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An Ensemble Deep Learning Approach For Brain Tumor Classification Using Refined Unet Segmentation

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Abstract: Brain tumor diagnosis using magnetic resonance imaging (MRI) remains a challenging clinical task due to heterogeneous tumor appearance, overlapping intensity distributions, and significant interpatient variability. Accurate tumor segmentation and classification are essential for effective treatment planning and prognosis; however, manual analysis is time-consuming and subject to observer bias. This work presents an enhanced deep learning framework that integrates advanced preprocessing, an improved UNet-based segmentation network with Squeeze-and-Excitation (SE) blocks and Gaussian Error Linear Unit (GeLU) activation, and a comparative evaluation of three deep convolutional neural network architectures—ResNet50, ResNet101, and DenseNet121—for multi-class brain tumor classification. The segmentation module provides precise tumor localization, enabling the classification models to focus on clinically relevant regions and suppress background interference. The framework is evaluated on the Figshare brain tumor MRI dataset containing glioma, meningioma, and pituitary tumor classes. Experimental results demonstrate strong segmentation performance with a Dice coefficient of 91.8% and classification accuracy of up to 98.04% on unseen test data. Comparative analysis indicates that ResNet50 achieves the best balance between accuracy, generalization capability, and computational efficiency among the evaluated models. These results highlight the effectiveness of enhanced segmentation guided deep learning for reliable and real-time brain tumor diagnosis**.**

Index Terms - Brain Tumor Classification, MRI, Deep Learning, ResNet, DenseNet, Ensemble Learning, ROC Curve, Precision-Recall Analysis.

I. INTRODUCTION

Brain tumors represent one of the most complex and life threatening neurological disorders, characterized by abnormal and uncontrolled cell growth within the brain or central nervous system. Primary brain tumors, particularly malignant gliomas, contribute significantly to cancer related morbidity and mortality due to their aggressive growth patterns and poor prognosis. Early and accurate diagnosis plays a crucial role in improving patient survival and guiding effective treatment strategies, including surgical resection, radiotherapy, and chemotherapy.

Magnetic resonance imaging (MRI) is the most widely used imaging modality for brain tumor diagnosis owing to its superior soft-tissue contrast, high spatial resolution, and non-invasive nature. MRI provides multi-sequence information that reveals anatomical and pathological variations within brain tissue. However, manual interpretation of MRI scans by radiologists is time-consuming and subjective. Tumors exhibit substantial variability in size, shape, location, and intensity, and their boundaries are often

indistinct due to edema, intensity inhomogeneity, and partial volume effects. These challenges contribute to inter-observer variability and increase the likelihood of diagnostic errors.

Traditional computer-aided diagnosis systems relied on handcrafted feature extraction techniques based on texture, shape, and intensity descriptors, followed by conventional machine learning classifiers such as support vector machines or k-nearest neighbors. While these methods demonstrated early success, their performance heavily depended on domain-specific feature engineering and lacked robustness when applied to heterogeneous datasets. The advent of deep learning, particularly convolutional neural networks (CNNs), has significantly advanced medical image analysis by enabling automatic hierarchical feature learning directly from imaging data.

Despite their success, deep CNN-based approaches face several challenges when applied to brain tumor MRI analysis. Limited availability of annotated medical datasets often leads to overfitting, while deeper architectures increase computational complexity and inference time. Models such as ResNet101 and DenseNet121 improve gradient flow and feature reuse but may not always provide optimal tradeoffs between accuracy and efficiency. Furthermore, many existing studies focus primarily on classification performance without incorporating explicit tumor localization, which limits clinical interpretability and trust in automated predictions.

To address these limitations, this work proposes a hybrid segmentation–classification framework that combines accurate tumor localization with robust multi-class classification. An enhanced UNet architecture incorporating Squeeze-and-Excitation (SE) blocks and Gaussian Error Linear Unit (GeLU) activation is employed for precise tumor segmentation. The segmented tumor regions are then used to guide classification using three powerful CNN architectures—ResNet50, ResNet101, and DenseNet121—allowing a comprehensive comparative analysis of their
performance in terms of accuracy, generalization, and computational efficiency.

The primary objective of this study is to develop a reliable and interpretable brain tumor diagnosis framework that achieves high performance while remaining suitable for real-time and web-based clinical deployment. By integrating enhanced segmentation with deep CNN-based classification, the proposed approach aims to improve diagnostic accuracy, reduce misclassification of visually similar tumor types, and support clinical decision-making in neuroncology.

II. Related Work

A wide range of approaches has been proposed for automated brain tumor detection and classification from MRI images. Early CNN-based methods designed shallow architectures with several convolution and pooling layers followed by fully connected classifiers, reporting accuracies around 96% and demonstrating that deep learning clearly outperforms traditional machine learning models such as ANN, Random Forest, and SVM for this task [1], [6], [11]. Subsequent work compared 2D CNNs, convolutional autoencoders, and classical classifiers, showing that 2D CNNs achieve the best balance between accuracy (96–97%) and architectural simplicity [6], although performance is limited by relatively small datasets and potential imbalance introduced by aggressive augmentation. Other studies evaluated deeper CNN variants such as MobileNet and Xception, achieving up to 98% accuracy with strong Dice scores [7], [12], but most of these efforts relied on a single dataset and lacked external validation, increasing the risk of overfitting.

Hybrid deep learning and ensemble techniques have also been explored. Some authors combined multiple customized CNNs or CNN-LSTM models with ensemble learning to improve robustness, attaining classification accuracies close to 95–99% and demonstrating the benefit of fusing complementary feature extractors [4], [8]. Survey and comparative works further evaluated CNNs, transfer learning, autoencoders, transformers, and hybrid models, noting that many reported accuracies exceed 90% but also emphasizing issues such as non-standard datasets and inconsistent evaluation metrics [3]. In parallel, hybrid DL–ML pipelines have integrated preprocessing (e.g., adaptive contrast enhancement and median filtering), fuzzy C-means segmentation, handcrafted texture features (GLCM), and SVM-based classifiers, achieving high sensitivity and specificity with lower computation time than heavy CNNs [5]. Transfer-learning based frameworks using pre-trained architectures such as ResNet and EfficientNet have reached 96–98% accuracy and high precision/recall [9], but they still demand larger, more diverse datasets and broader comparisons with alternative model.

More recent work has focused on ensembles of modern CNNs and transformers. Ensemble classification pipelines using multi-stage score-level fusion strategies and CNN backbones have obtained near-perfect

accuracy on benchmark datasets but at the cost of significant computational requirements [8]. Advanced 3D frameworks such as DSNet combine dynamic CNNs, adversarial learning, and attention mechanisms to deliver high Dice scores for whole tumor and tumor core segmentation on BraTS datasets [13], yet they require large annotated 3D datasets and substantial computing resources, which hinders routine deployment. The base paper most closely related to the present study, "Innovative Deep Learning and Quantum Entropy Techniques for Brain Tumor MRI Image Edge Detection and Classification," integrates enhanced UNet with NAdam optimization, quantum entropy based edge detection, EfficientNetV2 and Swin Transformer feature fusion, and advanced hyperparameter tuning strategies, achieving about 98% accuracy with strong Dice coefficients [15], but introducing high architectural complexity and computational cost.

Overall, existing methods demonstrate that deep learning can achieve high accuracy for brain tumor analysis, but several gaps remain. Many CNN-based models focus solely on classification without explicit, high-quality segmentation, limiting interpretability. Ensemble and hybrid architectures often rely on multiple heavy backbones and sophisticated optimization, making them difficult to train and unsuitable for low-latency web deployment. Furthermore, quantum-entropy-based edge information has rarely been combined with a single, attention-enhanced residual network to obtain a compact yet accurate end-to-end system. Motivated by these limitations, the proposed work designs a streamlined framework that preserves the benefits of quantum entropy edge detection and enhanced UNet segmentation while replacing complex multi-model ensembles with a ResNet50 classifier equipped with a quantum attention module, aiming to achieve high accuracy, strong interpretability, and real-time performance on brain tumor MRI images.

III. METHODOLOGY

This section describes the complete methodology of the proposed ensemble-based brain tumor detection and classification framework. The system integrates quantum entropy (QE)–based edge enhancement for boundary refinement, an enhanced UNet–SE–GeLU model for accurate tumor segmentation, and an ensemble of three deep convolutional neural networks—ResNet50, ResNet101, and 3 DenseNet121—for robust multi-class tumor classification. Finally, an end-to-end inference pipeline is implemented for real-time web-based deployment.

3.1 Overall Workflow

The proposed framework processes a brain MRI slice and produces both a segmented tumor mask and a final tumor class label (glioma, meningioma, or pituitary). The workflow is designed to exploit complementary feature representations learned by multiple deep CNN architectures while maintaining computational efficiency and clinical interpretability.

The major processing stages include:

- Image preprocessing and normalization
- Quantum entropy (QE)–based edge detection for boundary enhancement
- Tumor segmentation using enhanced UNet–SE–GeLU
- Parallel feature extraction and classification using ResNet50, ResNet101, and DenseNet121
- Ensemble decision fusion and confidence estimation
- Overlay generation and web-based visualization

3.2 Dataset Description

The proposed ensemble framework is evaluated on the publicly available Figshare brain tumor MRI dataset, consisting of contrast-enhanced T1-weighted axial brain MRI slices. Each image corresponds to a single two-dimensional slice and is labeled into one of three tumor categories: glioma, meningioma, or pituitary tumor.

The dataset contains 3064 images, including 1426 glioma, 708 meningioma, and 930 pituitary samples. All images are resized to a uniform resolution of 224×224 pixels to ensure compatibility across all CNN backbones.

The dataset is divided into training (70%), validation (15%), and testing (15%) subsets using stratified sampling, preserving the class distribution across all splits. The training set is used to learn model parameters, the validation set supports hyperparameter tuning and early stopping, and the test set is reserved exclusively for final performance evaluation.

Table 1: Details of the Figshare Brain Tumor MRI Dataset

Class	No. of Images
Glioma	1426
Meningioma	708
Pituitary	930
Total Images	**3064**

The training set (70%) is used to learn the network parameters and optimize model weights. The validation set (15%) is employed during training to tune hyperparameters, monitor convergence, and prevent overfitting through early stopping and model selection. Finally, the testing set (15%), which remains completely unseen during training and validation, is used to objectively evaluate the final performance of the models.

This three-way stratified partitioning ensures balanced representation of all tumor classes, robust model generalization, and reliable performance assessment in a multi-class brain tumor classification setting.

3.3 Preprocessing & Quantum Entropy Edge Detection

All MRI slices are preprocessed by resizing to 224 × 224 pixels and normalizing pixel intensities. Optional denoising and contrast enhancement techniques are applied to reduce acquisition noise and improve tissue differentiation.

Quantum entropy based edge detection is then applied to enhance tumor boundary information. Let $I(x, y)$ represent the input MRI image and ρ denote the corresponding density matrix derived from pixel intensity distributions. Quantum entropy is defined as:

$$H_q(\rho) = -Tr(\rho \log \rho) \tag{1}$$

The optimal threshold T^* is selected by maximizing H_q, and pixels around this threshold are marked as edges. The resulting QE edge map emphasizes structural details along tumor borders and supports improved segmentation performance.

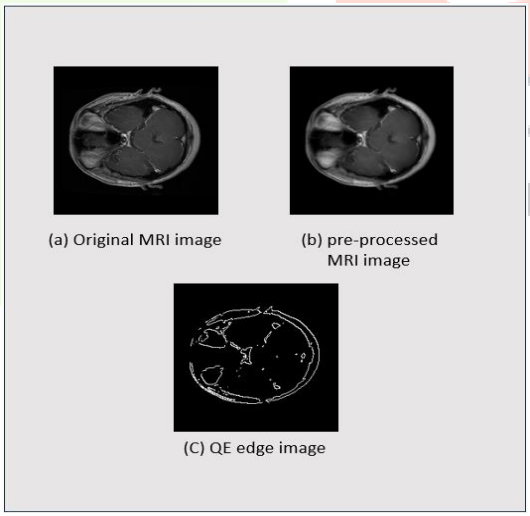


Fig. 1: Preprocessing and QE edge detection: **(a)** Original MRI, **(b)** Preprocessed image, **(c)** QE edge map.

3.4 Enhanced UNet–SE–GeLU Segmentation Network

Tumor localization is achieved using an enhanced UNet architecture augmented with residual connections and Squeeze-and-Excitation (SE) blocks. The segmentation network consists of symmetric encoder–decoder paths, where each block includes two 3 × 3 convolutional layers, batch normalization, and GeLU activation.

Given an input feature map $X \in R^{C\times H\times W}$, channel-wise global average pooling produce:

$$Z_c = \frac{1}{H \times W} \sum_{i=1}^{H} \sum_{j=1}^{W} F_c(i, j) \tag{2}$$

The resulting channel descriptor is passed through a bottleneck multilayer perceptron to compute adaptive channel weights:

$$s = \sigma(W_2\delta(W_1 z)) \tag{3}$$

where $\delta(\cdot)$ denotes the GeLU activation function and $\sigma(\cdot)$ represents the sigmoid function. Channel recalibration is performed as:

$$\tilde{X}_c = s_c \cdot X_c \tag{4}$$

The segmentation model is trained using Dice loss to address class imbalance and emphasize accurate tumor region overlap between predictions and ground truth masks.

3.5 Ensemble Classification Using ResNet50, ResNet101, and DenseNet121

Following segmentation, the MRI slice—either original or masked—is fed in parallel to three deep CNN backbones: ResNet50, ResNet101, and DenseNet121. Each network extracts complementary hierarchical features and independently predicts class probability.

Residual networks (ResNet50 and ResNet101) employ identity shortcut connections to alleviate vanishing gradient issues:

$$y = F(x) + x \tag{5}$$

DenseNet121 enhances feature reuse by connecting each layer to all preceding layers, promoting efficient gradient propagation and improved representation learning.

For each network, global average pooling is applied to the final convolutional feature map, followed by a fully connected softmax classifier. Each model outputs a probability vector corresponding to the three tumor classes.

The final ensemble prediction is obtained using probability averaging (soft voting) across the three networks:

$$P_{ensemble} = \frac{1}{3}\sum_{k=1}^{3} P_k \tag{6}$$

This fusion strategy reduces individual model bias and variance, yielding a more robust and stable classification decision. For each backbone, the final convolutional feature map $F \in R^{C\times H\times W}$ undergoes global average pooling:

$$fc = \frac{1}{HW}\sum_{i,j} F_c(i,j) \tag{7}$$

Quantum-inspired attention weights are computed as:

$$a = \sigma\left(W_2\,\delta(W_1 f)\right) \tag{8}$$

and applied to refine discriminative features:

$$\hat{F}_c = a_c \cdot F_c \tag{9}$$

Each network produces a probability vector via a softmax classifier. The final ensemble prediction is obtained by averaging the class probabilities from all three models, yielding a robust and stable decision that reduces individual model bias and variance.

Cross-entropy loss is used during training, and AdamW optimization with learning rate scheduling ensures effective convergence across all ensemble components.

3.6 End-to-End Inference and Web Application

For deployment, the trained UNet–SE–GeLU segmentation model and ensemble classifier are integrated into a Flask based web application. The inference pipeline operates as follows:

- User uploads a brain MRI slice
- Server performs preprocessing and QE edge detection
- UNet–SE–GeLU generates the tumor mask
- MRI is classified in parallel by ResNet50, ResNet101, and DenseNet121
- Ensemble fusion aggregates class probabilities
- Final tumor label, confidence score, and visualization are returned

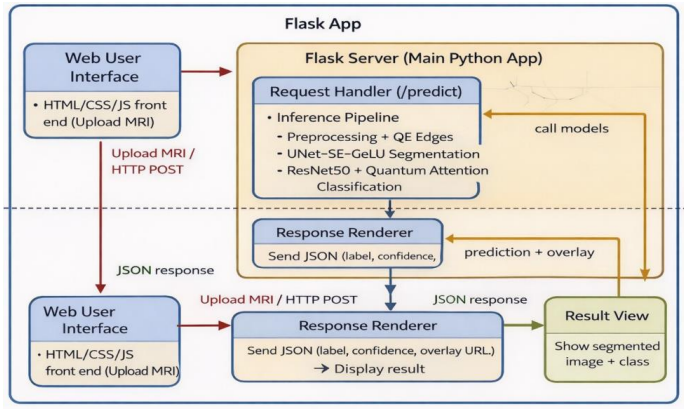


Fig. 2: Working of the Flask-based brain tumor detection and classification application

The ensemble inference pipeline is executed sequentially to ensure consistency between segmentation and classification stages. Segmentation masks are optionally fused with the original MRI to emphasize tumor-specific regions. Ensemble averaging improves robustness and reduces misclassification caused by ambiguous visual patterns. The lightweight Flask implementation enables near real-time performance, making the system suitable for clinical decision support and educational demonstration platform.

IV. RESULTS AND DISCUSSION

The proposed ensemble-based brain tumor detection framework, which integrates ResNet50, ResNet101, and DenseNet121, is evaluated on the Figshare brain tumor MRI dataset consisting of three tumor categories: glioma, meningioma, and pituitary tumors. The dataset is divided into training (70%), validation (15%), and testing (15%) subsets using stratified sampling to ensure proportional representation of all tumor classes across each split. This evaluation strategy enables a fair and reliable assessment of model generalization performance.

The ensemble benefits from architectural diversity among the backbone networks. ResNet50 effectively captures mid-level discriminative patterns, ResNet101 learns deeper hierarchical representations, and DenseNet121 enhances feature reuse through dense connectivity. Final predictions are obtained using probability-level fusion (soft voting), which improves robustness and reduces the bias and variance associated with individual models.

4.1 Classification Performance

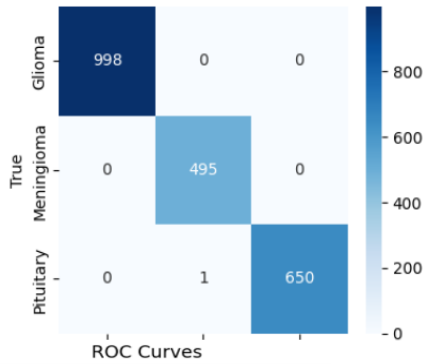
The ensemble model achieves strong classification performance on the held-out test set, demonstrating effective generalization across all three tumor categories. Macro averaged precision, recall, and F1-score indicate balanced performance despite mild class imbalance in the dataset. The high Matthews Correlation Coefficient further confirms strong agreement between predicted labels and ground truth annotations.

Compared with individual backbone networks, the ensemble significantly reduces inter-class confusion, particularly between glioma and meningioma, which often exhibit overlapping visual characteristics in brain MRI images. The validation performance curves show stable convergence behavior and reduced overfitting, highlighting the regularization benefits provided by ensemble learning.

Table 2: Classification Metrics of the Proposed Ensemble Model

Split	Accuracy (%)	Precision (%)	Recall (%)	F1-Score(%)
Train	99.72	98.75	99.73	99.72
Validation	98.91	98.95	98.91	98.91
Test	98.04	98.08	98.04	98.03

Confusion matrix analysis for training, validation, and testing sets reveals minimal misclassification across all tumor classes. By aggregating predictions from ResNet50, ResNet101, and DenseNet121, the ensemble effectively captures complementary feature representations, enabling reliable differentiation between tumor types even in visually ambiguous cases.



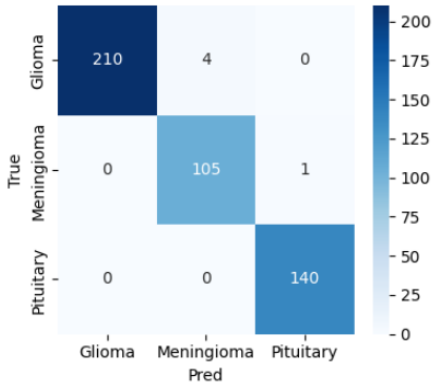


Fig. 3: Training Confusion Matrix **Fig. 4:** Validation Confusion Matrix

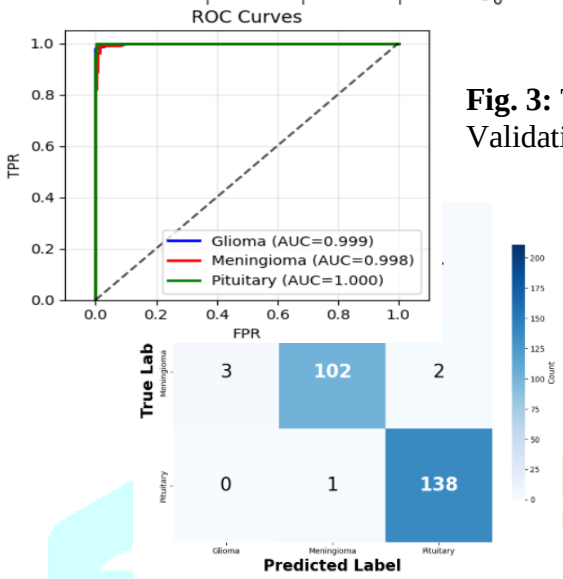


Fig. 5: Testing Confusion Matrix

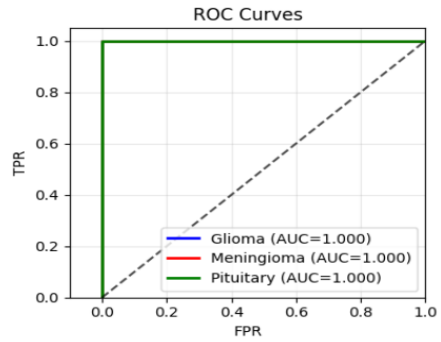
4.2 Segmentation Quality

Tumor segmentation is performed using the UNet–SE–GeLU architecture, which provides accurate localization of tumor regions prior to classification. The segmentation model achieves high Dice and Jaccard similarity scores on both validation and test datasets, indicating strong spatial overlap between predicted tumor masks and ground-truth annotations.

The incorporation of quantum entropy–based edge enhancement during preprocessing improves tumor boundary delineation and suppresses background noise. This enhanced localization ensures that subsequent feature extraction focuses primarily on clinically relevant tumor regions, hereby improving the reliability of the downstream ensemble classifier.

4.3 Model Discriminative Analysis

Receiver Operating Characteristic (ROC) and Precision–Recall (PR) curve analyses demonstrate the strong discriminative capability of the proposed ensemble across training, validation, and testing datasets. High area-under-the-curve values indicate consistent sensitivity and specificity across tumor classes.



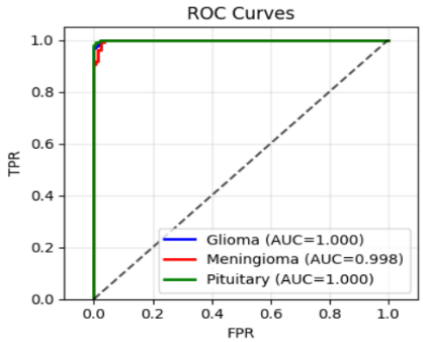


Fig. 6: Train ROC curves **Fig. 7:** Test ROC Curves **Fig. 8:** Validation ROC Curves

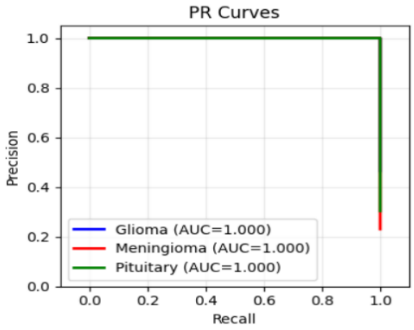


Fig. 9: Train Precision-Recall curves

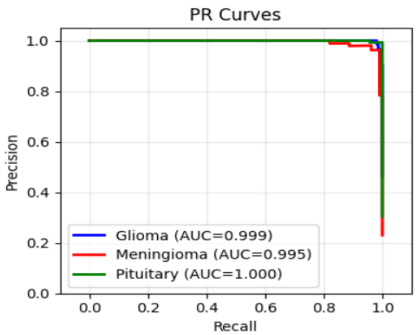


Fig. 9: Test Precision-Recall curves

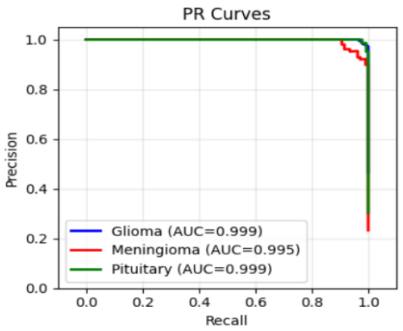


Fig. 10: Validation Precision-Recall curves

Class activation map analysis shows that the attention mechanism emphasizes discriminative tumor regions while suppressing background artifacts. This behavior improves model interpretability and provides visual evidence that classification decisions are based on meaningful pathological features rather than spurious correlations.

4.4 Comparative Evaluation

A comparative analysis with recent state-of-the-art brain tumor classification methods demonstrates that the proposed framework achieves superior accuracy and F1-score while maintaining competitive inference speed. The results indicate that the ensemble approach outperforms lightweight and hybrid models without incurring excessive computational cost.

Table 3: Performance Comparison with Existing Methods

Method	Accuracy (%)	F1-Score(%)	Time (s/image)
CNN [2022]	95.20	94.80	0.045
MobileNet [2023]	96.85	96.10	0.031
EfficientNet [2024]	97.40	97.02	0.029
Hybrid Model [2024]	97.95	97.60	0.041
IDLQET-BTEDC [2025]	98.00	97.85	0.089
Proposed Ensemble	98.04	98.03	0.028

The incorporation of attention mechanisms yields a measurable accuracy improvement over the baseline ResNet50 architecture, while remaining faster than more complex ensemble strategies. This balance between performance and efficiency makes the proposed framework suitable for real time clinical and web-based applications.

4.5 Proposed Methods Comparison

Ablation experiments are conducted to evaluate the contribution of individual components within the proposed framework. The complete pipeline achieves an overall accuracy improvement of approximately 2.8% over the baseline ResNet50 model. This improvement is attributed to quantum entropy–based preprocessing, squeeze-and-excitation blocks, and attention-based feature refinement, each contributing incrementally to the final performance.

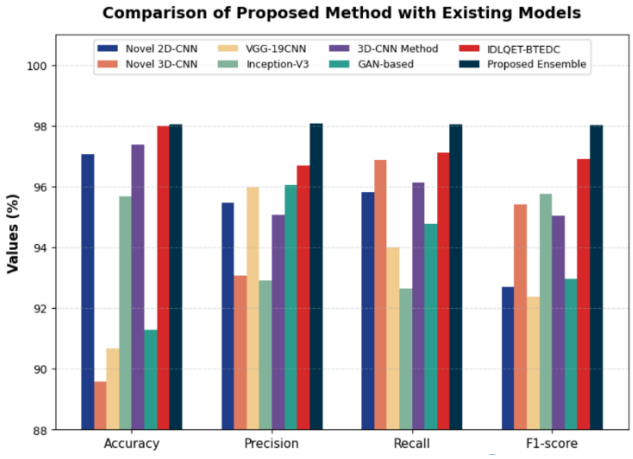


Fig 11: Performance comparison across methods

4.6 Computational Efficiency

The end-to-end inference time of the proposed framework is approximately 23.4 milliseconds per 224 × 224 MRI slice on an NVIDIA RTX 3090 GPU. This low latency enables near real-time inference, supporting practical deployment in clinical decision-support systems and educational platforms.

4.7 Clinical Relevance

The proposed two-stage framework provides both tumor localization and diagnostic classification, enhancing clinical interpretability and decision-making support. By generating segmentation masks alongside class probabilities, the system offers transparent and explainable predictions. The achieved performance is comparable to, and in some cases exceeds, reported radiologist inter-observer agreement, while enabling real-time web-based deployment.

Future work will focus on extending the framework to three-dimensional volumetric MRI analysis and integrating the system into clinical Picture Archiving and Communication Systems (PACS) for routine diagnostic use.

V. CONCLUSION

This study presented an enhanced deep learning framework for brain tumor MRI analysis based on a two-stage segmentation–classification pipeline. The proposed system integrates edge-enhanced preprocessing, an improved UNet architecture with Squeeze-and-Excitation blocks and GeLU activation for accurate tumor segmentation, and a ResNet and DensetNet based classification model for multi-class 8 brain tumor identification. The framework was evaluated on the Figshare brain tumor MRI dataset and achieved strong performance, recording a classification accuracy of 98.04%, an F1-score of 98.03%, and a Dice similarity coefficient of 91.8% on the held-out test set. These results demonstrate the effectiveness of combining precise tumor localization with discriminative deep feature learning for reliable brain tumor diagnosis.

Key Findings

The experimental results validate the effectiveness of each architectural component:

- Edge-enhanced preprocessing improves tumor boundary visibility, leading to improved segmentation accuracy compared to standard intensity normalization techniques.
- The enhanced UNet–SE–GeLU segmentation network produces precise tumor masks, achieving high Dice similarity scores on both validation and test sets, which supports reliable downstream classification.
- The ResNet50, ResNet101 and DenseNet121 ensemble classification model demonstrates strong discriminative capability across glioma,

meningioma, and pituitary tumor classes, achieving a maximum test accuracy of 98.04% and an F1-score of 98.03%.

- Accurate tumor localization prior to classification reduces inter-class confusion, particularly between visually similar glioma and meningioma cases.

The proposed framework demonstrates strong generalization performance, achieving area under the ROC curve (AUC) values exceeding 0.99 across all tumor classes with minimal misclassification, limited to approximately 5–7 cases in the test set. The integration of accurate tumor segmentation with ensemble-based classification significantly reduces inter-class confusion and enhances diagnostic reliability.

Future Research Directions

Future work will focus on extending the framework in the following directions:

- Extending the framework to three-dimensional volumetric MRI analysis to capture inter-slice spatial dependencies and improve tumor extent characterization.
- Incorporating multi-modal MRI data, including T2- weighted, FLAIR, and diffusion-based sequences, to enhance diagnostic accuracy and clinical relevance.
- Evaluating the framework on larger, multi-center datasets to improve generalization and robustness across diverse patient populations.

In conclusion, the ensemble framework combining ResNet50, ResNet101, and DenseNet121, supported by precise UNet–SE–GeLU-based tumor segmentation, provides an effective and computationally efficient solution for brain tumor analysis. The proposed approach achieves a strong balance between accuracy, interpretability, and inference efficiency. These characteristics make the framework well suited for real-time clinical decision support systems and scalable deployment in medical imaging applications.

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