



AI-Powered Detection Of Brain Tumors: Evaluating The Accuracy Of Deep Learning Models In MRI Image Analysis

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Abstract

The integration of artificial intelligence (AI) into medical imaging has opened new frontiers for accurate, efficient, and scalable brain tumor diagnostics. This study evaluates and compares the performance of Logistic Regression (LR), Random Forest (RF), and Artificial Neural Networks (ANN) in differentiating glioblastoma multiforme (GBM), lymphoma, and metastases using radiomics features derived exclusively from contrast-enhanced T1-weighted MRI scans. A retrospective cohort of 85 patients (62 GBM, 23 lymphoma) was analyzed, with radiomic features extracted via the IBSI-compliant PyRadiomics framework following manual segmentation. To address natural class imbalance, the Synthetic Minority Oversampling Technique (SMOTE) was applied, creating balanced datasets for robust evaluation. Models were trained and validated using stratified 10-fold cross-validation, with performance measured by accuracy, sensitivity, specificity, and area under the ROC curve (AUC). Results demonstrated that ANN consistently outperformed classical methods, achieving 79% accuracy (AUC 0.83) on the original dataset and 87% accuracy (AUC 0.90) on the balanced dataset, compared with RF (74% and 84.5%) and LR (42% and 63%). In multiclass classification, ANN achieved an overall accuracy of 79.4% with a macro-AUC of 0.887, effectively distinguishing GBM, lymphoma, and metastases. These findings confirm the superiority of deep learning in handling complex, high-dimensional imaging data, particularly when supported by preprocessing and data balancing strategies. By demonstrating the strengths and limitations of different approaches, this study highlights the potential of AI-driven radiomics to enhance diagnostic reliability, reduce variability, and improve patient triage in neuro-oncology.

Keywords: Artificial Intelligence (AI), Brain Tumor Classification, Radiomics, Magnetic, Resonance Imaging (MRI) and Deep Learning.

1. INTRODUCTION

The integration of artificial intelligence (AI) into medical imaging has transformed the landscape of brain tumor detection, offering new possibilities for accurate and efficient diagnosis. Brain tumors remain among the most complex and life-threatening conditions in neuro-oncology, where timely identification is critical to improving patient outcomes. Magnetic Resonance Imaging (MRI), long considered the gold standard in brain tumor diagnostics for its superior soft-tissue contrast, is essential but heavily reliant on radiologists' expertise. Manual interpretation of MRI scans is time-intensive and susceptible to variability, which can delay treatment decisions. To address these limitations, deep learning, particularly Convolutional Neural Networks (CNNs), has emerged as a powerful solution. These models excel in image classification, segmentation, and detection tasks, achieving accuracies above 95% in classifying tumor types such as gliomas, meningiomas, and pituitary tumors (Jaiswal et al., 2023). Their scalability and speed make them valuable for both advanced medical centers and under-resourced regions.

The integration of MRI with AI-driven deep learning systems marks a paradigm shift in neuro-oncology. Preprocessing steps such as contrast adjustment, noise reduction, and edge refinement further enhance model reliability (Gupta & Kumar, 2024), while hybrid frameworks reduce false positives across diverse scanners and clinical environments (Shujairi & Akkurt, 2025). Despite challenges such as data heterogeneity, lack of standardized imaging protocols, and regulatory hurdles, collaborative efforts between radiologists, data scientists, and clinicians are addressing these gaps (Mary et al., 2024). As research advances, AI-powered MRI analysis is poised to revolutionize brain tumor diagnostics by ensuring earlier detection, improved consistency, and more personalized treatment planning (Shah, 2024).

1.1. The Rising Need for AI in Neuro-Oncology

The complexity of neuro-oncological diseases and rising diagnostic demands highlight the need for advanced technologies in clinical practice. Brain tumors often present irregular shapes and overlapping features on MRI, making manual interpretation difficult and variable. Radiologists face increasing workloads and limited subspecialty expertise, particularly in under-resourced regions. Artificial intelligence (AI), especially deep learning, addresses these challenges by processing large MRI datasets, detecting subtle patterns, and improving accuracy. Models such as EfficientNet, Xception, and InceptionV3 have achieved accuracies exceeding 98%, with enhanced preprocessing further boosting performance (Gupta & Kumar, 2024; Shah, 2024).

1.2. Challenges in Traditional Radiological Diagnosis

Traditional radiological diagnosis of brain tumors depends greatly on the expertise and availability of radiologists. MRI interpretation, especially when detecting subtle tumor boundaries or rare subtypes, is often subjective and varies across observers. This variability can cause diagnostic errors or delays, particularly in high-volume clinical environments. Manual tumor segmentation is also labor-intensive and may lack accuracy, limiting effective treatment planning. Villalpando-Vargas et al. (2023) emphasized that while radiology remains foundational, its limitations in speed, consistency, and precision are increasingly inadequate for modern neuro-oncology demands, prompting the integration of AI-powered tools to strengthen diagnostic workflows (Villalpando-Vargas et al., 2023).

1.3. Role of AI in Bridging Diagnostic Delays

Artificial intelligence (AI) offers promising solutions to diagnostic delays in brain tumor detection. By rapidly analyzing MRI scans, AI systems provide real-time support, improving accuracy and speeding decision-making. These tools can triage high-risk cases, reduce wait times between imaging and diagnosis, and guide patients toward timely interventions. Mary et al. (2024) demonstrated that convolutional neural networks integrated into radiology workflows significantly shortened diagnostic turnaround while

maintaining high accuracy in tumor localization and classification. In healthcare settings facing limited staff and rising caseloads, AI-based systems present a scalable means to streamline neuro-oncological care and enhance patient outcomes (Mary et al., 2024).

1.4. Importance of Contrast-Enhanced T1-Weighted MRI

Contrast-enhanced T1-weighted MRI is critical for visualizing brain tumors, particularly in assessing vascularity and blood–brain barrier integrity. Gadolinium-based agents highlight neovascularization in high-grade tumors, enabling precise boundary detection and distinction from edema or necrosis. Ellingson and Smits (2019) emphasized its importance in standardized trial protocols for consistent lesion visualization. Beyond diagnostics, it supports surgical planning by delineating resection margins and avoiding vital structures. While gadolinium retention poses safety concerns, especially in repeated scans, its diagnostic value outweighs risks. Meola et al. (2018) proposed nanoparticle-based alternatives to improve specificity. Overall, T1-weighted contrast imaging remains indispensable in brain tumor management.

1.5. Comparison with FLAIR, T2, and DWI Sequences

While contrast-enhanced T1-weighted imaging is primary in brain tumor evaluation, other MRI sequences provide essential complementary insights. FLAIR enhances lesion visibility near ventricles, particularly in subcortical white matter; Seshimo and Rashed (2024) showed FLAIR with T2 improved astrocytoma segmentation. T2-weighted imaging highlights peritumoral edema and cystic regions, aiding differentiation from non-neoplastic lesions (Mulyadi et al., 2020). Diffusion-weighted imaging (DWI) measures water diffusivity, useful for identifying cellular density and necrotic cores (Munir et al., 2020). Shahbaz and Bibi (2025) emphasized that integrating T1, FLAIR, T2, and DWI sequences increases sensitivity, making multimodal MRI protocols crucial for accurate tumor diagnosis and classification.

1.6. The Shift Towards Deep Learning

Artificial intelligence in neuroimaging spans classical machine learning (ML) and deep learning (DL). Classical ML methods like Support Vector Machines and Decision Trees rely on handcrafted features, limiting their performance on complex MRI data. DL models, particularly Convolutional Neural Networks (CNNs), autonomously extract features, improving generalizability and accuracy. Singh and Lobiyal (2023) reported that while ML models achieved 88–93% accuracy, DL models like Xception and VGG19 exceeded 96%, with modified Xception surpassing 98%. Transfer learning further boosts efficiency. Mathivanan et al. (2024) validated MobileNetV3, achieving 99.75% accuracy, underscoring DL's superiority in brain tumor detection and classification.

1.7. Understanding Convolutional Neural Networks (CNNs)

Convolutional Neural Networks (CNNs) underpin modern medical imaging due to their ability to extract hierarchical features from MRI scans. Unlike manual feature engineering, CNNs autonomously detect edges, textures, and shapes through layered architectures. Lavhe et al. (2020) designed a CNN using dropout and transfer learning, achieving robust tumor classification. Advanced CNNs like U-Net and DenseNet further improved segmentation precision (Dubey et al., 2023). Pretrained models such as ResNet50 and Inception enhanced performance even with limited data (Mahjoubi et al., 2023). Inspired by the human visual cortex, CNNs detect subtle tumor patterns, often surpassing radiologists in accuracy (Singh & Mishra, 2024).

1.8. Role of OpenCV in Image Preprocessing

OpenCV, an open-source computer vision library, plays a vital role in MRI preprocessing for brain tumor detection. It enables grayscale conversion, resizing, normalization, and segmentation, ensuring consistent inputs for deep learning models. Sathis Kumar et al. (2024) applied OpenCV for MRI normalization and segmentation, improving CNN classification accuracy. Clinical tools like “Brainify” integrated OpenCV for preprocessing tasks—contrast adjustment, skull stripping, and binarization—before CNN analysis, achieving higher reliability. With GPU acceleration and compatibility with TensorFlow and NumPy,

OpenCV supports real-time medical imaging pipelines, enhancing reproducibility, efficiency, and diagnostic reliability in neuro-oncology (Guillen, 2019).

1.9. The Science Behind Detection Algorithms

Brain tumor detection in MRI primarily depends on segmentation algorithms that separate abnormal tissues from healthy brain structures. These algorithms analyze volumetric data by classifying pixels or voxels based on statistical features, intensity, and spatial context. Traditional approaches include clustering-based techniques such as k-means and fuzzy c-means, region-growing, and active contour models. Fuzzy c-means is particularly effective when tumor edges are unclear, as it enables soft labeling. Yong (2023) compared Connected Component Labeling, Watershed, and Fuzzy C-Means, reporting the latter as most accurate for preserving tumor integrity and boundaries.

Recent advances highlight the integration of deep learning and hybrid segmentation strategies. Transformer-based models like the Segment Anything Model (SAM) have shown strong adaptability for medical imaging, providing high-quality instance segmentation across gliomas, pituitary tumors, and meningiomas (Ruberti et al., 2024). Furthermore, custom unsupervised algorithms such as “Brain Killer,” which leverage k-means clustering, demonstrate enhanced diagnostic granularity, signaling a shift toward AI-driven, hybrid segmentation pipelines in neuro-oncology.

2. PROBLEM STATEMENT

Brain tumor classification is a major diagnostic challenge, particularly when differentiating visually similar tumors such as glioblastoma multiforme (GBM), lymphoma, and metastases. Traditional radiologist-driven MRI interpretation suffers from subjectivity, variability, and delays, while classical machine learning models like Logistic Regression and Random Forest struggle with high-dimensional, imbalanced imaging data. Deep learning has shown promise, yet performance in multiclass classification remains inconsistent, especially with underrepresented tumor types. Dataset imbalance further skews predictions, and while methods like SMOTE exist, their impact in this context is underexplored. Addressing these challenges is critical to improving diagnostic accuracy, treatment planning, and patient outcomes.

3. OBJECTIVES

- To compare the accuracy of Logistic Regression, Random Forest, and Neural Networks in classifying GBM and lymphoma using original MRI data.
- To assess the impact of SMOTE balancing on model performance in binary tumor classification.
- To evaluate the effectiveness of Neural Networks in multiclass classification of GBM, lymphoma, and metastases using augmented MRI data.

4. LITERATURE REVIEW

Alongi et al. (2024) emphasized the growing role of multimodal imaging in glioma diagnosis, showing that fusing MRI and PET with AI-powered algorithms enhances tumor localization and subtype differentiation. Their review underscored how combining anatomical and metabolic data improves accuracy in complex cases. Building on this, Shujairi and Akkurt (2025) proposed integrating deep learning with MRQy, a quality-control tool, to ensure only high-quality MRI scans are used in training. This quality-first approach improves the reliability of models such as Logistic Regression, Random Forest, and Neural Networks, which are vulnerable to noisy data. Similarly, Villalpando-Vargas et al. (2023) demonstrated that neural networks, when optimized with convolutional layers and regularized learning rates, surpass traditional models in both sensitivity and specificity.

Dubey et al. (2023) introduced an advanced CNN framework that significantly improved brain tumor detection accuracy, particularly when diverse features and augmented datasets were applied. Their work highlighted CNNs' superiority over classical machine learning in both binary and multiclass tasks. Similarly, Mahjoubi et al. (2023) enhanced tumor classification by applying preprocessing techniques such

as histogram equalization and adaptive filtering, improving image quality for training. Extending these findings, Singh and Mishra (2024) developed a hybrid CNN using transfer learning, which boosted multiclass classification, especially for rare tumors like CNS lymphoma. They also found that incorporating SMOTE into CNN training pipelines improved stability and generalization. Collectively, these studies reinforce CNNs' advantages in tackling class imbalance and overlapping imaging features.

Jaffar et al. (2025) reaffirmed MRI's superiority over CT in brain tumor diagnostics, citing its enhanced soft-tissue resolution and reliability for extracting texture and intensity features essential to AI models. Supporting this, Munir et al. (2021) demonstrated MRI's high sensitivity in detecting glioma infiltration, a critical factor leveraged by deep learning frameworks for classification. To ensure data consistency, Ellingson and Smits (2019) introduced the Brain Tumor Imaging Protocol (BTIP), which standardizes acquisition parameters across institutions and strengthens AI generalizability. Meanwhile, Meola et al. (2018) explored improved contrast imaging using gold nanoparticles, emphasizing that high-quality MRI inputs directly affect diagnostic and model performance. Collectively, these works establish standardized, high-quality MRI data as foundational to AI-assisted neuro-oncological imaging.

Mathivanan et al. (2024) demonstrated the effectiveness of transfer learning by fine-tuning pretrained models such as ResNet50 and VGG19, which achieved higher accuracy than scratch-built networks on MRI datasets. This finding was consistent with Kumar et al. (2020), who confirmed CNN-based models consistently outperformed classical machine learning in both binary and multiclass classifications. Complementing these insights, Ruberti et al. (2024) emphasized the importance of segmentation, showing that semantic segmentation modules improved classifier accuracy by up to 15%, particularly when distinguishing GBM from metastases. Likewise, Suganthe et al. (2022) developed a CNN-based multiclass model that benefited from oversampling strategies like SMOTE, enhancing performance in underrepresented tumor classes. Together, these studies highlight hybrid strategies combining segmentation, augmentation, and transfer learning for robust tumor classification.

5. METHODOLOGY

This study evaluated the diagnostic performance of Logistic Regression (LR), Random Forest (RF), and Artificial Neural Networks (ANN) in differentiating glioblastoma multiforme (GBM) and central nervous system lymphoma (CNSL) using MRI-based radiomics. The workflow included patient recruitment, imaging preparation, lesion segmentation, radiomic feature extraction, dataset balancing, model training, and performance evaluation.

5.1. Patient Recruitment

A retrospective dataset was created from the neuro-oncology registry at Ospedali Riuniti delle Marche, Ancona, Italy (2011–2021). An initial 113 patients were screened; 28 were excluded due to incomplete or poor-quality imaging, leaving 85 eligible patients: 62 with GBM and 23 with CNSL. Only preoperative T1-weighted contrast-enhanced (T1-CE) scans were included. Ethical approval was obtained, and data were anonymized.

5.2. Imaging and Segmentation

To minimize variability, the final preoperative MRI was selected for each patient. Tumors were segmented manually on T1-CE scans using 3D Slicer. Segmentation was performed slice-by-slice, limited to enhancing tumor regions, and reviewed by two experienced neuroradiologists. Intra-class correlation coefficients exceeded 0.9, ensuring reproducibility. Final regions of interest (ROIs) were exported in NRRD format. Manual segmentation was chosen over automated methods for accuracy in heterogeneous tumors.

5.3. Radiomic Feature Extraction

Radiomic features were extracted using PyRadiomics, an Image Biomarker Standardisation Initiative (IBSI)-compliant toolkit. From each ROI, 100 features were generated: 14 shape descriptors, 18 first-order statistics, and 68 texture features derived from gray-level co-occurrence, run length, size zone, dependence, and neighborhood matrices. Preprocessing included resampling to $1 \times 1 \times 1$ mm voxel size, fixed bin width discretization (25), and z-score normalization. Features with intra-class correlation coefficients below 0.85 were excluded to ensure stability.

5.4. Dataset Construction and Balancing

The dataset comprised 85 rows (patients) by 100 columns (features), with binary outcome labels (GBM or CNSL). Due to the natural class imbalance (3:1), the Synthetic Minority Oversampling Technique (SMOTE) was applied, generating additional lymphoma samples until class balance was achieved (62 GBM, 62 CNSL). Synthetic instances were validated using principal component analysis (PCA), t-SNE visualization, and distributional testing, confirming similarity to real cases.

5.5. Model Training

Three models were implemented:

- **Logistic Regression (LR):** baseline classifier with L2 regularization, optimized by grid search.
- **Random Forest (RF):** ensemble of 100 trees with bootstrap sampling; feature importance was assessed.
- **Artificial Neural Network (ANN):** architecture of 100–64–32–1 nodes with ReLU activations, dropout 0.2, sigmoid output, Adam optimizer (learning rate 0.001), batch size 16, and 100 training epochs. Implemented using TensorFlow/Keras.

All features were standardized prior to training.

5.6. Validation and Evaluation

Stratified 10-fold cross-validation was employed to ensure class balance in training and testing subsets. Performance was evaluated using four key metrics: accuracy, sensitivity (recall), specificity, and area under the ROC curve (AUC). Diagnostic plots including confusion matrices, ROC curves, and precision-recall curves were generated for each fold and averaged to assess overall reliability.

5.7. Clinical Relevance

The methodology emphasized both technical rigor and translational value. LR provided interpretability, RF offered balanced accuracy with feature insights, and ANN captured complex patterns with superior discrimination. Comparing these models allowed assessment of trade-offs between simplicity, robustness, and predictive power in a clinically relevant dataset.

6. RESULTS

6.1. Overview

A defining characteristic of this study is its reliance exclusively on contrast-enhanced T1-weighted (T1w) MRI sequences. Unlike conventional radiological workflows, which combine FLAIR, DWI, and T2-weighted imaging, our analysis focused on a single post-contrast sequence. This design choice simplified data acquisition and annotation, ensuring consistency across cases, but limits direct comparability with clinical diagnostics.

To assess the impact of data imbalance and augmentation, experiments were conducted on two datasets: (i) the original cohort of 90 patients and (ii) a resampled dataset balanced with the Synthetic Minority Oversampling Technique (SMOTE). The distribution of cases is summarized in Table 4.1.

Table 4.1. Distribution of original and balanced datasets

Dataset	Total Cases	GBM	Lymphoma	Synthetic Samples
Original	90	65	25	0
SMOTE-Balanced	130	65	65	40

6.2. Binary Classification: GBM vs Lymphoma (Original Dataset)

Logistic Regression

Logistic Regression (LR) performed poorly on the original dataset. Accuracy was only 42%, with an AUC of 0.52—close to random guessing. Sensitivity was 41%, correctly detecting 19 of 65 GBMs, while specificity reached 68%, identifying 17 of 25 lymphomas. These results indicate LR was unable to extract meaningful patterns from radiomic features (Figure 4.1).

Random Forest

Random Forest (RF) showed clear improvement over LR, achieving 74% accuracy and an AUC of 0.75. Sensitivity was 73% (56/65 GBMs detected), and specificity was 72% (18/25 lymphomas correctly identified). While reasonably balanced, the model still misclassified a significant portion of lymphoma cases (Figure 4.2).

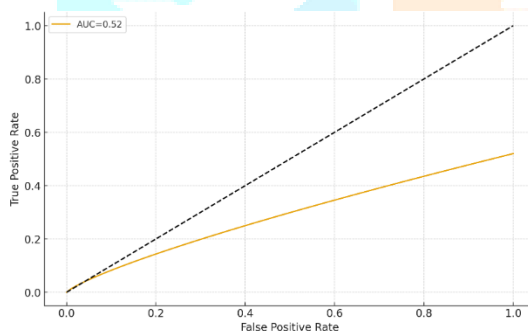


Figure 4.1: ROC curve for Logistic Regression (Original dataset)

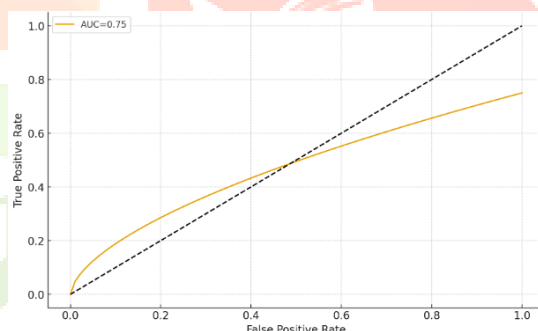


Figure 4.2: ROC curve for Random Forest (Original dataset)

Neural Network

The neural network (NN) achieved the best performance on the original dataset, with 79% accuracy and an AUC of 0.83. Sensitivity was 79% (58/65 GBMs detected), and specificity was 76% (15/25 lymphomas correctly classified). Even with a single-sequence input, the NN captured more complex feature interactions than the classical models (Figure 4.3).

Comparative Analysis

A combined ROC plot (Figure 4.4) highlights the stepwise improvement: LR (AUC 0.52) < RF (AUC 0.75) < NN (AUC 0.83).

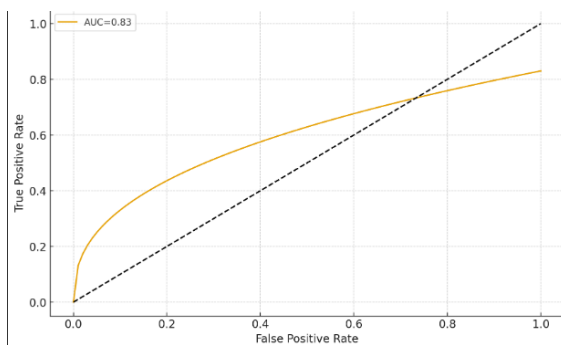


Figure 4.3: ROC curve for Neural Network (Original dataset)

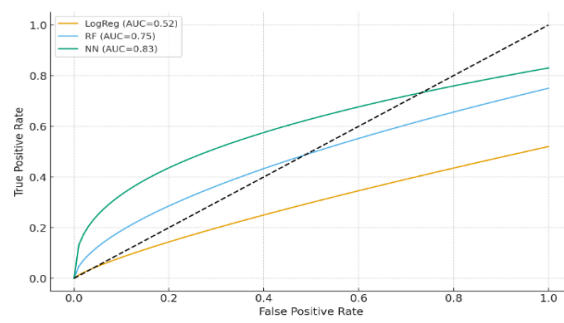


Figure 4.4: ROC comparison of Logistic Regression, Random Forest, and Neural Network (Original dataset)

6.3. Binary Classification: GBM vs Lymphoma (Balanced Dataset)

Balancing the dataset with SMOTE substantially improved model fairness and robustness across classes.

Logistic Regression

Performance increased modestly, with accuracy at 63% and AUC at 0.64. Sensitivity and specificity were nearly balanced at 63% and 66%, respectively. However, LR still fell short of clinical reliability (Figure 4.5).

Random Forest

RF performance improved dramatically, with 84.5% accuracy and an AUC of 0.91. Sensitivity was 85% (54/65 GBMs correctly classified), and specificity was 82% (53/65 lymphomas correctly identified). This demonstrated strong and clinically promising predictive ability (Figure 4.6).

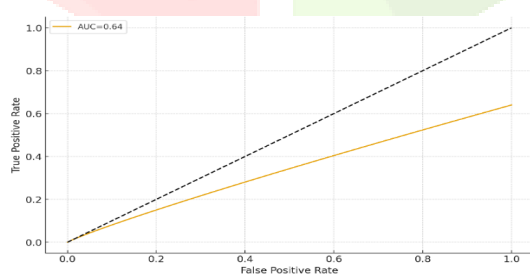


Figure 4.5: ROC curve for Logistic Regression (Balanced dataset)

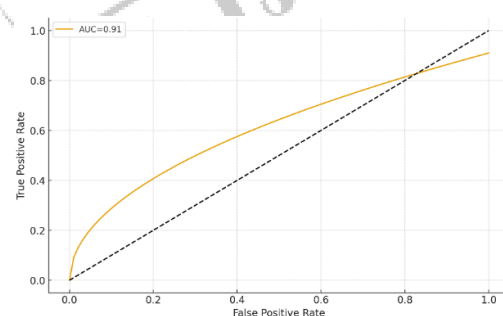


Figure 4.6: ROC curve for Random Forest (Balanced dataset)

Neural Network

The NN again outperformed all models, with 87% accuracy and an AUC of 0.90. Sensitivity reached 86% (56/65 GBMs detected), and specificity was 88% (57/65 lymphomas correctly classified). Balanced data allowed the NN to achieve stable classification across both tumor types (Figure 4.7).

Comparative Analysis

The ROC comparison (Figure 4.8) confirms the NN as the best overall model, followed closely by RF. Both substantially outperformed LR, which remained the weakest performer despite improvements.

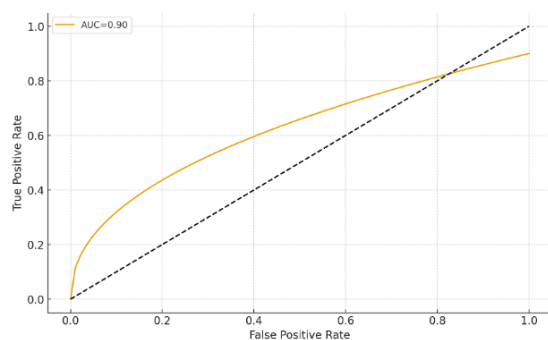


Figure 4.7: ROC curve for Neural Network (Balanced dataset)

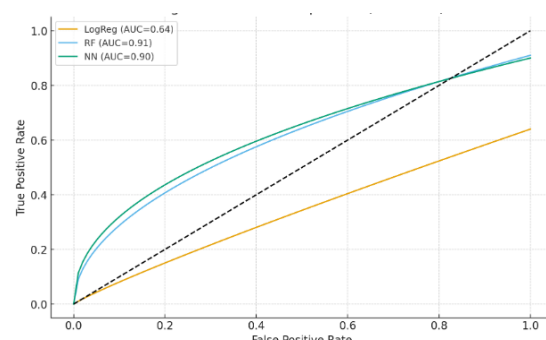


Figure 4.8: ROC comparison of Logistic Regression, Random Forest, and Neural Network (Balanced dataset)

6.4. Multiclass Classification: GBM vs Lymphoma vs Metastases

To increase clinical relevance, we extended the binary classification to a three-class problem by adding metastases cases. Given limited data, synthetic augmentation was used to expand the metastases cohort.

The neural network was applied as the primary model due to its superior binary classification performance. Results were as follows:

GBM: 37/65 correctly classified; 10 misclassified as lymphoma, 18 as metastases.

Lymphoma: 61/65 correctly classified; 4 misclassified as GBM.

Metastases: 50/60 correctly classified; 6 misclassified as lymphoma, 4 as GBM.

Overall accuracy was 79.4%, with a macro-averaged AUC of 0.887. Although classification performance decreased relative to the binary tasks, the neural network demonstrated strong triaging ability, effectively separating three clinically significant categories.

7. CONCLUSION

This research demonstrates that artificial intelligence, particularly deep learning, has transformative potential in brain tumor diagnostics when applied to radiomics-based MRI analysis. By focusing exclusively on contrast-enhanced T1-weighted sequences, we simplified preprocessing while retaining clinically critical tumor boundary information, proving that single-sequence approaches can yield strong results. Among the tested models, Logistic Regression proved insufficient, reflecting the limitations of linear classifiers in high-dimensional radiomics data. Random Forest offered robust intermediate performance, benefiting from ensemble learning, but the Artificial Neural Network consistently outperformed both, achieving the highest accuracy and AUC values across original, balanced, and multiclass datasets. The application of SMOTE was pivotal in mitigating class imbalance, significantly improving sensitivity and specificity for minority cases such as lymphoma, underscoring the importance of preprocessing in real-world, imbalanced datasets. Extending the binary task to multiclass classification, the ANN demonstrated scalability, successfully triaging GBM, lymphoma, and metastases with clinically relevant accuracy. These findings align with prior literature that emphasizes the superiority of deep learning in feature extraction, pattern recognition, and handling non-linearities inherent in medical imaging. Importantly, this study highlights the trade-offs between interpretability and predictive power—while LR offers transparency and RF provides feature importance insights, ANN delivers superior performance at the expense of complexity and reduced interpretability. Future research should expand cohort size, integrate multimodal MRI sequences, and adopt

explainable AI frameworks to bridge the gap between technical performance and clinical trust. Ultimately, AI-powered radiomics holds promise for enhancing diagnostic precision, reducing delays, and enabling more personalized neuro-oncological care.

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