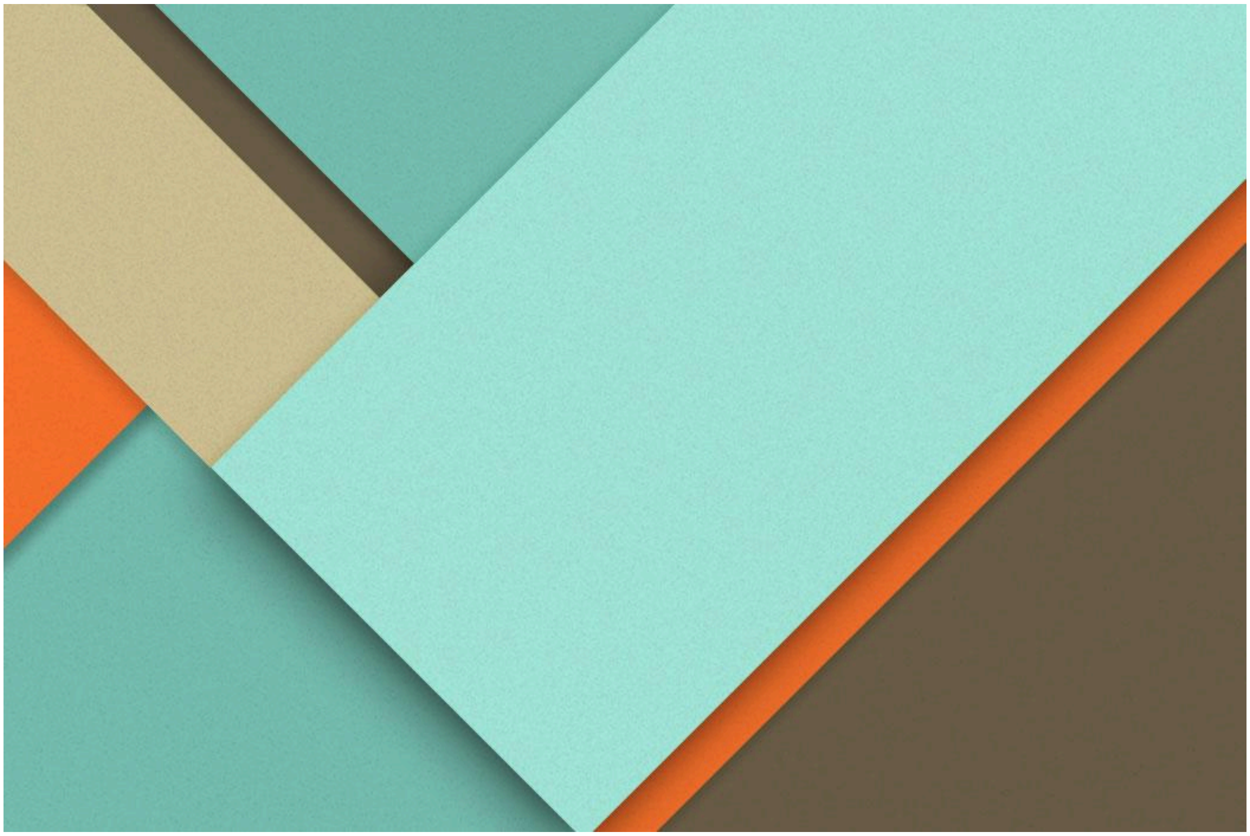

BrainTumor Identification & Classification

24.10.2024

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Ai&Ds-A

Objective

The project aims to develop and evaluate deep learning models, including CNN, CNN-LSTM, and U-Net architectures, for automated classification of brain MRI scans into four categories: Glioma, Meningioma, Pituitary tumor, and No Tumor. By leveraging these models, the project seeks to enhance accuracy, reduce diagnostic time, and provide a scalable solution for brain tumor detection.

Data Collection and Preprocessing

Dataset

This dataset combines three sources: Figshare,SARTAJ dataset, and Br35H. It comprises 7,023 MRI images of human brains, classified into four categories: glioma, meningioma, pituitary, and no tumor. Images for the no-tumor class were specifically taken from the Br35H dataset.

Gliomas, which account for about 33% of brain tumors, commonly affect elderly individuals, with higher prevalence in males. Gliomas range in grade, from low to high, based on cellular activity and aggressiveness. Low-grade gliomas, often found in children, are generally less aggressive, while nearly 80% of malignant brain tumors are gliomas. Grade I gliomas develop slowly and can sometimes be removed surgically. In contrast, Grade IV gliomas, or glioblastomas, grow rapidly, spread widely, and are notably challenging to treat due to their aggressive nature.

Preprocessing

- Loading and Resizing: MRI images are loaded from directories for each category (glioma, meningioma, pituitary, and no tumor), converted to grayscale, and resized to a uniform size.

- Normalization: Images are normalized by scaling pixel values to the range [0, 1], improving model performance.

- Label Encoding: Labels are one-hot encoded, transforming categorical labels into binary vectors for multi-class classification.

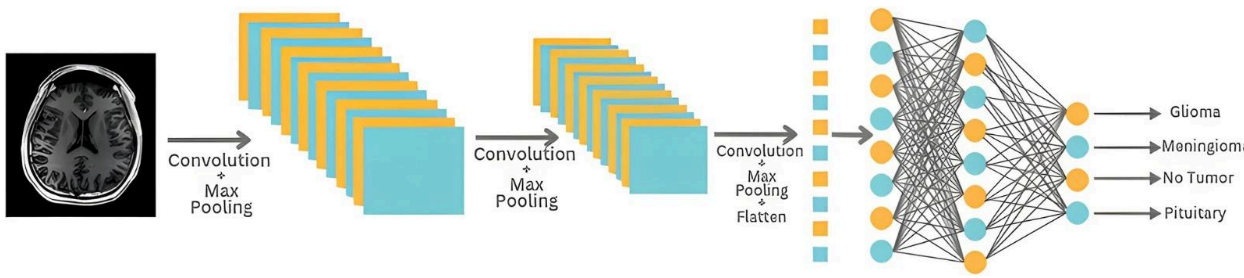
- Data Shuffling and Splitting: Training data is shuffled for randomness and split into training and validation sets to optimize model training.

- Test Data Processing: The test dataset undergoes identical processing to ensure consistency in evaluation.

- Evaluation: A confusion matrix visually compares true and predicted labels, providing insights into model accuracy across each class.

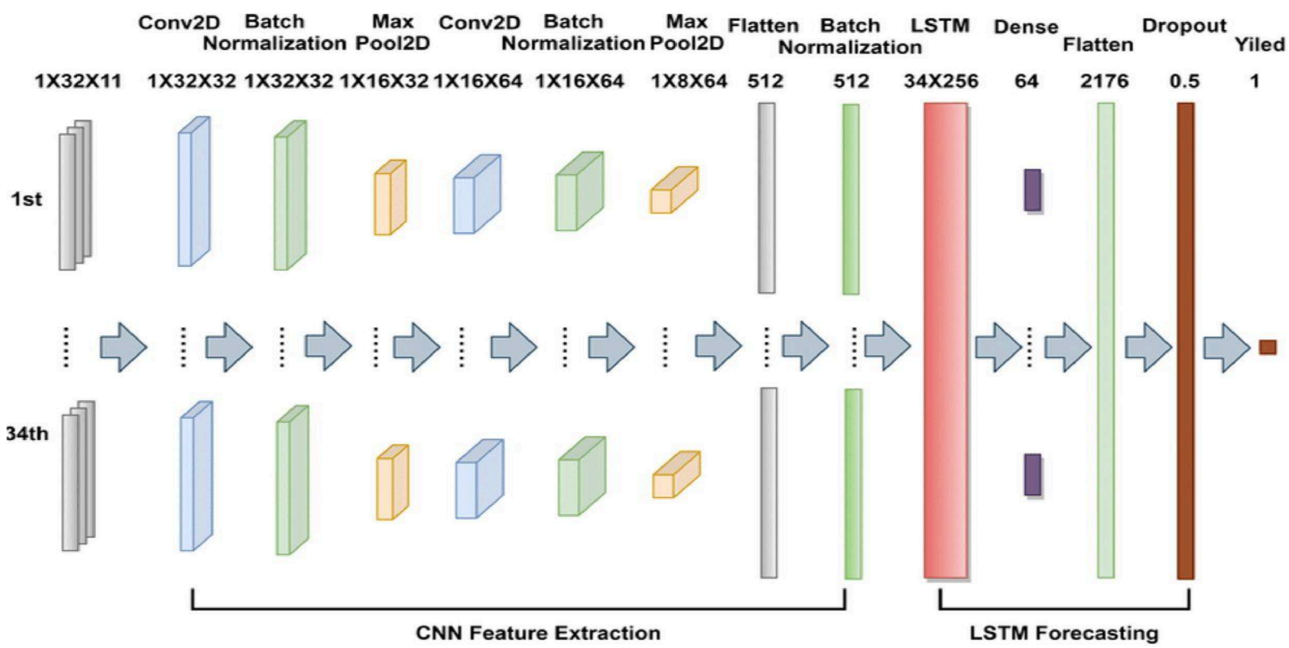
Model Architecture & Description

1. CNN-Architecture



The CNN architecture consists of two convolutional layers, each followed by max-pooling. The first layer applies 32 filters and the second 64 filters, both using 3x3 kernels with ReLU activation for feature extraction. Max-pooling layers downsample the feature maps, reducing dimensionality and computation. After flattening the feature maps, a fully connected dense layer with 128 neurons is applied for feature combination, followed by a softmax output layer for multi-class classification. The model is compiled using the Adam optimizer and categorical cross-entropy loss for optimal accuracy.

2. CNN + LSTM



(b)

The CNN+LSTM architecture used for brain tumor classification processes MRI image sequences as follows:

Input: Sequences of 10 MRI images, each resized to **100x100 pixels**, with 3 color channels (RGB).

-CNN Layers: Three convolutional layers with **32, 64, and 128 filters** (kernel size 3x3), each followed by **2x2 max-pooling**. These extract spatial features such as textures and edges from individual frames.

-LSTM Layer: A single LSTM layer with **128 units** captures temporal dependencies across the sequence of images.(tanh Activation)

- Dense Layers: A fully connected layer with **64 neurons** (ReLU activation) and Dropout (0.5) to prevent overfitting.

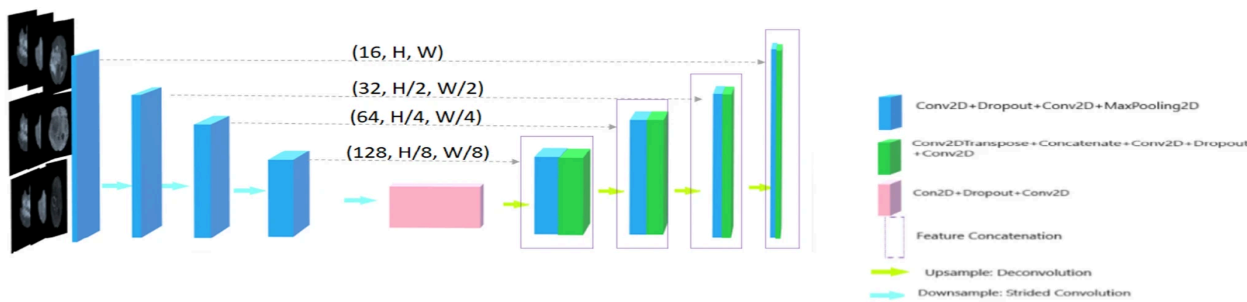
- Output Layer: A softmax layer outputs probabilities for the 4 classes (Glioma, Meningioma, Pituitary Tumor, No Tumor).

- Optimizer: Adam-Adaptive Moment Estimation(minimize the loss function during the training of neural networks)

- Loss Function: Categorical cross-entropy for multi-class classification.

This architecture effectively combines spatial and temporal analysis for accurate brain tumor detection across MRI sequences.

3.U-Net



This U-Net model, modified for brain MRI classification, uses an encoder-decoder structure to capture detailed spatial information in grayscale MRI images and classify them into four categories: Glioma, Meningioma, Pituitary Tumor, and No Tumor. Below is the breakdown of the model's architecture based on the provided code.

Input: 128x128 grayscale MRI images.

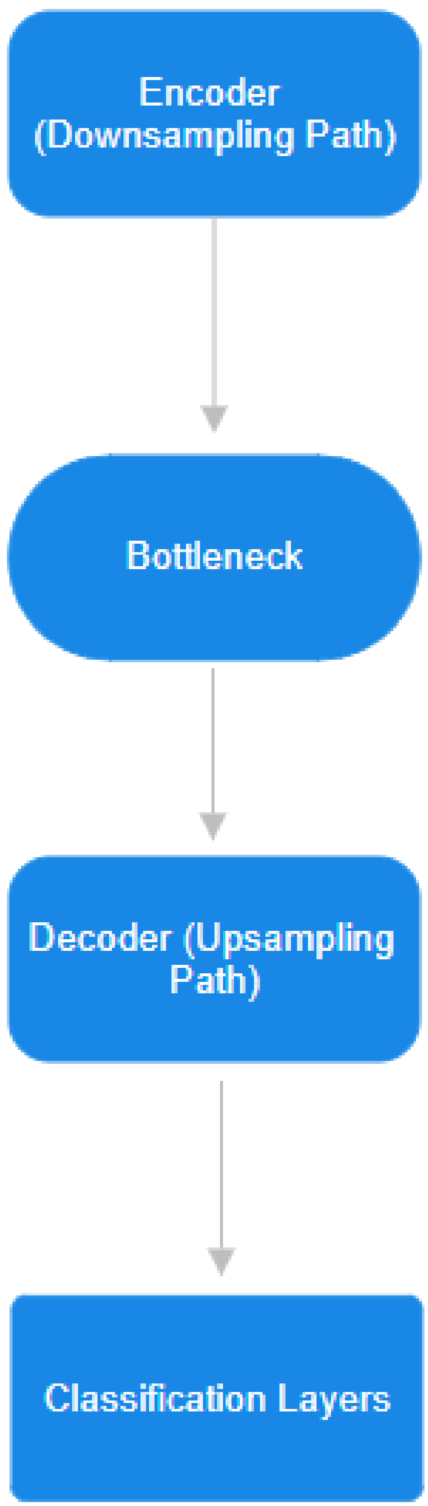
Encoder Path: Successive 3x3 convolutions (64 and 128 filters) with ReLU activation, followed by 2x2 max pooling to downsample and capture hierarchical spatial features.

Bottleneck: Two 3x3 convolutions with 256 filters, extracting core features for accurate tumor identification.

Decoder Path: Transposed convolutions (Conv2DTranspose) with 128 and 64 filters to upsample, with skip connections to corresponding encoder layers, preserving fine spatial details.

Classification Layers: Flattened decoder output, followed by fully connected layers with ReLU activation.

Output: A softmax layer for multi-class classification across four tumor types: Glioma, Meningioma, Pituitary Tumor, and No Tumor.


Encoder
(Downsampling Path)
Bottleneck
Decoder (Upsampling
Path)
Classification Layers

Aspect	CNN Model	CNN + LSTM Model	U-Net Model
Architecture	Sequential layers of convolution and pooling, focusing on spatial feature extraction.	Combines CNN for spatial feature extraction with LSTM for sequence learning, targeting both spatial and temporal dependencies.	Encoder-decoder structure with skip connections to capture both spatial features and context information.
Feature Extraction	Captures spatial features effectively.	Learns both spatial features and temporal sequences across frames.	Excels in capturing both spatial and contextual features across multiple scales.
Strengths	Efficient for single-frame classification; good at identifying spatial features.	Combines spatial and sequential learning, capturing changes over sequences; beneficial for dynamic image series.	High accuracy in pixel-level segmentation; useful for detailed boundary and region delineation in images.
Weaknesses	Limited to spatial analysis, lacking temporal understanding for sequences.	More computationally demanding and complex; requires larger datasets.	High memory and computational demand; may require extensive fine-tuning for optimal performance.
Accuracy (%)	94.2	83.08	86.08
Loss Rate (%)	27.27	75.3	58.6

Training process

1. **Model Compilation**:
   Each model (CNN, CNN+LSTM, U-Net) is compiled with the Adam optimizer and categorical cross-entropy loss, designed to support multi-class classification. The evaluation metric used is accuracy.
2. **Training and Validation Split**:
   The training data is further split into training and validation sets, ensuring that 20% of the data is reserved for validation. This allows the model to optimize while monitoring its performance on unseen data.

3. **Training Epochs**:
   Each model is trained over 10 epochs, during which the model iteratively learns patterns in the training data, minimizing loss and improving accuracy with each pass.
4. **Batch Size**:
   A batch size of 16 is used, meaning that 16 images are processed together in each forward and backward pass. This is chosen to balance memory constraints and model convergence speed.
5. **Model Evaluation**:
   After training, the model is evaluated on a separate test set. The test set undergoes the same preprocessing as the training set, allowing the model to be assessed on unseen data to measure its generalization performance.
6. **Results and Visualization**:
   Model performance is visualized using a confusion matrix, which provides insights into classification accuracy across different classes and helps highlight any misclassifications.

Real-Time Considerations

Latency

- Minimize inference time for quick predictions.
- Use optimization techniques (e.g., quantization, pruning) to reduce latency.

Accuracy and Reliability

- Maintain high accuracy, sensitivity, and specificity.
- Implement continuous learning for model adaptation.

Robustness

- Ensure the model handles variability in data (e.g., noise, resolution).
- Focus on generalization to unseen data.

Integration with Clinical Workflows

- Develop an intuitive user interface for healthcare professionals.
- Ensure seamless integration with existing hospital systems.

Evaluation Metrics

Accuracy: Overall correctness of predictions. Important for assessing general model performance.

Precision: Ratio of true positives to total predicted positives. Essential to minimize false positives in tumor detection.

Recall (Sensitivity): Ability to identify actual tumors. Critical to avoid missing any tumor cases.

F1 Score: Balances precision and recall, useful for handling class imbalances among tumor types.

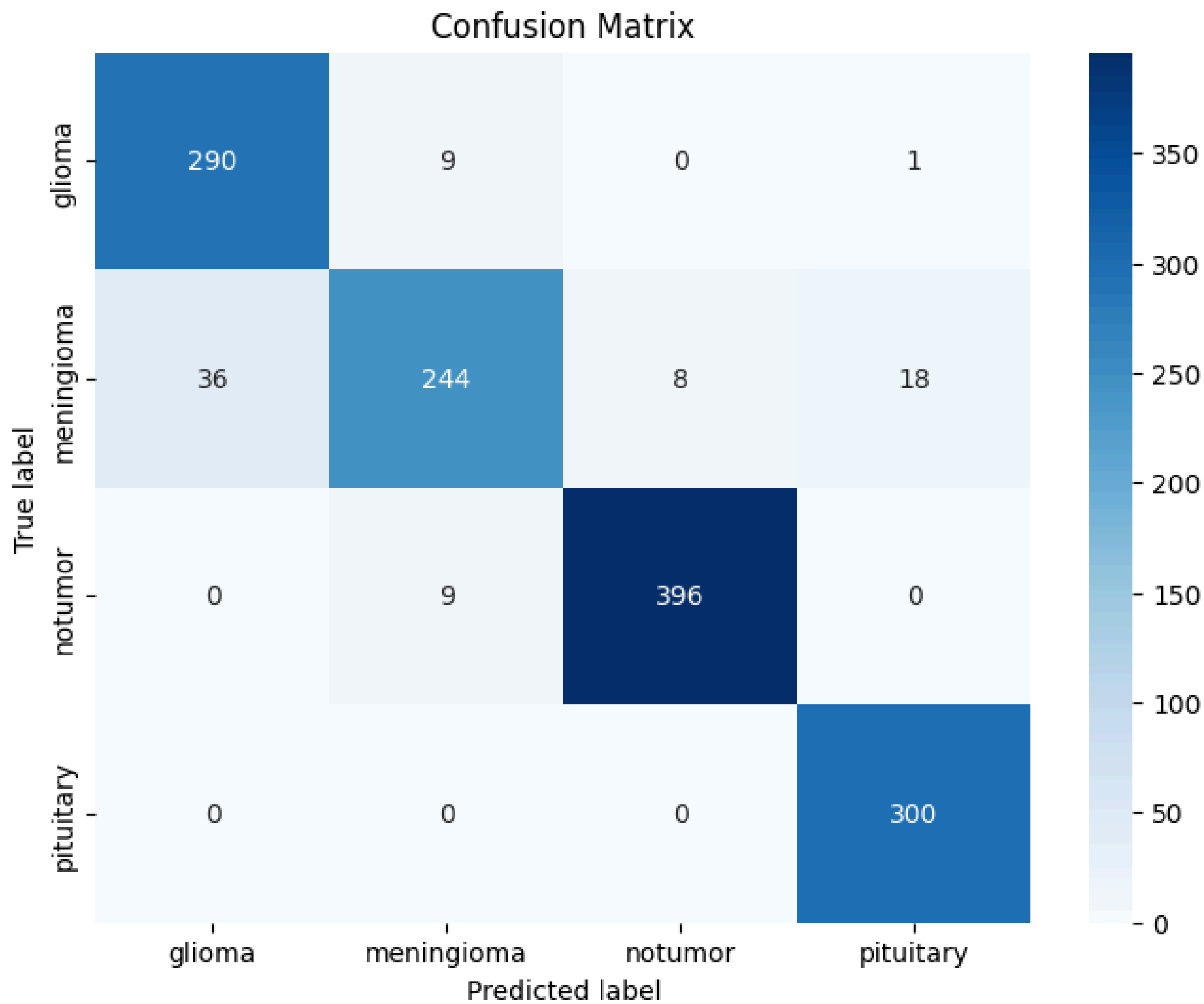
Confusion Matrix: Displays true positives, true negatives, false positives, and false negatives. Helps identify which tumor types are confused with others.

Output

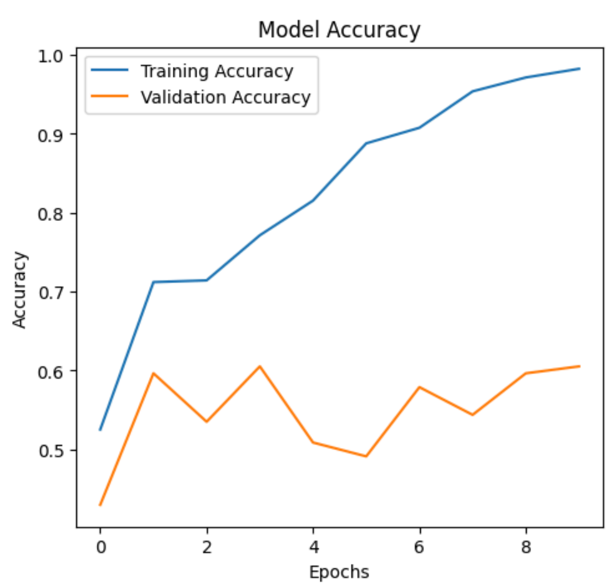
CNN Model:

```
Epoch 1/10
143/143 ━━━━━━━━━━━━━━━━━━━━ 15s 94ms/step - accuracy: 0.6016 - loss: 0.9034 - val_accuracy: 0.8705 - val_loss: 0.4095
Epoch 2/10
143/143 ━━━━━━━━━━━━━━━━━━━━ 13s 89ms/step - accuracy: 0.8675 - loss: 0.3511 - val_accuracy: 0.8889 - val_loss: 0.3054
Epoch 3/10
143/143 ━━━━━━━━━━━━━━━━━━━━ 13s 89ms/step - accuracy: 0.9193 - loss: 0.2197 - val_accuracy: 0.8793 - val_loss: 0.3103
Epoch 4/10
143/143 ━━━━━━━━━━━━━━━━━━━━ 13s 88ms/step - accuracy: 0.9480 - loss: 0.1502 - val_accuracy: 0.9283 - val_loss: 0.2282
Epoch 5/10
143/143 ━━━━━━━━━━━━━━━━━━━━ 13s 89ms/step - accuracy: 0.9798 - loss: 0.0694 - val_accuracy: 0.9204 - val_loss: 0.2827
Epoch 6/10
143/143 ━━━━━━━━━━━━━━━━━━━━ 13s 87ms/step - accuracy: 0.9864 - loss: 0.0406 - val_accuracy: 0.9221 - val_loss: 0.2389
Epoch 7/10
143/143 ━━━━━━━━━━━━━━━━━━━━ 13s 88ms/step - accuracy: 0.9854 - loss: 0.0443 - val_accuracy: 0.9361 - val_loss: 0.2585
Epoch 8/10
143/143 ━━━━━━━━━━━━━━━━━━━━ 13s 89ms/step - accuracy: 0.9931 - loss: 0.0222 - val_accuracy: 0.9379 - val_loss: 0.2608
Epoch 9/10
143/143 ━━━━━━━━━━━━━━━━━━━━ 13s 88ms/step - accuracy: 0.9983 - loss: 0.0096 - val_accuracy: 0.9318 - val_loss: 0.3096
Epoch 10/10
143/143 ━━━━━━━━━━━━━━━━━━━━ 13s 89ms/step - accuracy: 0.9991 - loss: 0.0056 - val_accuracy: 0.9318 - val_loss: 0.2815
```

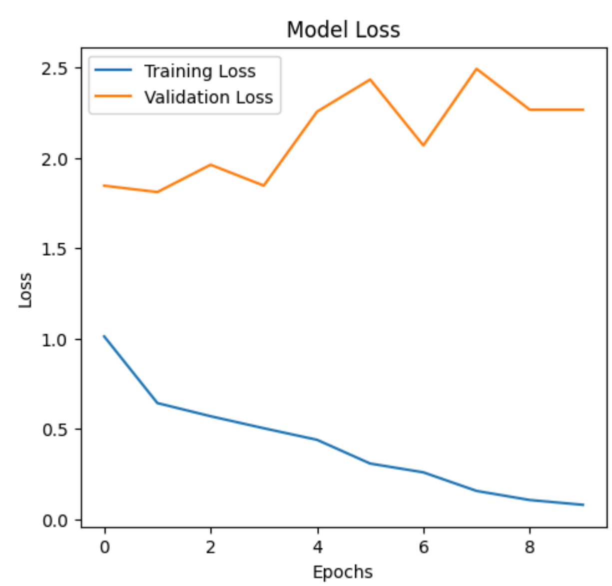
```
41/41 ━━━━━━━━━━━━━━━━━━━━ 1s 21ms/step - accuracy: 0.8993 - loss: 0.4803
Test accuracy: 94.28%
```



Confusion Matrix
True label
glioma
meningioma
notumor
pituitary
290
9
0
1
36
244
8
18
0
9
396
0
0
0
0
300
Predicted label
350
300
250
200
150
100
50
0



Model Accuracy
Training Accuracy
Validation Accuracy
Accuracy
Epochs
1.0
0.9
0.8
0.7
0.6
0.5
0
2
4
6
8

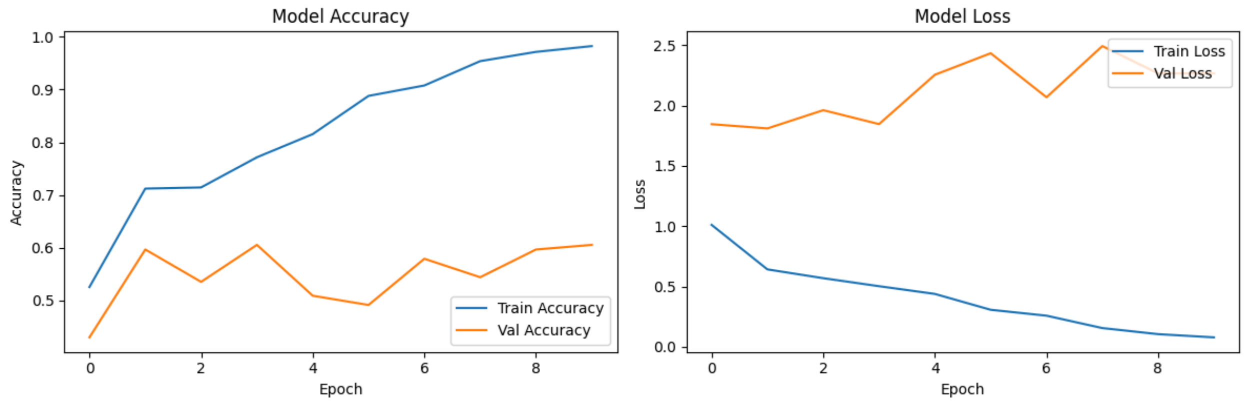


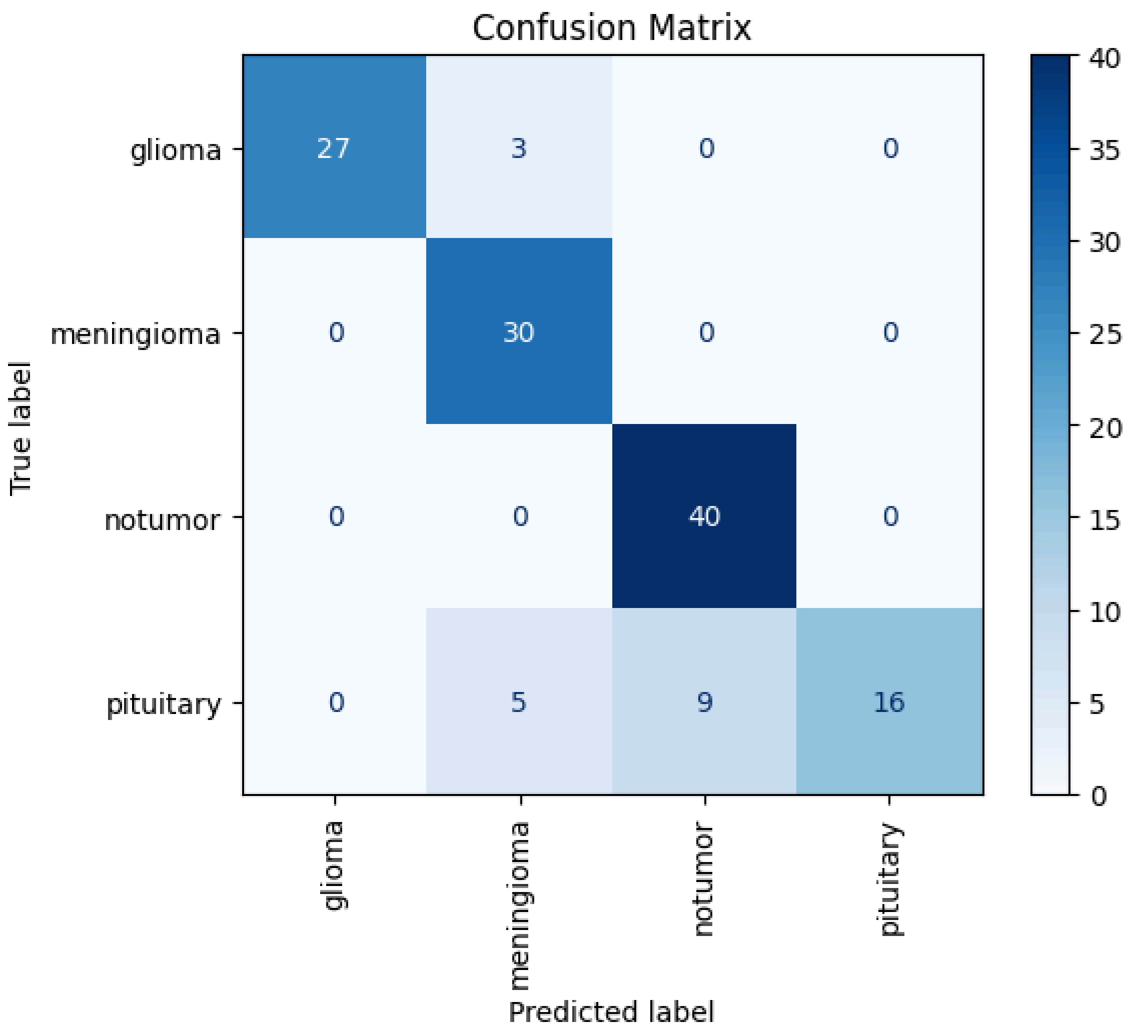
Model Loss
Training Loss
Validation Loss
Loss
Epochs
2.5
2.0
1.5
1.0
0.5
0.0
0
2
4
6
8

CNN+LSTM Model:

```
Epoch 1/10
29/29 ━━━━━━━━━━━━━━━━━━━━ 66s 2s/step - accuracy: 0.4206 - loss: 1.2123 - val_accuracy: 0.4298 - val_loss: 1.8454
Epoch 2/10
29/29 ━━━━━━━━━━━━━━━━━━━━ 53s 2s/step - accuracy: 0.6996 - loss: 0.6742 - val_accuracy: 0.5965 - val_loss: 1.8103
Epoch 3/10
29/29 ━━━━━━━━━━━━━━━━━━━━ 56s 2s/step - accuracy: 0.6698 - loss: 0.6364 - val_accuracy: 0.5351 - val_loss: 1.9615
Epoch 4/10
29/29 ━━━━━━━━━━━━━━━━━━━━ 53s 2s/step - accuracy: 0.7988 - loss: 0.4617 - val_accuracy: 0.6053 - val_loss: 1.8460
Epoch 5/10
29/29 ━━━━━━━━━━━━━━━━━━━━ 59s 2s/step - accuracy: 0.8252 - loss: 0.4532 - val_accuracy: 0.5088 - val_loss: 2.2552
Epoch 6/10
29/29 ━━━━━━━━━━━━━━━━━━━━ 56s 2s/step - accuracy: 0.8885 - loss: 0.2949 - val_accuracy: 0.4912 - val_loss: 2.4336
Epoch 7/10
29/29 ━━━━━━━━━━━━━━━━━━━━ 61s 2s/step - accuracy: 0.9069 - loss: 0.2507 - val_accuracy: 0.5789 - val_loss: 2.0684
Epoch 8/10
29/29 ━━━━━━━━━━━━━━━━━━━━ 55s 2s/step - accuracy: 0.9543 - loss: 0.1553 - val_accuracy: 0.5439 - val_loss: 2.4929
Epoch 9/10
29/29 ━━━━━━━━━━━━━━━━━━━━ 54s 2s/step - accuracy: 0.9753 - loss: 0.1086 - val_accuracy: 0.5965 - val_loss: 2.2663
Epoch 10/10
29/29 ━━━━━━━━━━━━━━━━━━━━ 48s 2s/step - accuracy: 0.9862 - loss: 0.0671 - val_accuracy: 0.6053 - val_loss: 2.2663
5/5 ━━━━━━━━━━━━━━━━━━━━ 2s 291ms/step - accuracy: 0.8668 - loss: 0.5015
5/5 ━━━━━━━━━━━━━━━━━━━━ 2s 392ms/step
```

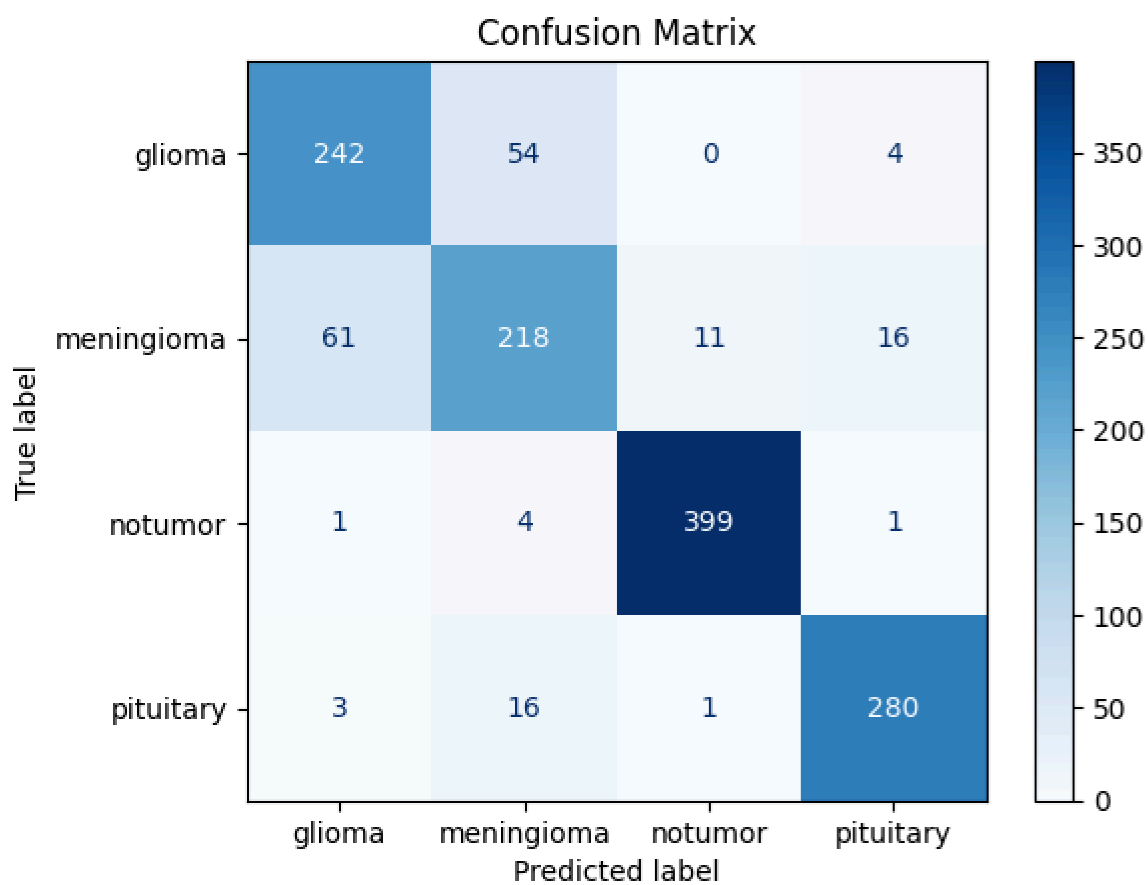
```
5/5 ━━━━━━━━━━━━━━━━━━━━ 2s 277ms/step - accuracy: 0.8668 - loss: 0.5015
Test Accuracy: 83.08%
Test Loss: 75.52%
```

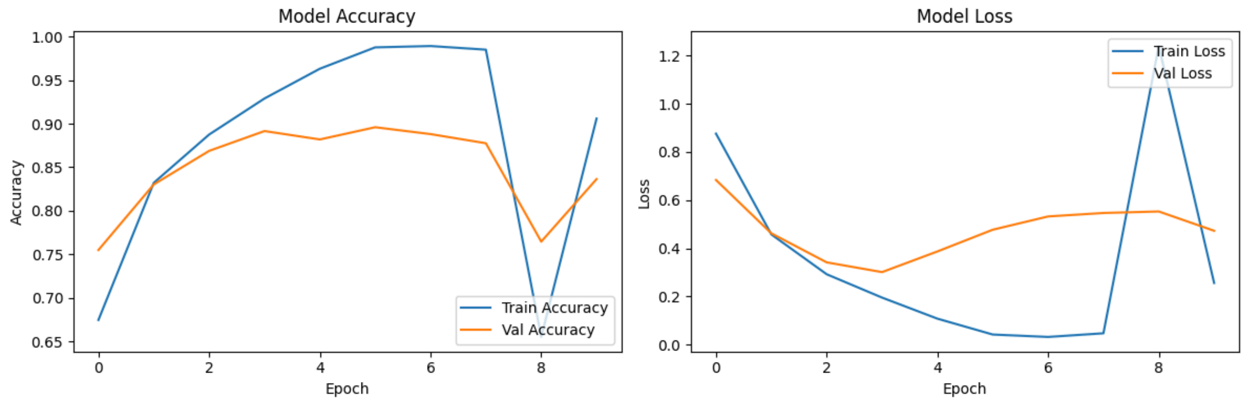

Model Accuracy
Accuracy
Epoch
Train Accuracy
Val Accuracy
Model Loss
Loss
Epoch
Train Loss
Val Loss


Confusion Matrix
True label
Predicted label
glioma
meningioma
notumor
pituitary
27
3
0
0
0
30
0
0
0
0
40
0
0
5
9
16

U-NET MODEL:

```
Epoch 1/10
286/286 ━━━━━━━━━━━━━━━━━━━━ 731s 3s/step - accuracy: 0.5480 - loss: 1.3440 - val_accuracy: 0.7550 - val_loss: 0.6838
Epoch 2/10
286/286 ━━━━━━━━━━━━━━━━━━━━ 760s 3s/step - accuracy: 0.8187 - loss: 0.4863 - val_accuracy: 0.8303 - val_loss: 0.4622
Epoch 3/10
286/286 ━━━━━━━━━━━━━━━━━━━━ 734s 3s/step - accuracy: 0.8838 - loss: 0.3005 - val_accuracy: 0.8688 - val_loss: 0.3417
Epoch 4/10
286/286 ━━━━━━━━━━━━━━━━━━━━ 732s 3s/step - accuracy: 0.9187 - loss: 0.2186 - val_accuracy: 0.8915 - val_loss: 0.3012
Epoch 5/10
286/286 ━━━━━━━━━━━━━━━━━━━━ 711s 2s/step - accuracy: 0.9678 - loss: 0.0893 - val_accuracy: 0.8819 - val_loss: 0.3870
Epoch 6/10
286/286 ━━━━━━━━━━━━━━━━━━━━ 712s 2s/step - accuracy: 0.9887 - loss: 0.0409 - val_accuracy: 0.8959 - val_loss: 0.4772
Epoch 7/10
286/286 ━━━━━━━━━━━━━━━━━━━━ 713s 2s/step - accuracy: 0.9864 - loss: 0.0370 - val_accuracy: 0.8880 - val_loss: 0.5323
Epoch 8/10
286/286 ━━━━━━━━━━━━━━━━━━━━ 715s 3s/step - accuracy: 0.9881 - loss: 0.0339 - val_accuracy: 0.8775 - val_loss: 0.5467
Epoch 9/10
286/286 ━━━━━━━━━━━━━━━━━━━━ 721s 3s/step - accuracy: 0.6828 - loss: 1.8012 - val_accuracy: 0.7647 - val_loss: 0.5529
Epoch 10/10
286/286 ━━━━━━━━━━━━━━━━━━━━ 729s 3s/step - accuracy: 0.9028 - loss: 0.2660 - val_accuracy: 0.8364 - val_loss: 0.4729
41/41 ━━━━━━━━━━━━━━━━━━━━ 46s 1s/step - accuracy: 0.8281 - loss: 0.5195
Test Accuracy: 86.88%
```





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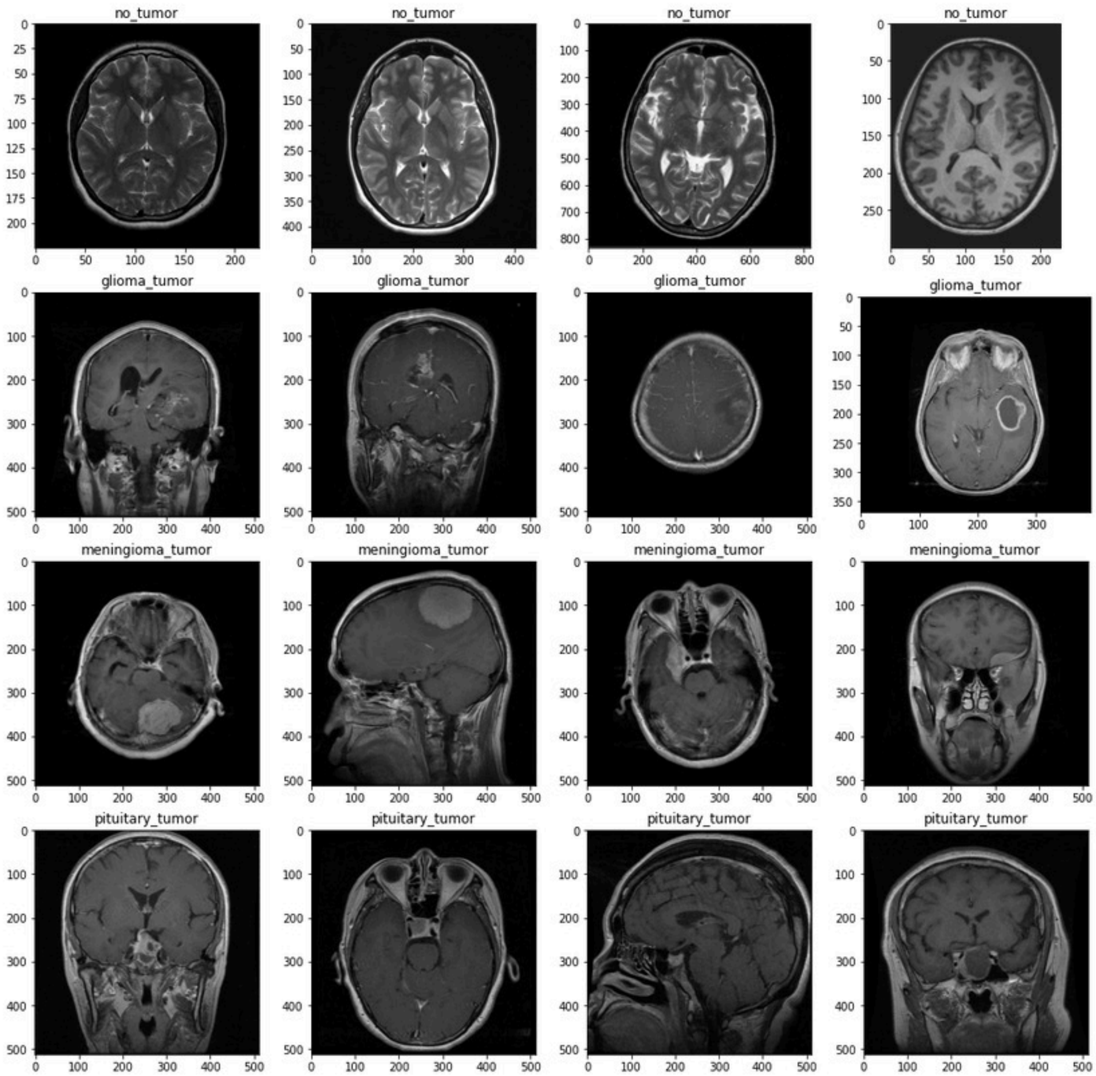
Result Analysis

- CNN Model: Achieved an accuracy of 94.2%, effectively extracting spatial features for static MRI frame classification. However, its lack of temporal awareness limits its effectiveness in scenarios requiring sequential context.

- CNN + LSTM Model: Demonstrated an accuracy of 83.08%, capturing both spatial and temporal dependencies across MRI frames. While its accuracy is lower than the CNN model, it excels in analyzing complex sequences, as indicated by improved recall and precision metrics.

- U-Net Model: Achieved an accuracy of 86.08% and is particularly effective in pixel-level segmentation. Its encoder-decoder architecture excels in detecting subtle distinctions in tumor classes, evidenced by high precision and recall scores, making it the best choice for detailed medical image analysis.



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Mohammad Zafer Khaliki & Muhammet Sinan Başarslan *Scientific Reports*

14, Article number: 2664 (2024)

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Ramdas Vankdothu a, Mohd Abdul Hameed b, Husnah Fatima c-
https://www.sciencedirect.com/science/article/abs/pii/S0045790622002361?fr=RR-1&ref=cra_js_challenge

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· Hadi Seyedarabi2

4.Kaggle

1.**Br35H :: Brain Tumor Detection 2020**

https://www.kaggle.com/datasets/ahmedhamada0/brain-tumor-detection?select=no

2.Figshare

https://figshare.com/articles/dataset/brain_tumor_dataset/1512427

Summary

This project focuses on automated brain tumor classification using MRI images, leveraging three deep learning models: CNN, CNN+LSTM, and U-Net. Each model is designed to analyze MRI scans to classify between tumor types (glioma, meningioma, pituitary) and non-tumor cases. The CNN extracts spatial features, CNN+LSTM integrates spatial and temporal features across MRI sequences, and U-Net uses segmentation principles to capture intricate details for improved classification.