MGMT Classification in MRI Images

Submitted By

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DEPARTMENT OF COMPUTER SCIENCE AND ENGINEERING

INSTITUTE OF TECHNOLOGY

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MGMT Classification in MRI Images

Major Project - II

Submitted in partial fulfillment of the requirements

for the degree of

Master of Technology in Computer Science and Engineering

Submitted By

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Guided By

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DEPARTMENT OF COMPUTER SCIENCE AND ENGINEERING

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Certificate

This is to certify that the major project entitled **"MGMT Classification in MRI Images"** submitted by **Divyang Makwana(21MCEC15)**, towards the partial fulfillment of the requirements for the award of degree of Master of Technology in Computer Science and Engineering of Nirma University, Ahmedabad, is the record of work carried out by him under my supervision and guidance. In my opinion, the submitted work has reached a level required for being accepted for examination. The results embodied in this major project part-II, to the best of my knowledge, haven't been submitted to any other university or institution for award of any degree or diploma.

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Statement of Originality

I, **Divyang Makwana**, Roll. No. **21MCEC15**, give undertaking that the Major Project entitled "**MGMT classification in MRI Images**" submitted by me, towards the partial fulfillment of the requirements for the degree of Master of Technology in **Computer Science & Engineering (Specialization in Computer Science)** of Institute of Technology, Nirma University, Ahmedabad, contains no material that has been awarded for any degree or diploma in any university or school in any territory to the best of my knowledge. It is the original work carried out by me and I give assurance that no attempt of plagiarism has been made.It contains no material that is previously published or written, except where reference has been made. I understand that in the event of any similarity found subsequently with any published work or any dissertation work elsewhere; it will result in severe disciplinary action.

Signature of Student
Date: 23/05/2023
Place: Ahmedabad

Endorsed by
Dr. Rupal A. Kapdi
(Signature of Guide)

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Divyang Makwana
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Abstract

A malignant brain tumor known as a glioblastoma is an extremely life-threatening condition. It has been demonstrated that a favourable risk factor and indication of how well patients respond to chemotherapy is the presence of a specific genetic sequence known as MGMT promoter methylation in tumours. The only way to determine the presence of MGMT promoters so far is through genetic analyses that require an operation. In order to reduce the number of operations, it would be helpful to develop an accurate method for determining the presence of MGMT promoters using only MRI.

Abbreviations

MGMT	O6-methylguanine-DNA-methyltransferase
DL	Deep Learning
AUC	Area Under Curve.
GBM	Glioblastoma
TMZ	Temozolomide

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Chapter 1

Introduction

Brain Tumour Radiogenomic Classification is a research project with the goal of creating sophisticated methods for classifying brain tumors using genomic data and radiological imaging. Because of the complexity and diversity of brain tumors, it is essential to classify them correctly in order to manage patients and develop appropriate treatments.

1.1 General Introduction

It is known as radio genomics when radiological imaging features are combined with genomic information, such as genetic mutations or molecular markers, to better understand tumor characteristics and increase diagnostic precision. Researchers can discover significant correlations between imaging symptoms and underlying genetic changes by integrating these two imaging modalities, allowing for the creation of more specialized and individualized treatment plans.

Specifically focused on the methylation state of the MGMT promoter region, the RSNA-MICCAI Brain Tumour Radiogenomic Classification challenge offers a dataset of brain tumour pictures coupled with accompanying genomic data. In glioblastoma, a particularly aggressive form of brain tumour, the MGMT promoter methylation status is an important biological biomarker that affects therapy responsiveness and patient outcomes.

In order to accurately categorise brain tumours based on their MGMT promoter methylation status, this research endeavour aims to use machine learning and deep learning algorithms to analyse radiological images and genomic data. Clinicians may be able to save time, lessen subjectivity, and increase the overall accuracy of tumour classification by automating this classification process.

The provided method uses the Fastai package to develop a deep learning-based strategy for the radiogenomic categorization of brain tumours. It entails preprocessing the DICOM pictures, standardising them, training a convolutional neural network (CNN) model on the prepared data, and measuring the model's effectiveness with the right metrics. The unobserved brain tumour images' MGMT promoter methylation status is then predicted using the trained model.

This study adds to the development of precision medicine by addressing the RSNA-MICCAI Brain Tumour Radiogenomic Classification challenge and equipping medical personnel with more precise and effective tools for the detection and management of brain tumours.

Chapter 2

Literature Survey

2.1 Summary of relevant papers

There are many classification algorithms are used to classify the status of MGMT in MRI Images. we are going to do the comparative survey of different existing research methodology of MGMT classification. The figure 2.1 and 2.2 shows the literature survey of most relevant papers for this title is mentioned.

In this[1] study, a quick and compact CNN is shown to be able to predict if MGMT promoter methylation would be found in MRI images. The authors feed a neural network using the median "middle-most" cross section of a FLAIR scan as the input. Rectified Linear Unit (ReLU) activation is utilized by the seven-layer CNN architecture. The Categorical Cross Entropy Loss function is used as the loss function, and the Adam Optimizer is the used as the optimizer. The model was trained utilizing GPU acceleration, and the authors were able to extrapolate data with good performance.

In this [2] study, authors examine the categorization of MGMT status in brain tumour MR images using deep learning. The MGMT status is crucial for figuring out how well chemotherapy works for glioblastoma patients. In order to overcome a scarcity of training information the scientists have applied a Transfer Learning Approach using video clip categorization network C3D. With the use of a locally linked layer, MRI sequences were combined. AUC for the public validation set is 0.689, the method proved successful in differentiating MGMT methylation from unmethylated patients. AUC was provided by 0.577 on the private test set. Additional research is required to evaluate clinical signifi-

cance and survival prediction accuracy.

The authors of this [3] paper suggest a technique for estimating the level of MGMT promoter methylation in high-grade gliomas using MR images. They use deep convolutional neural networks to segment the tumour, and they extract both radiomic and form data that were trained using a variational autoencoder. They use a typical machine learning methodology, which starts with feature selection and ends with training a random forest classification model, to get predictions. Before entering their predictions into the competition, they test and improve their methods using the RSNA-ASNR-MICCAI BraTS 2021 challenge dataset.

In order to enhance the categorization of MGMT promoter methylation directly from MRI images, a new preprocessing technique is presented in this study. In addition to MGMT promoter methylation identification, the suggested approach in this paper[4] can be useful for other purposes. Based on MRI scan analysis, the scientists created a technique they call Intermediate State Generator (IS-Gen), which can be customised for a variety of deep learning models. The IS-Gen method may be used for more than simply MRI images. It may be used to iteratively impute intermediary data layers to create a more continuous volumetric dataset from any three-dimensional dataset. In addition, the authors created four distinct models to analyse and contrast performance using the same unorganised dataset. The first two models utilised methods based on radiomic characteristics.

This paper [5] research offers a deep learning-based strategy employing Convolutional Neural Networks (CNN) to forecast MGMT methylation status in glioblastoma patients using non-invasive MRI data. The suggested method avoids laborious tumour segmentation, picture pre-processing, and feature extraction stages. By maximising the search space, Bayesian optimisation is used to find the hyperparameters that help with higher classification performance. The validation and testing area under curves (AUC) for the proposed technique were 0.718 and 0.477, respectively, according to the validation and testing datasets given by RSNA-MICCAI.

This [6] study suggests a deep-learning approach for analysing multi-modal MRI data to assess the MGMT promoter methylation status of gliomas. To improve classification performance overall, the suggested technique combines four sub-structures: multi-modal feature aggregation, light attention mechanism, separable embedding, and modal-wise shortcut. The performance of the existing MRI-based learning models for detecting MGMT methylation status is also reviewed in the research, and its results are contrasted with those of the suggested approach. In terms of accuracy and effectiveness, the suggested strategy performs better than the already used models. The proposed approach can be a non-invasive substitute for surgically removing brain tissue samples to ascertain the state of MGMT promoter methylation, according to the paper's conclusion.

The purpose of this [7] study is to evaluate the accuracy of noninvasive MGMT methylation status prediction using quantitative and qualitative imaging characteristics. Retrospective examination of MR images from GBM patients was done by the authors, who then used machine learning to create multivariate prediction models. On information from the The Cancer Genome Atlas (TCGA) database, they evaluated these models. The acquired results offer more proof that MGMT methylation status in GBM and common preoperative MRI variables are related.

The evaluation of cutting-edge techniques for the segmentation of intrinsically heterogeneous brain glioblastoma sub-regions in mpMRI scans and the evaluation of techniques to predict the MGMT promoter methylation status on the baseline scans prior to surgery are the main topics of this paper [8]. Participants in the challenge can use a dataset of 8,000 MRI scans from 2,000 glioma patients to refine their approaches and create segmentation labels for the various subregions of the tumour. The properties of the challenge data are also covered in the publication, along with the annotation procedure used to produce the challenge data, a thorough explanation of the challenge's requirements, and an assessment of how well each participating technique performed. The limits and currently being considered future directions are covered in the paper's conclusion.

Table 2.1: Literature Survey

Title	**year**	**Methodology**	**Summary**	**Accuracy**
Simple and Fast Convolutional Neural Network Applied to Median Cross Sections for Predicting the Presence of MGMT-Promoter Methylation in FLAIR MRI Scans[1]	2022	CNN	The computational complexity is reduced by focusing the training on the median cross sections of the FLAIR scans in the data set.	59.48
A Video Data Based Transfer Learning Approach for Classification of MGMT Status in Brain Tumor MR Images [2]	2022	CNN	In this paper, study conducted of MGMTstatus assessmentby multiparametric MRI scans and od the ability of deep learning for classification of this task.	57.70
Prediction of MGMT Methylation Status of Glioblastoma Using Radiomics and Latent Space Shape Features [3]	2022	CNN	In this paper, Method was proposed for predicting the status Of MGMTpromoter methylation in high-grade gliomas.	58.20
Optimizing Prediction of MGMT Promoter Methylation from MRI Scans using Adversarial Learning [4]	2022	CNN	study to detect the methylation status through noninvasive magneticre sonance imagining based machine learning model was conducted in this paper.	58.20

Table 2.2: Literature Survey

Title	**year**	**Methodology**	**Summary**	**Accuracy**
Radiogenomic prediction of MGMT using deep learning with bayesian optimized hyperparameters [5]	2022	CNN	They proposed a CNN model with Bayesian Optimized hyperparameters to classify MGMT methylation status in glioblastoma patients. Bays optimization is applied to obtained the hyperparameters for the CNN model.	47.70
An Attentive Multi-Modal CNN for Brain Tumor Radiogenomic Classification [6]	2022	CNN,SVM	A novelattentive deep-learning-based classification model that integrates multi-modal feature aggregation, and modal-wise shortcuts for performance improvement was proposed in this paper.	56.41
Learning MRI-based classification models for MGMT methylation status prediction in glioblastoma [7]	2022	CNN	The aim of this study was to assess the ability of quantitative and qualitative imaging variables in predicting MGMT methylation status Noninvoaseively.	58.00
The RSNA-ASNR-MICCAI BraTS 2021 Benchmark on Brain Tumor Segmentation and Radiogenomic Classification [8]	2022	CNN	The RSNA-ASNR-MICCAI BraTS 2021 challenge targets the evaluation of computational algorithms assessing the same tumor compartmentalization, as well as the underlying tumor's molecular characterization.	59.48

Chapter 3

Dataset

3.1 Introduction of Dataset

The RSNA and MICCAI provided a labeled dataset of MRI scans for a competition. The data was divided into three parts: training, validation, and testing data.

- Training
- Validation
- Testing

The data included the following kinds of scans:

- Fluid Attenuated Inversion Recovery
- T1-weighted pre-contrast
- T1-weighted post-contrast
- T2-weighted

The database used for the competition was a large and diverse dataset. It included MRI scans from a variety of patients with different conditions. This allowed the models to learn to identify a variety of different patterns in the MRI scan.
The use of a large and diverse dataset is important for training machine learning models. It allows the models to learn to identify a variety of different patterns in the data. This can improve the performance of the models on unseen data.

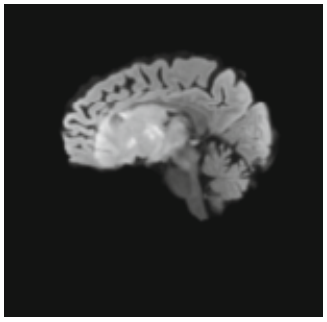

Figure 3.1: FLAIR

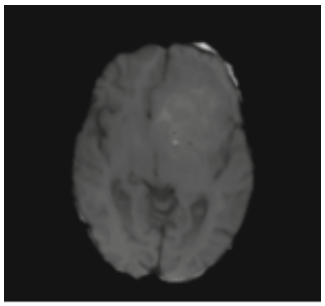

Figure 3.2: T1w

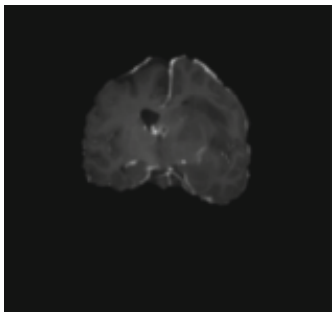

Figure 3.3: T1wCE

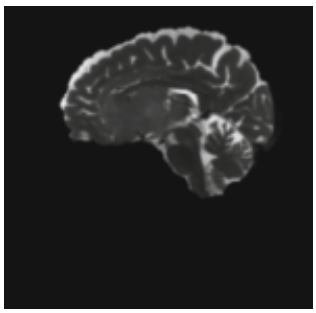

Figure 3.4: T2w

The testing data consisted of 400 directories, the validation data consisted of 87 directories, and the training data consisted of 582 directories of MRI scans. The images were in DCM format and had a resolution of 256 $\times$ 256 pixels. The training data was class-balanced, meaning that there was an equal number of images with and without the MGMT promoter.

Figures 3.5 and 3.6 show examples of MRI scans with and without the MGMT promoter. The MGMT promoter is highlighted with a value of 1 in images with the promoter present, and with a value of 0 in images without the promoter present.

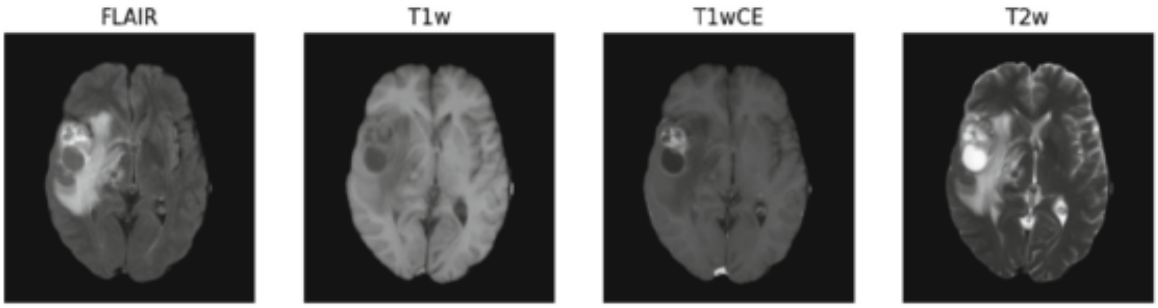

Figure 3.5: MGMT Status:0

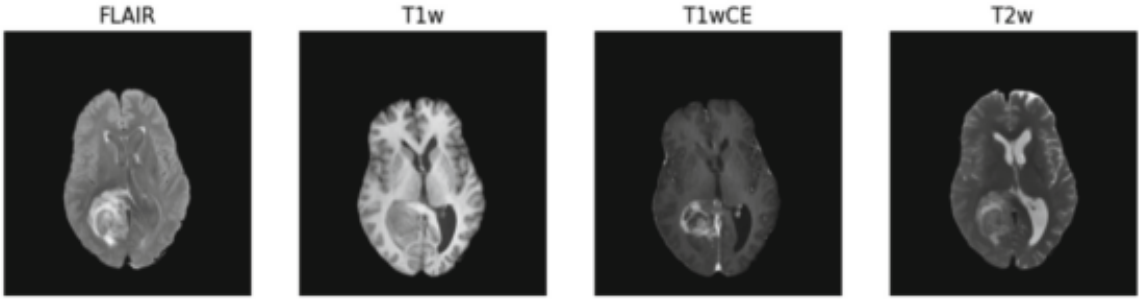

Figure 3.6: MGMT Status:1

The Brats dataset also contains clinical information on the patients, such as age, gender, and survival rates, in addition to the imaging data. Researchers are now able to investigate the connections between tumour characteristics, clinical variables, and imaging aspects.

The Brats dataset has gained international attention as a benchmark dataset in the field of medical image analysis. It makes it possible to create and assess cutting-edge algorithms for classifying, segmenting, and predicting brain tumours. The openness of the dataset promotes collaboration and advances in the identification and management of brain tumours.

Chapter 4

Proposed Method

Here, an algorithm that uses machine learning to classify brain tumour radiogenomic data is examined. To preprocess and analyse medical picture data, the code makes use of a variety of libraries and frameworks, including Torch, Fastai, Seaborn, Matplotlib, Pydicom, and Pandas. The ultimate objective is to forecast the MGMT gene promoter in patients with brain tumours.

The code begins by loading the required modules and libraries, including system-related utilities, image processing programmes, deep learning frameworks, and data visualisation tools. After that, it determines whether CUDA is available and initialises the random seed for repeatability.

The next stage is to process DICOM (Digital Imaging and Communications in Medicine) files, which contain information on medical imaging. The script takes the appropriate information from the DICOM files, makes the required adjustments, and saves the images in PNG format. The next classification challenge uses these transformed photos as its input.

4.1 Data Preparation

The script reads labels for the training data from a CSV file. Based on predetermined criteria, specific cases are excluded, and a count plot is used to show the distribution of the remaining data. The code then goes on to resolve DICOM files by converting them to PNG format and saving them in the relevant folders after creating separate folders for training and testing data.

4.2 Data Loading and Preprocessing

The code generates a DataLoaders object, which mixes the training and validation data, using the Fastai package. The loading and preprocessing of the data for the model are handled by this object.

All of the photos in the dataset are subjected to an image transformation to ensure uniformity in the input data. The photos are resized using the Resize transformation to a given size (in this case, 224x224 pixels). Prior to feeding the images into the neural network, this resizing phase is crucial to make sure that all of the images have the same proportions.

The batch size is set to 64. The amount of samples that will be sent through the network at once during training is referred to as the batch size. By processing more data simultaneously, a higher batch size can increase efficiency, but it also calls for more memory.

Information regarding the labels and filenames of the photos is needed by the DataLoaders object. The label col argument in this code is set to 1, indicating that the label data is kept in the DataFrame's second column (the "value" column). The third column of the DataFrame (the "file" column), where the filenames of the photographs are stored, is indicated by the value of the function col argument, which is set to 2.

The code invokes the show batch() function to display a batch of photographs from the dataset after creating the DataLoaders object. This offers a visual preview of the data that has been loaded and modified, assisting in verifying that the preparation processes have been appropriately applied.

Overall, the preprocessing and data loading stages make sure that the training and validation data are correctly prepared for the neural network model's training. The photos are scaled to a uniform size, and the DataLoaders object is given the appropriate label and filename data for quick handling and training.

4.3 Model Architecture

The PyTorch framework is used in the code to define a neural network model.

The Model has the following layers :

- 2 Convolutional layers
- 2 Max pooling layers

- 3 Fully connected layers

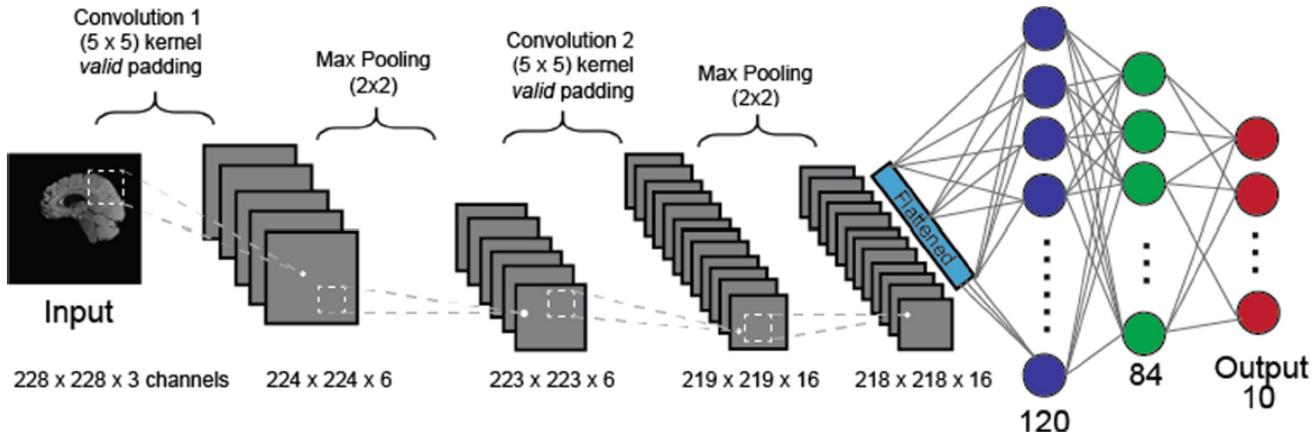

Figure 4.1: Neural Network Architecture [1]

Conv1 and Conv2 are the first two convolutional layers in the model, which extract features from the input images. These layers are defined using the PyTorch library's Conv2d class. Six feature maps are produced by the first convolutional layer from an input of three channels (representing the RGB colour channels of the images). Six input feature maps are used in the second convolutional layer to produce 16 output feature maps. The convolutional kernel for both layers is 5x5 , and after each convolution operation, a ReLU activation function is used.

The MaxPool2d class from PyTorch is used to perform a max pooling operation after each convolutional layer. The most significant characteristics are kept while the spatial dimensions of the feature maps are reduced using the max pooling process. In this code, the feature maps are downsampled using a 2x2 max pooling window with a stride of 2.

After the convolutional and pooling layers, there are three fully connected layers (fc1, fc2, and fc3). These completely connected layers receive input from the prior layers' flattened feature maps for categorization. These layers are defined using PyTorch's Linear class. The fully connected layers are divided into three groups with sizes of 120, 84, and 10, respectively.

The final fc3 produces the model's output. It describes the expected probabilities of the radiogenomic classification task for brain tumors. The ReLU activation function is not applied to the output layer.

The model is trained using the training dataset during the training phase. DICOM pictures that have undergone processing and been converted to PNG format make up the training data. The model is trained to recognize the patterns and traits that can be used to categorize different types of brain tumors.

The given below figure is demonstrating that 285 patients have 0 MGMT value while 300 patients have 1 MGMT value.

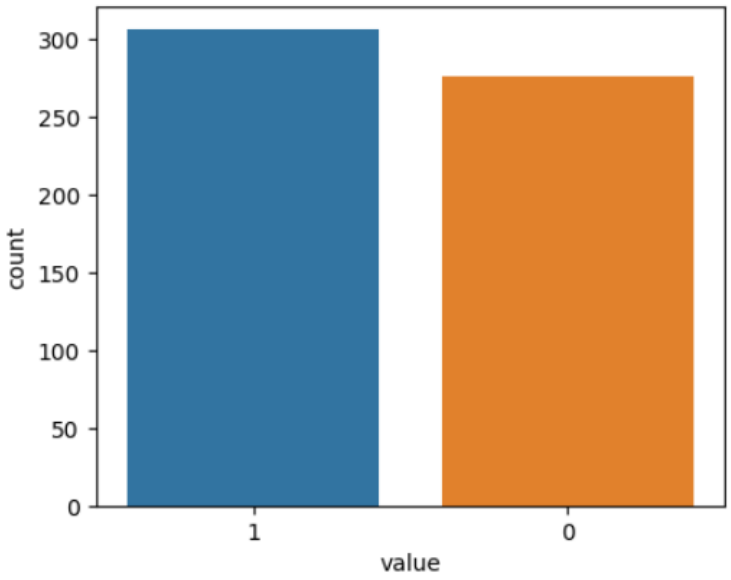

Figure 4.2: count plot

The learner object's fit one cycle method is used for training, and it uses backpropagation and gradient descent to optimize the model's parameters. A predetermined number of epochs (EPOCHS) are used to train the model, with each epoch denoting a complete run over the training dataset. To reduce the loss and enhance its predicting skills, the model modifies its weights and biases at the beginning of each epoch. The training progress is shown, together with data like accuracy and error rate, as well as the loss.

Examining Phase:

In the testing stage, the trained model's performance is assessed using test dataset data that has not yet been viewed. The test data is made up of DICOM images that have also undergone processing and PNG format conversion. Each test item's labels (probability of having MGMT promoter methylation) are predicted using the trained model.

A data frame (dfntest) with the anticipated probability has been created. The predictions of the model can be further examined and judged, for example by computing the lowest and maximum probability. For submission or further analysis, the final predictions are saved in a CSV file (submission.csv) with the necessary column names.

Chapter 5

Results and Analysis

The model was trained for 100 epochs, and the loss and accuracy curves show that the model is learning to fit the data and classify it correctly.

epoch	train_loss	valid_loss	error_rate	accuracy	time
0	1.282506	0.714728	0.474138	0.525862	00:04
1	1.232943	0.714091	0.474138	0.525862	00:03
2	1.198714	0.698580	0.448276	0.551724	00:04
3	1.156514	0.677973	0.474138	0.525862	00:04
....	.....	.....	....	...	....
95	0.697125	0.674066	0.431034	0.568965	00:04
96	0.695154	0.674723	0.439655	0.560345	00:04
97	0.694444	0.674971	0.431034	0.568965	00:04
98	0.696486	0.674824	0.422414	0.577586	00:04
99	0.697215	0.674732	0.431034	0.568965	00:04

Figure 5.1: Output

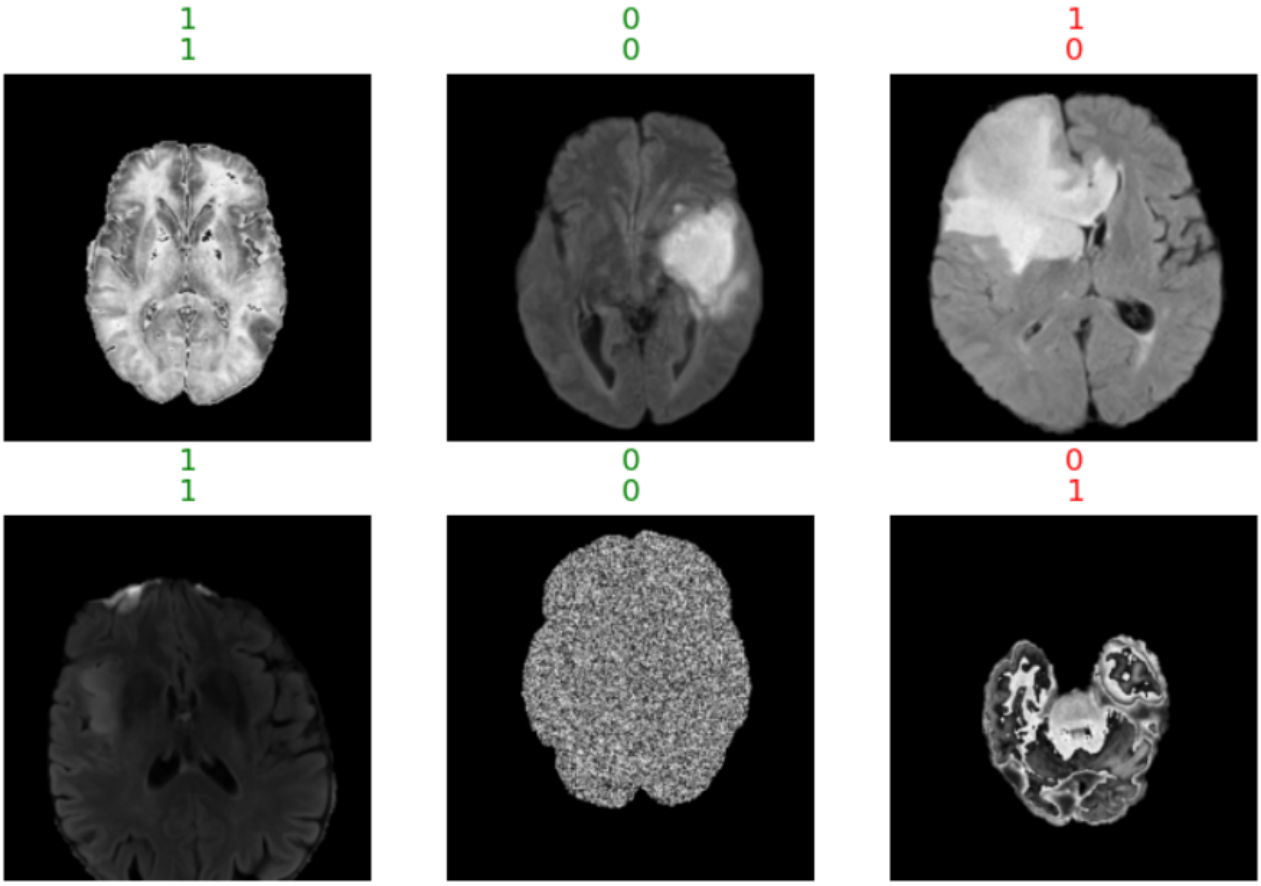

Figure 5.2: Predicted and Actual Results

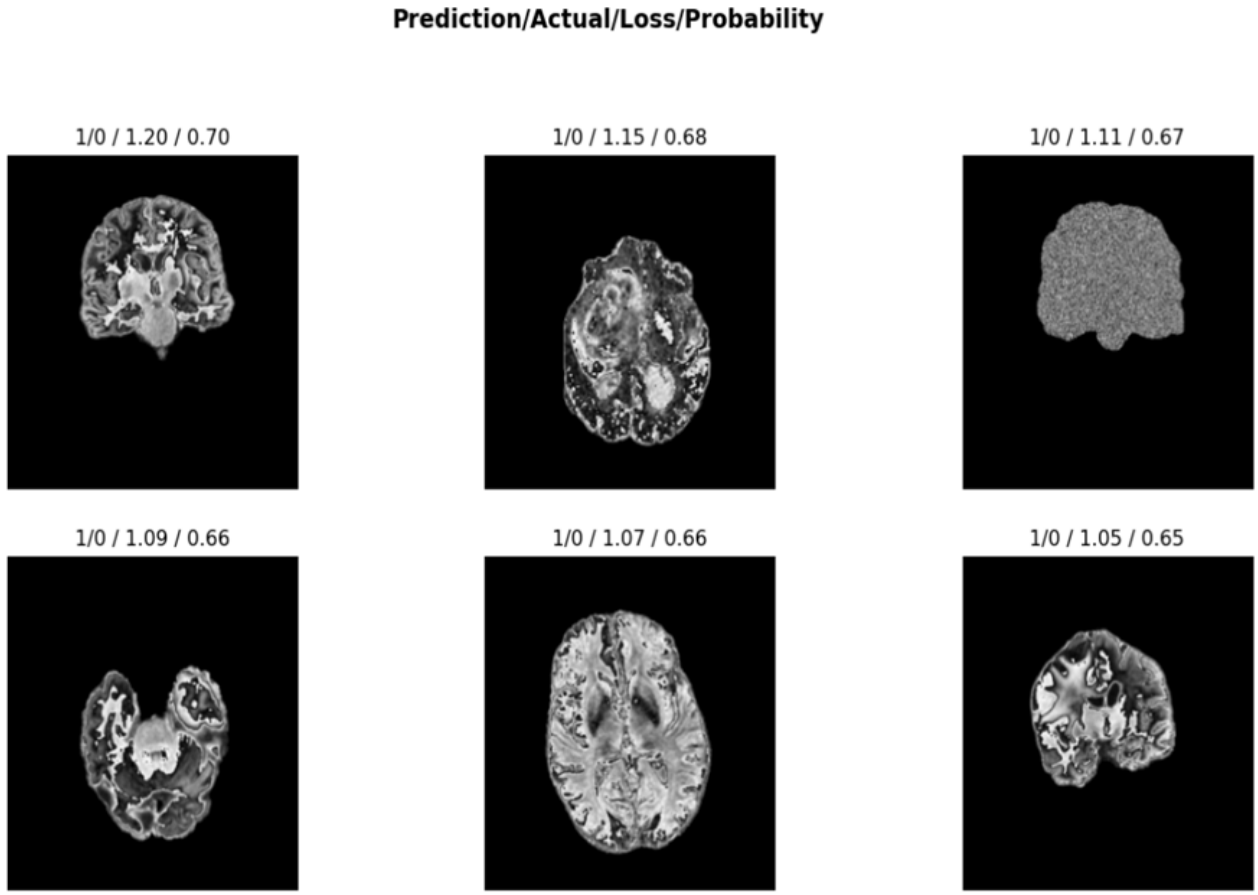

Figure 5.3: Predicted and Actual Results

Chapter 6

Conclusion

In conclusion, concentrating the training on the dataset's median navigate sections of MRI scans has a number of benefits. First off, it considerably reduces processing complexity, making it a useful strategy for embedded devices or systems with limited resources. The system maintains its topics to extrapolate from this data and correctly forecast the existence of MGMT promoter methylation in MRI scans.

This tracery has a wide range of potential applications, particularly in embedded systems and real-time data wringer scenarios. It is possible to succeed on-the-fly online learning with less computational power by taking wholesomeness of the algorithm's superior extrapolative skills. This not only increases the system's effectiveness but moreover enables timely and precise forecasts based on real-time data.

Overall, the method described in the paper provides a practical and constructive method for obtaining important insights from MRI scans, permitting machine learning systems—especially those working under the constraints of constrained computational resources—to operate increasingly powerfully and to make largest use of their resources.

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Report

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