Brain Tumor Classifier

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Abstract

In this work, we address the problem of brain tumor classification from Magnetic Resonance Imaging (MRI) using deep learning techniques. The dataset used consist of 6000 MRI scans (from (Fateh et al. 2025)), covering three types of tumor (glioma, pituitary, and meningioma) from three perspectives (coronal, sagittal, and axial). Our goal was to design a functioning pipeline capable of fine-tuning a pre-trained convolutional neural network for the multi-class classification task. We adopted ResNet18 ((He et al. 2015)) as the backbone architecture due to its efficiency in image recognition tasks. The system was then implemented in Python using PyTorch. The experiments demonstrated strong classification performance, with an accuracy confirming the model's reliability across different views. These results highlight the potential of deep learning frameworks in assisting medical diagnosis by providing accurate tumor detection from MRI data.

Introduction

Project Idea Inspired by the third Sustainable Development Goal, "Good Health and Well-being", we aimed to explore applications of AI in the medical domain. Recent research has shown that deep learning models, particularly those used in computer vision, are already capable of outperforming human specialists in specific diagnostic tasks (e.g. *Microsoft AI Diagnostic Orchestrator*[1]). This demonstrates how, in today's medical practice, machine intelligence can play a central role in illness recognition, supporting or even surpassing human expertise.

Project's goal In this project report we present how to build an efficient neural network to solve the task of multi-classification on a dataset of Mangnetic Resonance Imaging (MRI) images. The dataset was introduced in (Fateh et al. 2025). The goal of the project is to create a simple pipeline to fine tune a pre-trained neural network that achieves good performances on classifying 3 types of brain tumors.

Dataset overview The dataset consists of 6,000 MRI images, each categorized into one of four classes: glioma, pituitary, meningioma, or no tumor. For each class, images are acquired from multiple perspectives, covering the coronal, sagittal, and axial planes. This design ensures that the trained model generalizes effectively across different anatomical views. The inclusion of the no tumor class is essential, as it enables the model to distinguish between healthy and pathological brain scans.

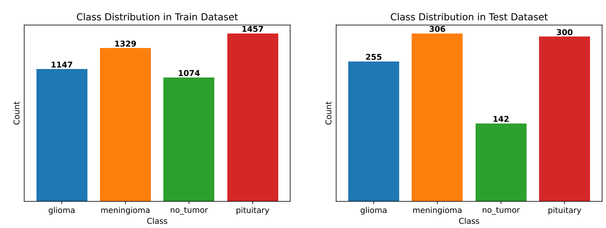

Figure 1: Dataset classes distribution.

Tool's overview In this paragraph we shortly introduce all the main tools used in the project. To solve the multi-classification task we have used a Deep Convolutional Neural Network, to be more precise we have used ResNet18 (He et al. 2015) which is a Residual Network. The network is composed by 18 layers with residual connections and contains 11.2 million parameters. Since our dataset is not large enough to train the entire model from scratch, we applied a technique called fine-tuning along with a simple data augmentation method.

The project was developed in python and the entire code is open source[2]. The python library used is Pytorch Lightning and the training of the model was done locally.

Processing Pipeline

In this section we describe the preprocessing pipeline that we've used to achieve the results that are reported in the following section.

Data augmentation The dataset was splitted in train (4000 images), validation (1000 images) test sets (1000 images). To enlarge the training set we've applied the following transformations:

[1] *https://time.com/7299314/microsoft-ai-better-than-doctors-diagnosis/*

[2] *https://github.com/Ultimi-Sumiti/Brain_Tumor_Classifier*

- Resize to shape 224×224 (to match the ResNet18 input shape).
- Random horizontal flip.
- Random rotation between range $[0°, 360°]$.
- (Optionally) Random zoom out.

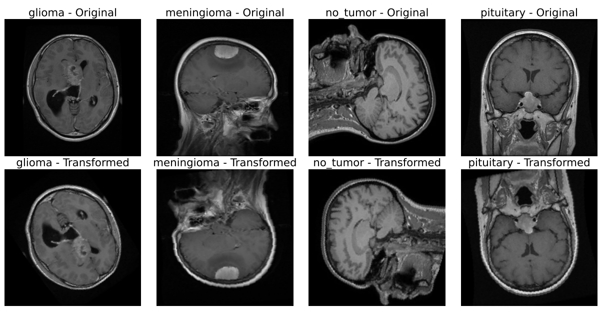

Figure 2: Comparison between original an transformed images.

Fine tuning the network After data augmentation we're ready to train the network. We have loaded an instance of ResNet18 pre-trained on the ImageNet dataset and we followed a common fine-tuning pipeline which consists in the following steps:

1. Copy the values of the ResNet18 pre-trained parameters into our model.
2. Change the size of the output layer to match the 4 classes.
3. Freeze all the parameters except for the ones in the layer added in the previous step.
4. Train the new layers only.
5. Un-freeze the previous layers and continue training on the entire network.

Using this strategy we were able to achieve good performances on the provided dataset.

Results

Here below we want to show some metrics and main results about the performances of our work.

Figure 6 shows the train and validation losses and train and validation accuracies during the first training phase (where only the last layer is un-frozen). As expected the validation loss decreases epoch by epoch until we reach the maximum of 35 epochs. In this situation the model has reached a validation accuracy of $\approx 80\%$.

In Figure 7 is shown how the losses and the accuracies evolve during the fine-tuning phase. Again we can see that the validation loss decreases until the training stops at epoch 16. The accuracy on the validation set reaches $\approx 98\%$.

After the fine-tuning phase, we evaluated the model on the test set. Table 1 reports the metrics computed on the test set; Figure 3 presents the confusion matrix; and Figure 4 displays the per-class scores (accuracy, precision, recall, and F1-score).

Metric	Value
Test Accuracy	0.979
Test Loss	0.056

Table 1: Accuracy and loss on the test set.

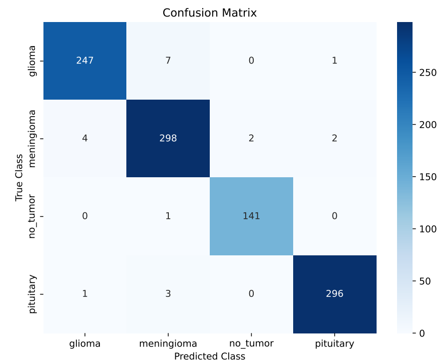

Figure 3: Confusion matrix on test set.

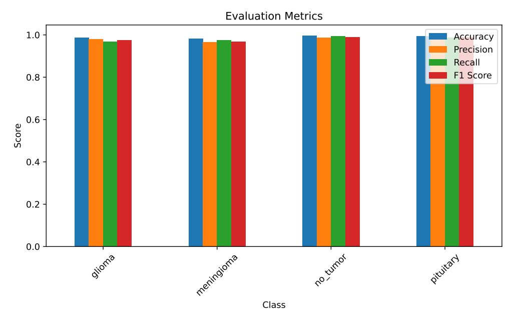

Figure 4: Per-class metrics plot.

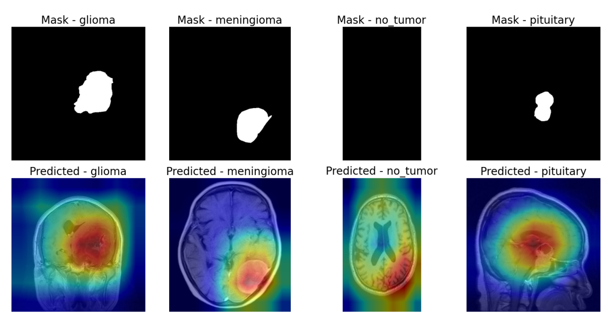

Figure 5: Class Activation Mapping (CAM).

Figure 5 shows the Class Activation Mapping (CAM) for each class. In the first row, we can see the ground-truth tumor masks, while in the second row the highlighted regions indicate the most important areas the trained model relies on when deciding the class of each image. The red regions indicate areas of high importance, while the blue regions correspond to areas of low importance. We can observe that the model is focusing on right spot to make the decisions.

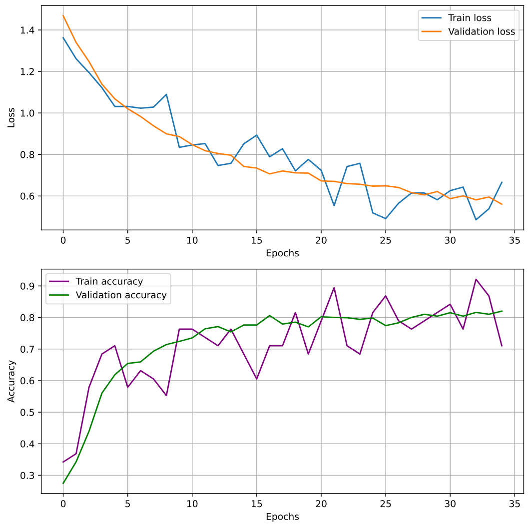

Figure 6: Initial training plots.

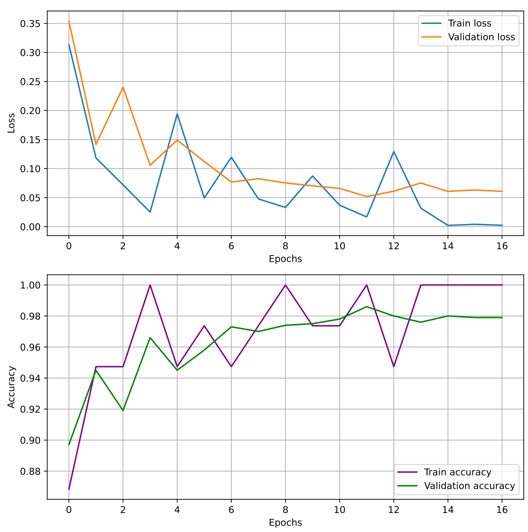

Figure 7: Fine-tuning plots.

Conclusions

Guided by the broader vision of sustainable development, we decided to focus our work on the intersection between artificial intelligence and healthcare, an area where technological innovation can have a tangible social impact. In particular, our study takes inspiration from the growing body of research showing how machine learning techniques, originally developed for generic computer vision tasks, can be effectively transferred to medical imaging. This context provided a solid ground to explore the potential of AI as a tool not only for improving diagnostic accuracy but also for contributing to more accessible and efficient healthcare solutions.

The project we have described can be extended to include different types of brain tumors. In addition, one could address the segmentation task: in this scenario, the model would not only classify the brain as healthy or determine the tumor type, but also localize the tumor region with pixel-level precision.

References

Fateh, A.; Rezvani, Y.; Moayedi, S.; Rezvani, S.; Fateh, F.; and Fateh, M. 2025. BRISC: Annotated Dataset for Brain Tumor Segmentation and Classification with Swin-HAFNet. arXiv:2506.14318.

He, K.; Zhang, X.; Ren, S.; and Sun, J. 2015. Deep Residual Learning for Image Recognition. arXiv:1512.03385.