Predict brain tumorredict brain tumor: Using Federated Learning



What is Brain Tumor?

A brain tumor is a collection, or mass, of abnormal cells in your brain. Your skull, which encloses your brain, is very rigid. Any growth inside such a restricted space can cause problems. Brain tumors can be cancerous (malignant) or noncancerous (benign). When benign or malignant tumors grow, they can cause the pressure inside your skull to increase. This can cause brain damage, and it can be life-threatening.

Introduction

Brain tumors pose a significant healthcare challenge, requiring accurate prediction for effective treatment strategies. In this context, Federated Learning (FL) emerges as a promising solution, particularly in healthcare, where data privacy is paramount.

FL enables collaborative model training across distributed datasets without the need to share sensitive patient information centrally. This decentralized approach not only safeguards patient privacy but also leverages the collective knowledge embedded in diverse datasets. Motivated by the imperative to protect patient confidentiality and the need for scalable solutions, we aim to develop a FL-based model for brain tumor prediction.

Our objective is to harness FL's potential to enhance the accuracy and efficiency of brain tumor diagnosis, paving the way for more personalized treatment approaches. By leveraging FL's privacy-preserving mechanisms and scalability, we aspire to contribute to the advancement of medical research and the improvement of patient outcomes in the domain of brain tumor diagnosis and treatment.

What is Federated Learning?

Federated Learning (FL) is a decentralized machine learning approach where model training occurs locally on distributed devices, such as smartphones or edge servers, without centralizing raw data. In this paper, FL is applied to develop a brain tumor prediction model using MRI images.

Each client device, representing different healthcare institutions, trains the model locally on its dataset while preserving data privacy. Model updates are then aggregated centrally to refine the global model. FL enables collaborative learning across diverse datasets without sharing sensitive patient information, thus ensuring privacy and scalability in healthcare applications.

Methodology:

Dataset: Brain Tumor MRI Dataset containing glioma, meningioma, no tumor, and pituitary images.

FL Approach: Explanation of federated learning framework and its implementation for brain tumor prediction.

Model: Description of the CNN architecture with VGG16 base for feature extraction and classification.

FL Implementation: Details on how model updates are aggregated across client devices while preserving data privacy.

Methods

The application of deep learning approaches in context to improve health diagnosis is providing impactful solutions. According to the World Health Organization (WHO), proper brain tumor diagnosis involves detection, brain tumor location identification, and classification of the tumor on the basis of malignancy, grade, and type. This experimental work in the diagnosis of brain tumors using Magnetic Resonance Imaging (MRI) involves detecting the tumor, classifying the tumor in terms of grade, type, and identification of tumor location.

This method has experimented in terms of utilizing one model for classifying brain MRI on different classification tasks rather than an individual model for each classification task. The Convolutional Neural Network (CNN) based multi-task classification is equipped for the classification and detection of tumors. The identification of brain tumor location is also done using a CNN-based model by segmenting the brain tumor.

Dataset Compilation

- The Brain Tumor MRI Dataset is compiled by integrating images from three primary sources: figshare, SARTAJ dataset, and Br35H.
- The dataset encompasses a total of 7023 MRI images of human brain classified into four distinct classes: glioma, meningioma, no tumor, and pituitary.
- Notably, the "no tumor" class images are sourced exclusively from the Br35H dataset.

1. FL Approach

- Explanation of Federated Learning: FL is a decentralized learning paradigm enabling model training across multiple edge devices without centralizing sensitive data.
- Implementation for Brain Tumor Prediction: FL is applied to our dataset by distributing model training across client devices while preserving data privacy.
- The FL framework facilitates collaborative learning by aggregating model updates from individual clients, thereby improving model performance without compromising data confidentiality.

Model Architecture

- Description of CNN Architecture: Our model utilizes a Convolutional Neural Network (CNN) with a VGG16 base for feature extraction and classification.
- The VGG16 base, pre-trained on the ImageNet dataset, serves as a powerful feature extractor, capturing intricate patterns in brain MRI images.
- Additional layers, including Dropout and Dense layers, are added for regularization and classification tasks, respectively.

FL Implementation Details

- Aggregation of Model Updates: Model updates from client devices are aggregated using federated averaging or similar techniques to update the global model.
- Preservation of Data Privacy: FL ensures data privacy by keeping raw patient data localized to client devices, thus preventing the need for centralized data storage.
- Client Participation: Client devices, representing different healthcare institutions or sources, contribute locally trained model updates while maintaining control over their data.

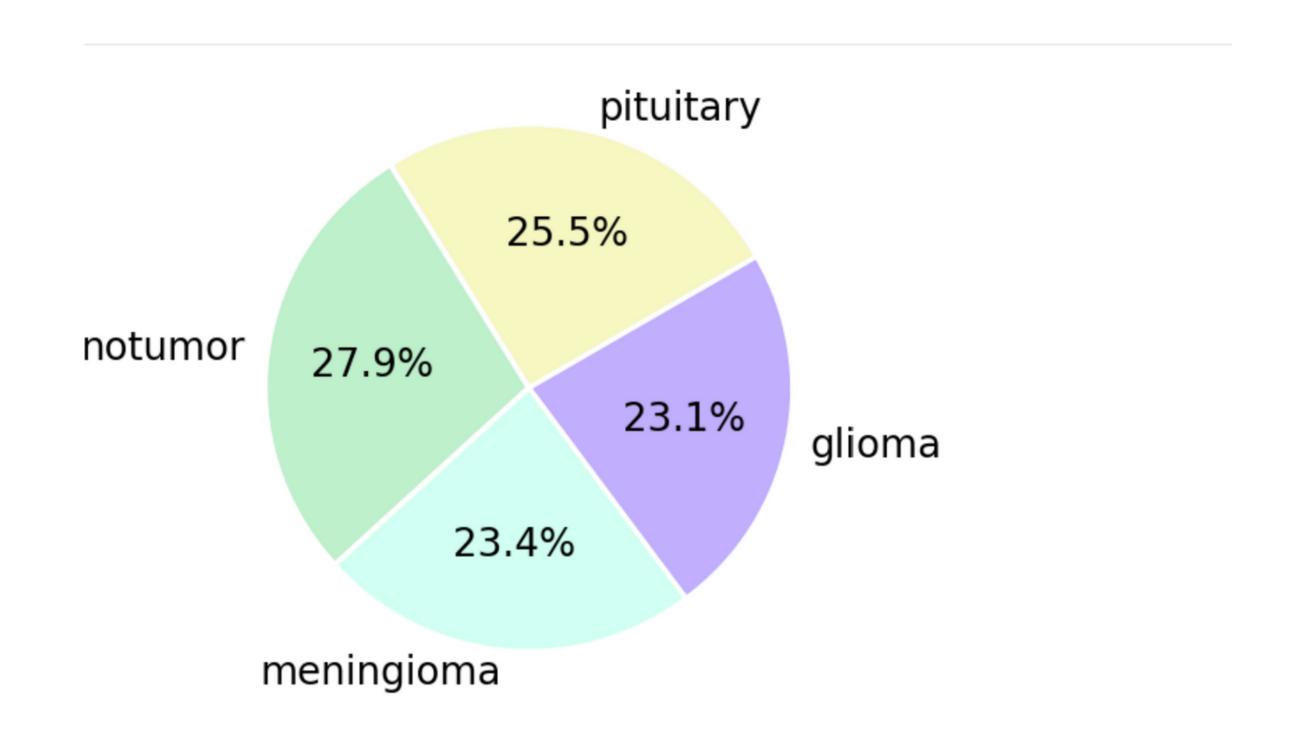
Model Architecture

Detailed CNN Architecture: Our model employs a Convolutional Neural Network (CNN) architecture built upon the VGG16 base.

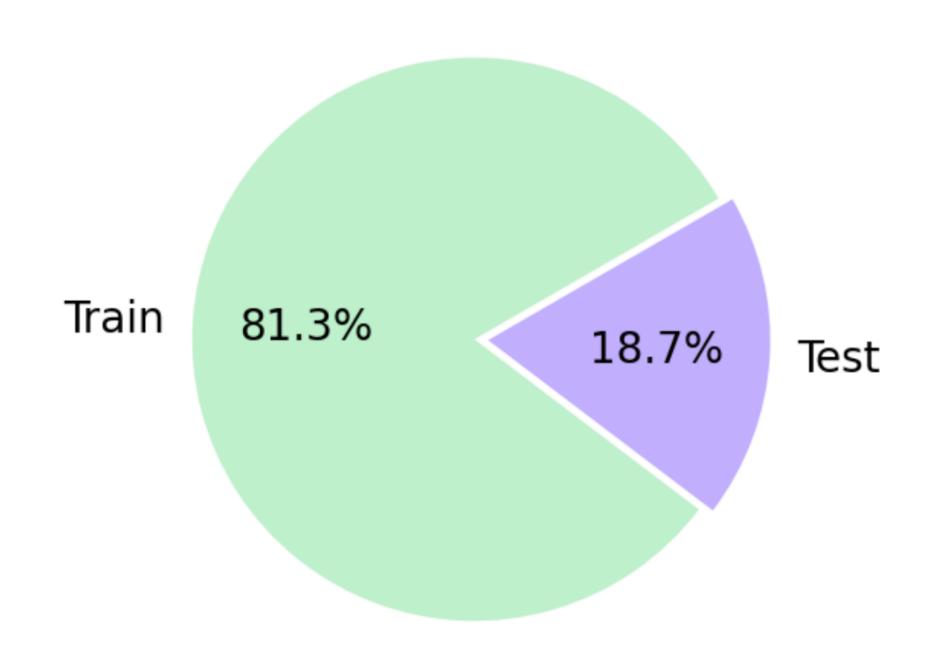
Explanation of Model Training in FL Framework: Model training in the Federated Learning (FL) framework involves distributing the model architecture to client devices.

Experiment Setup: The experiment is conducted using libraries such as TensorFlow, Keras, NumPy, and PIL. The hardware setup includes standard computational resources suitable for deep learning tasks.

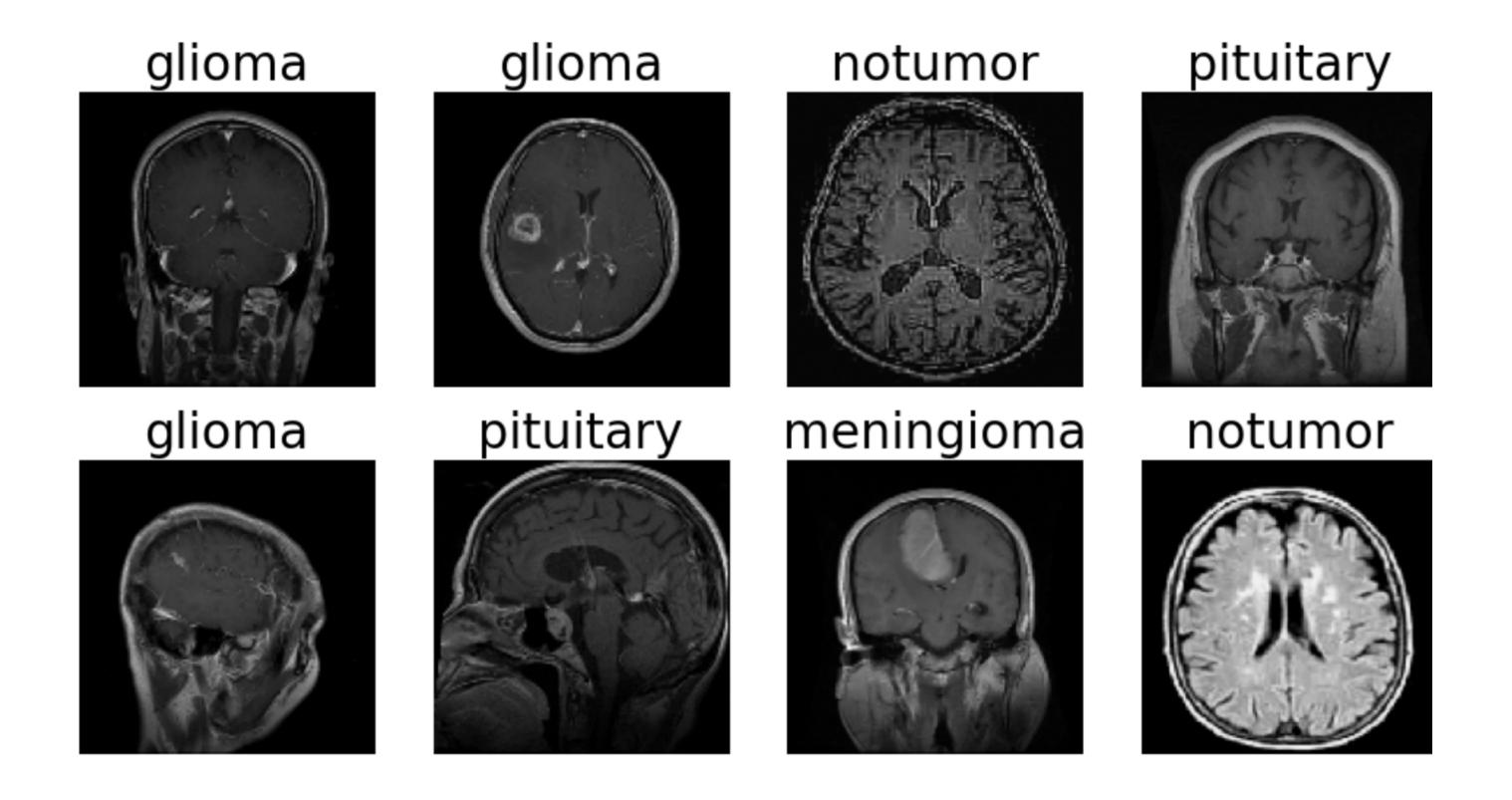
Plot of Dataset through visulatization



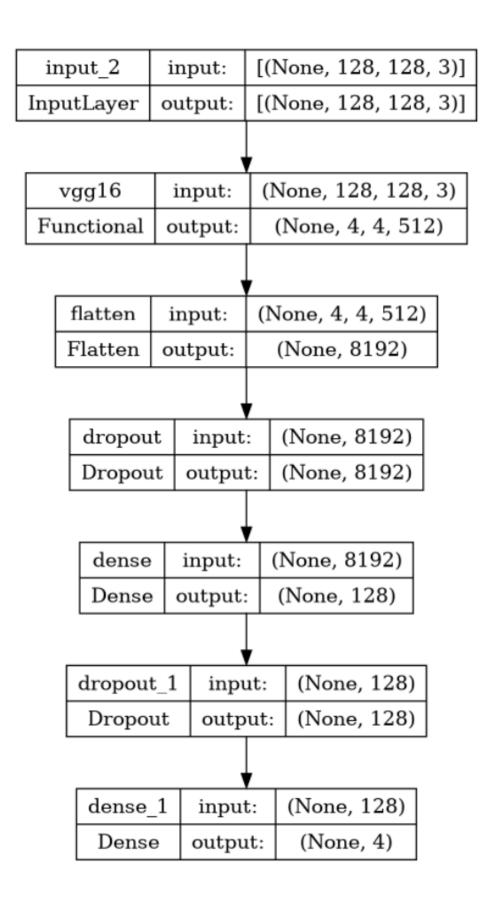
Testing and Training Set



Augmented Images with Labels



Model Architecture



Model Summary

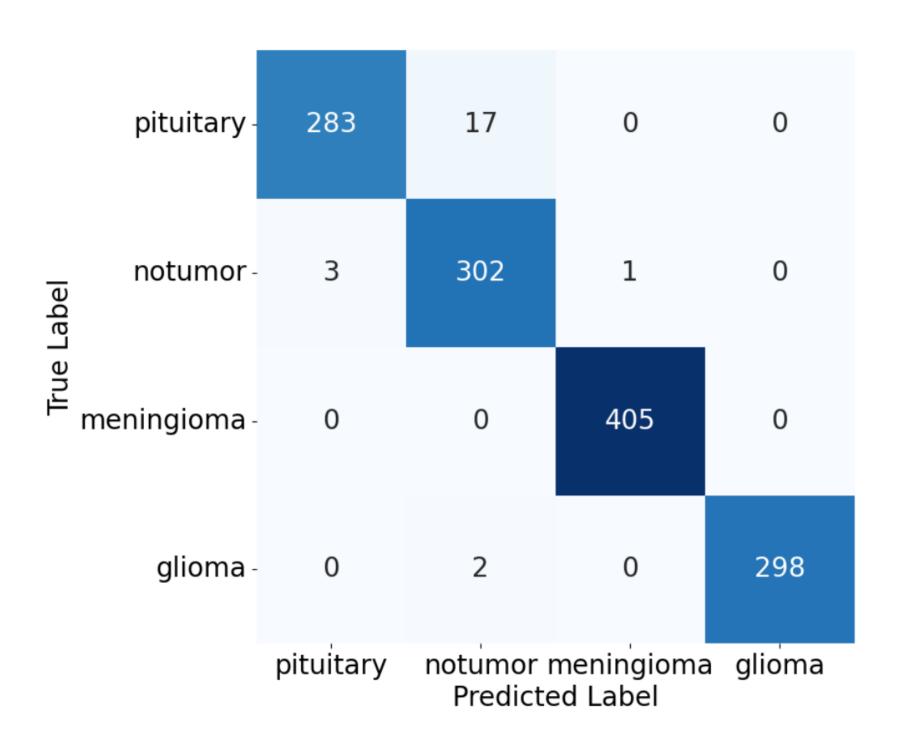
Model: "sequential"

Layer (type)	Output Shape	Param #
vgg16 (Functional)	(None, 4, 4, 512)	14714688
flatten (Flatten)	(None, 8192)	0
dropout (Dropout)	(None, 8192)	0
dense (Dense)	(None, 128)	1048704
dropout_1 (Dropout)	(None, 128)	0
dense_1 (Dense)	(None, 4)	516

Total params: 15763908 (60.13 MB)
Trainable params: 8128644 (31.01 MB)

Non-trainable params: 7635264 (29.13 MB)

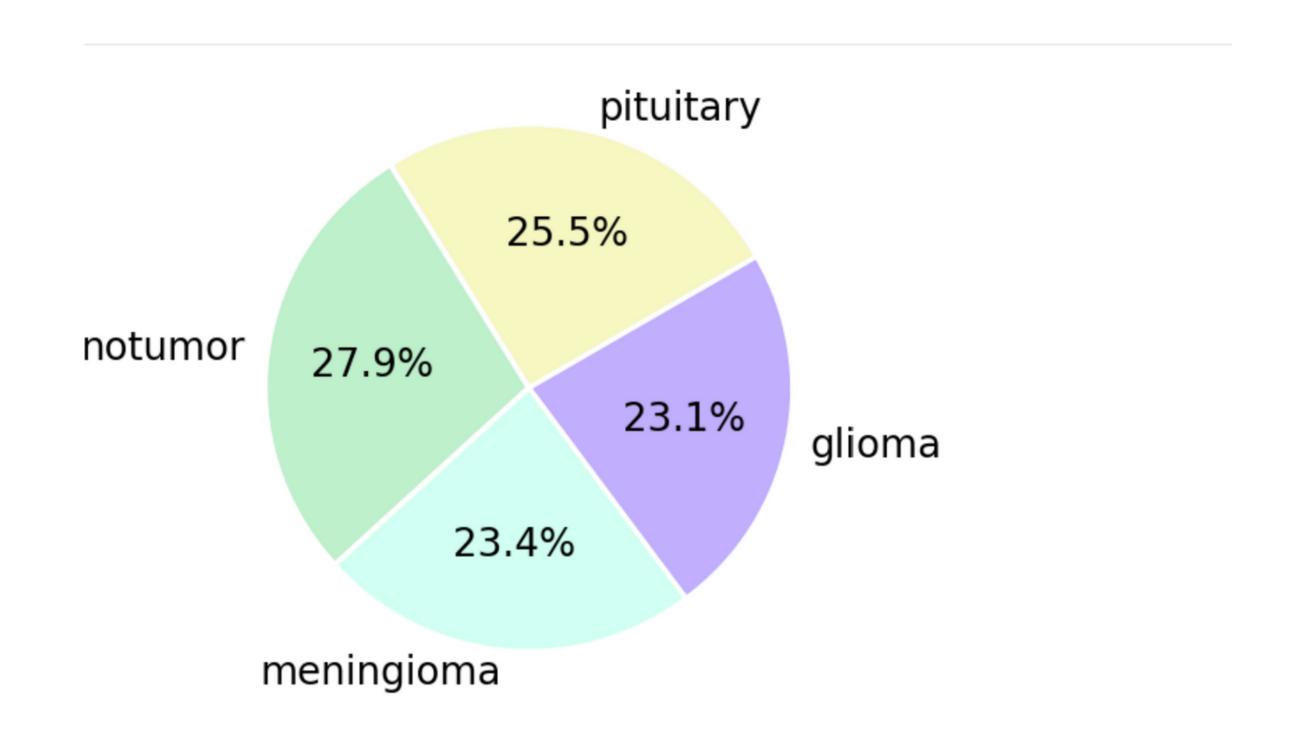
Confusion Matrix



Classfication Report

	precision	recall	f1-score	support
glioma	0.99	0.94	0.97	300
meningioma	0.94	0.99	0.96	306
notumor	1.00	1.00	1.00	405
pituitary	1.00	0.99	1.00	300
accuracy			0.98	1311
macro avg	0.98	0.98	0.98	1311
weighted avg	0.98	0.98	0.98	1311

Plot of Dataset through visulatization

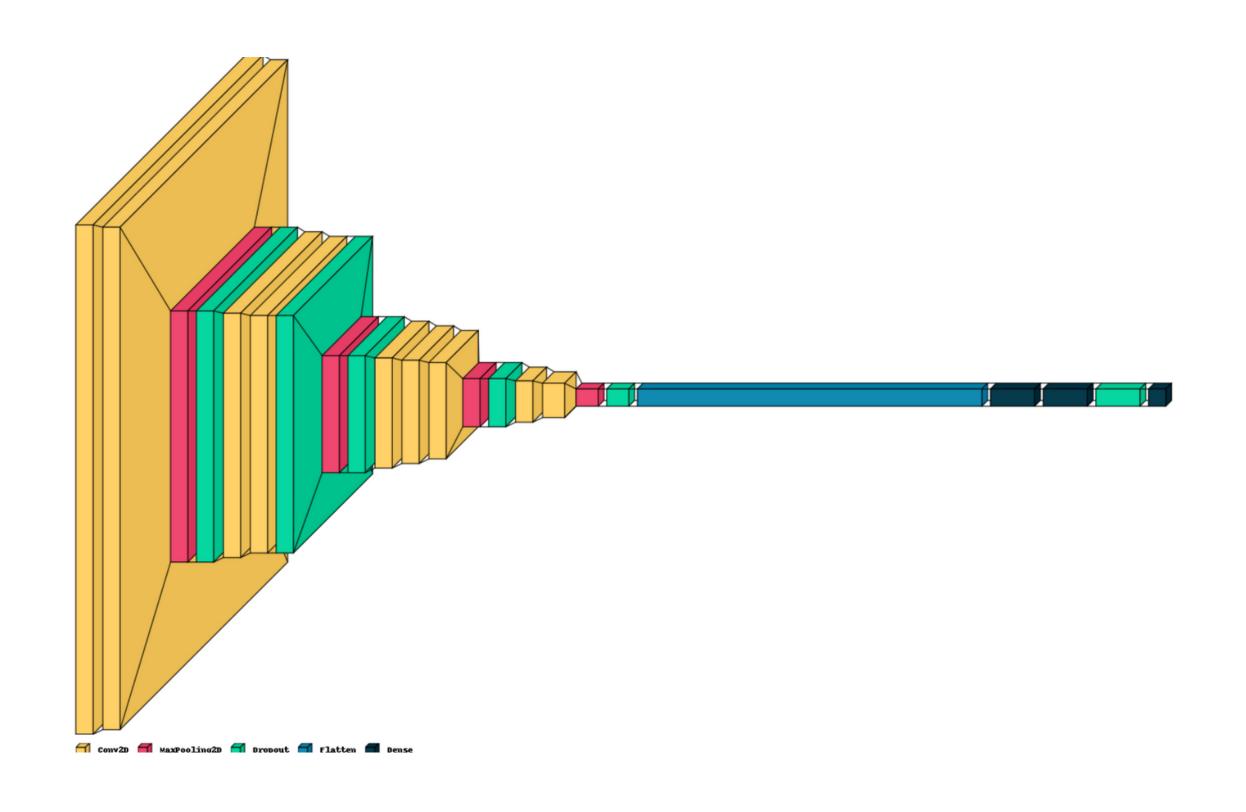


Accuracy of the model using FL

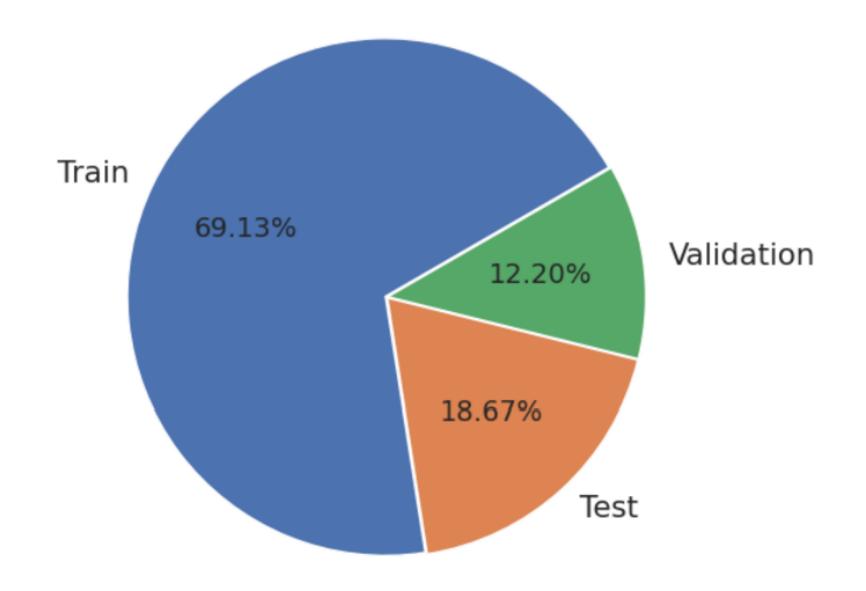
Test Loss: 0.08637356758117676

Test Accuracy: 0.983593761920929

Model 2: CNN+LSTM+BERT+Transformer



Testing and Training Set



Model Summary

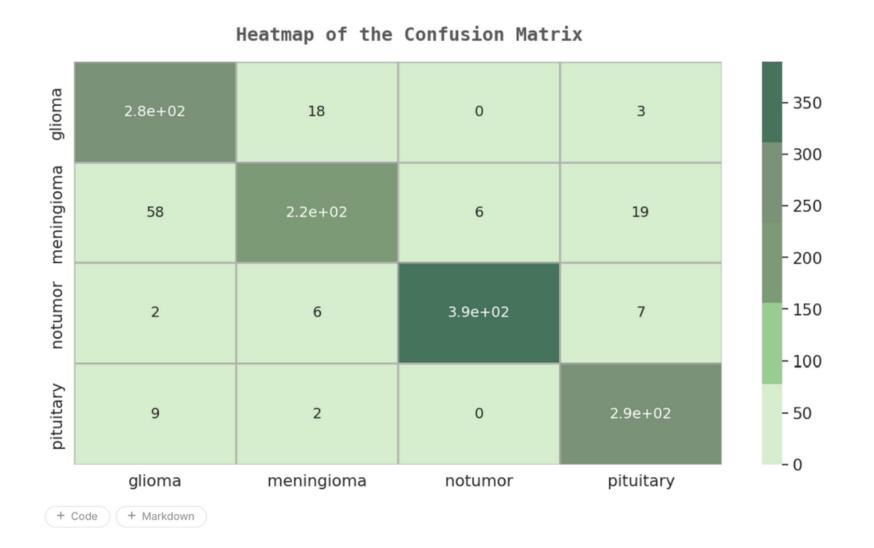
Model: "sequential"		
Layer (type) Ou	tput Shape	Param #
	lone, 148, 148, 128)	
conv2d_1 (Conv2D) (N	lone, 146, 146, 64)	73792
<pre>max_pooling2d (MaxPooling2D ()</pre>	None, 73, 73, 64)	0
dropout (Dropout) (N	lone, 73, 73, 64)	0
conv2d_2 (Conv2D) (N	lone, 71, 71, 64)	36928
conv2d_3 (Conv2D) (N	lone, 69, 69, 64)	36928
dropout_1 (Dropout) (N	lone, 69, 69, 64)	0
<pre>max_pooling2d_1 (MaxPooling (2D)</pre>	None, 34, 34, 64)	0
dropout_2 (Dropout) (N	lone, 34, 34, 64)	0
conv2d_4 (Conv2D) (N	lone, 32, 32, 128)	73856
conv2d_5 (Conv2D) (N	lone, 30, 30, 128)	147584
conv2d_6 (Conv2D) (N	lone, 28, 28, 128)	147584
<pre>max_pooling2d_2 (MaxPooling (2D)</pre>	None, 14, 14, 128)	0
dropout_3 (Dropout) (N	lone, 14, 14, 128)	0
conv2d_7 (Conv2D) (N	lone, 12, 12, 128)	147584
conv2d_8 (Conv2D) (N	lone, 10, 10, 256)	295168
<pre>max_pooling2d_3 (MaxPooling (2D)</pre>	None, 5, 5, 256)	0
dropout_4 (Dropout) (N	lone, 5, 5, 256)	0
flatten (Flatten) (N	lone, 6400)	0
dense (Dense) (N	lone, 512)	3277312
dense_1 (Dense) (N	lone, 512)	262656
dropout_5 (Dropout) (N	lone, 512)	0
dense_2 (Dense) (N	lone, 4)	2052

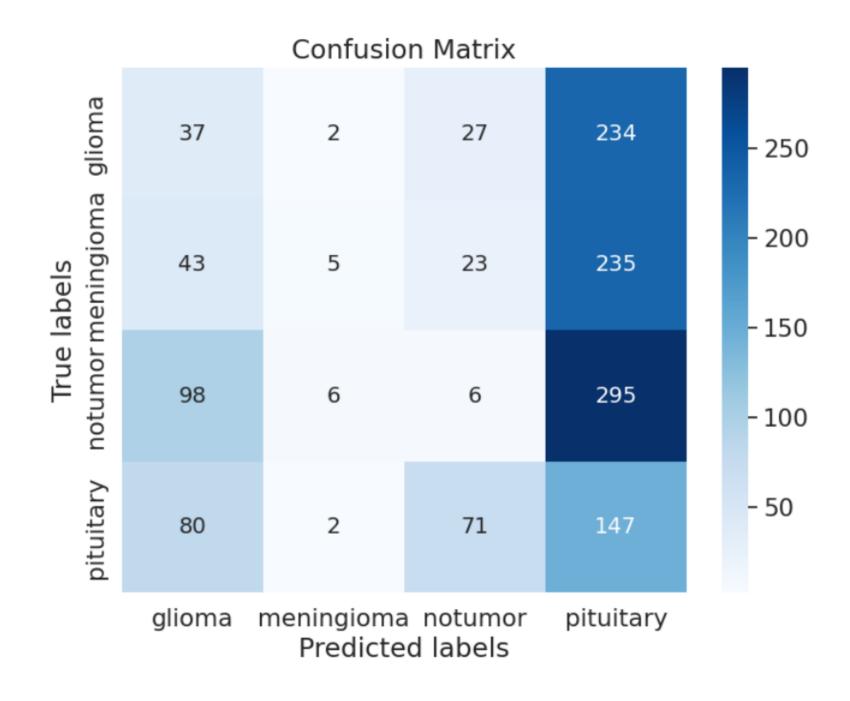
Total params: 4,505,028 Trainable params: 4,505,028 Non-trainable params: 0

Classfication Report

41/41 [=====	========		===] - 1s	20ms/step
	precision	recall	f1-score	support
glioma	0.14	0.12	0.13	300
meningioma	0.33	0.02	0.03	306
notumor	0.05	0.01	0.02	405
pituitary	0.16	0.49	0.24	300
accuracy			0.15	1311
macro avg	0.17	0.16	0.11	1311
weighted avg	0.16	0.15	0.10	1311

Confusion Matrix





Accuracy Table

Accuracy Table:

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	Precision	Recall	F1-score	Accuracy
glioma	0.143411	0.123333	0.132616	0.123333
meningioma	0.333333	0.016340	0.031153	0.016340
notumor	0.047244	0.014815	0.022556	0.014815
pituitary	0.161361	0.490000	0.242775	0.490000

Conclusion

The study successfully developed and compared two models for brain tumor prediction: one utilizing Federated Learning (FL) and the other using a Convolutional Neural Network (CNN). The FL-based model showed promising results, achieving competitive performance compared to the CNN model. Both models exhibited high accuracy and demonstrated their ability to predict brain tumor types accurately.