Radiogenomic Classification of Brain Tumor using MRI Sequences

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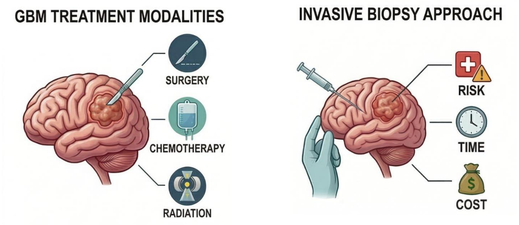
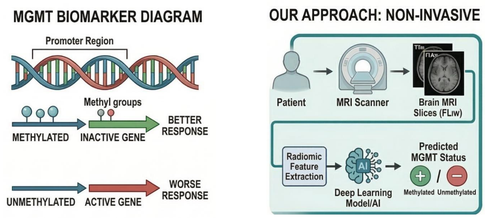
Background

- **Glioblastoma Multiforme (GBM)** is a highly aggressive brain tumor



- **O^6- methylguanine DNA methyltransferase (MGMT)** promoter methylation is a key biomarker for prognosis and treatment response.

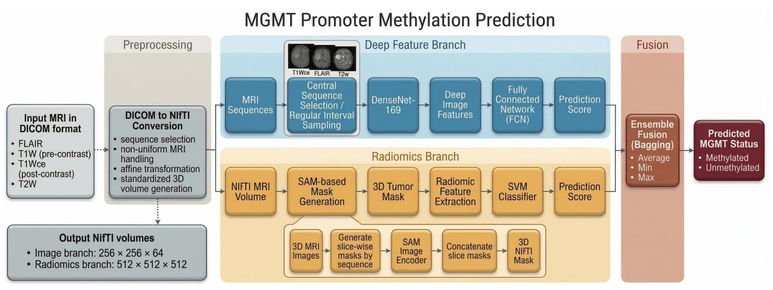


Objectives

- Develop a non-invasive framework to **predict MGMT promoter methylation** from brain MRI.
- Compare two feature extraction paths: radiomic features from SAM-generated masks and deep image features from DenseNet169.
- Evaluate whether ensemble learning can improve classification performance over individual models.

Methods

Proposed Framework

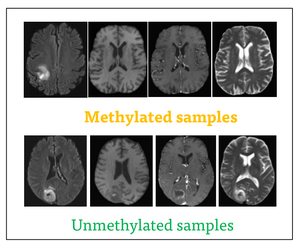


- **Preprocessing**
  - Convert MRI inputs from *DICOM* to *NIfTI* volumes.
  - Build 3D inputs using two slice-selection strategies:
    1. *Regular interval selection*
    2. *Central sequence selection*
- **Deep Feature Branch**: Create 3D stacks of size 256 × 256 × 64, extract image features using Densenet169 [3], and classify with a fully connected network using focal loss.
- **SAM Radiomics Branch**: Generate tumor masks slice by slice, reconstruct 3D masks, extract simple radiomic features (volume and energy), and classify with a linear SVM.
- **Fusion:** Fuse outputs using bagging ensemble methods: average, minimum, and maximum.
- **Predict MGMT Status**: Methylated / Unmethylated

Experiments

Dataset and Input

- Used the RSNA-MICCAI Brain Tumor Radiogenomic Classification dataset [1].
- Total 672 Patients Samples (Train-585, Test-87)



Training the Models

- *Focal Loss* to emphasizes hard/misclassified samples and down-weights easy/well-classified.
- DenseNet169 Setup: Image size 256, 64 images, batch size 1, learning rate 10e-6, LR decay 0.9, 150 epochs
- We used pretrained SAM [2].
- Experiments are done with 8 CPU cores, NVIDIA A100 80GB GPU, CUDA version 12.4, and PyTorch version 2.2.0

Evaluation Metrics

ROC Curve: A plot of **true positive rate (TPR)** versus **false positive rate (FPR)** across different classification thresholds. **TPR (Sensitivity)** measures the proportion of actual positives correctly identified.

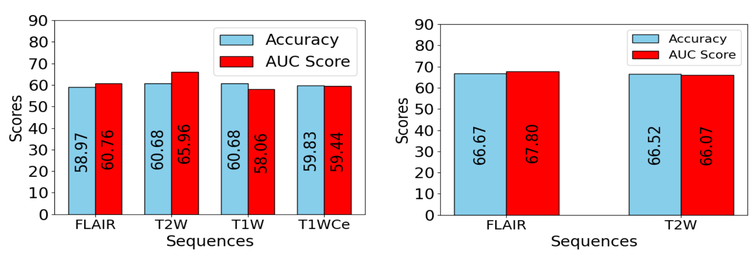
$$TPR = \frac{TP}{TP + FN} \qquad FPR = \frac{FP}{FP + TN}$$

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN}$$

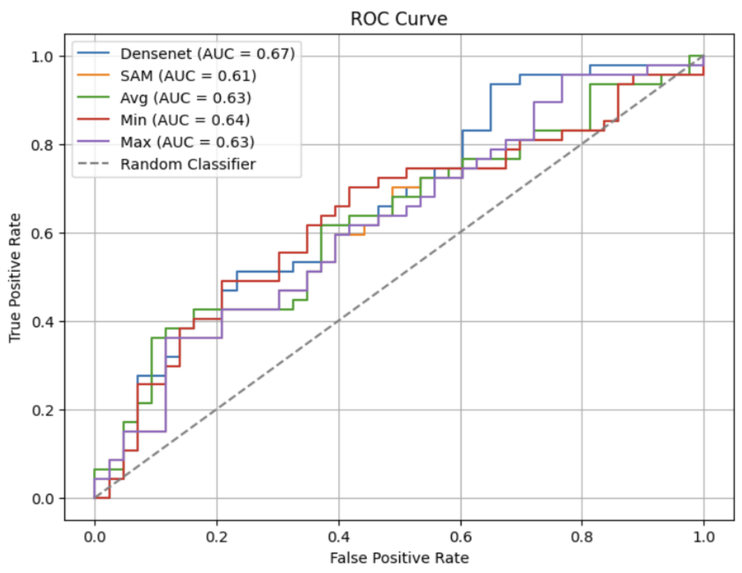
$$\text{AUC} = \sum_{i=1}^{m-1} \frac{(FPR_{i+1} - FPR_i) \cdot (TPR_i + TPR_{i+1})}{2}$$

Result

Densenet169 (Regular and Central Approach)



ROC curve of Densenet19 and SAM (regular Interval)



Conclusions

- Proposed a radiogenomic framework for **brain tumor classification** by predicting **MGMT promoter methylation** from multi-parametric MRI.
- Combined **SAM** and **DenseNet-169** to extract imaging information and classify MGMT status on the **RSNA-MICCAI dataset**.
- Achieved promising results, with **SAM reaching 61% AUC** and **DenseNet-169 reaching 67.54% AUC**, showing the effectiveness of the approach.

Future Works

- **Train SAM/MedSAM** on brain tumor MRI data to improve segmentation quality and downstream classification performance.
- **Replace DenseNet-169 with Vision Transformers (ViTs)** to explore stronger feature learning for MRI-based classification.
- **Use boosted ensembling**, keeping the best prediction probabilities during training and applying methods such as **AdaBoost**.

Impact

- Supports **non-invasive prediction** of MGMT methylation, reducing dependence on invasive diagnostic procedures.
- Contributes to **radiogenomics-driven precision medicine** by linking MRI patterns with clinically relevant genomic properties.
- Has the potential to assist **clinical decision-making and personalized treatment planning** for brain tumor patients.

References

[1] U. Baid et al., "The RSNA-ASNR-MICCAI BraTS 2021 Benchmark on Brain Tumor Segmentation and Radiogenomic Classification," arXiv preprint arXiv:2107.02314, 2021.

[2] A. Kirillov, E. Mintun, N. Ravi, H. Mao, C. Rolland, L. Gustafson, T. Xiao, S. Whitehead, A. C. Berg, W.-Y. Lo, et al., "Segment anything," in Proceedings of the IEEE/CVF International Conference on Computer Vision, pp. 4015–4026, 2023.

[3] G. Huang, Z. Liu, L. Van Der Maaten, and K. Q. Weinberger,

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