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An optimized deep learning framework for brain tumor classification using magnetic resonance imaging

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ABSTRACT

Accurate and interpretable classification of brain tumors in magnetic resonance imaging (MRI) scans plays a crucial role in early diagnosis and effective treatment planning. This study introduces a deep learning (DL) framework based on a customized YOLOv5m architecture integrated with a bidirectional feature pyramid network (BiFPN) for multi-class brain tumor classification. The integration of BiFPN enhances multi-scale feature fusion, improving detection across varied tumor types, while YOLOv5m ensures real-time inference capabilities. To mitigate class imbalance, a class-weighted cross-entropy loss is adopted. The model is evaluated on multiple performance metrics, achieving a test accuracy of 88.86%, precision of 88.70%, recall of 88.20%, and F1-score of 88.25%. It also reports a mean average precision (mAP@0.5) of 94.36%, with high class-wise average precision (AP) for glioma, meningioma, pituitary, and no-tumor categories. Computational time for training (12484.81 seconds) and testing (146.82 seconds) confirms the model's feasibility for real-time clinical deployment. To support interpretability, gradient-weighted class activation mapping (Grad-CAM) is integrated for visualizing class-discriminative regions, helping clinicians understand the model's predictions. A gradio-based user interface is also developed, enabling intuitive interaction with the system.

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1. INTRODUCTION

Brain tumors remain among the most critical and life-threatening neurological disorders, necessitating early and accurate diagnosis to improve patient outcomes. Magnetic resonance imaging (MRI) is the standard non-invasive modality for brain tumor detection due to its high spatial resolution and tissue contrast. However, manual interpretation of MRI scans is time-consuming and susceptible to inter-observer variability. To address these challenges, deep learning (DL) techniques have emerged as powerful tools for automating brain tumor classification and segmentation tasks.

Recent advancements in hybrid and transformer-based models have significantly improved classification accuracy and interpretability. Ahmed *et al.* [1] proposed a hybrid vision transformer (ViT) and gated recurrent unit (GRU) architecture for brain tumor detection in Southern Bangladesh, emphasizing explainable artificial intelligence (XAI) for clinical transparency. Sun *et al.* [2] explored a combination of

YOLOv8 and data efficient image transformer (DeiT) to achieve anomaly-aware diagnosis, demonstrating the potential of real-time object detection models in medical imaging. These innovations reflect a growing interest in leveraging object detection frameworks like YOLO for tumor localization and classification.

Traditional convolutional neural networks (CNNs) have dominated the literature from 2015 to 2020, as reviewed by Nazir *et al.* [3], but more recent architectures incorporate attention mechanisms and multiscale features. For example, IRNetv [4] and Arm-Net [5] use attention-guided modules and residual connections to extract richer representations of tumor regions. Solanki *et al.* [6] presented a comprehensive overview of intelligent techniques for brain tumor classification, highlighting the critical role of computational efficiency and diagnostic reliability. Talukder *et al.* [7] proposed a transfer learning-based approach for brain tumor categorization. Furthermore, deep semantic segmentation frameworks like DeepLabV3 [8] and optimized CNN variants such as ESRNet [9] have pushed the boundaries of automated brain tumor grading.

Despite these advancements, a gap remains in achieving a balance between detection speed, interpretability, and classification precision. To bridge this gap, our work integrates the YOLOv5m backbone with a bidirectional feature pyramid network (BiFPN) for enhanced feature fusion and tumor localization. The classification head is designed to handle multi-class brain tumor recognition, while gradient-weighted class activation mapping (Grad-CAM) is employed for visual explanation of model decisions, aligning with the growing demand for XAI in healthcare [10].

This study further incorporates weighted loss functions to address class imbalance. Its performance is evaluated using metrics such as accuracy, precision, recall, F1-score, and mean average precision (mAP@0.5). Compared to existing models, the proposed approach offers an effective trade-off between computational speed and classification accuracy, making it a viable solution for real-time brain tumor diagnosis in clinical settings.

The paper is structured as follows. Section 2 discusses related works. Section 3 outlines the proposed methodology, section 4 presents experimental analysis and findings, and section 5 concludes study.

2. RELATED WORKS

Brain tumor detection and classification using MRI images has garnered significant attention in recent years, especially with the advent of DL techniques. Numerous studies have proposed advanced models for improving diagnostic accuracy, efficiency, and interpretability. Ali *et al.* [11] introduced an evolutionary CNN to optimize feature learning for tumor detection, outperforming conventional CNN architectures. Similarly, Kumar *et al.* [12] presented a hybrid boosted ensemble learning approach that combined multiple deep learners to enhance the robustness of Alzheimer's analysis. The application of pure DL strategies has also been explored extensively. Liu and Wang [13] demonstrated the impact of advanced CNN architectures in MRI-based brain tumor classification, showing that model depth and data quality significantly affect performance. Pokhrel *et al.* [14] utilized deep CNNs specifically trained on MRI images for classification tasks, achieving high accuracy across multiple tumor types.

Bouhafra and Bahi [15] conducted a systematic review of DL techniques from 2020 to 2024, summarizing progress in classification, segmentation, and generalization across multiple datasets. Complementarily, Kumar *et al.* [16] reviewed a broader range of intelligent techniques, including CNNs, ensemble methods, and hybrid approaches. A variety of novel architectures have been proposed to tackle multi-class brain tumor classification challenges.

Beyond DL, earlier methods utilized traditional machine learning with handcrafted features and optimization strategies. For instance, the authors [17], [18] applied particle swarm optimization and artificial bee colony algorithms for MRI classification. Other notable approaches include wavelet-based support vector machine (SVM) classification [19], spider-web plotting techniques [20], genetic pattern search algorithms [21], and hybrid models combining optimization and neural networks [22]. Givian and Calbimonte [23] reviewed a non-invasive MRI-based approach for detecting neurocognitive disorders by extracting disease-specific feature vectors.

Napa *et al.* [24] introduced a meta-ensemble framework for brain tumor using independent region-of-interest (ROI) features extracted from T1-weighted MRI scans. By combining multiple classifier ensembles trained on anatomically defined ROIs, their approach achieved improved diagnostic performance and highlighted the most discriminative brain regions. Moreno *et al.* [25] proposed an ensemble-based brain tumor classification using transfer learning and an ensemble strategy.

Chauhan *et al.* [26] proposed a hybrid learning framework for cervical cancer diagnosis that integrates progressive image resizing, deep transfer learning, and principal component analysis for feature reduction. Their approach combines fine-tuned CNN models with classical machine learning classifiers using ensemble voting, achieving very high classification accuracy on whole slide images. The study highlights the effectiveness of hybrid deep–machine learning pipelines in enhancing diagnostic performance, particularly

when optimized feature selection and ensemble strategies are employed. Various ensemble methods have also shown promise in medical image analysis. The authors [27], [28] proposed fuzzy rank-based ensembles of CNNs for cytology and MRI segmentation. Another authors [29], [30] explored triplanar ensemble models for brain tumor segmentation and white matter hyperintensities.

The success of these approaches highlights the transition from handcrafted feature extraction to automated, high-dimensional DL methods. This transition has also led to a growing emphasis on model interpretability, computational efficiency, and multi-class classification capability. This study builds upon these insights by proposing a YOLOv5m-BiFPN-based brain tumor classification model integrated with Grad-CAM for visual explanation, emphasizing both accuracy and explainability in a real-time setting.

3. METHOD

The proposed methodology introduces a robust DL framework for multi-class brain tumor classification using a modified YOLOv5m architecture integrated with a BiFPN, as shown in Figure 1. The YOLOv5m backbone efficiently extracts rich spatial and semantic features from MRI images, while BiFPN refines and fuses multi-scale features through bidirectional pathways. This design enhances feature representation and enables effective handling of tumor size variability, complex structures, and heterogeneous textures in brain MRI scans.

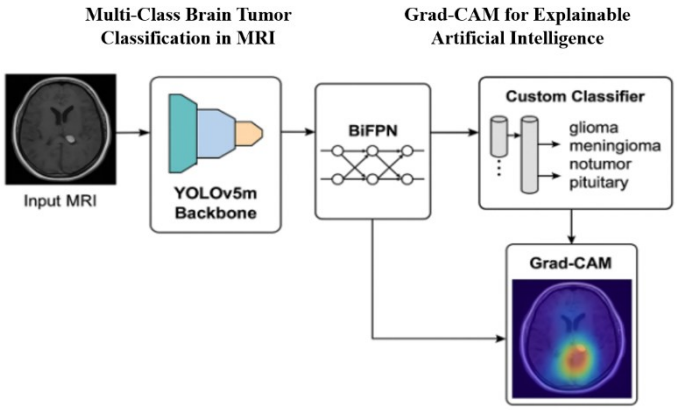


Figure 1. YOLOv5m with BiFPN and Grad-CAM visual interpretability framework

The experiments utilized the publicly available brain tumor MRI dataset [31] from Kaggle, consisting of two-dimensional MRI images categorized into four classes: glioma, meningioma, pituitary tumor, and no tumor. The dataset includes 7,023 images, divided using an 80%–20% split for training and testing. The training set contains 5,712 images, while the test set includes 1,311 images. Table 1 summarizes the dataset features, descriptions, and class-wise distribution.

Table 1. Dataset features, descriptions, and ranges

Feature	Description	Range/values
Training	Axial T1-weighted contrast-enhanced MRI scan of the brain	Grayscale or RGB, resolution varies (resized to 224×224)
Class label	Tumor category assigned to each image	glioma, meningioma, pituitary, notumor
Dataset split	Indicates whether the image is part of the training or testing set	Training, testing
File format	Image format of MRI scans	.jpg, .png
Image size	Dimensions of the original images (varies across samples)	Varies (standardized to 224×224 during preprocessing)
Intensity values	Pixel intensity values of MRI images	0–255 (normalized to -1 to 1 during preprocessing)

To enhance generalization and reduce overfitting, comprehensive data preprocessing and augmentation strategies were applied. All MRI images were resized to 224×224 pixels to satisfy the input requirements of the YOLOv5m backbone. During training, data augmentation techniques including random

horizontal flipping, rotations within ±15°, and brightness and contrast adjustments were employed to simulate variations commonly observed in MRI acquisition. Pixel values were normalized to the range [–1, 1] using a mean and standard deviation of 0.5, which ensured numerical stability and faster convergence. For the test set, only resizing and normalization were applied to maintain evaluation consistency. To address class imbalance, a class-weighted cross-entropy loss based on inverse class frequencies was used. The model was optimized using the Adam optimizer with an initial learning rate of 1×10^{-4}, and a step-based learning rate scheduler that reduced the learning rate by half every five epochs to promote stable training. Batch normalization layers further contributed to regularization and improved convergence. To evaluate robustness and generalizability, 10-fold cross-validation was performed, and performance metrics were averaged across folds. Model evaluation was conducted using accuracy, precision, recall, and F1-score, along with computational time analysis. The dataset was loaded using PyTorch's ImageFolder utility and processed in mini-batches to enable efficient graphics processing unit (GPU)-accelerated training.

Computational efficiency was assessed on a Google Colab environment equipped with an NVIDIA Tesla T4 GPU and 16 GB RAM. The model was trained for 20 epochs with a batch size of 32, achieving an average training time of 624.24 seconds per epoch and a total training time of 12,484.81 seconds. During inference, the model required 146.82 seconds to process the full test set of 1,311 images, corresponding to an average inference time of 0.11 seconds per image. Additionally, Grad-CAM was integrated to provide visual interpretability by highlighting discriminative tumor regions influencing predictions. A gradio-based interface was developed to enable real-time tumor classification and visualization, supporting clinical usability. Overall, the proposed framework achieves a strong balance between accuracy, interpretability, and computational efficiency, making it suitable for clinical decision support applications.

4. RESULTS AND DISCUSSION

4.1. Proposed model using YOLOv5m with BiFPN

This study presents an efficient DL framework for multi-class brain tumor classification that integrates the YOLOv5m architecture with a BiFPN. The proposed model is designed to address key challenges in MRI-based tumor analysis, including small lesion sizes, heterogeneous tumor morphology, low contrast, and class imbalance. YOLOv5m serves as a lightweight yet powerful backbone, enabling effective feature extraction and real-time inference, while BiFPN enhances multi-scale feature fusion to improve localization and discrimination of complex tumor structures across varying resolutions.

Unlike traditional CNN or patch-based approaches that may lose contextual information, the YOLOv5m–BiFPN framework processes full MRI images and leverages hierarchical feature representations to preserve both global and local context. The weighted fusion mechanism in BiFPN further improves robustness to scale variation and tumor heterogeneity. Experimental results demonstrate strong performance, achieving a test accuracy of 88.86%, an F1-score of 88.25%, and a mAP@0.5 of 94.36%. The low inference latency and moderate computational cost confirm the model's suitability for real-time clinical decision support systems.

As shown in Table 2, the YOLOv5m + BiFPN model exhibits balanced class-wise performance. It achieves excellent results for healthy cases (precision = 0.94, recall = 0.96) and pituitary tumors (precision = 0.88, recall = 0.97), indicating high reliability and minimal missed detections. Meningioma shows moderate performance (precision = 0.75, recall = 0.83), likely due to visual similarity with other tumors. Glioma achieves high precision (0.95) but comparatively lower recall (0.73), indicating the presence of occasional false negatives. From a clinical perspective, missed glioma cases are particularly critical, as delayed detection may affect treatment planning and patient outcomes. However, the high precision indicates that glioma predictions made by the model are highly reliable when detected. Therefore, the proposed framework is best suited as a clinical decision-support tool, assisting radiologists by highlighting suspicious regions rather than replacing expert judgment. macro- and weighted-average F1-scores (0.87 and 0.88) confirm balanced learning across classes.

Table 2. Performance metrics

Class	Precision	Recall	F1-score	Support
Glioma	0.95	0.73	0.82	300
Meningioma	0.75	0.83	0.79	306
No tumor	0.94	0.96	0.95	405
Pituitary	0.88	0.97	0.92	300
Accuracy			0.88	1311
Macro avg	0.88	0.87	0.87	1311
Weighted avg	0.89	0.88	0.88	1311

To validate the proposed framework, a comparative analysis (Table 3) was performed against CNN–transformer baselines, including DenseNet121 + ViT, DenseNet201 + ViT, InceptionV3 + ViT, and Xception + ViT, using identical data splits. DenseNet-based models achieved the lower accuracies (69% and 74%), while InceptionV3 + ViT and Xception + ViT reached 82% and 87% accuracy, respectively. The proposed YOLOv5m-BiFPN outperformed all baselines with 88% accuracy and an F1-score of 0.88, attributed to effective multi-scale feature fusion.

Table 3. Performance comparison with baseline DL models

Model	Accuracy	Precision	Recall	F1-score
DenseNet121 + ViT	0.69	0.81	0.67	0.61
DenseNet201 + ViT	0.74	0.83	0.71	0.64
InceptionV3 + ViT	0.82	0.88	0.80	0.82
Xception + ViT	0.87	0.88	0.86	0.87
YOLOv5m–BiFPN (Proposed)	0.88	0.89	0.88	0.88

To verify the statistical significance of the proposed YOLOv5m–BiFPN model's performance gains, a paired t-test was conducted using results from 10-fold cross-validation. Mean accuracy and F1-score values across folds were compared at a significance level of $p < 0.05$. The proposed model achieved statistically significant improvements in accuracy over DenseNet121–ViT ($p = 0.003$) and InceptionV3–ViT ($p = 0.012$), with corresponding significant gains in F1-score ($p = 0.004$ and $p = 0.018$). Performance improvements over Xception–ViT were also significant ($p = 0.041$), confirming that the gains stem from the effectiveness of the BiFPN-enhanced multi-scale feature fusion rather than random variation.

The detection performance is further supported by the strong mAP@0.5 results shown in Table 4. The model achieved an overall mAP@0.5 of 0.94, indicating high localization and classification capability across tumor classes. The no-tumor class recorded the highest average precision (AP) (0.98), followed by pituitary tumors (0.97), reflecting consistent structural patterns. Glioma achieved an AP of 0.94, while meningioma showed a lower AP (0.86), likely due to higher intra-class variability and overlapping visual features.

Table 4. mAP at IoU threshold 0.5 of the proposed model

IoU threshold 0.5 of the proposed model	AP
mAP@0.5 (multi-class)	0.94
AP@0.5 for glioma	0.94
AP@0.5 for meningioma	0.86
AP@0.5 for notumor	0.98
AP@0.5 for pituitary	0.97

Overall, the consistently high performance across classification and detection metrics validates the effectiveness of the BiFPN-enhanced YOLOv5m framework in extracting class-specific spatial and semantic cues from brain MRI scans, highlighting its robustness, reliability, and clinical applicability. An error analysis was conducted by reviewing representative misclassified MRI samples from the test set. Most errors occurred between glioma and meningioma due to overlapping visual characteristics such as similar intensity patterns, tumor locations, and irregular boundaries. Glioma exhibited high precision but lower recall, indicating that cases with heterogeneous textures or diffuse margins were occasionally missed. Some meningioma cases were confused with pituitary tumors because of comparable shape and contrast enhancement.

Grad-CAM analysis of misclassified samples showed that the model consistently focused on clinically relevant tumor regions, suggesting that errors were primarily due to inter-class feature ambiguity rather than incorrect spatial attention. Qualitative evaluation further revealed strong alignment between Grad-CAM heatmaps and visible tumor regions, particularly highlighting heterogeneous cores and infiltrative margins in glioma cases. Even when misclassified, attention remained on plausible pathological areas. These observations indicate that integrating multi-modal MRI sequences or 3D spatial context could further reduce misclassification and improve robustness. Table 5 depicts the comparison of the proposed model with previous studies.

Table 5. Performance metrics comparison with previous studies

Study	Dataset	Classifier	Accuracy (%)
Tuhin *et al*. [32]	Real-time MRI dataset	CNN and 3D CNN	85.0
Suter *et al*. [33]	BraTS2018	SVM with CNN	72.20
Hu and Xia [34]	BraTS2017 challenge	3D-based CNN	81.40
Present study	Kaggle MRI	YOLOv5m with BiFPN	88.86

4.2. Gradient-weighted class activation mapping visual interpretability

Interpretability is essential in medical image analysis to build clinician trust and ensure transparency in artificial intelligence (AI)-assisted diagnosis. To address this, the proposed YOLOv5m + BiFPN model incorporates Grad-CAM to provide visual explanations of its predictions. Grad-CAM generates heatmaps that highlight the most influential regions in an input MRI scan, allowing clinicians to verify whether the model's decisions are based on clinically meaningful features. As illustrated in Figure 2, Grad-CAM is applied to the BiFPN layer, which captures high-level multi-scale representations across different spatial resolutions.

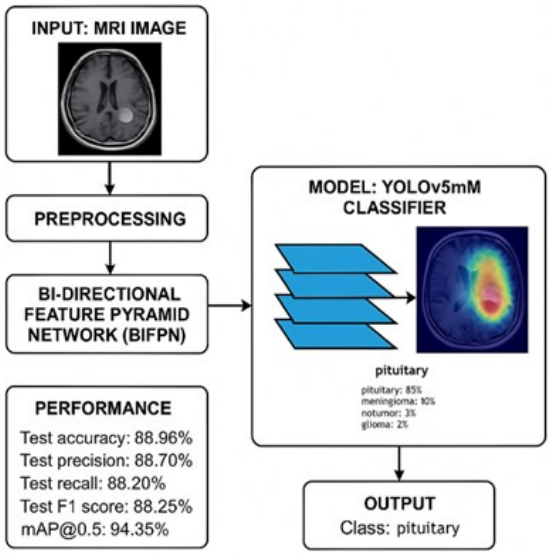
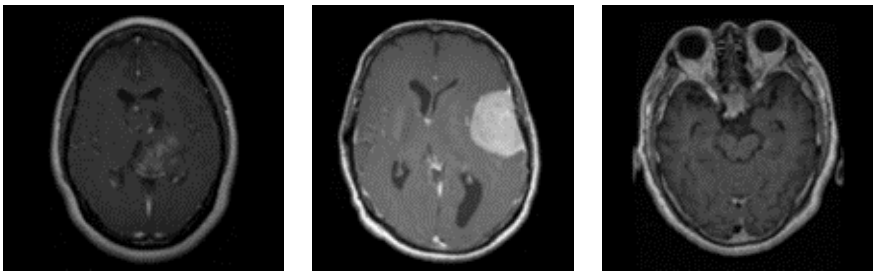


Figure 2. Process of Grad-CAM XAI

During inference, gradients of the predicted class with respect to BiFPN feature maps are averaged to compute feature importance, producing class-specific Grad-CAM heatmaps overlaid on MRI scans. These visualizations align well with clinically relevant tumor regions, especially in glioma and pituitary cases, confirming anatomically meaningful attention. A gradio interface further enables real-time prediction and visualization. Figure 3 shows the input MRI scan of a glioma, meningioma and pituitary cases.

Figure 3(a) shows the input MRI scan of a glioma case, while Figure 4 presents the corresponding prediction and Grad-CAM visualization generated by the YOLOv5m + BiFPN model. The model predicts glioma with 95% confidence, and the Grad-CAM heatmap highlights the central tumor region, confirming attention to clinically relevant features. Figure 3(b) shows the input MRI scan of a meningioma case, while Figure 5 presents the corresponding predictions and Grad-CAM visualizations. The YOLOv5m + BiFPN model predicts meningioma with 68% confidence, and the Grad-CAM heatmap highlights the well-defined lesion in the right hemisphere, confirming attention to clinically relevant tumor regions. Figure 3(c) shows the input MRI scan of a pituitary tumor, while Figure 6 presents the corresponding predictions and Grad-CAM visualizations. The YOLOv5m + BiFPN model classifies the scan as a pituitary tumor with 64% confidence, and the Grad-CAM heatmap highlights the lower central brain region, aligning with the anatomical location of the pituitary gland. These results emphasize the model's sensitivity to both the presence and absence of pathology, and demonstrate that even in ambiguous scenarios, it can reliably reject tumor predictions unless significant patterns are detected. The visual explanations provided by Grad-CAM support the clinical interpretability of such outcomes, allowing radiologists to validate the model's reasoning and further strengthening its potential for adoption in real-world diagnostic workflows.



(a) (b) (c)

Figure 3. Input MRI images of (a) glioma, meningioma, and (c) pituitary

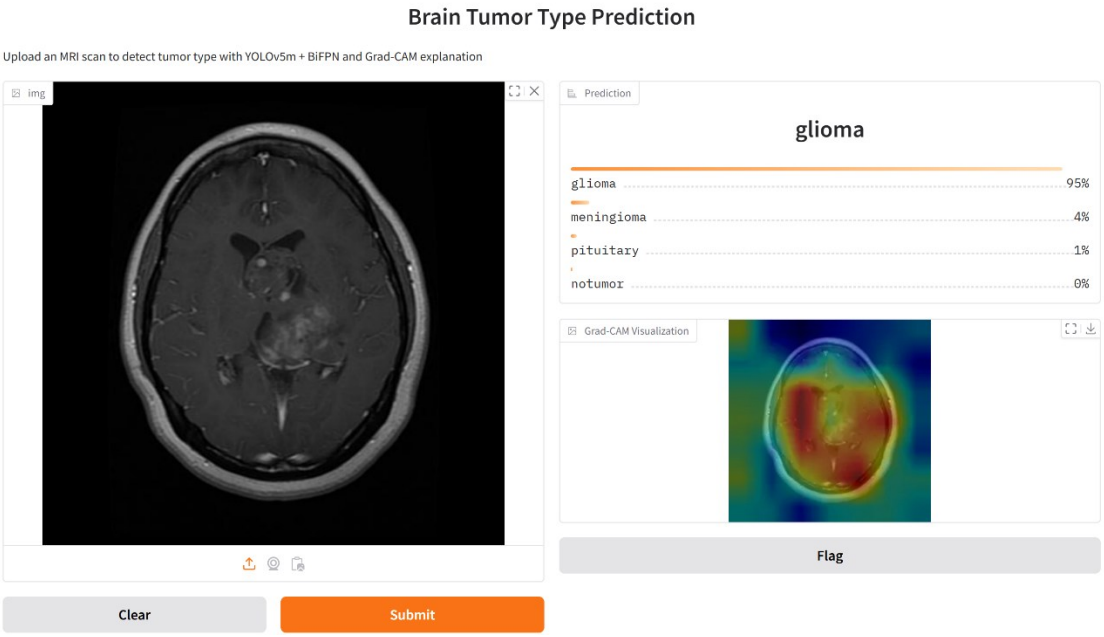


Figure 4. Brain tumor model prediction for glioma

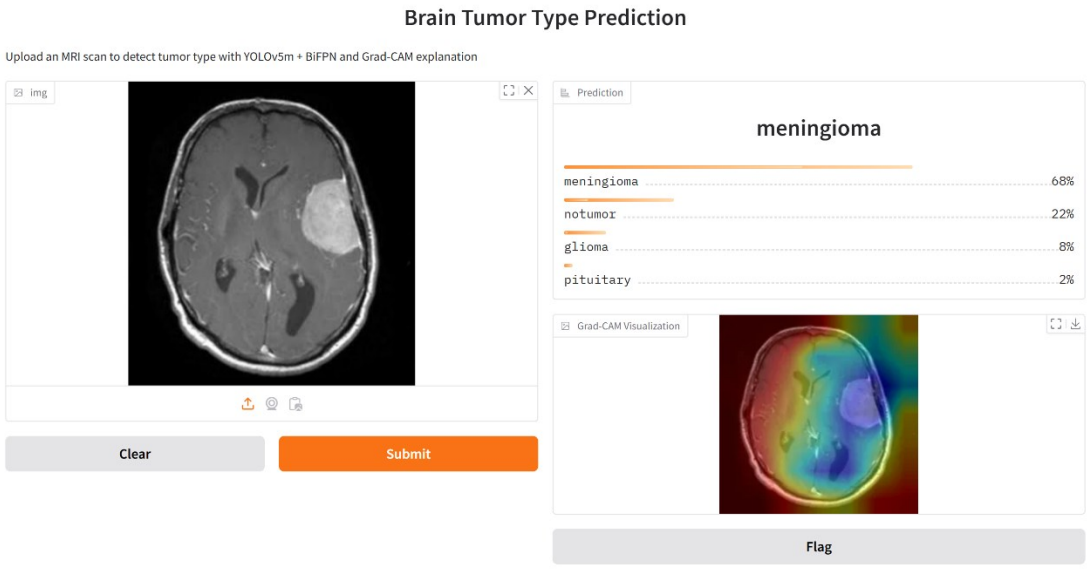


Figure 5. Brain tumor model prediction for meningioma

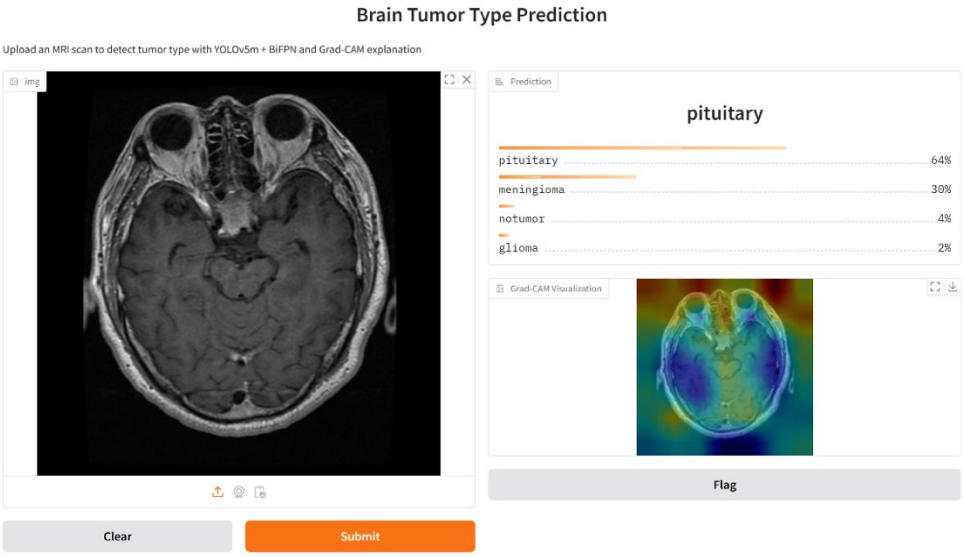


Figure 6. Brain tumor model prediction for pituitary

5. CONCLUSION

This study presents a robust and interpretable DL framework for multi-class brain tumor classification based on an enhanced YOLOv5m architecture integrated with a BiFPN. The model effectively addresses key challenges in brain MRI analysis, including tumor heterogeneity, size variation, and class imbalance. BiFPN facilitates efficient multi-scale feature fusion, enabling the network to capture both global context and fine-grained tumor details, while a class-weighted loss function ensures balanced learning across all tumor classes. The proposed approach achieved a test accuracy of 88.86% and demonstrated reliable class-wise performance, with an overall mAP@0.5 of 94.36%, reflecting strong multi-class detection capability. To improve transparency and clinical trust, Grad-CAM-based visual explanations were incorporated to highlight discriminative regions influencing predictions. Additionally, a gradio-based interactive interface was developed to enable real-time prediction and visualization. Overall, the framework offers a balanced combination of accuracy, efficiency, and explainability, making it suitable for clinical decision support.

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AUTHOR CONTRIBUTIONS STATEMENT

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

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Rajkumar Govindarajan		✓				✓		✓	✓	✓		✓		
Senthil Murugan		✓	✓	✓	✓				✓	✓	✓			
Janakiraman Jayanthi Arumugam		✓	✓	✓		✓	✓	✓		✓				

C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

CONFLICT OF INTEREST STATEMENT

Authors state no conflict of interest.

DATA AVAILABILITY

Data will be available upon reasonable request.

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