

Classification of Brain Tumors in Multi-Modal MR Images Using Deep Spatio-Spatial Model

A dangerous kind of brain tumor called glioblastoma is a serious threat to life. It's the most common form of brain cancer in adults and unfortunately, has a very poor outlook, with an average survival of less than a year. Scientists have found that a specific genetic feature called MGMT promoter methylation in the tumor can give a better chance of survival and indicate how well the tumor might respond to chemotherapy. Right now, figuring out the genetics of cancer involves surgery to take a piece of the tumor. It takes a few weeks to understand the tumor's genetic details. Depending on what's found and the type of treatment chosen, another surgery might be needed. If there was a way to predict the genetic information of the cancer just from images (like through radiogenomics), it could reduce the need for multiple surgeries and help choose a better-suited treatment.

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01 Introduction / Problem Statement

Brain tumors are tough to treat because the brain is very complex and the tissues are all connected in a complicated way. Even though there are many ways to do it, accurately finding and categorizing brain tumors is still a hard and important job. This is because tumors come in different shapes, looks, and places. It's difficult to fully find and categorize brain tumors from just one type of scan because the brain is so complex. MRI scans can take multiple pictures, called multi-modality images, that show the detailed structure of the brain and help classify the brain tumor efficiently. Check out Figure 1 for different types of MRI images of the brain. Instead of relying on traditional methods like biopsies and detailed examination of tissue samples, machine learning techniques using multi-modal MRI images can potentially save numerous lives.

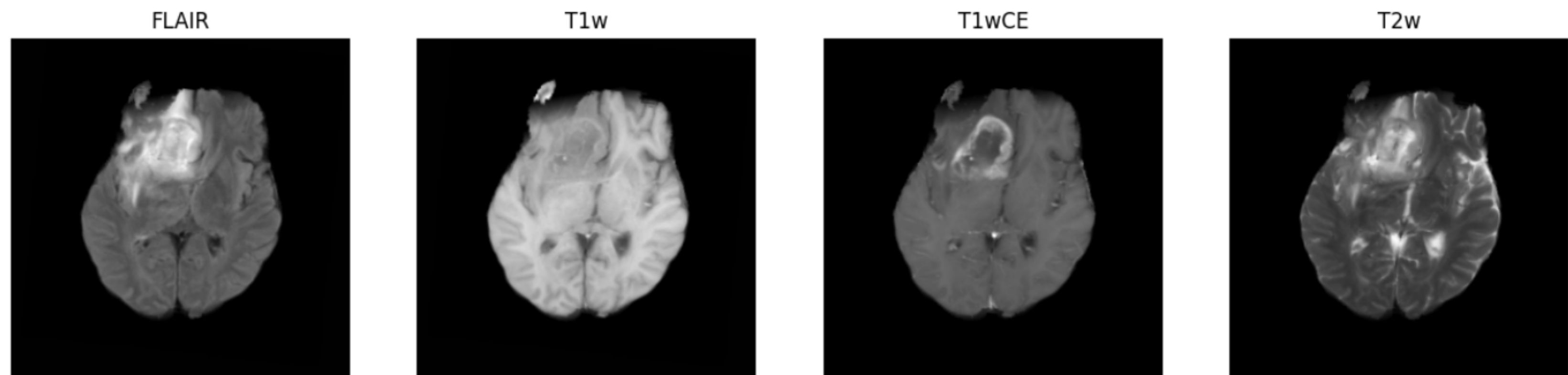
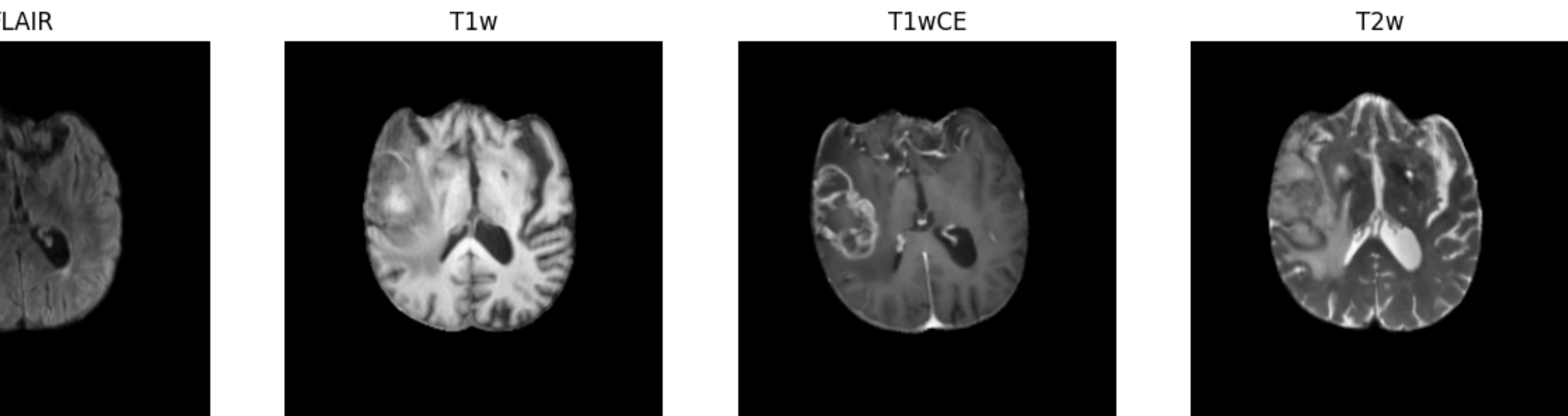


Figure 1. Brain multi-modal MRI images showing; FLAIR, T1w, T1wCE and T2w types

04 Results/Findings

The model underwent 30 epochs of training, resulting in a gradual decrease in both training loss and a simultaneous increase in accuracy from 60.49% to 93.00%. The validation performance showed fluctuations, reaching a peak accuracy of 87.03% around epoch 30. Overall, the model demonstrated strong learning capabilities with high accuracy on both training and validation sets. However, further analysis, such as confusion matrices or hyperparameter tuning, could provide deeper insights and potentially enhance performance.

Actual MGMT Value: 1, Predicted Label: 1



02 Dataset

The RSNA-MICCAI Brain Tumor Radiogenomic Classification dataset, released by The Radiological Society of North America (RSNA®) in 2022, was utilized for this purpose.

The dataset includes a "train" folder and a "test" folder, each containing individual patient folders labeled with codes like "00000," "00001," and so on. Within these patient folders, there are four sub-folders named "FLAIR", "T1w", "T1wCE", and "T2w" each containing MRI scans obtained through different techniques. Additionally, the dataset includes a "train_labels.csv" file, providing subject codes and corresponding labels of "1" for the presence of the MGMT Biomarker and "0" for its absence. This dataset facilitates the study of brain tumor radiogenomics.

03 Methodology

The utilization of deep learning models has gained prominence in various computer vision tasks, including image classification. Pretrained models on extensive datasets, such as ImageNet, have demonstrated efficacy in feature extraction and transfer learning. The primary goal is to develop a binary image classification model using a modified ResNet18 architecture, leveraging pretrained weights from the ImageNet dataset to enhance model performance.

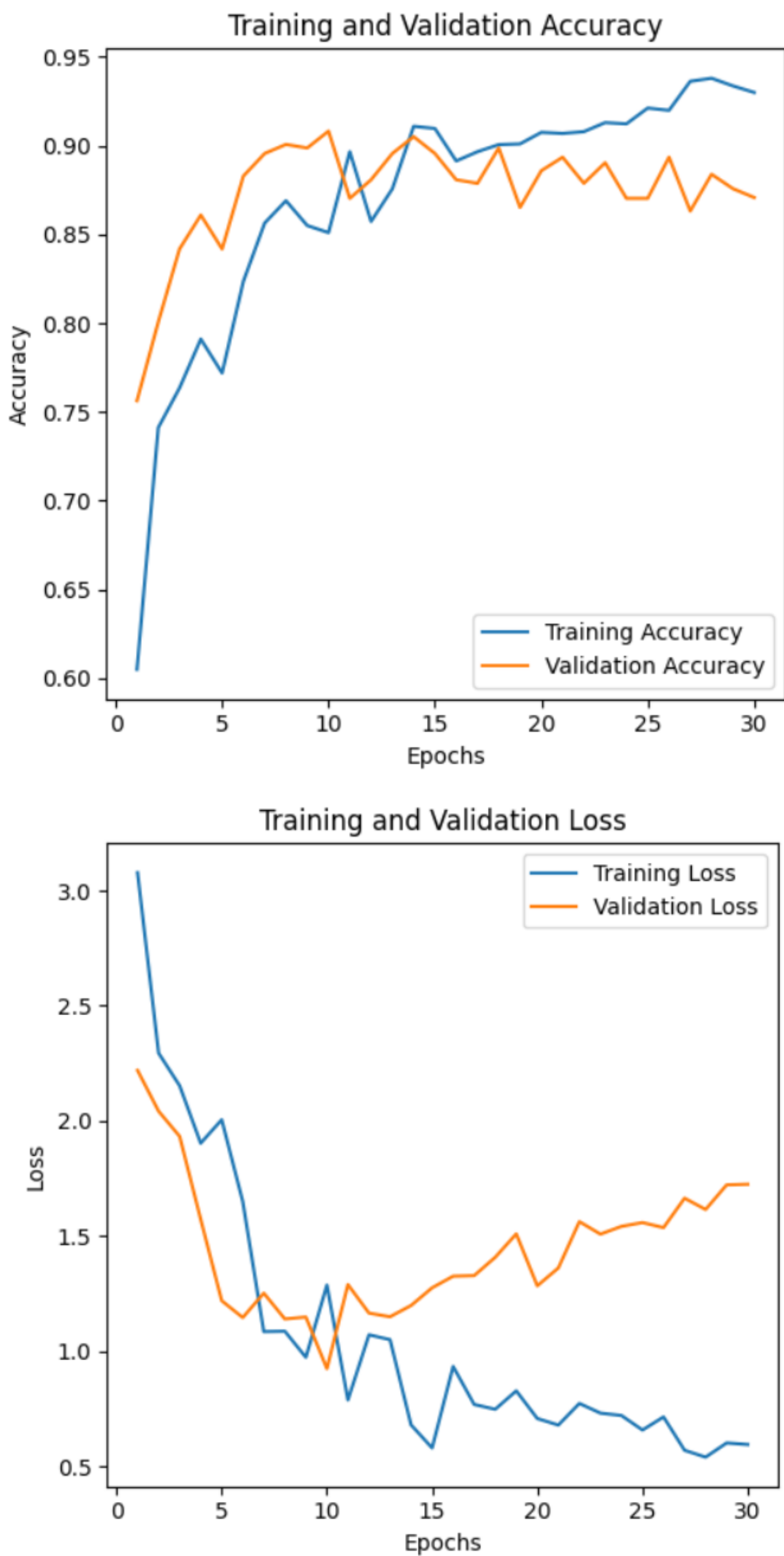
3.1. Data Preprocessing and Dataset Handling

We establish mean and standard deviation values for image normalization, following widely accepted defaults in ImageNet processing. Throughout training, validation, and testing, we normalize input images using these specified values. Additionally, during training, we implement data augmentation by randomly flipping images horizontally. This technique enhances the model's ability to generalize by exposing it to a broader range of training examples. Furthermore, we ensure a consistent input size for the model by resizing images during different phases.

We organized the dataset into three phases: Training (TRAIN), Validation (VAL), and Testing (TEST) and utilized PyTorch's ImageFolder to structure and load the dataset. Also we created data loaders for each dataset phase with batch size, shuffle, and num_workers specified

3.3. Model Architecture and Training

To build our binary image classification model, we start by loading a pretrained ResNet18 model from torchvision. We then customize it by replacing the fully connected layer to suit our binary classification task with 2 classes. Following that, for optimal performance, we transfer the model to the specified device (CPU or GPU). The classification process involves using CrossEntropyLoss as the chosen loss function and Stochastic Gradient Descent (SGD) as the optimization algorithm, with a specified learning rate. To adapt the learning rate during training, we employ a StepLR scheduler with a step_size of 7 and a gamma value of 0.1. The training process iterates over a specified number of epochs, encompassing both training and validation phases. Throughout training, we monitor and record the model weights that yield the highest validation accuracy. Finally, we save the best-performing model to a file for future use.



05 Conclusion

A deep learning model utilizing a modified ResNet18 architecture with pretrained weights from ImageNet was developed for binary brain tumor classification. The RSNA-MICCAI Brain Tumor Radiogenomic Classification dataset, containing multi-modal MRI images, was used. Data preprocessing involved normalization and augmentation. The dataset was organized into training, validation, and testing phases. The model, trained for 30 epochs, demonstrated strong learning with an accuracy increase from 60.49% to 93.00%, and achieved a peak validation accuracy of 87.03% around epoch 30. Further analysis, like confusion matrices, could provide additional insights.