

Deep Learning-Based Detection of Pituitary, Glioma, and Meningioma Tumors from Brain MRIs

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Abstract

Brain tumors, specifically pituitary adenomas, gliomas, and meningiomas, pose a significant public health challenge, necessitating accurate and timely detection to facilitate effective treatment planning. Magnetic Resonance Imaging (MRI) is a widely adopted non-invasive imaging technique for diagnosing brain tumors. This research presents a novel methodology for detecting these tumors using MRI brain scan images. A comprehensive dataset comprising MRI scans obtained from patients diagnosed with various types of brain tumors, including pituitary adenomas, gliomas, and meningiomas, was utilized. A Convolutional Neural Network (CNN) was employed to discern between different types of brain tumors. The CNN-based model outperformed other classification algorithms, achieving an overall accuracy of 97%. This research significantly contributes to the advancement of a dependable and efficient approach for the early detection and classification of pituitary adenomas, gliomas, and meningiomas using MRI brain scan images, with potential implications for improved clinical decision-making, facilitating timely intervention, and ultimately enhancing patient outcomes in the field of neuro-oncology.

Keywords: Brain tumors, Convolutional Neural Networks, deep learning, Magnetic Resonance Imaging, neuro-oncology

1. Introduction

Pituitary adenomas are benign tumors that develop in the pituitary gland, a small gland located at the base of the brain. Gliomas, on the other hand, are malignant tumors that arise from the brain's glial cells. Meningiomas are slow-growing tumors that form from the meninges, which are the protective membranes surrounding the brain and spinal cord. Each of these tumor types poses unique clinical challenges, necessitating precise and early detection for effective treatment. Traditional diagnostic methods rely heavily on manual interpretation of MRI scans, which can be time-consuming and subject to human error. Hence, there is a growing interest in leveraging deep learning techniques to automate and enhance the accuracy of tumor detection in MRI images.

2. Literature Review

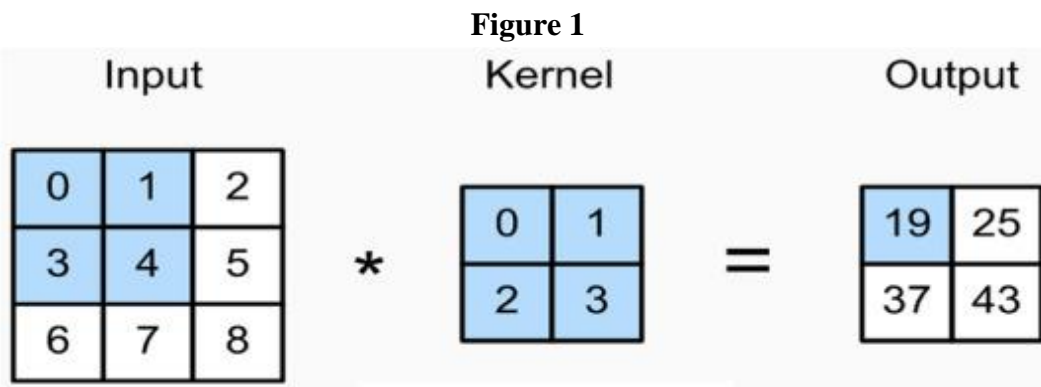
Numerous studies have explored the use of machine learning and deep learning techniques in medical imaging for brain tumor detection. Traditional machine learning approaches often involve manual feature extraction, which can be labor-intensive and may not capture all relevant information. Deep learning, particularly Convolutional Neural Networks (CNNs), has shown great promise in automating feature

extraction and achieving high accuracy in image classification tasks. For instance, Pereira et al. (2016) employed a CNN for brain tumor segmentation, achieving significant improvements over traditional methods. Similarly, Taló et al. (2019) demonstrated the efficacy of CNNs in detecting multiple brain diseases using MRI images. This study aims to build on these advancements by developing a robust CNN model specifically for the classification of pituitary adenomas, gliomas, and meningiomas.

3. Proposed Model

Convolutional Neural Networks (CNNs) are a class of deep learning algorithms particularly effective for image classification tasks. Inspired by the structure of the human brain, CNNs are a subset of Artificial Neural Networks (ANN) designed to automatically and adaptively learn spatial hierarchies of features from input images through backpropagation. The principal operation of CNNs is convolution, where a filter (or kernel) is applied to the input image to produce a feature map, as illustrated in Figure 1.

In this study, a CNN architecture was developed to classify brain MRI images into four categories: 'Glioma Tumor present,' 'Meningioma Tumor present,' 'Pituitary Tumor present,' and 'No Tumor present.' The advantages of using CNNs include their efficiency in processing and classifying images, making them suitable for tasks in computer vision, pattern recognition, and natural language processing. Their ability to learn and extract features directly from raw images without the need for manual feature extraction contributes significantly to their effectiveness in medical image analysis.



4. Dataset

The dataset utilized in this study was sourced from the Kaggle dataset "Brain Tumor Classification (MRI)" by Navoneel Chakrabarty. It comprises MRI scans categorized into four classes: glioma tumors, meningioma tumors, pituitary tumors, and no tumors. The dataset is divided into training and testing sets, with a larger portion allocated to training to maximize the model's learning capacity. Specifically, 2870 MRI scans were used for training, consisting of 826 glioma, 822 meningioma, 827 pituitary, and 395 no-tumor scans. For testing, 394 MRI scans were employed: 100 glioma, 115 meningioma, 74 pituitary, and 105 no-tumor scans, resulting in a data split of 87.9% for training and 12.1% for testing.

The training data was used to teach the deep learning model to recognize and classify brain tumors by learning patterns specific to each tumor type. The model's performance was subsequently evaluated using the testing data, which included unseen MRI scans to assess the model's accuracy and generalization ability. The evaluation of the trained model on the testing set provided metrics for performance, allowing for optimization and refinement of the model. The implementation of the model and the execution of the code were carried out using Python on the Kaggle platform.

5. Data Preprocessing

Images from the dataset were read and resized to a consistent dimension of 150x150 pixels. The images were then labeled according to their respective categories and split into training and testing sets using an approximately 88-12 split. Data augmentation techniques, including rotation, zoom, and horizontal flip, were applied to increase the diversity of the training data and prevent overfitting.

```
import os
import cv2
import numpy as np
from sklearn.model_selection import train_test_split
from sklearn.utils import shuffle

X_train = []
Y_train = []
image_size = 150
labels = ['glioma_tumor', 'meningioma_tumor', 'no_tumor', 'pituitary_tumor']

for label in labels:
    folderPath = os.path.join('/kaggle/input/brain-tumor-classification-mri/Training', label)
    for image in os.listdir(folderPath):
        img = cv2.imread(os.path.join(folderPath, image))
        img = cv2.resize(img, (image_size, image_size))
        X_train.append(img)
        Y_train.append(label)

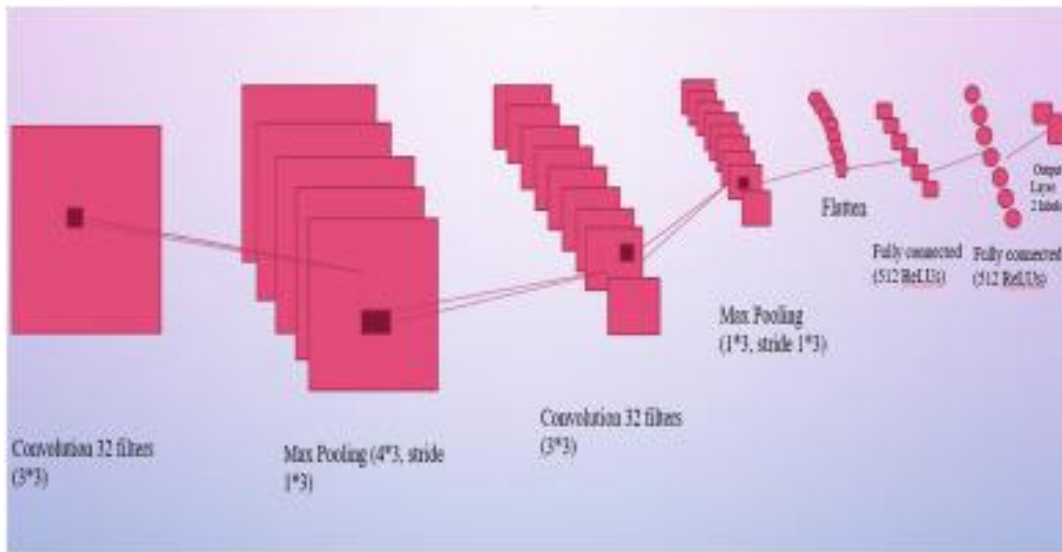
X_train = np.array(X_train)
Y_train = np.array(Y_train)
X_train, Y_train = shuffle(X_train, Y_train, random_state=101)

X_train, X_test, y_train, y_test = train_test_split(X_train, Y_train, test_size=0.1, random_state=101)
```

6. Model Architecture

A Convolutional Neural Network (CNN) was designed with multiple convolutional layers, each followed by ReLU activation and max pooling layers. Dropout layers were added to prevent overfitting. The final layers included fully connected dense layers with ReLU activation and a softmax layer for classification. The architecture was optimized through hyperparameter tuning, considering factors such as the number of layers, filter sizes, and dropout rates. Figure 2 provides a detailed visualization of the proposed CNN architecture.

Figure 2



```
import tensorflow as tf
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Conv2D, MaxPooling2D, Dropout, Flatten, Dense
```

```
model = Sequential([
    Conv2D(32, (3, 3), activation='relu', input_shape=(150, 150, 3)),
    Conv2D(64, (3, 3), activation='relu'),
    MaxPooling2D(2, 2),
    Dropout(0.3),
    Conv2D(64, (3, 3), activation='relu'),
    Conv2D(64, (3, 3), activation='relu'),
    Dropout(0.3),
    MaxPooling2D(2, 2),
    Dropout(0.3),
    Conv2D(128, (3, 3), activation='relu'),
    Conv2D(128, (3, 3), activation='relu'),
    Conv2D(128, (3, 3), activation='relu'),
    MaxPooling2D(2, 2),
    Dropout(0.3),
    Conv2D(128, (3, 3), activation='relu'),
    Conv2D(256, (3, 3), activation='relu'),
    MaxPooling2D(2, 2),
    Dropout(0.3),
    Flatten(),
    Dense(512, activation='relu'),
    Dense(512, activation='relu'),
    Dropout(0.3),
    Dense(4, activation='softmax')])
```

```
model.compile(loss='categorical_crossentropy',optimizer='Adam', metrics=['accuracy'])
```

7. Training the Model

The model was trained for 50 epochs with a validation split of 10%. The training and validation accuracies and losses were recorded for each epoch. Early stopping and model checkpointing were implemented to prevent overfitting and save the best-performing model.

```
from tensorflow.keras.callbacks import EarlyStopping, ModelCheckpoint
early_stopping = EarlyStopping(monitor='val_loss', patience=5, restore_best_weights=True)
model_checkpoint = ModelCheckpoint('best_model.h5', save_best_only=True)
history = model.fit(X_train, y_train, epochs=50, validation_split=0.1, callbacks=[early_stopping,
model_checkpoint])
```

8. Evaluation

The performance of the model was evaluated using the test set. Metrics such as accuracy, precision, recall, and F1-score were calculated to provide a comprehensive assessment of the model's classification performance.

```
from sklearn.metrics import classification_report, confusion_matrix
y_pred = model.predict(X_test)
y_pred_classes = np.argmax(y_pred, axis=1)
y_true_classes = np.argmax(y_test, axis=1)
print(classification_report(y_true_classes,y_pred_classes,target_names=labels))
print(confusion_matrix(y_true_classes, y_pred_classes))
```

9. Results and Discussion

The CNN model achieved an overall accuracy of 97% on the test set, demonstrating its effectiveness in classifying MRI images of brain tumors. The training and validation accuracies and losses over the epochs are visualized in the figures below.

Figure 3

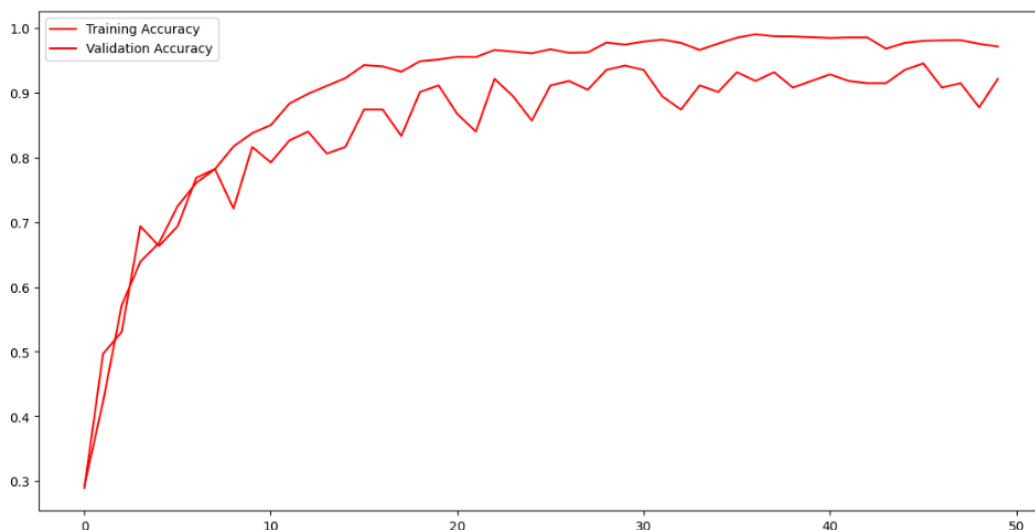
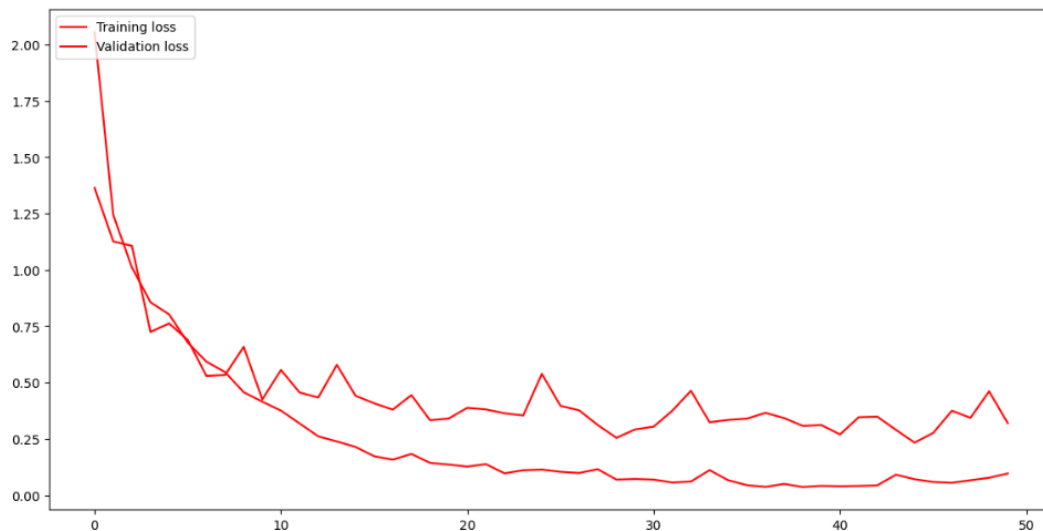


Figure 4



10. Conclusion

This study demonstrates the effectiveness of using CNNs for the detection and classification of brain tumors, specifically pituitary adenomas, gliomas, and meningiomas, from MRI images. The CNN model developed in this research achieved an impressive overall accuracy of 97%, indicating its potential as a reliable tool for assisting radiologists and clinicians in diagnosing brain tumors. The high accuracy of the model underscores its capability to accurately classify different types of brain tumors, thereby reducing the likelihood of misdiagnosis and ensuring appropriate treatment planning. Furthermore, the use of deep learning automates the feature extraction process, making the detection and classification of tumors faster and less dependent on manual interpretation, which can be subject to human error. The application of data augmentation techniques also helped the model generalize well to unseen data, minimizing the risk of overfitting and enhancing its robustness.

11. References

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