation masks.

5.3 Convergence and Generalization Performance

In order to study the optimization path as well as the generalizability of the proposed model, the learning behavior was analyzed using the graph of the sum of BCE and Dice loss functions over 100 epochs as presented in Fig.6

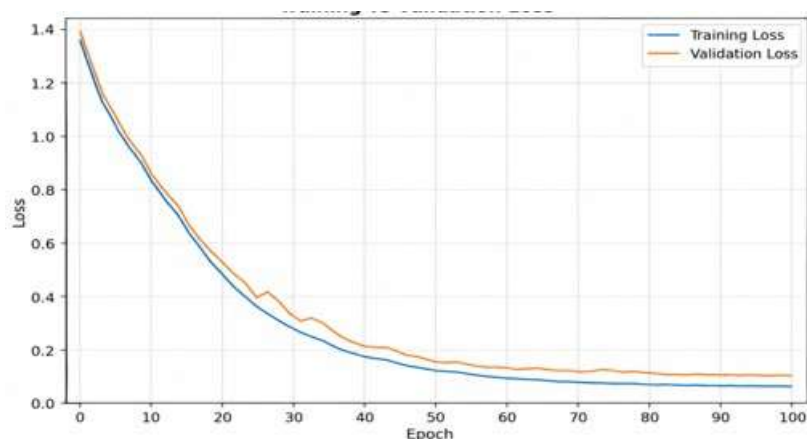


Fig. 6. Loss Curve of the Proposed Framework

As seen from the above figure, the train and validation loss curves show a monotonic reduction in a synchronized manner from an initial value of 1.36 and 1.40, respectively. This simultaneous reduction clearly indicates that the combined loss function was able to guide the optimization process in gradient descent to minimize the classification error by using the BCE loss and maximize the structural similarity using the Dice coefficient. Although some temporary fluctuations can be seen in the validation curve between epochs 22 and 35, caused due to mini-batch variance during spatial boundary optimization, the entire curve is highly stable. Most importantly, there is no sign of asymptotic divergence or upward inflexion in the validation curve compared to the training curve, which implies that the network successfully addressed the overfitting problem. After the 60th epoch, both the curves reach the plateau phase, implying that the structure of the network became converged with minimized compound losses of 0.08. The relatively small generalization gap observed after training indicates consistent performance across the training and validation sets.

5.4 Training and Validation Dice Performance

The curve Fig. 7 shows the dice coefficient for training and validation during 100 epochs indicates how the learning model learns and generalizes. In the early epochs, the Dice score is observed to rise slowly as the learning model learns the spatial features of the tumor regions in the brain. After more training, the Dice score for training rises further until it attains a very high value, thus learning the tumor boundaries and features. Both the curves tend to converge after about 95 epochs, although the variations are minimal. The fact that the gap between the training and validation Dice values is relatively small implies that there is little or no overfitting and that the model generalizes well.

6. ABLATION STUDY

The ablation study shown in the Table. 6 was conducted to quantify the individual contribution of the principal modules of the proposed framework. The baseline CNN configuration was progressively enhanced by introducing the lightweight feature extraction/encoder, shared feature extraction, segmentation branch, feature-fusion mechanism, and explainability module. The comparison demonstrates the effect of each architectural module on classification and segmentation performance. The lightweight encoder is additionally evaluated in terms of parameter count and computational complexity to verify the reduction in model complexity. The dual-task configuration assesses whether joint learning of tumor classification and localization provides complementary information, whereas the feature-fusion configuration evaluates the benefit of combining spatial and semantic representations. The final configuration integrates all proposed modules.

7. COMPUTATIONAL COMPLEXITY

The computational efficiency of the proposed framework was evaluated in terms of the number of trainable parameters, floating-point operations (FLOPs), model size, inference time as shown in Table 7. The proposed architecture employs lightweight feature extraction and shared representations for segmentation and classification, thereby avoiding the computational redundancy associated with independently trained segmentation and classification networks.

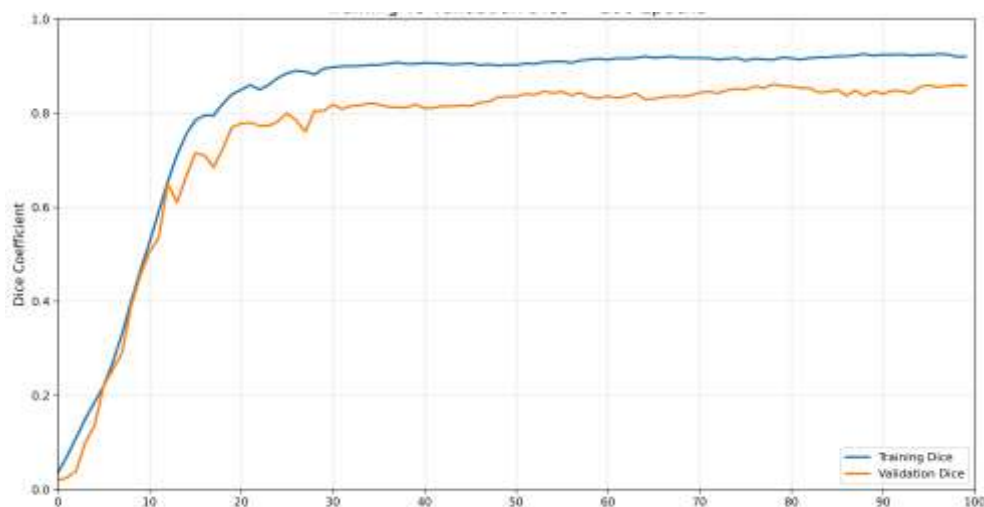


Fig.7. Training and Validation Dice Curve

The classification head operates on compact high-level representations, while the segmentation decoder reconstructs the tumor localization map using progressively up-sampled features. The explainability module is applied to the learned representations to generate visual explanations and does not introduce additional trainable parameters. Overall, the reduced parameter counts and FLOPs indicate that the proposed framework is computationally suitable for resource-constrained medical-imaging applications while retaining the capability to perform tumor segmentation and classification within a unified architecture.

Table 6. Ablation Study of the Proposed Framework

Configuration	Accuracy (%)	Precision (%)	Recall (%)	Specificity (%)	F1-Score (%)	IoU (%)
Baseline CNN	92.66	94.12	94.94	93.96	93.34	92.45
+LFE	93.18	95.12	95.36	94.14	93.87	93.18
+JSE	94.12	95.46	95.89	94.76	94.12	93.97
+LFE+JSE	95.89	96.49	96.78	95.89	95.67	95.31
Proposed	98.34	98.02	97.72	98.55	97.32	96.56

Table 7. Computational Complexity Analysis

Method	Parameters (M)	FLOPs (G)	Model Size (MB)	Inference Time (ms/image)
DenseNet	31.04	32.21	28.59	32.81
CNN	25.56	27.12	27.57	28.65
PCANet	15.48	15.22	21.06	18.78
R-CNN	10.32	11.4	19.23	13.58
Proposed	7.81	9.84	17.81	11.23

8. LIMITATIONS AND CLINICAL IMPLICATIONS

Although there have been encouraging outcomes on the BRISC 2025 benchmark dataset, some constraints need to be taken into consideration. The dataset is comprised of MRI images belonging to four diagnostic classes; however, this dataset might not reflect the patient population variance, imaging protocols, machines used, appearance of the tumors, and scanning conditions used in practice. While a stratified 80:20 division was made for the training of the classification data, stratification does not prevent possible class imbalance, which is not covered by the current study. In addition, the testing was conducted through the use of the test dataset from the same benchmark dataset, and there was no validation test done on an external dataset.

Thus, the presented results should not be taken as a sign of the method's usability in practice. In terms of computations, the developed light-weighted model includes 7.81 million of parameters, needs 9.84 GFLOPs, has a model size of 17.81 MB, and takes an average of 11.23 ms per inference under the presented experimental conditions. It means that the computational efficiency is shown; however, real-life performance will depend on hardware settings. As for the segmentation, the obtained Dice and IoU scores show good overlap with reference masks; however, the overlap-based metrics cannot fully measure local boundary errors. Localized boundary errors can occur near irregular, low contrast, or poorly defined tumor boundaries, which means that boundary-specific evaluation has to be used in further studies. The same concerns the Grad-CAM algorithm, as it provides information about regions of interest in the case of the predicted classes.

Lastly, the high performance of the framework under the benchmark scenario should be separated from clinical diagnostic performance. Current results show the performance of the model under the current experimental setup but not its safety and reliability. In future work, external validation, analysis of class imbalance, assessment of boundary-aware segmentation performance, robustness testing under different imaging conditions, expert comparison, and clinical trial will be conducted.

9. CONCLUSIONS

In this research work, an efficient and interpretable novel lightweight and explainable deep learning approach was introduced for automatic brain tumor segmentation and classification using MR images. The introduced approach uses a combination of lightweight feature extraction and shared learning architecture to carry out segmentation and classification in one single framework. According to the results obtained from experiments, the model is capable of accurately identifying the tumors and giving reliable tumor class predictions at the same time. Compared to the existing methods, the accuracy rate reached 98.34% by the proposed method, which shows an enhanced performance in classification. Training and Validation Dices curves for 100 Epochs show the learning behaviour of the network with convergence and with minimum difference between training and validation showing the ability of the network to generalize on unseen images of MRI. Explainable AI can be used to improve the interpretation of the results of the network by pointing out those regions of the images which influence the decisions made by the network. In conclusion, the framework suggested is an efficient one for computer-aided brain tumor analysis. Future scope includes validation with larger and multi-center datasets.

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AUTHOR CONTRIBUTIONS

Sudhansu Bhusan Kar: Investigation, Methodology, Laboratory Analysis, Writing & Review

Jibanananda Mehena: Conceptualization, Data Curation, Formal Analysis, Supervision.

CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

ETHICS STATEMENT

Ethical approval was not required for this study.

DATA AVAILABILITY STATEMENT

Data supporting the findings of this study are available from the corresponding author upon reasonable request.

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