Deep Learning for Brain Tumor Detection: A High-Precision Approach

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ABSTRACT

This paper aims to enhance efficiency in the healthcare field by applying deep learning to tumor diagnostics. Approximately 20 million people are diagnosed with tumors yearly. Suspected brain tumor patients are diagnosed manually through visual analysis of a magnetic resonance imaging (MRI) scan, which is classified as either glioma, meningioma, pituitary, or no tumor. Manual diagnosis performed by doctors costs thousands of dollars, presenting a burden to public health agencies and health insurance members. Therefore, optimizing the process with novel technologies presents the perfect opportunity to increase healthcare efficiency. Deep learning artificial intelligence (AI) models, specifically convolutional neural networks (CNNs), enable extremely fast image classification with almost no inference cost, making implementation at multiple sites straightforward. These models are trained on a dataset, and their parameters are adjusted automatically until the model's performance on the training dataset is optimal. This paper applies the technology of CNNs using the batch normalization technique to the problem of brain tumor classification and presents the results of the trained model. The model was trained on publicly available datasets and achieved a validation accuracy of 93.5% with a high level of confidence in correct classifications. This surpasses the current state-of-the-art models at 92.1%; however, dataset differences may contribute to this discrepancy. Overall, this paper demonstrates a novel application of CNN models to enhance efficiency in tumor diagnostics, while also considering ethical concerns.

Introduction

Artificial intelligence (AI), specifically deep learning, has transformed medical imaging and diagnostics by enabling faster, more accurate, and expandable solutions. Among its many applications, AI has been adopted for medical image analysis. Certain deep learning algorithms, such as the convolutional neural network (CNN), excel at analyzing medical images, including computerized tomography (CT) scans and X-rays (Hetmat, 2025). They can detect and locate abnormalities with high precision, often matching or surpassing the accuracy of human diagnostics (Rana, 2022).

Brain tumors are categorized as benign (non-cancerous) and malignant (cancerous), and each requires its own treatment procedure. Malignant tumors, such as gliomas, are highly invasive and rapidly growing, meaning treatment must begin as soon as possible after diagnosis. Benign tumors, such as meningiomas and pituitary adenomas, grow slowly and often have well-defined borders, making them easier to surgically remove (McFaline-Figueroa, 2018). However, even benign tumors can be life-threatening if they compress vital brain structures. Therefore, an accurate diagnosis of these tumors is life-saving, as it directly determines treatment efficiency and patient survival. A misdiagnosis, due to interpretive errors, can cause permanent damage or death (Mukherjee, 2023).

Current brain tumor diagnostics are costly and resource-intensive due to the lack of fully automated systems with expert-level accuracy (Abiwinanda, 2018). The absence of reliable tools contributes to a problem of diagnostic variability among experts, where studies show that even experienced radiologists may disagree on tumor boundaries and subtypes in ~15-20% of cases (Louis, 2021), prompting rescans or second opinions. These inefficiencies can inflate health care expenses due to unnecessary treatments or delayed therapy. Automated systems with radiologist-level accuracy could drastically reduce costs by reducing scan interpretation time, minimizing repeat imaging, and optimizing treatment planning.

Convolutional Neural Networks

Recent advancements in the field of deep learning have developed highly efficient CNNs to infer classifications from images. Machine learning is a mathematical technique based on the use of back propagation to optimize a model based on a training dataset. Several advanced CNNs like EfficientNet have successfully created generalized image classification models (Tan, 2019).

Compared to traditional neural networks, CNNs are better at processing images because they use convolutions at the beginning rather than neurons. Convolutions extract localized features, which can be repeated across the whole image to extract certain kinds of features like edges, corners, and points (Yamashita, 2018). Repeated convolutions allow the model to condense image information down into important key features. Then, the convolution results are flattened and sent through dense layers to create the final classification (Li, 2021).

A typical convolutional neural network uses interleaved convolutional layers and max-pooling layers. Convolutions apply a filter to the image, and max-pooling removes irrelevant data (Gu, 2018). After repeated layers, the data is then flattened and sent through fully connected networks with traditional neurons. The diagram of this structure is reproduced in Figure 1.
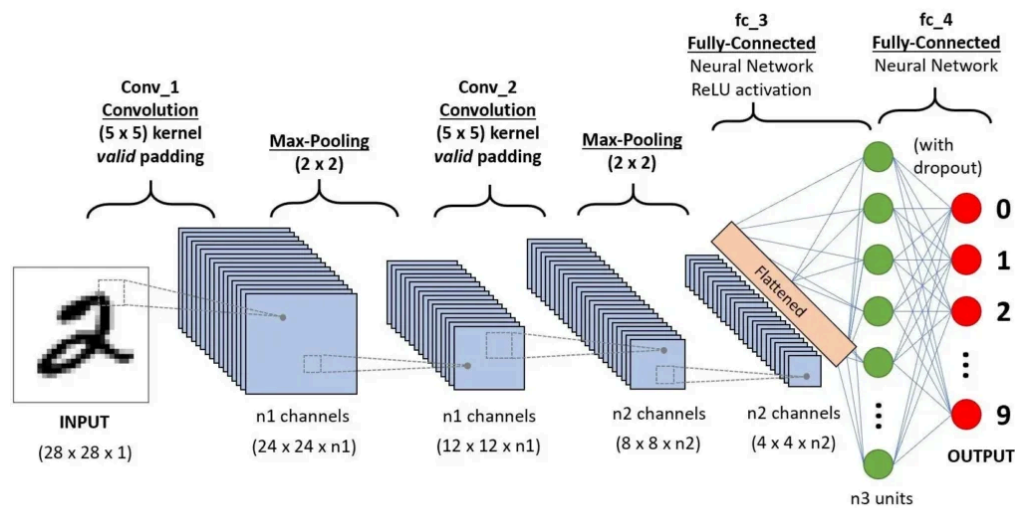

Figure 1. Diagram of a convolutional neural network

A technique sometimes used to prevent the gradient explosion problem is batch normalization, which subtracts the mean pixel intensity from all pixels in each image (Bjorck, 2018). This ensures the image is normalized to be centered on zero. Batch normalization is particularly effective on MRI data because many images tend to vary in the average pixel value. An additional technique, which is necessary to prevent overfitting, is dropout (Srivastava, 2014). Dropout layers randomly remove some information during training, which prevents overfitting on the data because the model must learn overall features rather than training on individual pixels. Using both dropout and batch normalization is expected to increase the maximum attainable model accuracy dramatically.

Magnetic Resonance Imaging

Magnetic resonance imaging (MRI) is a non-invasive medical imaging technique that uses radio waves and strong magnetic fields to generate detailed images of the body's internal structures, particularly soft tissues like the brain. Different MRI sequences can highlight specific features to help radiologists identify abnormal masses (Cha, 2006).

A publicly available MRI image dataset from Kaggle was used (Nickpavar, 2021). This dataset includes classification labels for four different kinds of images: glioma, meningioma, pituitary, and no tumor. The dataset has 7022 images total, and all are stored in the JPG format. Many are taken from different machines and represent

different layers of the brain, so the images are not as uniform as a controlled measurement of thousands of brains would produce. This means batch normalization is likely to be more effective on this dataset than on others. Example images are displayed in Figure 2 and Figure 3.
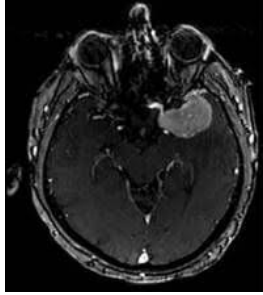

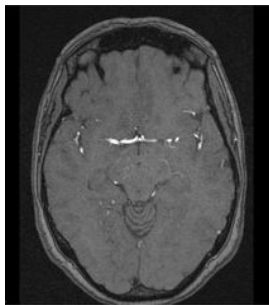**Figure 2.** Sample image with meningioma

Figure 3. Sample image with no tumor

However, the rise of AI-driven diagnosis raises ethical concerns, particularly regarding accountability and patient safety (Islam, 2024). If an AI system misdiagnoses a brain tumor, determining liability becomes complex. It is difficult to tell whether responsibility should fall on the developers, the healthcare providers using the tool, or the executive bodies that approved it. In other cases, patients may not consent to their MRI scans being used to train an AI model. However, ethical concerns about machine learning models should be reserved for their application, not for their research.

Related Work

Arunkumar et al. developed an artificial neural network with a final layer using a support vector machine. This segmentation model attained 92.1% accuracy and classified each pixel as a region of interest or a non-region of interest (Arunkumar, 2020). However, this model only classified between tumor and non-tumor, so it lacks important information about the kind of brain tumor present. This model also used important image filtering techniques like batch normalization.

Salçin et al. used a recurrent neural network (RNN) to earn a 92% accuracy (Salçin, 2019). However, the segmentation model was not trained on images of brains without tumors, so it would only be relevant for classifying what kind of tumor rather than detecting whether one is present or not.

In the research paper "Intraoperative brain tumour identification with deep learning," Martini et al. developed a CNN and attained a 91.3% accuracy on a dataset of brain tumor images (Martini, 2020). This paper is similar to the technique presented in the current paper; however, the process of batch normalization will be used to improve upon the accuracy.

Methods

The publicly available brain tumor dataset on Kaggle was used. Because of the nature of this problem, a CNN was developed to fit the specifications of the MRI image. The model was developed using a Google Colab instance with Python 3.12 and the TensorFlow 2.16 library with Keras. Images were imported through Keras's ImageDataGenerator library to convert image files into Python dataframes.

Training data was split from validation data with a ratio of 0.8, meaning 80% of the files in the dataset were used to train the model, while the other 20% of the files in the dataset were used to confirm its accuracy. After splitting the data into two datasets, the model runs on a continuous cycle of training and optimizing through a batch size of 32 until it exhausts the training dataset. This represents the end of epoch 1. Then, the model is tested on the validation dataset continuously to ensure there is no overfitting. This process is repeated through several epochs until the validation and training accuracy reach a steady state. A diagram of the training process is shown in Figure 4.
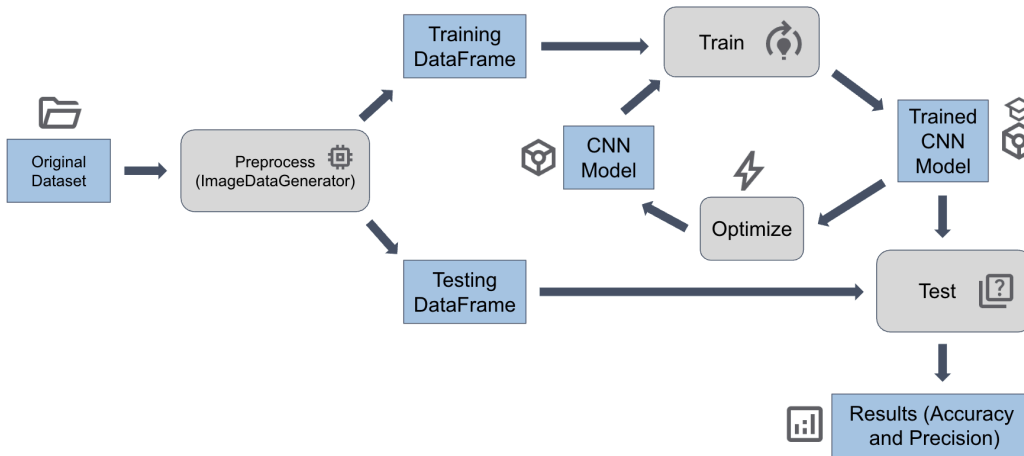

Figure 4. Data flow while training convolutional neural networks. Data is represented in blue and processes are described in grey.

Additionally, the techniques of batch normalization and dropout were implemented to increase the model accuracy. These were developed using vector math available in the PyTorch library. The batch normalization procedure took the mean pixel intensity of the image and subtracted that number from every pixel in the image. Then, dropout was employed by randomly removing information from the vectors between each layer in the model.

Results

The model performed better than expected, attaining a training accuracy of 95.2% and a validation accuracy of 93.6%, higher than the previous state-of-the-art 92.1% accuracy. The confusion matrix made with Matplotlib 3.4 is displayed in Figure 5 and shows which predicted and actual labels the model got confused. Surprisingly, the accuracy on "notumor" images was 100%, meaning the model is extremely accurate at detecting the absence of a tumor. The two kinds of tumors most frequently confused were glioma and meningioma, which is likely because both can appear near the edge of the brain and are roughly spherical. However, accuracy was still above 90% for these two tumors.
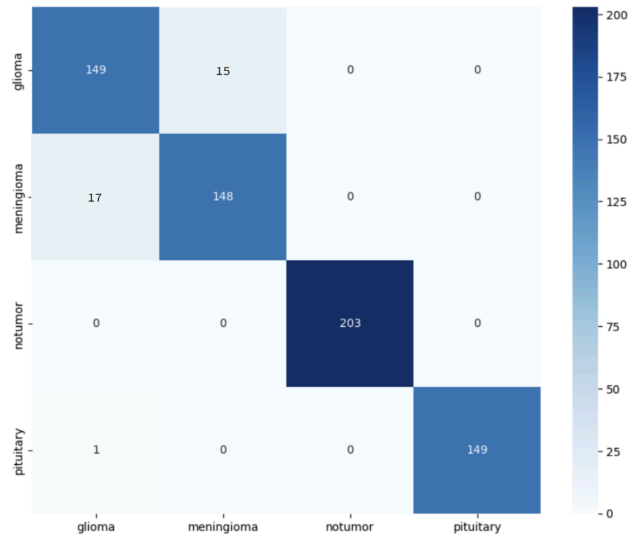
Figure 5. Confusion Matrix of predicted and actual labels. Each row is a predicted label, and each column is the actual label.

On most tumors, the model was extremely confident in the type of tumor classified, often giving a confidence value of more than 0.9. A sample graph showing model confidence on a meningioma image is displayed in Figure 6. Additionally, the accuracy over epochs graph shows strong convergence onto the final accuracy value, meaning the model was trained easily on the datasets.
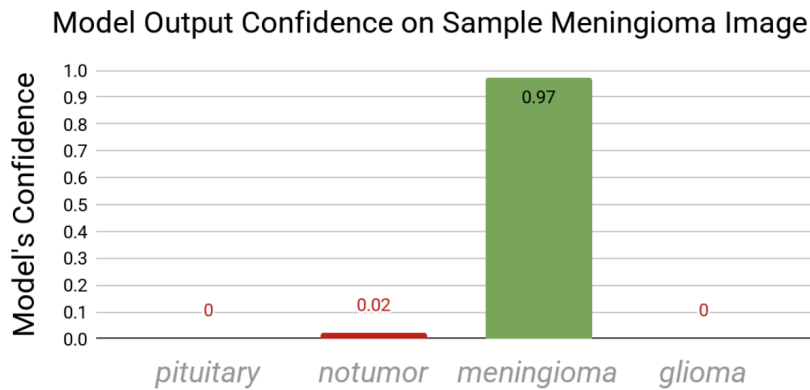

Figure 6. Meningioma sample image confidence

The training and validation accuracies for each epoch are recorded in Table 1 and Figure 7. These figures show strong learning a convergence onto certain training and validation accuracies. Additionally, we can conclude the model was not overfitting on the data because the difference between final training accuracy and final validation accuracy was negligible. Since the training and validation accuracy approach an asymptote, it is unlikely that more epochs would increase the final accuracy.

Epochs completed	Traning accuracy	Validation accuracy
1	0.514	0.32
2	0.798	0.681

3	0.912	0.780
4	0.921	0.911
5	0.945	0.923
6	0.946	0.923
7	0.944	0.926
8	0.951	0.933
9	0.952	0.936
10	0.949	0.934

Table 1. Training and validation accuracy across epochs
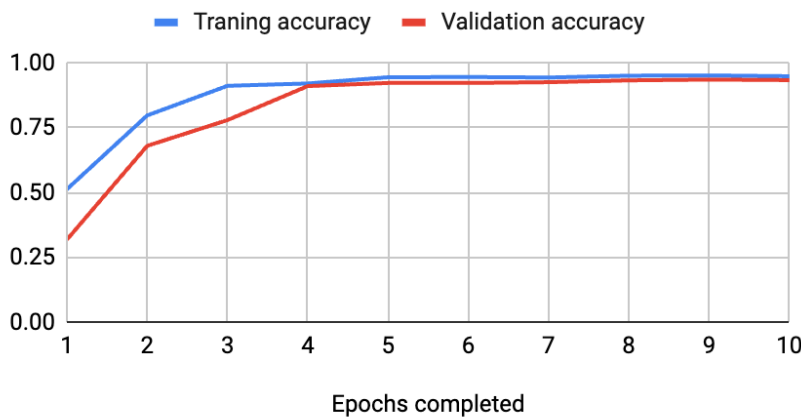

Figure 7. Graph of training and validation accuracy across epochs

Discussion

This project, however, still faces numerous limitations due to current technology. The publicly available Kaggle dataset does not include variation in age, meaning the model is unlikely to work well on MRI scans of youth. It is also limited in terms of the kinds of tumors, including only four different tumor classifications. Additionally, the unavailability of balanced, annotated medical image datasets and the need for improved trustworthiness in AI systems hinder widespread adoption (Dhar, 2023). Compared to other fields, medical imaging lacks many publicly available datasets due to the sensitivity of patient information.

In future work, deep learning models like this can be embedded into websites, enabling global access to brain tumor diagnostic services. With a more diverse dataset, future models will need even more CNN-related training tools like batch normalization to reach the same levels of accuracy. Thankfully, more advanced models, such as EfficientNet, have been developed and pre-trained on large image datasets, meaning their first few layers are already optimized to analyze images. The application of EfficientNet to a new brain tumor image dataset holds high prospects for reducing healthcare burdens globally.

An additional pathway to developing machine learning models that classify brain tumors is to use the entire 3D MRI scan as input. The current model uses a two-dimensional flat image. With a three-dimensional data set, a large convolutional neural network has the potential to outperform all other current models.

Conclusion

By advancing AI-driven solutions for brain tumor detection, this project aims to bridge gaps in accessibility and accuracy, offering a transformative approach to medical diagnostics. The final CNN model achieved a training accuracy of 95.2% and a validation accuracy of 93.6%, indicating strong generalization and minimal overfitting. Precision and recall metrics were similarly high, confirming that the model consistently identified tumor types with a low error rate. The model demonstrated robust learning, with minimal accuracy drop between training and validation.

The use of multiple convolutional layers with batch normalization and max-pooling effectively captured tumor-specific features. Compared to manual diagnoses and previous AI models, this solution offers greater accuracy and efficiency. While similar studies reported accuracies around 85-90%, this model's performance represents a significant advancement, enabling faster, more reliable tumor detection.

The project exceeded expectations, delivering a state-of-the-art model that could enhance diagnostic accuracy and reduce costs in real-world medical applications. Despite the challenges of working with undiversified datasets, AI holds immense promise in reducing diagnostic errors, automating decision-making, and lowering healthcare costs.

Acknowledgements

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