**Brain Tumor Radiogenomic Classification**

**Running instructions**

* First enable GPU within the notebook(we used Kaggle).
* Add competition named **RSNA-MICCAI Brain Tumor Radiogenomic Classification** to the notebbok for accessing input.
* Now continue with running the code

**Project Overview**

Glioblastoma is a highly aggressive form of brain cancer with a very poor prognosis. A critical genetic marker MGMT promoter methylation has been identified as a favorable prognostic factor and a predictor of chemotherapy responsiveness. Traditionally, determining this marker requires invasive surgery followed by genetic analysis.

This project aims to develop a deep learning model that predicts the MGMT promoter methylation status using MRI scans alone a step towards non-invasive radiogenomic diagnostics. It was built for the RSNA-MICCAI Brain Tumor Radiogenomic Classification challenge on Kaggle, using a ResNet10 model to predict patients responsiveness to chemotherapy .

**Dataset Details**

The dataset contains multi-parametric MRI scans for each patient, structured as follows:

- FLAIR (Fluid Attenuated Inversion Recovery)

- T1w (T1-weighted pre-contrast)

- T1Gd (T1-weighted post-contrast)

- T2w (T2-weighted)

Each patient's scan is stored in a dedicated folder named with a unique 5-digit ID. Each scan type is stored in its sub-folder with images in DICOM (.dcm) format.

**Example folder structure:**

data/train/00000/

│

├── FLAIR/

├── T1w/

├── T1wCE/

└── T2w/

The goal is to predict the probability that a tumor has MGMT promoter methylation (`MGMT\_value`) based solely on these MRI sequences.

**Model Workflow**

The model training and evaluation pipeline is implemented in `braintumor-final.ipynb` and follows these major steps:

**1. Data Preprocessing**

- DICOM file loading and conversion to Numpy arrays

- Resampling and resizing slices

- Normalization and stacking of modalities

**2. Model Architecture**

- A lightweight ResNet10 model tailored for 3D imaging input

- Binary classification head outputting a probability

**3. Training**

- Loss: Binary Cross-Entropy

- Optimizer: Adam

- Validation split for performance evaluation

**4. Prediction**

- Inference pipeline for test cases

- Output formatting for submission

**Sample Test Cases**

|  |  |  |  |
| --- | --- | --- | --- |
| Test Case ID | Patient ID / Input File | MGMT Value / Description | Result Description |
| |  | | --- | | TC01 |  |  | | --- | |  | | 762 | 0.5423619225621223 | Chemo Recommended |
| TC02 | 1 | 0.543903037905693 | Chemo Recommended |
| TC03 | 229 | 0.543903037905693 | Chemo Recommended |
| TC04 | 190 | 0.4979252964258194 | Chemotherapy not suitable |
| TC05 | 125 | |  | | --- | |  |  |  | | --- | | 0.45046495646238327 | | Chemotherapy not suitable |
| TC06 | brain1.png | Invalid Input - MRI data required (Detected format: PNG) |  |
| TC07 | Heart.jpg | Not a brain scan – it is a Heart scan! Expected brain scan |  |
| TC08 | brainjpg1.jpeg | Invalid Input - MRI data required (Detected format: DICOM - Non-MRI) |  |
| TC09 | spine.dcm | Not a brain scan – it is a Spine scan! Expected brain scan |  |
| TC10 | brainjpg1.dcm | Invalid Input - MRI data required (Detected format: DICOM - Non-MRI) |  |
| TC11 | lungs.png | Not a brain scan – it is a Lung scan! Expected brain scan |  |
| TC12 | brain1.dicom | Invalid Input - MRI data required (Detected format: DICOM - Non-MRI) |  |
| TC13 | ct.dcm | Invalid Input - MRI data required (Detected format: DICOM - Non-MRI) |  |

**Results**

**Training accuracy**

MAE: 0.034934

MSE: 0.001750

RMSE: 0.041835

Accuracy using MAE: 96.50658616877121

Accuracy using MSA: 99.82498434392868

Accuracy using RMSE: 95.81651274567116

**Testing accuracy**

MAE: 0.04683

MSE: 0.002480

RMSE: 0.049803

Accuracy using MAE: 95.31472755803001

Accuracy using MSA: 99.75196843706364

Accuracy using RMSE: 95.01972327137985