RSNA-MICCAI Brain Tumor Radiogenomic Classification

Deep Learning for Medical Image Analysis - UB - UPC

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Clinical background

Glioblastoma
(malignant tumor in the brain)

- Most common form of **brain cancer**
- **Median survival < 1 year**

The presence of the specific MGMT genetic sequence is an important prognostic factor and a strong predictor of responsiveness to chemotherapy.

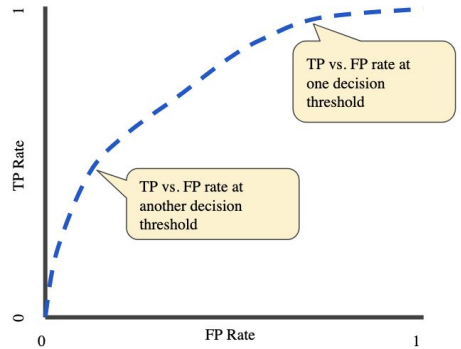
Problem: Genetic analysis of cancer **requires surgery** to extract a tissue sample.

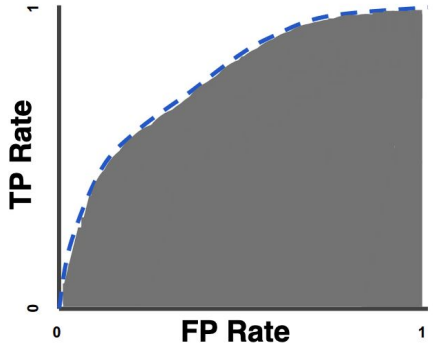
Challenge: Develop an accurate method to **predict the genetics of the cancer through imaging** such as radiogenomics, thus, minimizing the number of surgeries and refining the type of therapy required.

Result summarization

Evaluation metrics: **Area under the ROC curve (AUC)**, accuracy, FScore and Matthew's Correlation Coefficient.

The AUC is a metric that measures the overall discriminatory capacity of a model.





No straightforward clinical meaning

Results

Members	Score
	0.62174
	0.61881
	0.61732
	0.61562
	0.60751

Winning approach - AUC: 0.6217

Approach	3D CNN
Architecture	ResNet10
Loss	Binary Cross Entropy
Optimizer	Adam
Epochs	15
Learning Rate	lr = 0.0001 (epochs: 1->10) | lr=0.00005 (epochs: 10->15)
Batch Size	8
General Information	• Small trick: The best central image trick • One epoch -> 1 minute and 20 seconds using an RTX 3090.

Other approaches (2°) - AUC: 0.6188

Approach	2D CNN - LSTM - DICOM images to PNG
Architecture	CNN: EfficientNet B0 - LSTM: From scratch.
Loss	Binary Cross Entropy
Optimizer	Adam
Epochs	15
Learning Rate	0.0001
Batch Size	8
General Information	• Cross Validation • 2D convolution to map the 4-channel image into a 3-channel feature map • Data augmentation

Some thoughts

- Simpler models obtained in general better results
- The lack of straightforward clinical meaning is concerning **(AI Explainability problem)**