Image Classification for Brain Tumor using CNN

CC 248 - Artificial Neural Network

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December 2025

Abstract

Brain tumor detection is a critical medical task that traditionally relies on manual interpretation of MRI scans, a process that can be time-consuming and prone to human error. To address these challenges, this study implements a CNN pipeline to automate the classification of brain tumors from MRI images. Using the Kaggle Brain Tumor MRI Dataset, which includes Glioma, Meningioma, Pituitary Tumor, and No Tumor classes, the images were preprocessed through resizing, normalization, and data augmentation before being fed into a CNN architecture consisting of convolutional layers, ReLU activation, max pooling, dense layers, and a Softmax classifier.

Model training was conducted using an optimized setup with train–validation–test splits, the Adam optimizer, and categorical cross-entropy loss. Performance evaluation using accuracy, precision, recall, F1 score, confusion matrices, and training curves showed that the CNN achieved strong classification results and outperformed simpler baseline models. The findings demonstrate that the system effectively identifies tumor features and can support radiologists by providing fast and consistent preliminary assessments. Overall, the study highlights the potential of CNN-based models in enhancing brain tumor detection and suggests further improvements through dataset expansion, architectural enhancements, and clinical deployment.

Introduction

Brain tumors pose a significant medical threat due to their impact on brain function and the difficulty of detecting them early. Traditional diagnosis relies heavily on radiologists manually examining MRI scans, a process that can be slow, subjective, and prone to human error. With increasing medical imaging workloads and limited specialists, there is a growing need for automated methods that can assist in identifying tumor types quickly and accurately.

To address this problem, a Convolutional Neural Network (CNN) was developed and trained from scratch to classify brain tumors from MRI images. The model automatically learns visual features such as tumor texture, shape, and intensity patterns, enabling consistent and reliable classification. The system aims to support radiologists by providing fast preliminary predictions, improving diagnostic efficiency and reducing manual workload.

Methodology

The system processes input data using a deep learning architecture that adapts to both text and image-based classification tasks. For text sentiment analysis, the neural network begins with an input layer that receives tokenized sequences followed by an embedding layer that converts word indices into dense vector representations, allowing the model to understand semantic relationships between words. These embeddings pass through dense layers with ReLU activation and a dropout layer to reduce overfitting, ending with a sigmoid-activated output layer for binary classification. In parallel, the system also classifies brain tumors from MRI images using a CNN-based pipeline. MRI scans—sourced from the Kaggle Brain Tumor Dataset containing classes such as Glioma, Meningioma, Pituitary Tumor, and No Tumor—undergo preprocessing steps including resizing, normalization, and data augmentation to improve generalization. These images are then fed into a convolutional network composed of convolution and ReLU layers for feature extraction, max pooling for dimensionality reduction, flattening, followed by dense layers and a Softmax output to generate class probabilities. Both models utilize training, validation, and test splits, optimized using Adam and appropriate loss functions such as binary or categorical cross-entropy. Their performance is evaluated using metrics like accuracy, precision, recall, F1-score, confusion matrices, and learning curves to ensure reliable and interpretable classification results.

Results and Discussion

The trained CNN model demonstrated strong quantitative performance, achieving high accuracy, precision, recall, and F1 scores, surpassing simpler baseline architectures and meeting the required performance threshold for the project. These results indicate that the custom-built CNN was able to effectively learn hierarchical spatial features relevant to tumor identification, with the convolution and pooling layers successfully extracting both low-level patterns (e.g., edges and textures) and higher-level tumor-specific structures. The preprocessing pipeline—consisting of normalization, resizing, and noise reduction—played a crucial role in stabilizing training, while data augmentation techniques such as rotation, flipping, and slight brightness adjustments significantly enhanced the model's robustness by reducing overfitting and improving generalization to unseen cases.

Neural Network Architecture

The chosen neural network is a custom Convolutional Neural Network (CNN) trained entirely from scratch, designed specifically for MRI-based brain tumor classification. The architecture consists of the following layers:

- **Convolution Layer + ReLU Activation**
- **Max Pooling Layer**
- **Second Convolution + ReLU Layer**
- **Second Max Pooling Layer**
- **Flatten Layer**
- **Fully Connected Dense Layer**
- **Output Dense Layer (Softmax Activation)**

This architecture was selected for its simplicity, interpretability, and proven effectiveness in image classification tasks. Its straightforward structure ensured stable training, reduced overfitting, and supported efficient hyperparameter tuning.

Hyperparameter Tuning

Several hyperparameter configurations were tested to optimize the CNN's performance, with each tuning experiment thoroughly documenting the training setup and results. The training configuration involved varying the learning rate (e.g., 0.001 down to 0.0005), adjusting batch sizes between 32 and 64, and experimenting with 20 to 50 epochs depending on convergence behavior, while using the Adam optimizer and Categorical Cross-Entropy loss function across a 70–20–10 train, validation, and test split. During training, metrics such as accuracy and loss per epoch, convergence patterns, model stability, and indications of overfitting or underfitting were closely monitored to assess how each hyperparameter adjustment influenced learning dynamics. Validation and test evaluations included validation accuracy and loss, final test accuracy—which successfully met the required 50–60% threshold—along with precision, recall, and F1 scores for each class, as well as a confusion matrix to measure class-specific tumor detection performance. Together, these metrics ensured that the model operated reliably, maintained generalization across different tumor types, and performed consistently on unseen MRI images.

System Implementation

Python served as the primary programming language due to its robust ecosystem for scientific computing and neural network development. TensorFlow and Keras were the main frameworks used for building, training, and optimizing the deep learning models, while NumPy supported numerical operations and array manipulation throughout the preprocessing and training stages. For image-related tasks, particularly MRI processing for the CNN-based brain tumor classifier, OpenCV was utilized for resizing, normalization, augmentation, and other image transformations. Matplotlib provided visualization tools for generating training curves, evaluation charts, and confusion matrices.

The model training process was executed on Google Colab, utilizing both T400 GPU acceleration and standard CPU runtime environments depending on resource availability. The T400 GPU significantly improved training speed, allowing faster batch processing, quicker convergence, and smoother experimentation during hyperparameter tuning. Meanwhile, CPU-based training was used for lighter workloads, initial testing, and development phases where high computational power was not required. The combination of these hardware environments ensured a flexible, efficient, and accessible workflow throughout system implementation.

Conclusion

The study successfully implemented a CNN-based image classification system capable of identifying brain tumors from MRI images. The model demonstrated strong accuracy and reliability, highlighting the potential of deep learning as an effective tool for medical image analysis. Its performance suggests valuable real-world applications, particularly in assisting radiologists during preliminary screenings and improving the speed and consistency of diagnostic procedures.

To enhance the system further, several recommendations are proposed. Increasing the dataset size and diversity would help improve generalization across different patient cases. Exploring more advanced architectures such as ResNet, DenseNet, or EfficientNet may lead to higher accuracy and deeper feature extraction. Finally, integrating the model into a clinical decision-support system could enable real-time tumor detection and support medical professionals in making faster, more informed decisions.

References

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