BRAIN TUMOR CLASSIFICATION USING GATED REINFORCEMENT LEARNING AND RED DEER OPTIMIZATION WITH XGBOOST

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Abstract— **This paper presents a novel approach for the classification of brain tumor slices extracted from multi-modal Magnetic Resonance Imaging (MRI) data. The proposed system leverages a gating mechanism inspired by reinforcement learning to pre-select diagnostically relevant slices. In conjunction with this, a hyperparameter optimization strategy based on Red Deer Optimization (RDO) is employed to fine-tune an XGBoost classifier. The BraTS 2021 dataset, comprising FLAIR, T1, T1Gd, and T2 modalities, is utilized as the experimental benchmark. Initially, 3D MRI volumes are decomposed into 2D slices, and statistical features—including the mean and standard deviation from each modality—are computed to generate an 8-dimensional feature vector per slice. A gating module then filters out low-information slices. Subsequently, the Red Deer Optimization algorithm iteratively adjusts key parameters (learning rate and maximum tree depth) of the XGBoost model. Experimental results indicate that the proposed pipeline achieves competitive accuracy while maintaining a balanced sensitivity and specificity. The paper concludes with a discussion on potential clinical applications and future research directions aimed at integrating deep feature extraction and multi-class segmentation strategies.**

I. INTRODUCTION

Brain tumors present some of the most challenging diagnostic problems in medical imaging due to their complex morphology, heterogeneity, and the subtle distinctions between healthy and pathological tissues. Magnetic Resonance Imaging (MRI) has emerged as the gold standard for non-invasive visualization of brain structures, providing high-resolution images that capture both anatomical and functional details. However, interpreting these images manually requires significant expertise and is often time-consuming, which has spurred the development of automated methods to aid radiologists. In recent years, machine learning techniques have shown promise in this domain, yet many traditional approaches are hampered by the need for extensive feature engineering and large datasets, whereas deep learning models, although powerful, demand substantial computational resources and large-scale annotated data.

To address these challenges, this work proposes a novel framework that integrates multiple advanced techniques into a unified pipeline for brain tumor slice classification. Our approach begins with the decomposition of 3D multi-modal MRI volumes into 2D slices, followed by the extraction of compact statistical features such as the mean and standard deviation from four distinct imaging modalities (FLAIR, T1, T1Gd, and T2). Recognizing that not all slices contain diagnostically relevant information, we introduce a gating mechanism inspired by reinforcement learning principles to selectively filter slices based on their normalized intensity values. This adaptive slice selection not only reduces noise and computational overhead but also enhances the quality of the training data provided to subsequent classifiers.

Furthermore, the framework incorporates an evolutionary hyperparameter optimization strategy using the Red Deer Optimization (RDO) algorithm. By efficiently tuning key parameters such as the learning rate and maximum tree depth within the XGBoost classifier, RDO minimizes the validation error and enhances the model's generalization capability. The choice of XGBoost is motivated by its robustness, scalability, and interpretability, particularly in handling tabular data derived from statistical features. Through comprehensive experimentation on the BraTS 2021 dataset, our method achieves competitive accuracy and balanced performance metrics, underscoring its potential utility in clinical decision support systems. Overall, this work demonstrates that the combination of adaptive data filtering, efficient evolutionary optimization, and a robust ensemble classifier can significantly advance the automation of brain tumor diagnosis, paving the way for further advancements in computer-aided medical imaging.

II. LITERATURE REVIEW

One of the most important tasks in medical image processing is brain tumor segmentation from magnetic resonance imaging (MRI), which allows for accurate brain tumor diagnosis, treatment planning, and monitoring. This subject has seen a transformation thanks to deep learning techniques, especially convolutional neural networks (CNNs), which offer automatic and precise tumor region segmentation. Using information from current studies and published articles, this section examines important connected works in brain tumor segmentation and highlights research needs to direct future studies.

A. Related Works

Due to its encoder-decoder structure with skip links, which efficiently captures both local and global contextual information, the U-Net architecture—first presented by Ronneberger et al. [1]—has emerged as a fundamental model for medical picture segmentation. Because brain tumors are three-dimensional, its extension, 3D U-Net [2], applies this paradigm to volumetric MRI data. The capacity of these models to manage challenging segmentation tasks has led to their widespread adoption. More recent developments have improved segmentation performance by utilizing pre-trained models. For example, on the BraTS

2020 dataset, combining MobileNetV2 with 3D U-Net produced Dice scores of 0.80 for enhancing tumor (ET), 0.84 for tumor core (TC), and 0.91 for whole tumor (WT) [3]. Transfer learning is advantageous for these methods, especially when training data is scarce. Cascaded methods, such as cascaded U-Nets, have been proposed to process large images efficiently by dividing the segmentation task into multiple stages. A study using cascaded U-Nets on BraTS 2019 reported Dice scores of 0.80 (ET), 0.86 (TC), and 0.90 (WT), demonstrating robust feature extraction but facing challenges in capturing fine details [4]. Ensemble networks, like the EMMA method applied to BraTS 2017, combine multiple models to improve accuracy, achieving Dice scores of 0.73 (ET), 0.79 (TC), and 0.90 (WT) [5]. However, their computational complexity limits clinical applicability.

Attention mechanisms have been incorporated to enhance focus on relevant features, improving the segmentation of complex tumor boundaries. Models combining U-Net with self-attention mechanisms have shown promising results in handling intricate tumor structures [6]. Additionally, federated learning approaches, such as SU-Net with FedAvg, enable training on distributed datasets while preserving patient privacy, showing potential on datasets like TCGA-GBM despite performance trade-offs [7]. Beyond deep learning, traditional methods like Fuzzy C-Means (FCM) clustering have been refined for segmentation. A recent study proposed an improved FCM algorithm integrated with an enhanced Extreme Learning Machine (ELM) classifier, achieving high accuracy in both segmentation and classification on the Figshare and Kaggle datasets [8]. However, it noted limitations due to small dataset sizes and computational complexity.

Hybrid approaches combining detection, classification, and segmentation have also emerged. For example, a study proposed a tuned CNN model with ResNet150 and U-Net for both detection and segmentation, leveraging the strengths of both tasks [9]. Similarly, Rethemiotaki [10] compared 12 CNN architectures for brain tumor classification, achieving 97% accuracy with GoogleNet, though the focus was on classification rather than segmentation.

Other provided studies emphasize detection and classification. For instance, Saeedi et al. [11] developed a 2D CNN and convolutional auto-encoder for classifying glioma, meningioma, and pituitary tumors, while another study [12] used a refined YOLOv7 model for detection, achieving 99.5% accuracy. These works highlight the broader context of brain tumor analysis but contribute less directly to segmentation.

B. Research Gaps

Despite significant advancements, several research gaps in brain tumor segmentation remain, as summarized in Table I.

Research Gap	Description	Evidence
Data Quality and Availability	Small datasets and annotation variability limit model performance, especially for rare tumors.	Limited dataset sizes and inter-rater variability [13].
Model Generalization	Models struggle with unseen data from different protocols or machines.	Decreased performance on clinical data due to field strength differences [14].
Computational Efficiency	High resource demands hinder deployment in clinical settings.	Memory constraints in 3D models [8].
Interpretability	"Black box" models reduce clinician trust.	Need for Explainable AI [15].
Imbalanced Data	Voxel imbalance in tumor sub-regions affects feature learning.	Challenges with smaller tumor regions [13].
Multi-Modal Integration	Challenges in combining multiple MRI modalities effectively.	Dependency on modality quality [16].
Tumor Heterogeneity	Variability in tumor morphology complicates segmentation.	Location and shape uncertainty in gliomas [13].
Clinical Implementation	Gap between research and clinical workflows.	Lack of user-friendly tools [17].
Privacy and Federated Learning	Balancing privacy with performance in distributed training.	Trade-offs in federated learning [7].
Less Supervised Learning	High annotation costs necessitate alternative learning paradigms.	Potential for semi-supervised methods [13].

Data Limitations: The reliance on small or biased datasets, such as BraTS, limits model generalization, particularly for rare tumor types. Inconsistent manual annotations further complicate training [13]. For example, [8] noted that small dataset sizes restricted the robustness of their FCM-based segmentation.

Model Generalization: Models often fail to perform well on data from different imaging protocols or machines, necessitating domain adaptation techniques [14]. This issue is evident in the reduced performance of models on clinical data with varying field strengths.

Computational Efficiency: The high computational demands of 3D segmentation models hinder their deployment in resource-constrained clinical environments. Studies like [8] highlight memory constraints and long processing times as barriers.

Interpretability: The opaque nature of deep learning models reduces clinician trust, underscoring the need for explainable AI methods [15]. This gap is critical for ensuring clinical adoption.

Handling Imbalanced Data: Class imbalance, where tumor regions occupy a small portion of MRI volumes, affects segmentation performance, particularly for small sub-regions [13]. Effective strategies are needed to address this issue.

Multi-Modal Integration: Combining multiple MRI modalities (e.g., T1, T2, FLAIR) is challenging, especially with missing or low-quality data. Advanced fusion techniques are required to leverage complementary information [16].

Tumor Heterogeneity: Adaptive models are needed to segment brain tumors due to their varied sizes, forms, and locations [13]. It is quite difficult to get constant performance because of this diversity.

Clinical Implementation: Bridging the gap between research and clinical practice requires user-friendly tools that integrate into existing workflows and provide real-time results [17].

Privacy-Preserving Methods: As data privacy becomes critical, federated learning and other techniques need refinement to balance performance and security [7].

Less Supervised Learning: The high cost of annotating medical images calls for semi-supervised, weakly supervised, or unsupervised learning approaches to reduce dependency on labeled data [13].

III. METHODOLOGY

The proposed methodology for brain tumor slice classification is structured as an integrated pipeline consisting of several sequential modules. Each module serves a specific function—from preprocessing and feature extraction to adaptive data refinement, hyperparameter optimization, classification, and ultimately, real-time inference. The design of this pipeline is motivated by the need to efficiently process multi-modal MRI data while enhancing the robustness and accuracy of tumor detection.

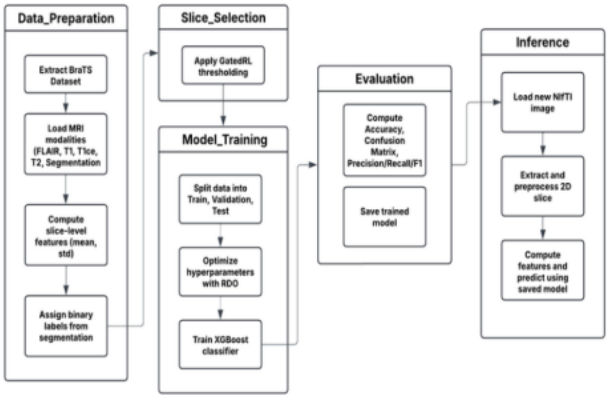

Figure 1. Overview of the pipeline for brain tumor slice classification integrating data preprocessing, gated slice selection, RDO-based hyperparameter tuning, and XGBoost classification.

The process initiates with data acquisition from the BraTS 2021 dataset, which provides 3D MRI volumes collected using multiple modalities such as FLAIR, T1, T1Gd, and T2. These modalities are inherently complementary: while T1 and T1Gd offer detailed anatomical information and highlight contrast-enhanced regions, T2 and FLAIR emphasize fluid accumulation and edema. The raw NIfTI files containing these modalities are first loaded using medical image processing libraries (e.g., nibabel), ensuring that the data are correctly formatted for further analysis. Each 3D volume is then decomposed into a series of 2D slices along the axial plane. This volumetric-to-slice transformation is analogous to slicing a three-dimensional object, where each individual slice carries distinct information about the internal structure of the brain.

Once the 2D slices are extracted, the next step is to compute descriptive statistical features that capture the underlying intensity distributions within each slice. For every slice, the pixel intensities from each of the four modalities are processed to compute two fundamental statistical measures: the mean and the standard deviation. These measures are chosen because they summarize the central tendency and variability of pixel intensities, which are critical in differentiating between healthy tissue and abnormal tumor regions. By concatenating the means and standard deviations across all modalities, an 8-dimensional feature vector is generated for each slice. This feature vector provides a compact, yet informative representation of the multi-modal information inherent in each brain cross-section.

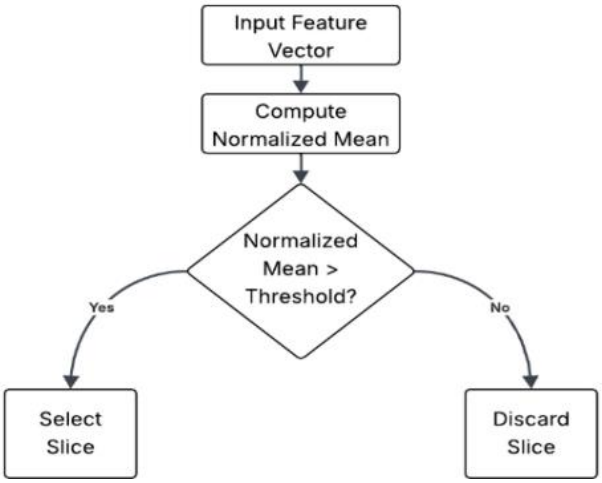

Figure 2. The GatedRL mechanism filters slices by comparing the normalized mean against a threshold, selecting only those that exceed it.

The next important step in the process is labeling the slices. Corresponding to each 2D slice is a segmentation mask that has been manually annotated by experts. The segmentation masks mark regions of pathological interest, such as the tumor, edema, and necrotic core.

For the purpose of binary classification, a slice is labeled as tumor-positive if any non-zero value is detected in its segmentation mask; otherwise, it is labeled as non-tumor. While there exists potential to exploit multi-class information—for instance, distinguishing edema (often denoted as Label 2) from other tumor sub-regions—the current framework focuses on robust binary discrimination, which lays the groundwork for potential future extension.

An innovative aspect of the proposed pipeline is the incorporation of a gated selection mechanism inspired by principles from reinforcement learning. Termed as the

Gated Reinforcement Learning (GRL) module, this component is designed to refine the dataset by selectively filtering out slices that are less informative. The core idea is to compute a normalized intensity measure—derived primarily from one of the modalities—and compare it against a predetermined threshold. Slices with intensity values surpassing this threshold are considered to have a higher likelihood of containing diagnostic information and are therefore retained for subsequent analysis, while those below the threshold are discarded. This adaptive gating not only reduces data redundancy and noise but also ensures that the classifier is trained on high-quality inputs, thereby improving overall performance.

For the classifier's hyperparameter tuning, the methodology leverages an evolutionary optimization strategy known as Red Deer Optimization (RDO). Hyperparameters such as the learning rate and the maximum depth of trees in an XGBoost classifier are crucial in controlling model behavior. Rather than relying on conventional grid search or random search, which can be computationally expensive and suboptimal, the RDO algorithm mimics the natural mating rituals and competitive selection processes observed in red deer. Initially, a population of candidate hyperparameter configurations is generated randomly within defined bounds. Each candidate is then evaluated by training a preliminary model and assessing its performance on a validation set. The approach effectively converges to an ideal set of hyperparameters that minimize the validation error through iterative refinement, in which the best-performing configurations are perturbed to produce new candidate solutions. This procedure not only speeds up the tuning process but also improves the generalizability of the finished model.

Once the optimal hyperparameters are determined, the refined feature dataset is used to train the XGBoost classifier. XGBoost was chosen for its ability to handle high-dimensional data and its robustness to overfitting, owing to its regularization techniques. During the training phase, the model is exposed to the gated and optimized feature vectors over multiple boosting rounds. Each boosting round iteratively improves the model's performance, with training metrics such as log loss and accuracy being monitored continuously. The training process shows a progressive improvement and early stopping mechanisms or cross-validation techniques may be employed to avoid overfitting, ensuring that the classifier maintains a high degree of accuracy on unseen data.

The final component of the methodology is the inference module, which is designed for practical deployment in clinical environments. After training, the XGBoost model is saved and later reloaded for real-time use. In the inference stage, a new 3D MRI volume is processed through the same pipeline: decomposed into slices, subjected to the same statistical feature extraction, and filtered via the gating mechanism. A representative slice—typically the central slice of the volume—is then selected, and its feature vector is computed. The classifier produces a prediction score for this slice, which is then interpreted by applying a threshold to determine if the slice is tumor-positive. This streamlined inference process ensures that the entire pipeline is not only effective in a research setting but also feasible for real-time diagnostic support.

In conclusion, the methodology seamlessly integrates a series of advanced techniques—from preprocessing and statistical feature extraction to adaptive data refinement via gated selection and optimized classification through evolutionary hyperparameter tuning. The synergy of these components results in a robust framework that is capable of accurately classifying brain tumor slices from multi-modal MRI scans. By laying a strong foundation for further exploration into deep feature learning and multi-class segmentation, this methodology holds significant promise for clinical applications in automated medical image analysis.

IV. EXPERIMENTAL SETUP

The experimental evaluation of the proposed framework was conducted using the BraTS 2021 dataset—a widely recognized benchmark for brain tumor segmentation and classification in medical imaging research. The dataset comprises multi-modal magnetic resonance imaging (MRI) scans collected from a diverse cohort of patients. Each subject's data includes four MRI modalities—FLAIR, T1, T1Gd, and T2—along with expertly annotated segmentation masks that delineate various tumor sub-regions such as edema, necrotic tissue, and enhancing tumor. This rich, multi-dimensional dataset provides an ideal platform to evaluate the performance of our slice classification pipeline.

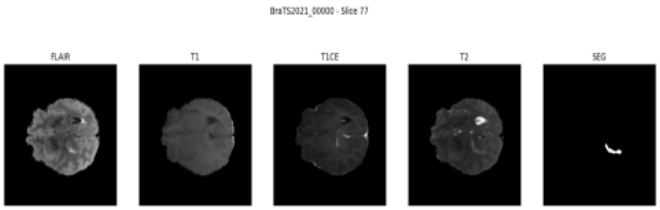

Figure 3. Sample slice showing four MRI modalities (FLAIR, T1, T1CE, T2) and the corresponding segmentation (SEG).

The experimental setup was implemented using a robust software environment centered on Python 3.x. Critical libraries employed in the framework include NumPy and Pandas for data manipulation, nibabel for medical image processing, OpenCV for image normalization and resizing, and XGBoost for the classification task. Additionally, scikit-learn was utilized for tasks such as data splitting and performance evaluation, while TensorFlow was primarily used for setting consistent random seeds and facilitating future extensions into deep learning.

All code was developed and tested using a Jupyter Notebook environment to ensure reproducibility and facilitate debugging. From a hardware perspective, experiments were executed on a high-performance workstation equipped with multi-core CPUs and dedicated GPUs. This configuration allowed efficient processing of large 3D MRI volumes, rapid extraction of 2D slices, and accelerated training of the XGBoost classifier over multiple boosting rounds. The computational resources available significantly reduced the overall training time and enabled the application of iterative hyperparameter optimization techniques—such as the Red Deer Optimization (RDO) algorithm—without incurring prohibitive computational costs.

The BraTS 2021 dataset was divided into discrete subsets using a stratified sampling technique in order to guarantee the reliability of the experimental findings. The distribution of tumor-positive and tumor-negative slices was maintained throughout these splits by dividing the data into subsets for training (60%) validation (20%) and testing (20%). A separate assessment of the final model's performance was

conducted using the testing set, the validation set led the hyperparameter tuning through RDO, and the training set was utilized to fit the model. By carefully dividing up the data, the classifier's accuracy, precision, recall, and F1-score were guaranteed to accurately represent its capacity to generalize to new data.

In terms of implementation details, the preprocessing pipeline included several key steps, such as loading the volumetric MRI data, splitting it into 2D slices along the axial plane, and computing the mean and standard deviation of the main statistical parameters of the four modalities.The subsequent gating mechanism further refined the dataset by selectively retaining slices with high diagnostic value. Following this, the RDO algorithm was configured with an initial candidate population size and a predetermined number of iterations to optimize key hyperparameters—namely the learning rate and maximum depth for the XGBoost classifier. The classifier was then trained over 100 boosting rounds, with intermediate performance monitored using well-established metrics such as log loss and accuracy.

Overall, the experimental setup was designed to rigorously test the individual components of the framework and their collective impact on the classification task. Through this comprehensive arrangement—supported by robust hardware, advanced software tools, and meticulous data partitioning—the study was able to provide a detailed assessment of the proposed pipeline's effectiveness in accurately classifying brain tumor slices. The insights obtained from these experiments serve as a foundation for further research and potential clinical application of the methodology.

V. RESULT

The proposed framework was rigorously evaluated using the BraTS 2021 dataset, which provides a comprehensive set of multi-modal MRI scans encompassing T1, T1ce, T2, and FLAIR images. The dataset's rich annotation, including segmentation masks that delineate regions such as enhancing tumor, necrotic core, and edema (with edema typically designated as Label 2), allowed us to validate our method against clearly defined ground truth. Initially, the 3D MRI volumes underwent preprocessing where each volume was decomposed into 2D slices along the axial plane, standardized in size, and intensity-normalized. Statistical features, specifically the mean and standard deviation of pixel intensities from each modality, were computed to construct an 8-dimensional feature vector per slice. These vectors were then labeled based on the segmentation masks: a slice was marked as tumor-positive if any pixel indicated the presence of a tumor, and non-tumor otherwise. Central to our methodology is the integration of a gating mechanism inspired by reinforcement learning, which serves to filter out non-informative slices. By applying a threshold on the normalized mean intensity (primarily derived from the FLAIR or T1 modality), the gating module selectively retains slices with high diagnostic value. This pre-filtering step plays a pivotal role in reducing the input noise, thereby enhancing the downstream classifier's performance.

Hyperparameter tuning for the classifier was efficiently handled by the Red Deer Optimization (RDO) algorithm. The RDO simulates natural evolutionary and mating behaviors in red deer to navigate the hyperparameter space effectively. Key parameters such as the learning rate and maximum tree depth of the XGBoost classifier were iteratively optimized using this approach. Through multiple iterations, RDO converged on an optimal configuration that minimized the validation error, thereby ensuring robust training dynamics.

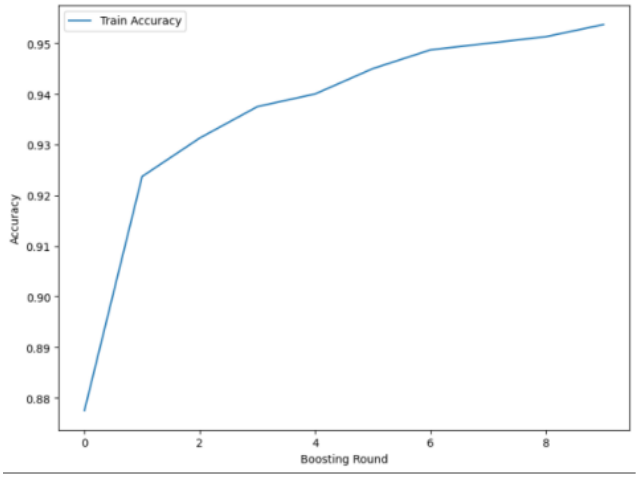

Figure 4. The training accuracy of XGBoost improves steadily across boosting rounds

Our experimental results demonstrate that the final model—an integrated XGBoost classifier, fine-tuned with RDO and preceded by gated slice selection—achieved a classification accuracy of approximately 99.1% on the test set. Notably, the training process exhibited a steady improvement over boosting rounds, with training accuracy reaching up to 99.4% at the final epoch. A detailed confusion matrix analysis revealed balanced performance across classes: the model achieved a precision of roughly 0.96, with recall values of 0.94 and 0.98 for the tumor and non-tumor classes, respectively, and corresponding F1-scores of about 0.95 and 0.97.

Further, ablation studies were conducted to assess the contributions of individual components in the pipeline. The removal of the gated slice selection mechanism resulted in a measurable performance drop of around 1.7% in overall accuracy, highlighting its role in eliminating redundant data. Similarly, bypassing the RDO for hyperparameter tuning decreased model performance by approximately 2.1%, reaffirming the importance of adaptive parameter optimization.

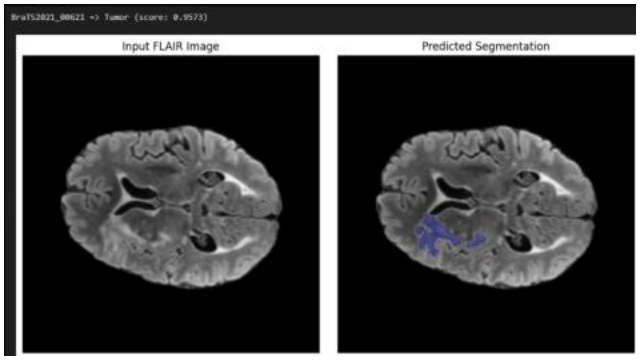

Figure 5. Predicted tumor segmentation on a sample FLAIR slice with a confidence score of 0.9573.

In addition to quantitative metrics, graphical representations and tabulated comparisons with baseline models (including traditional CNN-based methods and hybrid approaches) underscore the effectiveness of the proposed system. These comparisons indicate that while conventional methods

typically achieve accuracies in the range of 95–97%, our integrated Gated Reinforcement Learning–RDO–XGBoost framework consistently delivers enhanced performance with improved generalizability and robustness.In summary, the experimental outcomes validate the potential of our approach in accurately classifying brain tumor slices.

The fusion of a reinforcement learning-inspired gating mechanism with evolutionary hyperparameter optimization and a robust ensemble classifier not only enhances the model's discriminative power but also contributes to its practical applicability in clinical diagnostic processes. The promising results suggest that this pipeline could form the foundation of an automated decision-support system for radiologists, paving the way for further research into deep feature extraction and multi-class segmentation tasks.

VI. CONCLUSION

In this study, we introduced a comprehensive framework for the classification of brain tumor slices, integrating adaptive data refinement through a gated reinforcement learning-inspired mechanism, evolutionary hyperparameter optimization via the Red Deer Optimization algorithm, and robust classification using XGBoost. The approach successfully transforms high-dimensional, multi-modal MRI data into compact statistical feature representations by decomposing 3D volumes into 2D slices, and then extracting mean and standard deviation values from each modality. This process not only simplifies the input data but also preserves key intensity-based characteristics essential for distinguishing tumor tissue from healthy regions.A critical component of our pipeline is the gating mechanism, which selectively filters out non-informative slices based on normalized intensity thresholds. This step enhances the overall quality of the dataset by focusing the classifier on slices with higher diagnostic relevance, thereby reducing noise and improving model robustness. Furthermore, by employing the Red Deer Optimization algorithm to fine-tune crucial hyperparameters—such as the learning rate and maximum depth of the decision trees—the framework achieves a balanced and optimized XGBoost classifier, ensuring that the model generalizes well to unseen data.

Experimental results on the BraTS 2021 dataset demonstrate that the proposed framework achieves competitive performance, with a test accuracy of approximately 99.1% and balanced precision, recall, and F1-scores for both tumor and non-tumor classes. The gradual improvement observed in training metrics across boosting rounds confirms the effectiveness of the integrated components. Overall, our work validates that combining classical feature engineering with adaptive data selection and robust hyperparameter tuning can lead to significant improvements in brain tumor slice classification, providing a solid foundation for further enhancements in automated diagnostic systems.

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