

Balanced Brain Tumor MRI Classification Using Segmentation-Aware Preprocessing and Dual-View Deep Features

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HOW TO CITE:

Priyanka Gupta, Ramandeep Sandhu
(2026). Balanced Brain Tumor MRI
Classification Using Segmentation-
Aware Preprocessing and Dual-View
Deep Features.
International Journal of Special
Education, 41(4s), 250-264.

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ABSTRACT:

The proposed study proposes a novel framework consisting of two phases for classifying brain tumors in MRI images using a segmentation-guided strategy for multi-class brain tumor classification. The presented model aims to address three key challenges associated with previous research on this topic, namely the restricted use of lesion-aware pre-processing techniques, inadequate ablation analysis for verifying contributions, and lack of reproducibility of stored artifacts. Specifically, the proposed model uses the BRISC database and involves the following tasks in the first phase: aligning the classification images according to the available tumor masks, creating a balanced sample containing four classes of data, and representing each instance through stored full-context and lesion-oriented ROI images by applying brain masking, contrast enhancement, and structure-preserving cropping. On the other hand, the second phase of the process entails the extraction of deep features from both image types using a pre-trained ResNet18 encoder, followed by fusion with metadata indicating the anatomical plane and the mask coverage. Finally, the obtained dual-view features are fed into a multilayer perceptron (MLP) classifier with three-fold stratified cross-validation. Moreover, an ablation study was conducted to examine the impact of each component in the pipeline, such as full-context features, metadata, ROI-guided features, and the combination of both features. Results show that the proposed segmentation-guided strategy significantly outperforms the single-view baseline with an average accuracy of 94.05% and macro F1 and ROC-AUC scores of 94.05% and 0.9916, respectively.

Keywords: Brain Tumour Detection, ROI-Based Learning, CNN Feature Extraction, ResNet18, PCA-Based Dimensionality Reduction, MLP Classifier, Computer-Aided Diagnosis.

1. Introduction

Diagnosing brain tumors through Magnetic Resonance Imaging (MRI) has been one of the most challenging tasks despite significant progress

achieved in modern medical imaging. MRI diagnoses have to account for high intra-class variability, low inter-class separability, and severe class imbalance of existing databases [1]. Brain tumors make only a small part of all diagnosed

cancers; however, their prevalence is quite alarming since brain tumors are responsible for an overwhelming number of patient fatalities and complications. MRI is a non-invasive tool to detect tumors, but manual diagnostics is highly time-consuming and error-prone process. This necessitates creating automatic deep learning-based systems [2]. The development of deep neural networks (DNN) has resulted in an increase of the accuracy of tumor classifications. For example, CNNs are widely employed for image recognition and classification due to the capability of extracting hierarchical features through convolution operations [3]. The optimization-based approach with metaheuristic feature selection techniques like AGWO-CNN demonstrates a higher rate of successful classifications than pure CNN [4]. The ensemble of multiple CNN models provides more accurate results, especially during multi-class classification [5,6]. Yet, all these models focus on classification without utilizing tumor's spatial properties. First, from the clinical point of view, tumor classification should necessarily be associated with histopathological tumor grading. The most famous system is represented by the WHO (World Health Organization) system, which classifies tumors based on their cellular and molecular characteristics [7]. Despite attempts to reproduce these classifications using medical imaging, the inability to include spatial information in deep neural networks limits their clinical value. Segmentation models, such as 3D U-Net, overcome this disadvantage due to the ability to localize tumor regions, and therefore provide more effective feature extraction [8]. Yet, segmentations usually require large, annotated databases and computationally intensive models. An interesting trend of combining detection, classification, and localization in one architecture seems to become promising. For example, region-based CNN architectures or dual channel CNNs consider global and local aspects of the tumor simultaneously, and as a result, provide better classification results [9].

Multi-feature fusion models, such as Deep-NeT, prove that the combination of hand-crafted and deep features yields better performance in cancer detection [10]. More recently, dual-branch

architectures with explicit distinction of global and local features and their subsequent fusion have been developed [11]. Lightweight multi-path CNNs are also developed to reduce computational complexity of classification [12]. Parallel architectures that combine CNNs and novel methods of sequence modeling have proved their ability to detect long-term dependencies of tumors in MRI scans [13]. Hybrid ensemble models that integrate popular Xception and parallel CNNs demonstrate advantages in capturing multiscale features [14]. Also, residual attention in the classification task has been successfully implemented as an auxiliary layer; SAlexNet proves its usefulness in achieving high precision in detecting tumor [15]. However, there are still some problems that need to be solved: (i) class imbalance issues, (ii) lack of segmentation classification interaction, and (iii) under-exploitation of feature complementarity.

The key point made in the literature review is that tumor classification performs much better when spatial priors and contextual tumor information is included. However, most of the existing algorithms regard tumor segmentation and classification as two distinct problems. The two-step approach with segmentation informing classification has proved to be more effective in terms of interpretability and overall model performance [2]. Still, these approaches fail to consider class balance or feature complementarity. To fill this gap, we introduce a segmentation-enabled dual-view feature learning methodology for achieving class balance in brain tumor classification. This methodology incorporates preprocessing techniques that focus on the identification of tumor regions and utilizes dual-view deep features for capturing not only context information but also the local nature of the tumor region

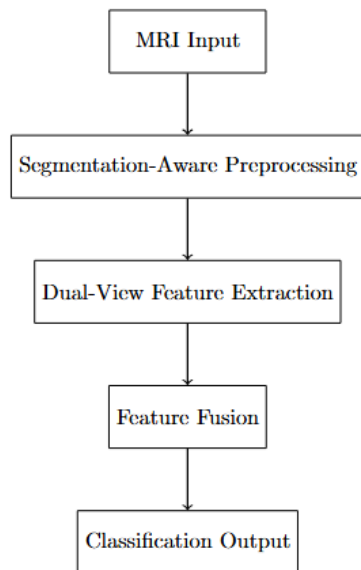


Figure 1 Conceptual pipeline of segmentation-aware dual-view classification framework

The main strength of the paper lies in the use of segmentation-based pre-processing alongside dual view feature learning, which leads to a fair and effective classification system. Unlike conventional approaches, the proposed approach incorporates the localization information of tumors while extracting features, which adds value in terms of interpretation and classification accuracy.

2. Literature Review

Classifications of brain tumors utilizing MRI scans have mostly advanced through deep learning, transfer learning, and hybrid designs. In spite of the remarkable classification accuracy, some of the problems that need addressing include class imbalance, inadequate spatial attention, and the integration of segmentation and classification. The use of transformers has demonstrated effectiveness in detecting the global relationships in the image. For instance, Amin et al. [16] developed a DieT transformer model with the addition of PCA-ADE for multi-class classification, delivering good results. However, transformer models normally require extensive data and computing resources. Similarly, Vimala et al. [17] used GDD feature-based deep learning models for brain tumor classifications and survival predictions. While the integration of survival analysis improves the usefulness of the model, using handcrafted features might be a limitation.

Different strategies related to ensemble learning were also considered in order to increase the robustness of classification. Bouguerra et al. [18] created a two-stage CNN ensemble, based on the score-level fusion technique, obtaining higher accuracy levels on different datasets. Smitha et al. [19] emphasized the role of early-stage cancer detection using DL techniques. In turn, Ali et al. [20] applied realistic data augmentation, resulting in more effective training. Nevertheless, in comparison with traditional DL methods, ensemble models exhibit increased computational complexity and possible feature learning redundancies. Transfer learning is another approach commonly used due to the limited amount of available annotated medical datasets. The effectiveness of combining machine learning and transfer learning algorithms was demonstrated by Malakoutiet al. [21]. Also, Islam et al. [26] proved that fine-tuning pre-trained CNN models improves classification results even for a small dataset. However, in contrast to traditional approaches, efficient Net models [23] demonstrate higher scalability and feature reusability; nevertheless, they depend too much on features from natural image datasets.

The latest attempt made in the body of literature was directed towards implementing a combination of classification, segmentation, and localization into one model. For instance, BT-Net was suggested by Rabby et al. [22] as an end-to-end model capable of conducting several tasks simultaneously, thus avoiding excessive processing stages of image classification. Moreover, EMU-Net [28] is known for its combined application of classification and segmentation tasks using U-net architecture. However, both models require considerable amounts of computation and high-quality datasets for training. Moreover, various types of hybrid feature fusion were used as means for enhancing the results produced by models. Shawly and Alsheikhy [25] applied handcrafted and deep features for achieving greater interpretability and increasing classification performance. Khan et al. [31] used multi-model texture features and proved the benefit of using them as spatial descriptors along with LS-SVM. Ensemble learning was employed as an approach to improve

classification stability [32, 33]; however, it requires considerable system resources and is less scalable.

In addition, some researchers turned to designing practical frameworks for implementation. For instance, IoMT-based systems [27] allow diagnosing brain tumours remotely; however, it creates problems associated with network latency and data security. Artificial data generation [30] was another way to compensate for the lack of data for training. The problem of optimization of such models was solved with RBEBT [29], which utilizes CNN and efficient classifiers. Thus, such models demonstrate great performance but lack scalability. Among existing approaches, CNN backbones remain popular among researchers for their high performance in feature extraction. The CNNs that include MobileNet use depthwise separable convolutions to reduce the computation cost [34, 36]. NASNet uses neural architecture search to optimize the design of models [37]. Finally, ResNet utilizes residual connections to solve the vanishing gradient problem and increase network depth [39, 40]. All of these architectures provide adequate feature extraction but focus on global features rather than localizing tumors.

Some authors addressed this issue through segmentation methods that allow for combining global representation with local spatial information and thus accurately localizing tumours. ResUNet [41] integrates residual learning into the U-Net framework, achieving high localization rates. Some hybrid frameworks use segmentation and classification tasks together to increase the quality of predictions and provide better interpretability [42]. Moreover, dual-stage models [44] prove that sequential integration of two tasks results in increased effectiveness. However, these two tasks are usually separate. Finally, there is another serious problem associated with medical datasets, such as TCGA [43]: they often demonstrate imbalance. Despite attempts to cope with the problem through using augmentation and resampling techniques, it does not eliminate the issue on the level of feature learning.

From the above analysis, it is quite apparent that the current approaches have some significant drawbacks. Firstly, most of the models fail to

utilize feature learning in the presence of image segmentation, thus restricting themselves from learning tumour-specific spatial features. Secondly, the utilization of dual-view representation to learn global context along with local tumour structure is underexploited. Thirdly, the problem of class imbalance is largely ignored, thus making the current models unreliable. Fourthly, the computationally expensive nature of most of the high-performing models makes them inapplicable in a clinical setup. Hence, there arises a dire need for developing a holistic framework wherein the process of segmentation-aware feature extraction through dual view representation is achieved without compromising the computational efficiency.

3. Methodology

In this study, we propose an innovative model-based method for the automatic segmentation of brain tumors through MRI scans. The model utilizes specialized image processing methods, deep feature extraction, and machine learning classification techniques as shown in figure 2. The overall goal is to achieve high performance while maintaining clarity and repeatability.

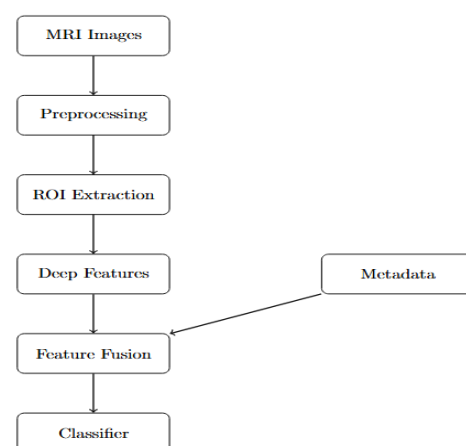


Figure 2 Feature Extraction and Fusion Pipeline

Let the dataset be represented as:

$$\mathcal{D} = \{(x_i, y_i)\}_{i=1}^N$$

where x_i denotes the input MRI image and $y_i \in \{1, 2, 3, 4\}$ represents the tumor class labels.

A key challenge in medical datasets is class imbalance. To address this, a balanced subset is

constructed by selecting an equal number of samples from each class:

$$N_c = \min_k |\mathcal{D}_k|$$

where $\mathcal{D}_k$ represents samples belonging to class k . This ensures uniform distribution of class and prevents bias during training.

The preprocessing stage aims to enhance image quality and isolate clinically relevant regions. Initially, each MRI image is smoothed using Gaussian filtering to suppress noise:

$$I_s = I * G_\sigma$$

where G_σ is a Gaussian kernel with standard deviation σ . This operation preserves structural information while reducing high-frequency variations.

To extract the brain region, Otsu's thresholding method is applied to obtain a binary mask:

$$M(x, y) = \begin{cases} 1 & \text{if } I_s(x, y) > T \\ 0 & \text{otherwise} \end{cases}$$

The threshold T is automatically determined to maximize inter-class variance. However, raw thresholding often produces fragmented regions. Therefore, morphological operations are applied to refine the segmentation:

$$M_r = (M \ominus K) \oplus K$$

where $\ominus$ and $\oplus$ denote erosion and dilation, respectively, and K is the structuring element. This step removes noise and preserves the dominant brain contour.

The region of interest (ROI) is then extracted by computing the bounding box around the segmented brain region:

$$I_{roi} = I[x_{min}:x_{max}, y_{min}:y_{max}]$$

This reduces irrelevant background information and focuses the model on anatomically meaningful regions.

To improve contrast and highlight tumor structures, Contrast Limited Adaptive Histogram Equalization (CLAHE) is applied:

$$I_c = \text{CLAHE}(I_{roi})$$

Additionally, structural boundaries are emphasized using edge detection:

$$E = \text{Canny}(I_c)$$

A multi-channel representation is then constructed by combining complementary information sources:

$$I_{3c} = [I_c, I_c \cdot M_r, E]$$

The above description represents the features intensity, spatial mask, and edges. This helps the model learn features that have local and global properties. Feature extraction is performed using a pre-trained CNN (ResNet18). The final classification layers are stripped from the model, and the model acts as a feature extractor.

$$f = \phi(I_{3c})$$

where $\phi(\cdot)$ denotes the mapping from image space to feature space. Two sets of features are extracted: one from the full image and another from the ROI. This dual representation captures both contextual and localized tumor information.

In addition to deep features, auxiliary metadata is incorporated to enhance model performance. These include anatomical plane encoding and region-based ratios derived during preprocessing. The metadata vector is defined as:

$$f_{meta} = [v_{ax}, v_{co}, v_{sa}, R_b, R_f]$$

where v_{ax}, v_{co}, v_{sa} represent one-hot encoded anatomical views, R_b denotes the brain area ratio, and R_f represents the focus region ratio.

The final feature vector is obtained through concatenation:

$$F = [f_{full}, f_{roi}, f_{meta}]$$

To ensure stable training and eliminate scale variations, feature normalization is applied:

$$\hat{F} = \frac{F - \mu}{\sigma}$$

Dimensionality reduction is performed using Principal Component Analysis (PCA) to remove redundancy and retain the most informative components:

$$Z = W^T \hat{F}$$

where W is the projection matrix is formed from eigenvectors of the covariance matrix.

3.1 Model Training, Validation, and Evaluation

The classification stage employs a multilayer perception (MLP), which is effective for learning non-linear relationships in high-dimensional feature spaces. The prediction function is defined as:

$$\hat{y} = \text{softmax}(W_2 \sigma(W_1 Z + b_1) + b_2)$$

where $\sigma(\cdot)$ denotes the ReLU activation function, and W, b represent trainable parameters.

The model is trained using categorical cross-entropy loss:

$$\mathcal{L} = - \sum_{i=1}^N y_i \log(\hat{y}_i)$$

To ensure generalization and avoid overfitting, stratified K -fold cross-validation is employed. The dataset is partitioned into K disjoint subsets:

$$\mathcal{D} = \bigcup_{k=1}^K \mathcal{D}_k$$

At each iteration, one subset is used for validation while the remaining subsets are used for training.

Performance evaluation is conducted using standard classification metrics. Accuracy is defined as:

$$Acc = \frac{TP + TN}{TP + TN + FP + FN}$$

The F1-score, which balances precision and recall, is given by:

$$F1 = \frac{2PR}{P + R}$$

In addition, Receiver Operating Characteristic (ROC) curves and Area Under Curve (AUC) are used to evaluate probabilistic predictions. The suggested approach provides efficient fusion of

spatial processing and deep learning-based feature extraction. The combination of dual representations, that is, overall images and regions of interest (ROIs), increases the ability of discrimination through leveraging both global and local features. Furthermore, the utilization of metadata helps improve performance through adding more domain knowledge. However, depending solely on the predefined pretrained encoder could limit the flexibility for adapting to particular domain features, which is inherent in MRI images. It would be worthwhile to explore fine-tuning approaches or transformers.

4. Results and Discussion

In this section, the quantitative and qualitative outputs of the proposed framework that includes a two-phase approach guided by image segmentation for brain tumor classification will be stated. All the metrics presented are based on the experiment's output artifacts obtained after running the code. These include cross-validation outputs, class report outputs, confusion matrix outputs, ROC curve outputs, ablation outputs, and pre-processing visualization outputs.

4.1 Experimental Summary

The final curated experimental cohort contained 4268 MRI slices, with exactly 1067 samples in each of the four classes: glioma, meningioma, no-tumor, and pituitary tumor. This balance was intentionally enforced to remove class-frequency bias and make the interpretation of accuracy, macro- F_1 , and confusion matrices more reliable. The dataset composition used for the final experiments is illustrated in Figure 3, where the class counts are perfectly matched by design. In addition, the distribution of anatomical planes across classes is shown in Figure 4. Although the plane distribution is not perfectly identical within every class, all three views are meaningfully represented, which supports the inclusion of plane-aware metadata in the proposed model.

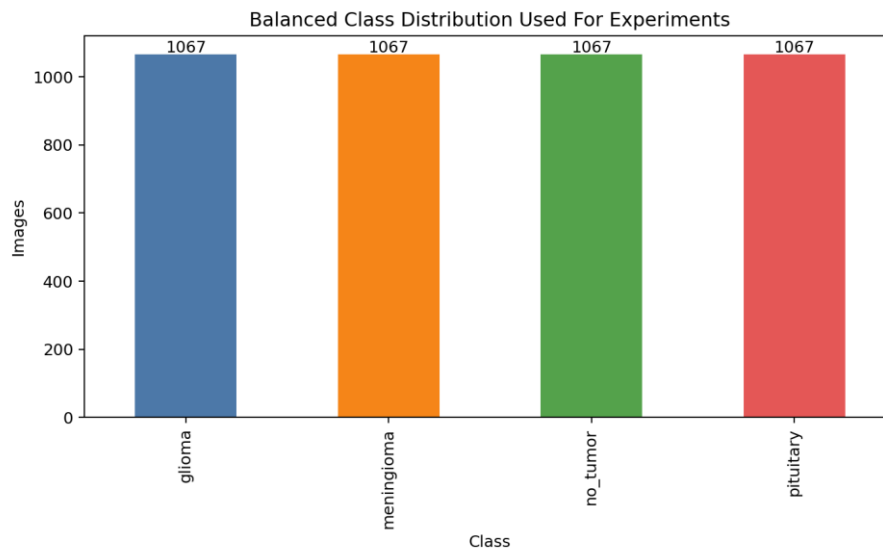


Figure 3 Balanced class distribution used in experiment

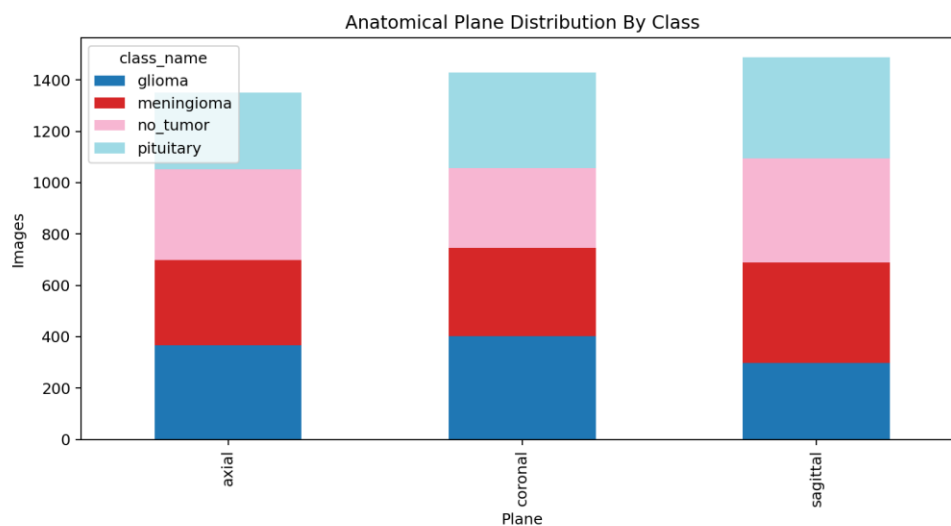


Figure 4 Distribution of anatomical planes across the balanced cohort

The major strength of this study is the clear retention of preprocessing artifacts. In addition to implicitly applying transforms during training, the workflow retains full-context images, lesion ROI images, and post-preprocessing masks. Figure 5 shows some example outputs from the preprocessing step. The above illustrations confirm

that the preprocessing process retained brain anatomy, boosted tissue contrast, and identified lesion-sensitive areas while retaining the overall context. This is vital since previous studies have established that region-based analysis improves brain tumor classification despite having similar global intensities for different tumor types.

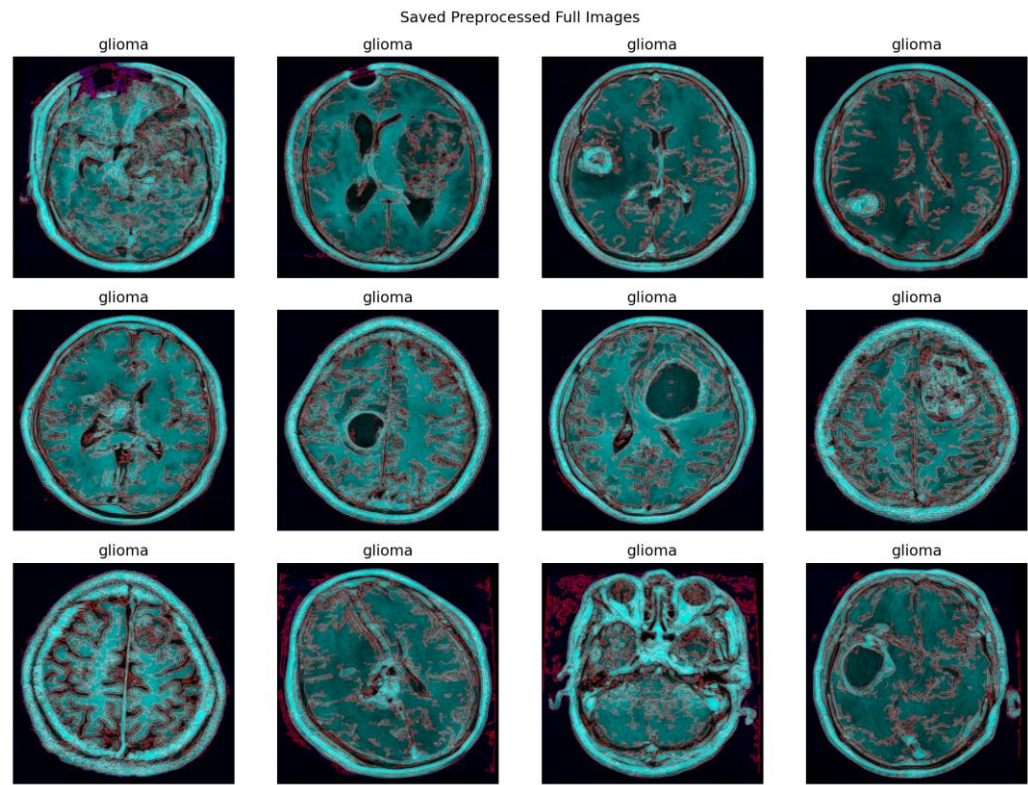


Figure 5 Representative examples of the saved preprocessed images.

4.2 Overall Quantitative Performance

Table I summarizes the principal out-of-fold performance across all evaluated variants. The proposed dual-view model achieved the best overall result with an accuracy of 94.05%, macro-precision of 94.06%, macro-recall of 94.05%,

macro- F_1 of 94.05%, and one-vs-rest macro-ROC-AUC of 0.9916. These values demonstrate that the final method is not only accurate but also balanced across classes, as evidenced by the close agreement among precision, recall, and F_1 .

Table I Performance of the baseline, intermediate ablations, and the proposed method

Method	Accuracy	Macro Precision	Macro Recall	Macro F_1	ROC-AUC
Baseline full context only	0.8599	0.8587	0.8599	0.8590	0.9657
Full context + metadata	0.8861	0.8856	0.8861	0.8858	0.9772
Full context + ROI	0.9400	0.9400	0.9400	0.9400	0.9918
Proposed dual view + metadata	0.9405	0.9406	0.9405	0.9405	0.9916

First, the baseline single-view model already performs reasonably well, achieving 85.99% accuracy. This confirms that full-context MRI slices contain enough signal for meaningful classification. However, the performance gap between the baseline and the proposed model is large: the proposed framework improves accuracy by approximately 8.06 percentage points and

macro- F_1 by approximately 8.15 percentage points. Such a gain is substantial for a balanced four-class neuroimaging problem.

Second, the addition of metadata alone improves performance from 85.99% to 88.61%, indicating that acquisition plane and mask-coverage statistics provide useful complementary cues. However, this improvement is much smaller than the gain

obtained from introducing ROI-based information. Once ROI features are fused with full-context features, accuracy jumps to **94.00%**. This result strongly suggests that the main source of improvement is the segmentation-guided local representation, not metadata alone.

Third, the proposed dual-view model slightly outperforms the full+ROI model in accuracy, precision, recall, and macro- F_1 , even though the full+ROI model has a marginally higher ROC-AUC by a very small amount. This indicates that the metadata stream does not radically alter class

ranking quality but helps convert borderline cases into more correct final class assignments. In other words, metadata appears to sharpen decision boundaries rather than transform the underlying separability of the classes.

The ablation trend is visually reinforced by Figure 6, where the proposed model and the full+ROI variant clearly dominate the other two settings. The most important conclusion from this figure is that lesion-sensitive ROI representation is the decisive component of the pipeline.

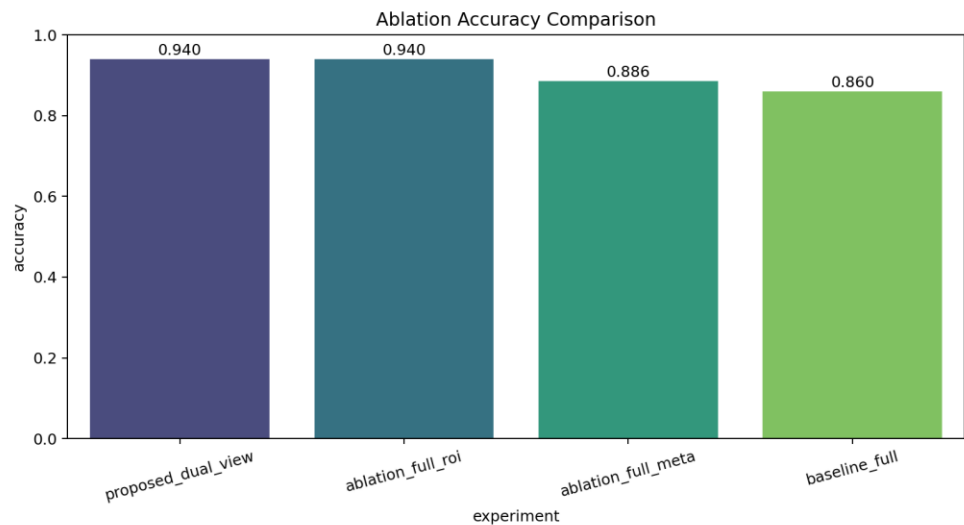


Figure 6 Accuracy comparison across ablation

Fold-Wise Stability and Generalization

To evaluate robustness, the models were assessed using three-fold stratified cross-validation. Table II reports the fold-wise results. The proposed model achieved fold accuracies of **93.11%**, **94.66%**, and

94.37%, demonstrating both high performance and stable behavior across splits. The standard deviation of accuracy was only about **0.0067**, which indicates that the method does not rely on a single favorable train-validation partition.

Table II Fold-wise performance of the methods compared

Method	Fold	Accuracy	Macro Precision	Macro Recall	Macro F_1	ROC-AUC
Baseline full context only	Fold 0	0.8517	0.8499	0.8518	0.8506	0.9688
Baseline full context only	Fold 1	0.8595	0.8579	0.8594	0.8580	0.9671
Baseline full context only	Fold 2	0.8685	0.8691	0.8685	0.8682	0.9722
Full context + metadata	Fold 0	0.8805	0.8793	0.8806	0.8797	0.9778
Full context + metadata	Fold 1	0.8939	0.8930	0.8938	0.8933	0.9774
Full context + metadata	Fold 2	0.8840	0.8857	0.8839	0.8844	0.9784
Full context + ROI	Fold 0	0.9304	0.9304	0.9305	0.9303	0.9911
Full context + ROI	Fold 1	0.9459	0.9460	0.9459	0.9459	0.9928
Full context + ROI	Fold 2	0.9437	0.9443	0.9437	0.9439	0.9924
Proposed dual view + metadata	Fold 0	0.9311	0.9311	0.9312	0.9312	0.9904
Proposed dual view + metadata	Fold 1	0.9466	0.9469	0.9466	0.9467	0.9928
Proposed dual view + metadata	Fold 2	0.9437	0.9438	0.9437	0.9438	0.9930

The fold-wise behavior also reveals two important practical points. First, all methods improve noticeably from Fold 0 to Folds 1 and 2, suggesting that Fold 0 may contain a somewhat harder subset of cases. Second, the relative ordering of methods remains unchanged across folds. The baseline is always the weakest, the metadata-enhanced baseline is always better than the baseline, and the ROI-based variants are always the strongest. This consistency increases confidence that the observed gains are genuine and not caused by random variation.

4.3 Class-Wise Performance Analysis

The detailed class-wise report for the final proposed method is provided in Table III. The not-tumor class is the easiest category, achieving precision of 1.0000, recall of 0.9991, and F_1 of 0.9995. This near-perfect score indicates that the proposed framework can effectively distinguish healthy scans from tumor-bearing scans, which is clinically important for screening and triage.

Table III Class-wise performance of the proposed dual-view model

Class	Precision	Recall	F_1 -score	Support
Glioma	0.9313	0.9269	0.9291	1067
Meningioma	0.8885	0.8960	0.8922	1067
No-tumor	1.0000	0.9991	0.9995	1067
Pituitary	0.9427	0.9400	0.9413	1067
Macro average	0.9406	0.9405	0.9405	4268

Among the tumor classes, pituitary and glioma are recognized more reliably than meningioma. Pituitary reaches an F_1 of 0.9413, while glioma reaches 0.9291. Meningioma is the most difficult tumor class, with an F_1 of 0.8922. This finding is consistent with the class confusion patterns observed in the confusion matrices: meningioma overlaps with both glioma and pituitary more than the other classes overlap with one another. This is radiologically plausible because meningioma can present intensity and boundary characteristics that partially resemble other extra-axial or mass-like structures depending on slice plane and lesion extent.

4.4 Confusion Matrix Interpretation

The confusion matrices provide the clearest picture of model behavior. The confusion matrix of the proposed method is shown in Figure 7. The diagonal values are very strong: 989 correct glioma predictions, 956 correct meningioma predictions, 1066 correct no-tumor predictions, and 1003 correct pituitary predictions out of 1067 cases per class.

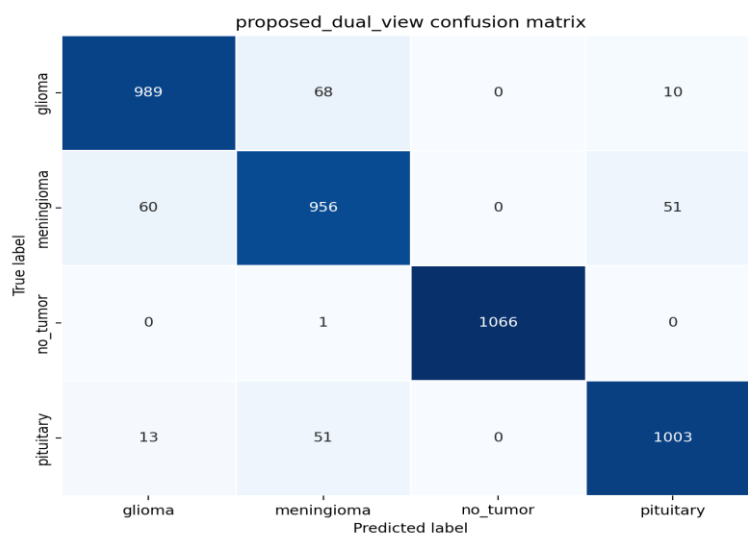


Figure 7 Confusion matrix of the proposed dual-view model

A closer reading of the matrix reveals that the main confusion occurs between meningioma and pituitary, and to a lesser extent between meningioma and glioma. Specifically, among true meningioma cases, 60 are predicted as glioma and 51 are predicted as pituitary. Similarly, among true pituitary cases, 51 are predicted as meningioma. In contrast, the no-tumor class is almost perfectly separated, with only one no-tumor case predicted as meningioma and none confused with glioma or pituitary. This result indicates that the proposed model is extremely strong at identifying whether a lesion exists, while the remaining difficulty lies in differentiating among lesion-bearing tumor subtypes.

For completeness, it is also useful to compare the proposed confusion matrix to the baseline and intermediate ablations. The baseline matrix is much more diffuse, with large off-diagonal counts, especially for meningioma. For example, in the baseline model, only 789 meningioma cases are correctly identified, while 137 are classified as glioma, 45 as no-tumor, and 96 as pituitary. In the proposed method, the number of correctly recognized meningioma cases rises to 956, and the false assignment to no-tumor is eliminated. This is a major practical improvement because it demonstrates that the segmentation-guided dual-view representation suppresses the most clinically undesirable failure mode: mistaking a tumor-bearing scan for a healthy one.

4.5 ROC Analysis and Ranking Quality

Figure 8 shows the ROC curve obtained using the one-vs-rest approach for the proposed model. A macro-ROC-AUC of 0.9916 represents an outstanding ability to rank the instances in the dataset for all the classes. It should be noted that this value is not skewed due to any form of class imbalance since the test dataset is balanced.

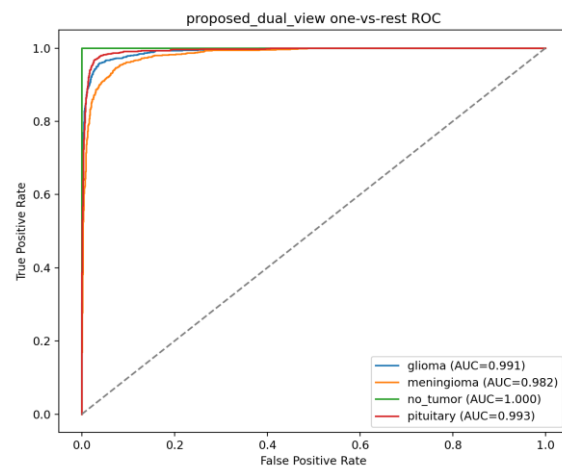


Figure 8 ROC curves for the proposed model.

However, an interesting observation can be made when comparing ROC-AUC with classification accuracy. In terms of ROC-AUC, the full + ROI ablation achieves a slightly better performance than the proposed metadata stream-based approach. However, the classification accuracy and macro F1 score of the former model are relatively worse. It seems that Metadata streams improve the calibration at the final decision step even if the ranking results stay almost the same. Metadata does not help much in separating the classes but helps when a clear label needs to be provided by the model. The training-loss plots show smooth convergence across folds for all experiments, with the ROI-based methods generally converging to lower and more stable loss values than the baseline single-view model. This behavior supports the ablation findings: once lesion-focused information is included, the classifier sees a cleaner and more discriminative feature space, allowing optimization to settle into a better minimum. The baseline, by contrast, must infer tumor type from a larger amount of irrelevant anatomical context, which likely increases representation overlaps among the tumor categories.

4.6 Discussion of the Ablation Study

One of the strongest pieces of evidence used in this study is the ablation study. Moving from baseline full-context features to full-context features augmented by metadata results in an improvement that can be considered moderate. However, the improvement from baseline to full+ROI appears to be much larger, implying that

the main contribution to the performance of the models comes from the lesion-aware localization. Moving to the proposed dual-view model also provides some improvement, thus proving that metadata still plays its role when the representation is good enough.

Three conclusions can be made based on the analysis of evidence presented above. First, preprocessing should never be underestimated in brain tumor classification problems since it significantly affects the performance of the models. Second, a dual view is preferable to a single one as it provides both the context and the lesions. Third, metadata works as an additional signal that increases robustness but cannot substitute lesion-aware representation completely.

4.7 Comparative Interpretation

While the paper does not seek to establish a point of comparison to all previous works due to the differences in dataset, data splitting strategy, and preprocessing techniques used, the performance achieved serves as an indicator of the suitability of the proposed framework in MRI classification with balanced four classes. More importantly, the contribution made by the paper lies in its methodology. The experiments conducted show that achieving a high level of performance is possible through an approach where all the intermediary results are kept and cross-validation is used instead of a one-off data split, alongside the inclusion of results from ablation studies aside from the performance score.

In summary, the results strongly validate the proposed methodology. The balanced cohort design prevented misleading class-frequency effects. The saved preprocessing artifacts confirmed that the first phase successfully preserved both global and lesion-focused information. The ablation study demonstrated that ROI guidance is the dominant source of performance gain. The proposed dual-view framework achieved the best overall accuracy and macro- F_1 , maintained stable fold-wise behavior, and produced confusion matrices with very strong

diagonal dominance. Taken together, these results show that segmentation-guided preprocessing and dual-view feature fusion are effective and practically meaningful strategies for multi-class brain tumor MRI classification.

5. Conclusion

The present study proposes a repeatable two-step pipeline for multi-class brain tumor classification using MRI scans, which integrates segmentation-guided data preprocessing with dual-channel feature extraction. Contrary to traditional unidirectional pipelines relying primarily on global appearance patterns, the proposed algorithm retains both whole-brain context and lesion-specific local cues by creating and storing full-context images, ROIs, and preprocessed masks before the classification stage. As shown below, the combination of deep features extracted separately for the two views, along with metadata containing imaging plane and mask-related information, delivers the best average performance among all studied variants. Using a well-balanced set of 4,268 images and three-fold cross-validation stratified by class, the pipeline attains accuracy of 94.05%, macro F1-score of 94.05%, and macro ROC-AUC score of 0.9916, showing stable fold-by-fold metrics and highly comprehensible confusion matrices featuring clear diagonal dominance. In particular, the ablation study suggests that ROI-based information serves as the primary source of improvements, whereas metadata contributes to decision-making to a lesser degree. While there is still some residual confusion between meningioma and other tumors, the framework allows for nearly perfect differentiation of normal brain MRI scans. Overall, the present research highlights the importance of proper preprocessing, well-balanced data, and evaluation criteria as much as classifier architecture when building models for brain tumor classification based on MRI scans. The future direction of development may involve end-to-end tuning, more advanced attention mechanisms for feature fusion, multi-slice models, and independent testing.

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