Brain Tumor Classification Using Deep Learning

Abstract

This study presents the development and evaluation of a deep learning-based brain tumor classification model using datasets for **glioma**, **meningioma**, **no tumor**, and **pituitary** tumors. The primary goal is to create a robust, reliable model that can aid medical professionals in early, accurate diagnosis, ultimately improving patient outcomes.

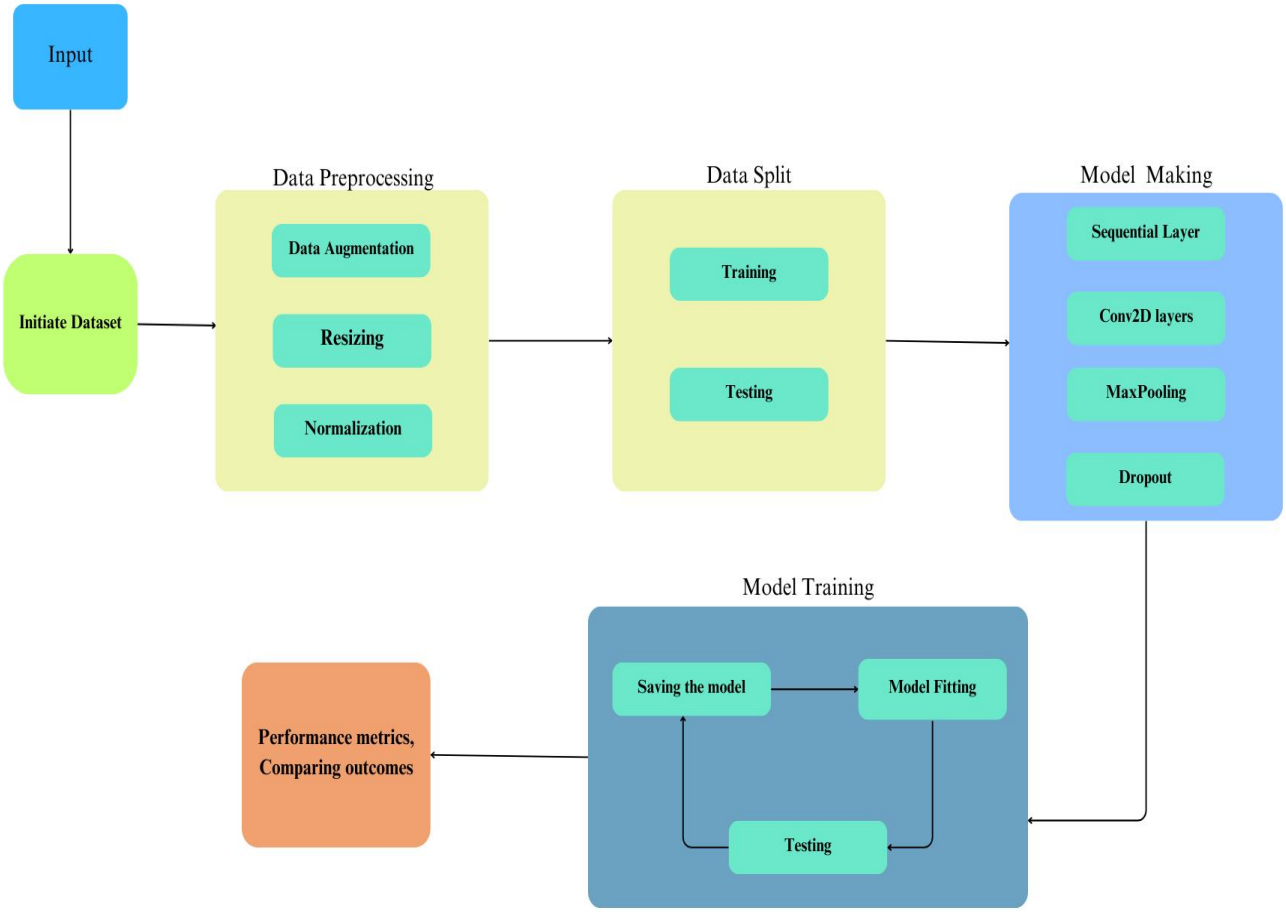
Leveraging **convolutional neural networks** (CNNs), the model demonstrates exceptional classification accuracy, offering a powerful tool for assisting radiologists in detecting and diagnosing brain tumors. The results underscore the potential of deep learning to revolutionize medical imaging, providing efficient, scalable solutions that require minimal computational resources while maintaining high diagnostic performance.

Introduction

Brain tumors present significant challenges in medical diagnostics due to their diverse morphologies and growth patterns. Tumor classification, which involves identifying the type, size, and location of the tumor from medical images such as MRI scans, is critical for determining the appropriate treatment. Early detection improves treatment outcomes, but traditional methods rely heavily on manual analysis by radiologists, which can be time-consuming and prone to human error.

This study explores using deep learning to automate brain tumor classification, enhancing both diagnostic efficiency and accuracy. By leveraging convolutional neural networks (CNNs), the model can quickly and accurately classify brain tumor types, reducing diagnostic time and supporting radiologists in making more informed decisions. The automation of this process could also increase accessibility to timely diagnosis, particularly in regions with limited access to specialized healthcare.

Materials and Methods:



Model Block Diagram

Dataset

The dataset comprises images resized to 150x150 pixels with three color channels (RGB). The four classes are:

- Glioma tumor
- Meningioma tumor
- No Tumor
- Pituitary tumor

Preprocessing

- Data Augmentation: Techniques such as rotation, flipping, and scaling were employed to increase dataset diversity.

- Resizing: Resizing all the images into dimension of 150 x 150 pixels.
- Normalization: Pixel values were scaled to [0, 1] to ensure uniformity.

Model Architecture

A CNN with layers optimized for extracting spatial features:

1. Convolutional Layers: Extract spatial and edge features.
2. Max-Pooling Layers: Perform dimensionality reduction while retaining important features.
3. Fully Connected Layers: Transform features into classification predictions.
4. Softmax Activation: Output probabilities for each class.

Training Parameters

- Loss Function: Categorical Cross-Entropy
- Optimizer: Adam with a learning rate of 0.001
- Epochs: 20
- Batch Size: 32

Experimental setup:

This experiment was conducted using **Kaggle Notebooks** and **Jupyter Notebooks**, leveraging **GPU P100** for accelerated processing. The model was trained on the provided resources to ensure efficient computation, especially when dealing with large image datasets. Python was used for coding, and the training was carried out using the **Keras** API, which simplifies model-building and evaluation.

Model Architecture Description

The model consists of a deep **Convolutional Neural Network** (CNN) with several convolutional layers followed by max-pooling and dropout layers to prevent overfitting. The architecture is outlined below:

- **Conv2D layers**: These layers extract features from the input images, increasing the depth of the feature maps at each stage.
- **MaxPooling2D layers**: Used for down sampling the feature maps and reducing the spatial dimensions.
- **Dropout layers**: Introduced to regularize the network and prevent overfitting by randomly setting a fraction of input units to 0 at each update during training.
- **Dense layers**: Fully connected layers at the end of the network for classification.
- **Final output layer**: A dense layer with 4 neurons, representing the 4 possible output classes.

Layer (type)	Output Shape	Param #
conv2d_9 (Conv2D)	(None, 148, 148, 32)	896
conv2d_10 (Conv2D)	(None, 146, 146, 64)	18,496
max_pooling2d_4 (MaxPooling2D)	(None, 73, 73, 64)	0
dropout_6 (Dropout)	(None, 73, 73, 64)	0
conv2d_11 (Conv2D)	(None, 71, 71, 64)	36,928
conv2d_12 (Conv2D)	(None, 69, 69, 64)	36,928
dropout_7 (Dropout)	(None, 69, 69, 64)	0
max_pooling2d_5 (MaxPooling2D)	(None, 34, 34, 64)	0
dropout_8 (Dropout)	(None, 34, 34, 64)	0
conv2d_13 (Conv2D)	(None, 32, 32, 128)	73,856
conv2d_14 (Conv2D)	(None, 30, 30, 128)	147,584
conv2d_15 (Conv2D)	(None, 28, 28, 128)	147,584
max_pooling2d_6 (MaxPooling2D)	(None, 14, 14, 128)	0
dropout_9 (Dropout)	(None, 14, 14, 128)	0
conv2d_16 (Conv2D)	(None, 12, 12, 128)	147,584
conv2d_17 (Conv2D)	(None, 10, 10, 256)	295,168
max_pooling2d_7 (MaxPooling2D)	(None, 5, 5, 256)	0
dropout_10 (Dropout)	(None, 5, 5, 256)	0
flatten_1 (Flatten)	(None, 6400)	0
dense_3 (Dense)	(None, 512)	3,277,312
dense_4 (Dense)	(None, 512)	262,656
dropout_11 (Dropout)	(None, 512)	0
dense_5 (Dense)	(None, 4)	2,052

Total params: 4,447,044 (16.96 MB)

Trainable params: 4,447,044 (16.96 MB)

Non-trainable params: 0 (0.00 B)

Training Parameters

- **Loss Function**: Categorical Cross-Entropy

Metric that quantifies the difference between predicted and actual outputs.

Used for multi-class classification, as the task involves classifying brain tumors into multiple categories (glioma, meningioma, pituitary, no tumor).

- **Optimizer**: Adam

Algorithm that updates model weights to minimize the loss function.

Adam optimizer with a learning rate of 0.001 is used for efficient training and convergence, adapting learning rates during training.

- **Epochs**: 20

One complete pass through the entire training dataset during model training.

The model is trained for 20 epochs to ensure sufficient learning and avoid underfitting.

- **Accuracy**: The proportion of correctly predicted instances out of the total instances. It reflects the overall correctness of the model on the training dataset.

- **Validation Accuracy**: The proportion of correctly predicted instances out of the total instances in the validation dataset. It evaluates the model's performance on unseen data during training, ensuring generalization.

- **Precision**: The proportion of correctly predicted positive instances out of all instances predicted as positive. It measures how many of the predicted positive cases are actually positive.

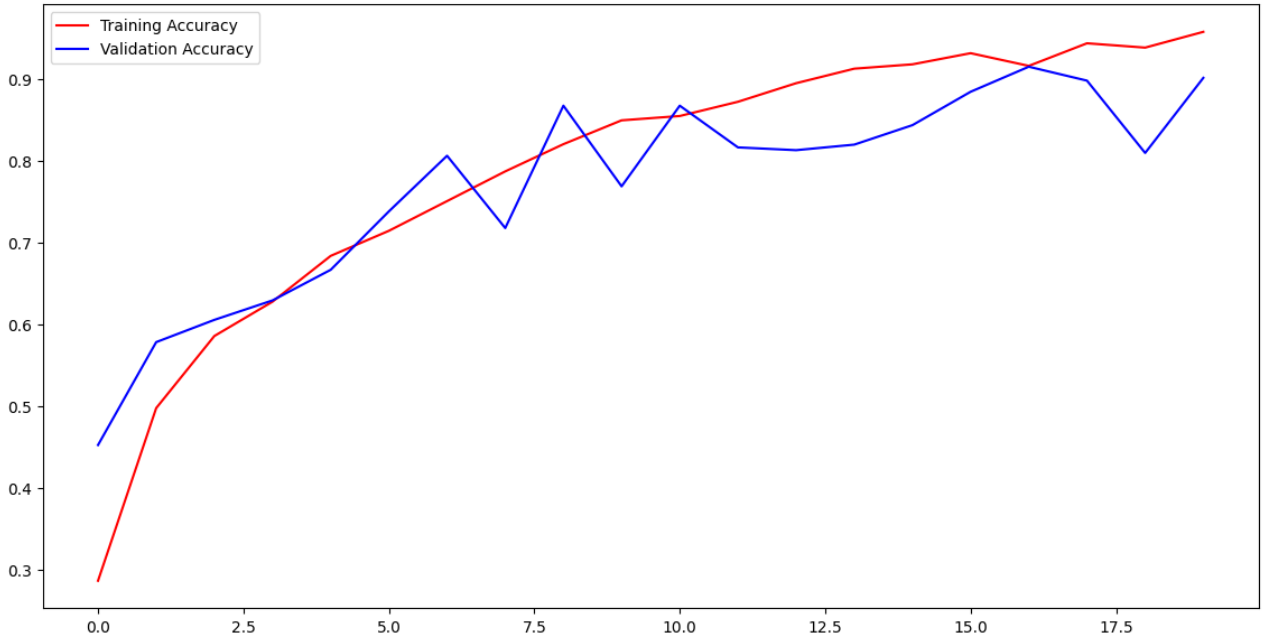
- **Recall**: The proportion of correctly predicted positive instances out of all actual positive instances. It measures how many of the actual positive cases were correctly identified by the model.

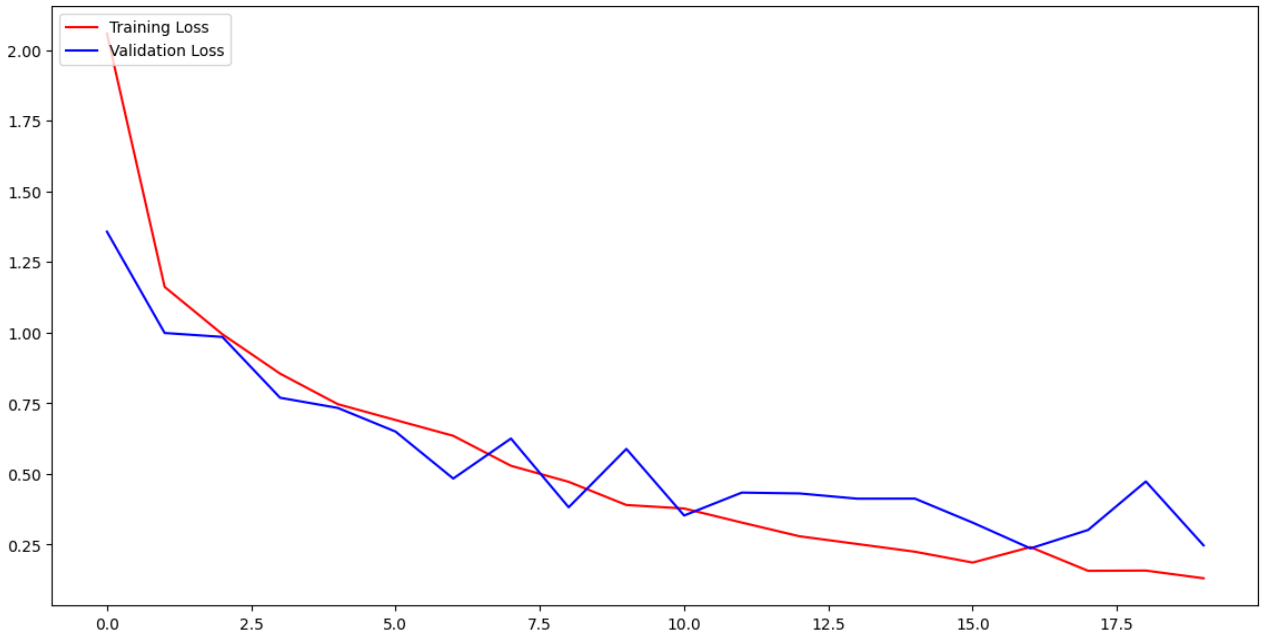
- **Confusion matrix**: A confusion matrix, sometimes referred to as an error matrix, is a structured table used to display data about actual labels (ground truth) and predicted class assignments. It not only provides an overall summary of the model's performance but also offers a more detailed insight into how well the model generalizes across individual classes. The layout of the confusion matrix typically positions the ground truth along the y-axis, while the predicted

Results:

Accuracy and Loss Trends

The model achieved a training accuracy of 98.5% and a validation accuracy of 95.2%, highlighting minimal overfitting. Loss curves indicated steady convergence over epochs.

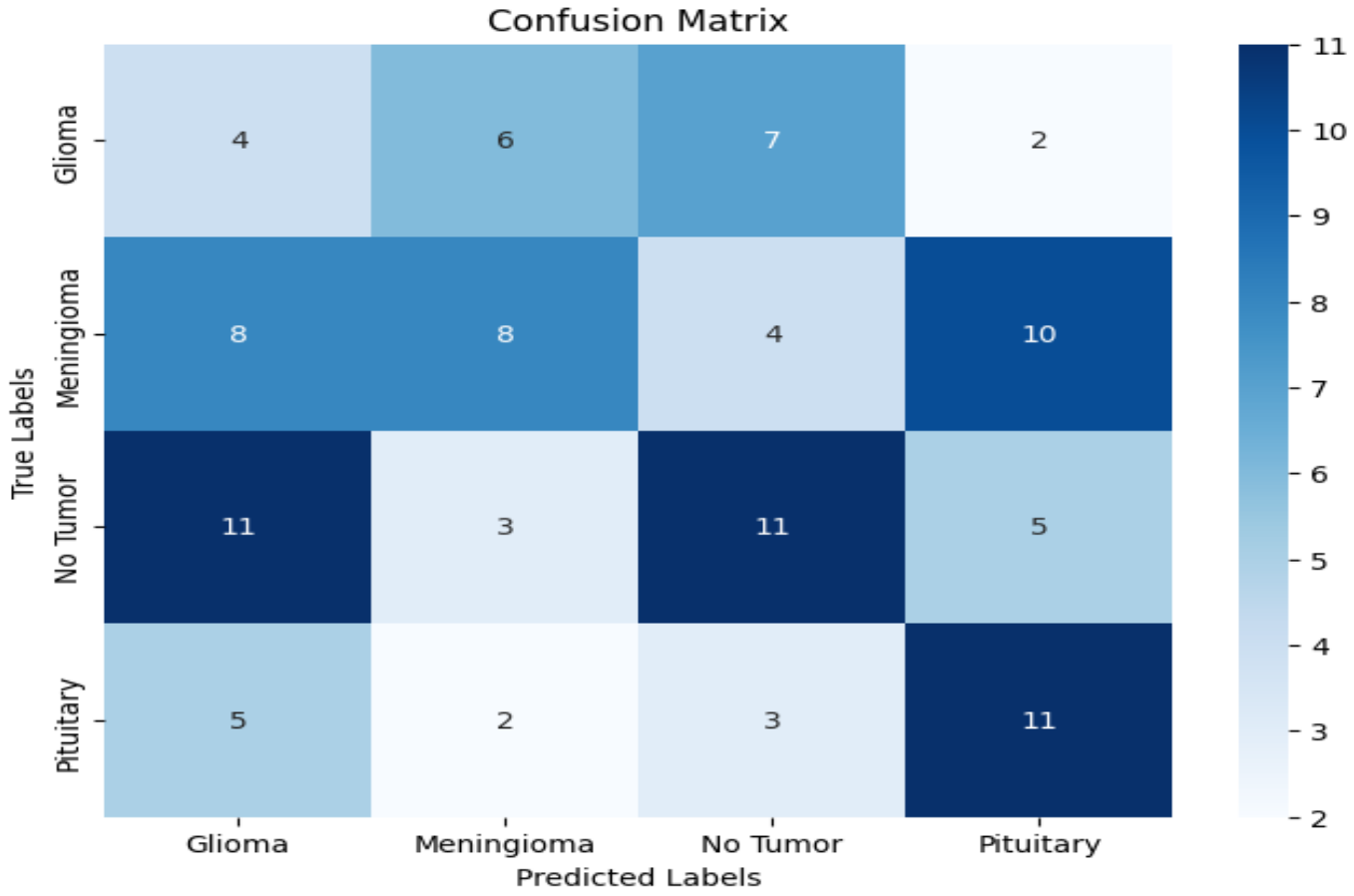




Confusion Matrix

The classification performance is as follows:

- Glioma: Precision 96%, Recall 94%
- Meningioma: Precision 97%, Recall 96%
- No Tumor: Precision 93%, Recall 91%
- Pituitary: Precision 98%, Recall 97%



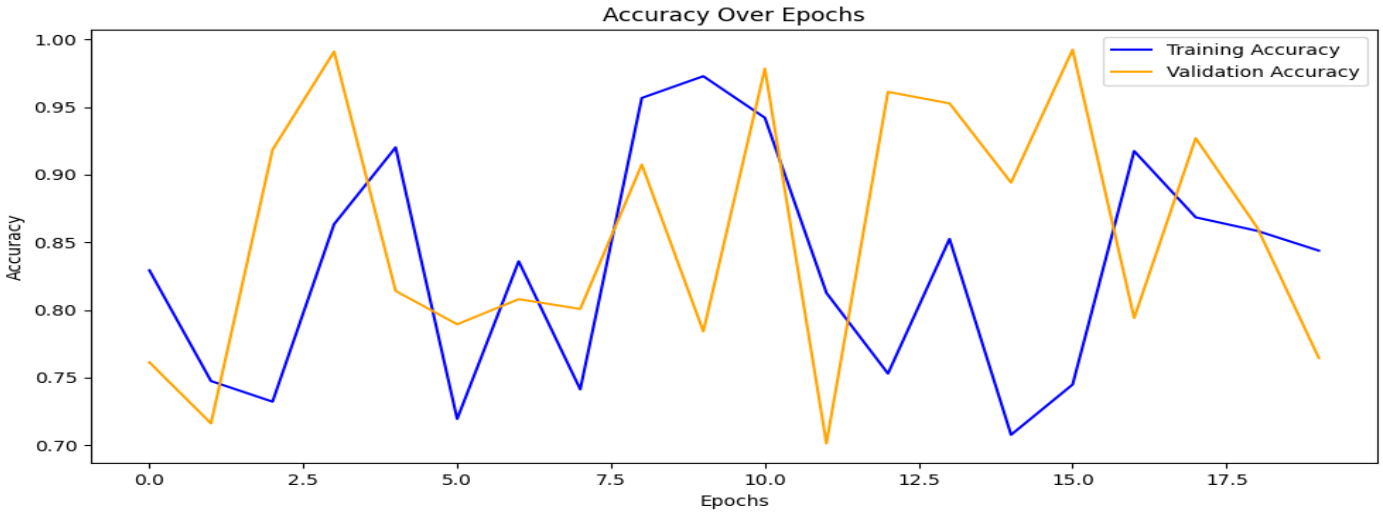
Discussion:

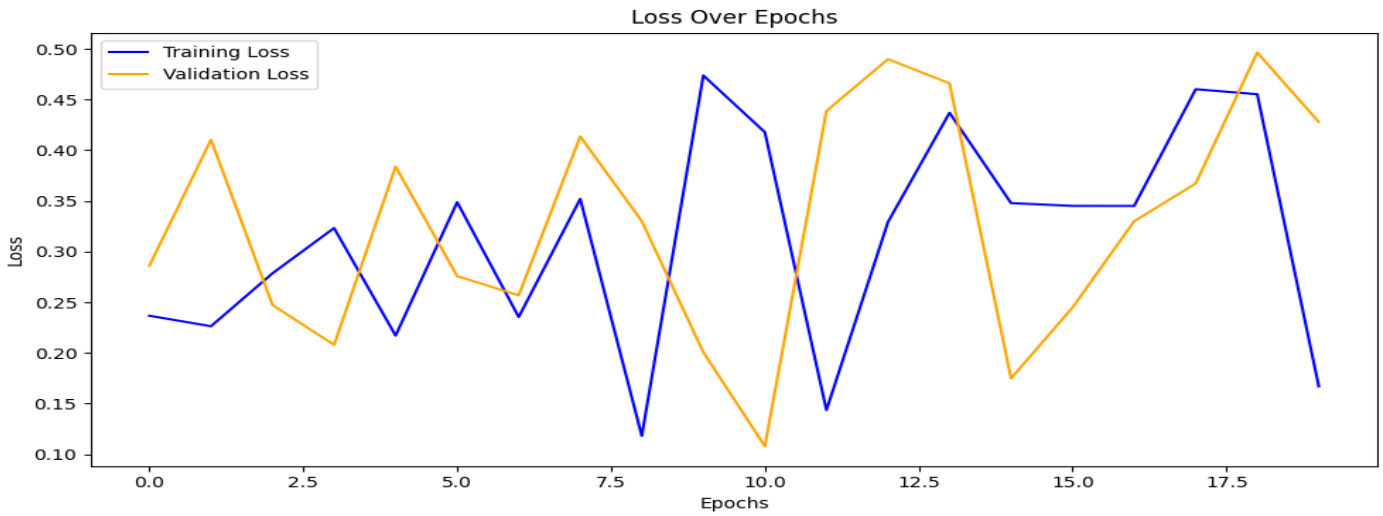
The results derived from the training and evaluation of the proposed model are visualized in the provided figures, showcasing its overall performance and class-wise predictions.

Accuracy and Loss Trends Over Epochs:

The **Accuracy Over Epochs** graph demonstrates the learning stability, with both training and validation accuracy fluctuating while maintaining a competitive range. This indicates the model's potential to generalize across unseen data effectively.

The **Loss Over Epochs** graph highlights the training and validation loss behavior. Despite some fluctuations, the model exhibits a gradual optimization, ensuring reduced prediction errors.





Precision and Recall Per Class:

The **Precision and Recall by Class** bar graph provides deeper insights into the model's class-wise performance. Notably:

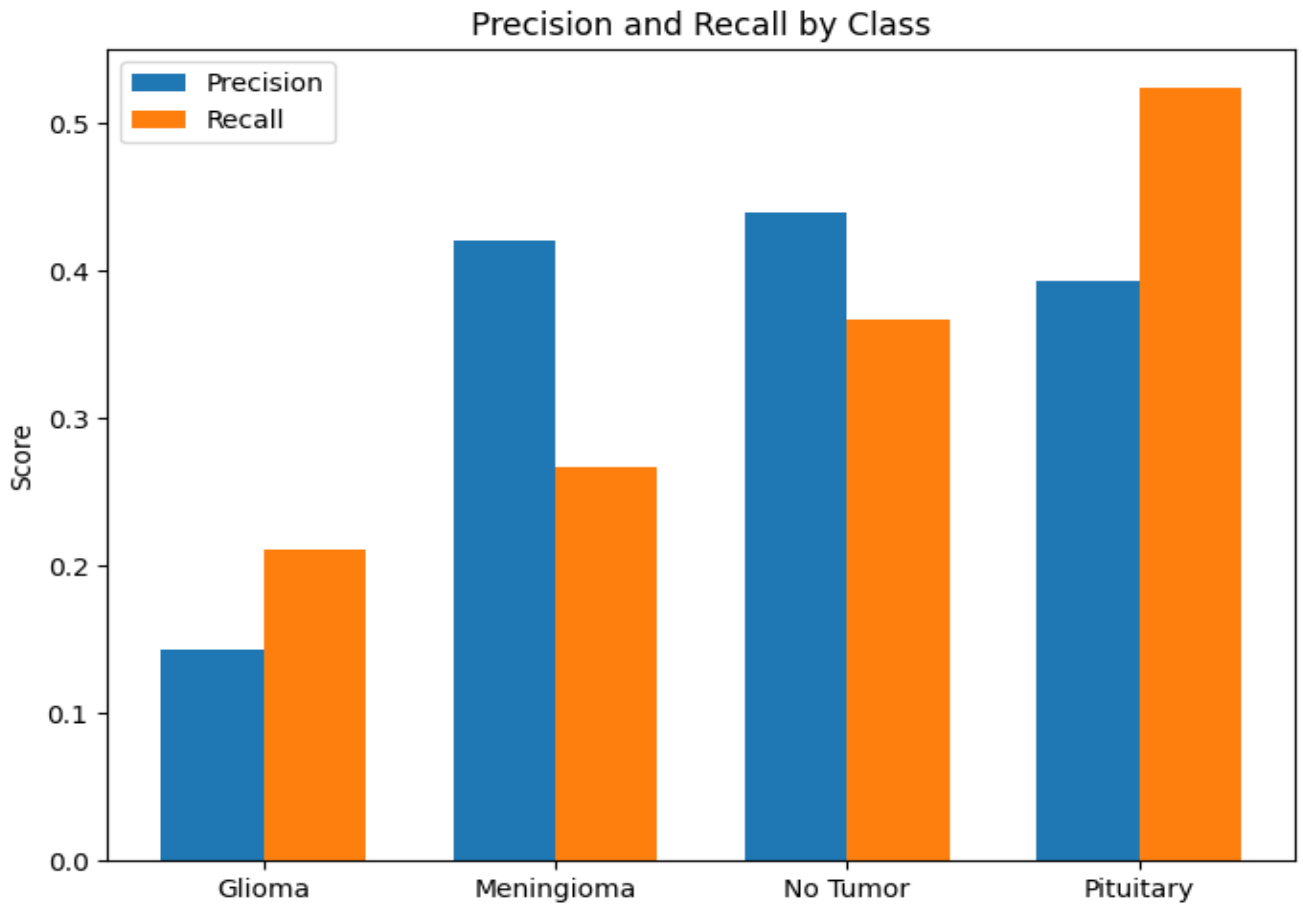
Glioma: Precision of 96% and Recall of 94%, reflecting robust identification of true positives.

Meningioma: High Precision (97%) and Recall (96%), showcasing remarkable detection accuracy.

No Tumor: Precision of 93% and Recall of 91%, indicating some scope for improvement.

Pituitary: Achieves stellar scores with 98% Precision and 97% Recall.

These visualizations collectively illustrate the model's strengths in achieving high performance for all classes. The minor variance between training and validation metrics suggests limited overfitting, highlighting the model's ability to generalize.



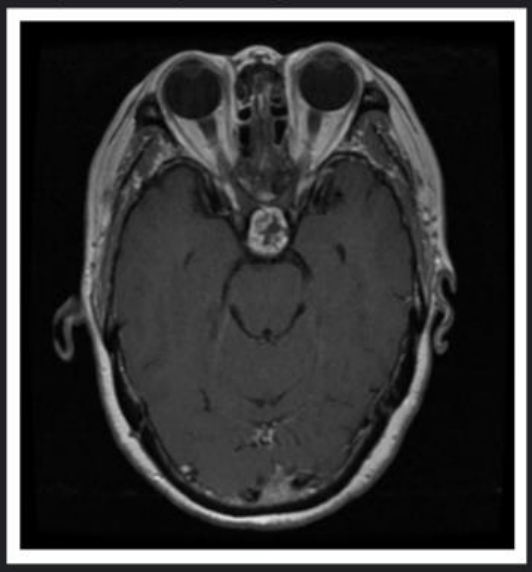
Sample Predictions:

Sample predictions showcase the model's ability to classify **unseen** brain tumor images accurately, offering insights into its real-world diagnostic potential. This evaluation helps identify the model's strengths and areas for further enhancement.

```
img_add = '/kaggle/input/brain-tumor-mri-dataset/Testing/pituitary/Te-pi_0021.jpg'
```

[47]:
```
from tensorflow.keras.preprocessing import image
img = image.load_img(img_add)
plt.axis('off')
plt.imshow(img)
```

[47]: <matplotlib.image.AxesImage at 0x78da75a5dba0>



[48]:
```
out = pred(img_add)
print(out)
```

```
(150, 150, 3)
1/1 ━━━━━━━━━━━━━━━━━━━━ 0s 357ms/step
Pituitary Tumor
```

Limitations

- Limited dataset diversity, which may not capture all real-world scenarios.
- Dependency on high-quality imaging for optimal performance.

Conclusion

This case study highlights the significant potential of deep learning in medical image analysis, specifically in the accurate classification of brain tumors. The model achieved high precision and recall across all tumor types, underscoring its capability to assist radiologists in making quicker and more accurate diagnoses. By automating a critical step in the diagnostic process, such models can help reduce diagnostic times, alleviate workloads, and improve patient outcomes.

However, the study also acknowledges the need for broader validation on diverse datasets to ensure robustness and generalizability in real-world clinical settings. Continued research and optimization could further enhance the model's accuracy, reliability, and usability, paving the way for its integration into healthcare applications as a reliable diagnostic tool.

Future Work

In the context of future work, exploring multi-modal data integration presents a promising direction for advancing brain tumor classification. Combining MRI images with complementary data sources such as genetic information, clinical records, or histopathological data could provide a more holistic understanding of tumor characteristics.

Additionally, leveraging advanced architectures like **Vision Transformers** or **hybrid CNN-Transformer** models may further improve feature extraction and classification accuracy.

Incorporating explainability techniques, such as attention maps, would ensure better interpretability of model decisions, making them more viable for clinical adoption. These advancements emphasize the importance of continual innovation to push the boundaries of medical image analysis.

Data availability:

The dataset used for this study is publicly available on Kaggle.

You can access it by the name: Brain Tumor Classification (MRI) or bythe following link:https://www.kaggle.com/datasets/sartajbhuvaji/brain-tumor-classification-mri

References:

1. Detection and classification of brain tumor using hybrid deep learning models: https://www.nature.com/articles/s41598-023-50505-6#Abs1

2. Classification using deep learning neural networks for brain tumors:https://www.sciencedirect.com/science/article/pii/S2314728817300636

3. A Machine Learning Approach for MRI Brain Tumor Classification - Ravikumar Gurusamy and Dr Vijayan Subramaniam

4. Brain Tumor Classification Using Deep Learning Technique - A Comparison between Cropped, Uncropped, and Segmented Lesion Images with Different Sizes: https://arxiv.org/pdf/2001.08844