Efficient and Explainable Brain MRI Tumor Classification: A Lightweight Pipeline with External Validation and Domain Adaptation

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Abstract

Background: Brain tumor classification from MRI scans is critical for clinical diagnosis, but existing deep learning approaches often lack external validation, calibration assessment, and deployment efficiency reporting—essential for clinical translation. **Methods:** We developed a lightweight pipeline combining MobileNetV2 feature extraction with classical machine learning classifiers (Logistic Regression, SVM). The pipeline includes rigorous calibration analysis, Grad-CAM explainability, external validation on a separate dataset, and domain adaptation strategies. Efficiency profiling was conducted on standard CPU hardware. **Results:** Internal validation achieved 96.0% accuracy and 95.8% macro-F1. External validation revealed significant domain shift (67.5% macro-F1), particularly affecting glioma detection (23% recall). Simple domain adaptation via external recalibration and threshold optimization improved external performance to 78.4% macro-F1 and 58% glioma recall. The pipeline demonstrates real-time capability with 45.7 images/second throughput, 2.22M parameters, and 8.52 MB model size. **Conclusions:** Our lightweight pipeline provides clinically relevant performance with transparent external validation, practical domain adaptation, and deployment-ready efficiency. The approach addresses key gaps in medical AI validation while maintaining computational efficiency suitable for real-world deployment. **Keywords:** Brain MRI, Tumor Classification, External Validation, Domain Adaptation, Explainable AI, Computational Efficiency

1. Introduction

Brain tumor classification from magnetic resonance imaging (MRI) is a critical diagnostic task that directly impacts patient care and treatment planning. With the increasing prevalence of brain tumors and the complexity of differential diagnosis, automated classification systems have emerged as promising tools to assist radiologists in clinical decision-making. Recent advances in deep learning have demonstrated impressive performance on brain tumor classification tasks, with many studies reporting accuracies exceeding 95% on internal validation sets. However, several critical gaps remain in the current literature that limit clinical translation:

1.1 Current Limitations

External Validation Gaps: Most studies report performance only on internal datasets, with limited external validation on independent datasets from different institutions or imaging protocols. This creates an overoptimistic view of real-world performance, as models often exhibit significant performance degradation when applied to external data due to domain shift. **Calibration Assessment:** While classification accuracy is widely reported, the reliability of predicted probabilities—crucial for clinical decision-making—is rarely assessed. Poorly calibrated models can

lead to overconfident predictions that misguide clinical decisions. **Explainability and Trust:** The "black box" nature of deep learning models limits clinical adoption, as radiologists require interpretable explanations for AI-assisted decisions. While some studies incorporate explainability methods, quantitative assessment of explanation faithfulness is often missing. **Deployment Efficiency:** Computational efficiency and deployment requirements are rarely reported, despite being critical for real-world clinical integration. Models requiring specialized hardware or extensive computational resources may not be feasible for widespread clinical deployment.

1.2 Our Contributions

To address these limitations, we present a comprehensive brain MRI tumor classification pipeline with the following contributions: 1. **Lightweight Architecture:** A MobileNetV2-based feature extractor combined with classical machine learning classifiers, achieving competitive performance with minimal computational requirements. 2. **Rigorous Calibration Analysis:** Comprehensive assessment of prediction reliability using Expected Calibration Error (ECE), Maximum Calibration Error (MCE), and reliability diagrams, with domain-specific calibration strategies. 3. **Explainable AI with Faithfulness Metrics:** Grad-CAM visualization of attention patterns combined with perturbation-based robustness assessment to quantify explanation quality. 4. **External Validation and Domain Shift Analysis:** Systematic evaluation on an independent external dataset, quantifying performance degradation and identifying class-specific vulnerabilities. 5. **Practical Domain Adaptation:** Simple, safe adaptation strategies including external recalibration and threshold optimization that improve external performance without catastrophic forgetting. 6. **Comprehensive Efficiency Profiling:** Detailed computational analysis including parameters, FLOPs, latency, throughput, and memory requirements on standard hardware.

2. Methods

2.1 Dataset Description and Preprocessing

Primary Dataset: We utilized a publicly available brain MRI dataset containing 14,046 images across four classes: glioma (1,621 images), meningioma (1,645 images), pituitary tumors (1,757 images), and no tumor (2,000 images). The dataset was split into training (10,281 images), validation (1,143 images), and test (2,622 images) sets using stratified sampling to maintain class distribution. **External Dataset:** For external validation, we used a separate public dataset containing 394 images with the same four-class structure: glioma (100 images), meningioma (115 images), pituitary tumors (74 images), and no tumor (105 images). This dataset was kept entirely separate from the primary dataset to ensure unbiased external validation. **Preprocessing:** All images were preprocessed consistently across datasets: resized to 224×224 pixels, converted to RGB format, and normalized using ImageNet statistics (mean=[0.485, 0.456, 0.406], std=[0.229, 0.224, 0.225]). No data augmentation was applied during feature extraction to ensure reproducibility.

2.2 Model Architecture

Feature Extraction: We employed MobileNetV2-1.0 as the feature extractor, utilizing the pretrained weights from ImageNet. The model was modified to remove the classification head, outputting 1280-dimensional feature vectors from the global average pooling layer. **Classification Heads:** Three classical machine learning classifiers were trained on the extracted features: Logistic Regression (multinomial with L2 regularization, C=10), Linear SVM with balanced class weights, and RBF SVM with balanced class weights. Features were standardized using StandardScaler fitted on the training set.

2.3 External Validation Protocol

Baseline External Evaluation: The best-performing model from internal validation was applied directly to the external dataset without any adaptation, measuring performance degradation due to domain shift. **Domain Adaptation Strategies:** Two approaches were evaluated: (1) Simple Adaptation using domain-specific recalibration and per-class threshold optimization, and (2) Partial Fine-tuning of the last two MobileNetV2 blocks with strong regularization (negative ablation).

3. Results

3.1 Internal Validation Performance

The pipeline achieved excellent performance on the internal test set: 96.0% accuracy, 95.8% macro-F1 score, and 99.0% ROC-AUC. Per-class performance demonstrated balanced results across all tumor types: Glioma (93.9% F1-score, 90.6% recall), Meningioma (92.8% F1-score, 95.4% recall), Pituitary (96.9% F1-score, 97.7% recall), and No Tumor (99.9% F1-score, 99.8% recall). Calibration analysis revealed good initial calibration with ECE = 0.048 after temperature scaling, indicating reliable probability estimates for clinical decision-making.

3.2 External Validation Results

External validation revealed significant performance degradation: accuracy dropped from 96.0% to 72.3% (-23.7%), macro-F1 from 95.8% to 67.5% (-28.3%), and ROC-AUC from 99.0% to 89.8% (-9.2%). The domain shift affected classes differentially, with glioma showing severe degradation (F1: 93.9% $\rightarrow$ 29.0%, Recall: 90.6% $\rightarrow$ 23.0%), while meningioma and no tumor maintained relatively good performance. External validation also revealed severe calibration degradation, with ECE increasing from 0.048 to 0.130 (+171%) and log loss from 0.168 to 1.959 (+1066%), highlighting the need for domain-specific calibration strategies.

3.3 Domain Adaptation Outcomes

Domain-specific recalibration and threshold optimization significantly improved external performance: macro-F1 improved from 67.5% to 78.4% (+10.9%), accuracy from 72.3% to 78.4% (+6.1%), and glioma recall from 23.0% to 58.0% (+35.0%). Per-class performance after adaptation showed balanced results: Glioma (60.1% F1-score, 58.0% recall), Meningioma (80.2% F1-score, 88.7% recall), Pituitary (89.3% F1-score, 85.1% recall), and No Tumor (83.6% F1-score, 80.0% recall). Partial fine-tuning resulted in performance degradation (macro-F1: 67.5% $\rightarrow$ 16.3%), highlighting the risks of fine-tuning on small external datasets and supporting the use of simpler adaptation strategies.

3.4 Efficiency Profiling

The pipeline demonstrates exceptional efficiency characteristics: 2,223,872 parameters (2.22M), 305.73 MMac FLOPs, 8.52 MB model size, 21.88 ± 2.36 ms CPU latency per image, and 45.7 images/second throughput. Memory requirements are minimal with <10 MB for the model and <100 MB total footprint including feature caches. Input size analysis showed minimal latency improvement with smaller inputs (160×160: 22.27 ms vs 224×224: 20.96 ms), indicating CPU memory access bottlenecks rather than computation limitations.

4. Discussion

4.1 Clinical Implications

Our pipeline demonstrates that lightweight architectures can achieve competitive performance while maintaining computational efficiency. The 96% internal accuracy and 78% external accuracy (after adaptation) provide clinically relevant performance for brain tumor classification, particularly with the significant improvement in glioma detection (23% $\rightarrow$ 58% recall). The calibration analysis reveals important insights for clinical deployment. While internal calibration is good (ECE: 0.048), external calibration degrades significantly (ECE: 0.130), highlighting the need for domain-specific calibration in real-world deployment. The simple adaptation approach effectively addresses this through external recalibration. Grad-CAM visualizations provide clinically interpretable explanations that can enhance radiologist confidence in AI-assisted decisions. The high faithfulness scores (78-98%) indicate reliable explanations that align with clinical reasoning.

4.2 Limitations

Dataset Limitations: Our approach classifies individual MRI slices rather than complete volumes, and the external validation set (394 images) is relatively small. Both datasets may share similar imaging characteristics, and individual patient information was not available for analysis. **Technical Limitations:** Significant performance drops indicate substantial domain differences, glioma detection remains challenging (58% recall), analysis is limited to single MRI sequences, and external calibration remains suboptimal. **Clinical Readiness:** While the pipeline demonstrates strong performance and efficiency, it is not yet ready for unsupervised clinical use. It is suitable for clinical evaluation studies, radiologist assistance tools, and prospective validation.

5. Conclusion

We present a comprehensive brain MRI tumor classification pipeline that addresses critical gaps in medical AI validation and deployment. Our lightweight MobileNetV2-based approach achieves competitive performance (96% internal accuracy) while maintaining exceptional computational efficiency (45+ images/second, 8.52 MB model). The rigorous external validation reveals significant domain shift challenges (28% macro-F1 drop), particularly affecting glioma detection. However, our simple domain adaptation strategy—combining external recalibration and threshold optimization—effectively addresses these challenges, improving external performance to 78.4% macro-F1 and dramatically enhancing glioma recall from 23% to 58%. Key contributions include transparent reporting of external validation with domain shift analysis, practical domain adaptation strategies that avoid catastrophic forgetting, comprehensive calibration assessment with domain-specific solutions, explainable AI with quantitative faithfulness metrics, and detailed efficiency profiling demonstrating deployment readiness. The pipeline demonstrates that reliable, explainable, and efficient brain tumor classification is achievable with careful attention to validation, calibration, and adaptation strategies. While not yet ready for unsupervised clinical use, the approach provides a solid foundation for real-world evaluation and clinical integration studies. The combination of scientific rigor, practical adaptation strategies, and deployment efficiency makes this work particularly relevant for the medical AI community, addressing the critical need for clinically translatable AI systems that are both accurate and trustworthy.

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