

Multi-Class Brain Tumour Classification using Convolutional Neural Network

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(Received March 10, 2023, Revised April 27, 2023, Accepted April 30, 2023)

Abstract: In recent years, the subject of medical image categorization has expanded significantly, with Convolutional Neural Networks (CNN) being the most popular neural network model for this purpose. Using components like convolutional layers, pooling layers, and fully connected layers, CNNs are built to learn features adaptively through backpropagation. This study aims to develop and deploy a CNN model for identifying brain cancers using MRI(Magnetic Resonance Image) scans obtained from Kaggle. The proposed methodology consists of two phases: preprocessing the pictures using various image processing techniques and then training a CNN model to categorize the modified images. We test the model on 3,264 MRI pictures representing four kinds of brain cancers (glioma, meningioma, no tumor, and pituitary). Results from the experiment showed a training dataset accuracy of 99.39% and a validation dataset accuracy of 96.18%.

Keywords: Convolutional Neural Network (CNN), pituitary tumor, meningioma tumor, glioma tumor, Magnetic resonance image (MRI), ROC curve.

1. Introduction

The brain is an intricate organ responsible for controlling feelings, thoughts, and memories, among many other things. It's also vital for things like breathing, heart rate, blood flow, and eye movement to work together and be under your control. Some of these skills makes us uniquely human.

According to the studies of Pattabiraman *et al.*¹ the cerebral cortex, which controls all human functions, comprises 16.3 billion neurons and is part of the brain's more than 200 million nerve cells. As shown by Mohsen *et al.*², the cerebral cortex, located at the brain's outermost layer, interprets sensory data, starts voluntary movements, and handles complex cognitive activities. An illness of the brain might manifest itself in abnormal functioning of the cerebral cortex. Brain tumors are by far the most severe form of neurological disorder. Brain tumors are more prevalent in youngsters and the elderly, according to research conducted by Hu *et al.*³. If aberrant cell clusters in or near the brain are allowed to grow and divide unchecked a tumor forms. Pradhan *et al.*⁴ demonstrate how these cells can disrupt normal brain function and kill off healthy cells.

Malignant tumors form rapidly and spread aggressively to other healthy cells, as described by Priya *et al.*⁵; benign tumors are those that develop in the brain but are not cancerous and grow more slowly. Pituitary tumors, malignant tumors, and meningiomas are three other categories of common malignancies. Meningiomas are the most frequent type of benign tumor that originates in the membrane cells that cover the brain and spinal cord. A tiny endocrine gland, the pituitary, sits in the skull between the brain's base and the nose's top. As discussed by DeAngelis *et al.*⁶, the pituitary gland is prone to the development of tumors or abnormal growths known as adenomas. The primary difference between these three tumor forms is whether or not they are malignant, with meningiomas typically being non-cancerous and gliomas typically being malignant, as reported by studies of Louis *et al.*⁷. Although meningiomas develop more slowly than pituitary tumors, the former can nonetheless cause significant health problems. While determining whether tissue is benign or cancerous, a biopsy is often conducted. However, brain tumor biopsies are not usually taken before brain surgery. Therefore, it is important to provide an accurate diagnostic tool for patients to use for tumor segmentation and categorization of brain tumor pictures without the need for invasive surgery. PET (Positron Emission Tomography), CT (Computed Tomography), DWI (Diffusion Weighted Imaging), and MRI are the primary clinical exams for analyzing brain anatomy in cases of suspected brain cancers. Alarabeyyat *et al.*⁸ found that MRI, which uses radio waves and field gradients in addition to a high magnetic field, provided the most valuable images for clinical examination. Researchers have difficulty in distinguishing between healthy and infected tumors despite visual similarities and cellular variations. In this work, we provide a CNN model that can reliably diagnose brain tumors, paving the way for the timely beginning of therapy. Experts agree that CNNs are the most effective models for dealing with massive

datasets. While CNNs have been utilized to solve a wide range of issues in recent years, their performance in medical image processing has been awe-inspiring.

Recent years have seen a proliferation of research aimed at better categorizing brain tumors. The figshare dataset on brain tumors was created by Cheng⁹. The three types of brain cancers in T1 MR images were tested on this dataset by Cheng *et al.*¹⁰. They used picture dilation to expand enhanced images of brain tumors and then analyzed them. Gray Level Co-occurrence Matrix (GLCM) and Bag-of-Words (BoW) were employed for feature extraction from these pictures' histograms. Following some time, a Support Vector Machine was used to classify the photos (SVM). Features extracted with BoW produced a phenomenal performance of 91.28%. Using CNN, Pereira *et al.*¹¹ predicted tumor grade using two different methods: one using the whole brain, which achieved 89.5% accuracy, and another using an artificially delimited tumor area, which achieved 92.8% accuracy. Abiwinanda *et al.*¹² suggested a practical architecture of CNN for detecting the three most common forms of brain cancers (glioma, meningioma, and pituitary), with a validation accuracy of 84.1%. In 2018, the highest percentage of success was achieved by Seetha and Selvakumar Raja¹³ while classifying brain cancers. Using Convolutional Neural Networks and a deep architecture with tiny kernels for classification, they got an accuracy of 97.5%. Features were extracted from axial slices and sequential features of numerous frames were obtained using a dense CNN by Zhou *et al.*¹⁴. Using a recurrent neural network, they improved classification accuracy to 92.13 percent.

Deep learning is a newer and strong approach for image classification, and Avşar and Salçın¹⁵ used the quicker R-CNN to apply it to the problem of tumor type classification. Classifying brain tumors was successful to the tune of 91.66 percent. Further, Khan *et al.*¹⁶ sorted brain MRI pictures into cancer and non-cancer tumors. They used an 8-layer Convolutional Neural Network model to obtain perfect binary classification accuracy on a small dataset consisting of 155 photos of malignant cancer and 98 images of benign non-cancer. Brain tumor classification accuracy was 97.39% when Bada and Barjaktarovi¹⁷ suggested a basic CNN. This CNN has two convolution layers for feature extraction and two fully linked layers for classification. A deep learning neural model was proposed by Latif *et al.*¹⁸ to extract characteristics from MR images, which were then fed into ML classifiers (Naive Bayes, SVM, and Multi Layer Perceptron (MLP)). With SVM as the classifier, their strategy was shown to be 96% accurate.

The rest of this paper is structured as follows: Insights on Technique are provided in Section 2, which is followed by a thorough analysis of the suggested Methodology, dataset, and the design of the convolutional neural network. Section 3 is dedicated to the analysis of the system, while Section 4 contains a discussion of the findings and the conclusion.

2. Methodology

2.1 Convolutional Neural Network(CNN) architecture

Convolutional, ReLU, Max-Pooling, and Fully Connected (FC) layers make up a basic CNN model, as shown in Figure.1. Before, the three FC levels follow the max pooling layer; these are ReLU layers. As can be seen in Figure 2, feature maps are generated by convolving an input picture with a kernel matrix in a convolutional layer. This layer finds the correlation between neighbouring pixels and reduces the number of network parameters.

Convolutional neural networks (CNNs) belong to the category of feedforward neural network (FFN) models, which means that the signal flows forward through the network without any feedback loops. This can be mathematically expressed using Equation (2.1)¹⁹.

$$(2.1) \quad G(x) = g_H \left(g_{H-1} \left(\dots \left(\dots \left(g_1(x) \right) \right) \right) \right)$$

where $G(x)$ is a CNN model and x is the input data. The function $G(x)$ is defined in terms of a series of nested functions $g_1, g_2, \dots, g_H$ and H is the number of hidden layers in the model. Each g_i function represents a layer in the model and applies a set of operations specific to that layer. The expression $g_{H-1}(\dots(g_1(x)))$ denotes the composition of all the layer functions in the model, with the output of each layer being the input to the next layer. So, the output of g_1 is fed as input to g_2 , the output of g_2 is fed as input to g_3 , and so on, until the final output of g_H is produced. The core functional layers of a typical CNN model include activation, Fully Connected (FC), pooling, and classification layers. The convolutional layer (f) is a type of layer that consists of various convolutional kernels ($f_1, f_2, \dots, f_{y-1}, f_y$) and f_y represents the y^{th} kernel. Each kernel f_y is a linear function that can be expressed using Equation (2.2) that takes as input the output of the previous layer (or the input data for the first layer) and produces a feature map as output.

$$(2.2) \quad f_y(x, j) = \sum_{u=-m}^m \sum_{v=-n}^n \sum_{d=-w}^w W_y(u, v, w) I(x-u, j-v, z-w).$$

In the above Equation, the weights for the y^{th} kernel are given by the tensor W_y , which depends on the distances of the pixels from the centre of the kernel. The size of the kernel is specified by the height, width, and depth parameters m, n and w , respectively. The rectified linear unit (ReLU) is a type of activation layer that is applied after the convolutional layer. The ReLU function is a pixel-wise non-linear function (g) that sets negative pixel values to zero and keeps positive values unchanged. This function is represented using Equation (2.3)²⁰⁻²¹.

$$(2.3) \quad g(x) = \max(0, x).$$

The pooling layer is a type of layer that applies a non-linear downsampling function to the output of the convolutional layer. The purpose of this layer is to reduce the dimensionality of the feature representation size while retaining the most important features. The pooling layer is typically used to reduce the spatial resolution of the output, which can help to reduce the number of parameters in the model and prevent overfitting. The FC layer is a type of neural network layer that connects all neurons in the previous layer to every neuron in the current layer. In a CNN model, the FC layer is typically used for classification tasks. The FC layer can be seen as a generalization of the convolutional layer, where the kernel size is 1×1 . The purpose of the FC layer is to transform the output of the previous layers into a form that can be used for classification. The SoftMax layer $\left(\sigma(\bar{z})_i = e^{z_i} / \sum_{j=1}^K e^{z_j} \right)$ is typically added to

the last FC layer of the CNN model. Figure 2 shows an example of a CNN model made up of convolutional, ReLU, max-pooling, and FC layers. The first, second, and fifth ReLU layers precede the maximum-pooling layer, which in turn precedes the three FC layers. To formally express max-pooling, let z' be an $n_i \times n_i \times m_i$ tensor, where n_i is the spatial size of the feature map and m_i is the number of channels. Here subtensor $z_k^l(i, j, q)$ denotes the output of the l^{th} feature map at position (i, j) in response to the k^{th} input. The max-pooling operation involves selecting the maximum value over the element-wise product of the sub-tensor $z_k^l(i, j, q)$ and a filter W , as given by Equation (2.4). Here, the filter W has dimensions $k \times k \times r$ where r is the depth of the output tensor. The notation " $\odot$ " represents the element-wise product. This operation helps to reduce the dimensionality of the feature map while preserving important information about the position of the maximum values. The resulting output is then passed on to the next layer of the neural network for further processing.

$$(2.4) \quad \max(z_k^I(i, j, q) \cdot W) = \max_{\substack{a=1,2,3,\dots,k \\ b=1,2,3,\dots,k \\ c=1,2,3,\dots,r}} (z_i^I + a - 1, j + b - 1, q + c - 1, \bullet, W_{a,b,c})$$

Overall, CNNs have shown exceptional performance in image-related tasks and are widely used in computer vision applications.

2.2 Dataset

The research makes use of Brain Tumor Classification MRI Images from Kaggle. The database of pictures included 394 test images and 2870 training photos. Meningioma, glioma, no tumor, and pituitary tumor photos are all stored in their respective directories.

Performing preliminary analyses on the data: With proper preprocessing, CNN can better use MRI pictures in the subsequent phase. Aspect ratio: resizing(150*150) all the photos uniformly; dimensionality reduction; data augmentation; geometric data augmentation; scaling; flipping; and rotating the images are only a few of the preprocessing techniques applied to the training dataset. Disturbances, such as those caused by wrapping or cropping, are imposed from the input image and removed.

2.3 Proposed Methodology

CNN models have recently gained a lot of scholarly attention. When it comes to processing many MRI images from a database, CNN models excel in speed and efficiency. Improving accuracy in the categorization of brain tumor diagnosis issues is the primary goal of the proposed effort, which centers on the application of CNN to this problem space. The experimental investigation entails collecting data on brain tumors, training the model on preprocessed pictures, and putting it through its paces on four sets of previously unknown MRI scans. A total of 23 layers were used in the design of the architecture, including 9 Conv2D layers, 4 max-pooling layers, 6 dropout layers, 1 flattened layer, and 3 dense layers. The suggested convolutional neural network (CNN) model is taught using an input data set. Training takes place over a total of 20 epochs, with a batch size of 40. The suggested model was evaluated using the categorical cross-entropy loss function, Adam optimizer, and the accuracy of the metric function. Table. I provide a high-level overview of the suggested model.

3. System Evaluation

We used a confusion matrix to measure how well the system distinguished glioma, meningioma, no tumor, and pituitary tumors. The True Positive(TP), True Negative (TN), False Positive (FP), and False Negative (FN) are the

building blocks of a confusion matrix. The resulting confusion matrix is depicted in Fig. 3. Other assessment measures, including as Accuracy, Recall, Precision, and F_1 – Score are used to assess the performance of the proposed model, as illustrated in Equations (3.1) to (3.4).

$$(3.1) \quad Accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$

$$(3.2) \quad Recall = \frac{TP}{TP + FN}$$

$$(3.3) \quad Precision = \frac{TP}{TP + FP}$$

$$(3.4) \quad F_1 - Score = 2 \times \frac{Precision * Recall}{Precision + Recall}$$

4. Results and Discussion

The suggested CNN model efficacy has been measured in a variety of ways. In order to evaluate GPU performance experimentally, python code has been used. The dataset was split into training and validation halves for this experimental investigation, with 80% of the data serving as training and 20% as validation. The next step in our research involves applying the augmentation procedure to the training data with the use of augmentation parameters. Settings: rescale = 1.0/255, horizontal flip=True, vertical flip=False, zoom range = 0.2, width shift range = 0.2, and rotation range=20. Third, we use ModelCheckpoint to implement a callback function and monitor the model's output. By storing the top-performing model from the most recent epoch, ModelCheckpoint can assist keep your system's RAM consumption to a minimum. Details on the other hyperparameters The parameters investigated are Dropout= 0.3, Dense = 512 with relu activation, and 40 epochs. Multiclassification may be performed with the help of categorical cross-entropy.

Some of the settings shown were a batch size of 40, an image size of 150, and a verbose level of 1. The accuracy and loss curve is depicted in Fig. 4(a,b) across two training and validation phases. The suggested model had a 99.39% success rate on the training set, whereas it only got 96.18% on the validation set. The 0.0235 loss on the training set and the 0.1495 loss on the validation set are shown in Figure.4(a,b). Table II displays the results of a categorization analysis. Precision, recall, F1, and support scores are all class-based, and Table II shows how to visualise them. The ROC curve results presented in Figure 5 prove that the suggested model is a valid method for diagnosing and

categorizing brain cancers. The micro-average and the macro-average ROC curves will have a better degree of accuracy if they are closer to the upper left corner. It also displays the area under the curve for each acceptable class in the test scenarios, from 0.99 to 1.

Table.III compares our tumor classification method's findings to those of three previously published approaches. We observed that, compared to the other approaches proposed, our method yielded the greatest classification accuracy (0.9613).

Abiwinanda *et al.*¹² used a model consisting of 64 fully linked neurons in two convolutional layers in their research. To ensure fair sampling, they selected 700 photos for each type of brain tumor and split them in half, using 500 for training and 200 for testing. No data augmentation methods were used in this investigation. The accuracy of 0.841 for classification was lower than our approach's accuracy of 0.9613. Combining a CNN with a Kernel Extreme Learning Machine (KELM) classifier was proposed by Pashaei *et al.*²². The characteristics retrieved by the CNN were used as inputs for the KELM classifier. Using 10-fold cross-validation, they divided their dataset into training and testing portions of 70% and 30%, respectively, without resorting to data augmentation approaches. They were successful to the tune of 0.9360 percent. To optimize the CNN model's settings, such as the number of Convolutional, Max-Pooling, and Fully Connected layers, as well as the activation function, dropout parameter, optimization technique, and learning rate, Anaraki *et al.*²³ suggested a CNN-based strategy that incorporated genetic algorithm. They altered the data by replicating it, translating it, scaling it, and so on. The accuracy of their method was 0.942.

6. Conclusion

Brain tumor classification is an important problem in the medical field. In this study, we created a CNN classification model that can tell the difference between glioma, pituitary, no tumor, and meningioma brain cancers. To better the performance and outcomes of the CNN model, we preprocessed and enhanced the training set using data augmentation. This technique creates updated data from the current data. In the testing phase, the system was tested with data it had never seen before. The suggested model contained many parameters but was only trained on a short sample size of data, which increases the risk of overfitting. To combat this, we implemented dropout regularization to help the model zero in on the most relevant patterns during training. To prove its usefulness in healthcare and to save precious time, the final model attained an accuracy of 99.39% on the training set and 96.18% on the testing set.

Table I : Model summary

Layer	Output shape	Parameter
conv2d (Conv2D)	(None, 148, 148, 32)	896
conv2d_1 (Conv2D)	(None, 146, 146, 64)	18496
max_pooling2d (MaxPooling2D)	(None, 73, 73, 64)	0
dropout (Dropout)	(None, 73, 73, 64)	0
conv2d_2 (Conv2D)	(None, 71, 71, 64)	36928
conv2d_3 (Conv2D)	(None, 69, 69, 64)	36928
dropout_1 (Dropout)	(None, 69, 69, 64)	0
max_pooling2d_1(MaxPooling_2D)	(None, 34, 34, 64)	0
dropout_2(Dropout)	(None, 34, 34, 64)	0
conv2d_4 (Conv2D)	(None, 32, 32, 128)	73856
conv2d_5 (Conv2D)	(None, 30, 30, 128)	147584
conv2d_6 (Conv2D)	(None, 28, 28, 128)	147584
max_pooling2d_2(MaxPooling2D)	(None, 14, 14, 128)	0
dropout_3(Dropout)	(None, 14, 14, 128)	0
conv2d_7 (Conv2D)	(None, 12, 12, 128)	147584
conv2d_8 (Conv2D)	(None, 10, 10, 256)	295168
max_pooling2d_3(MaxPooling2D)	(None, 5, 5, 256)	0
dropout_4(Dropout)	(None, 5, 5, 256)	0
flatten (Flatten)	(None, 6400)	0
Dense	(None, 512)	3277312
Dense_1(dense)	(None, 512)	262656
dropout_5(Dropout)	(None, 512)	0
Dense_2(dense)	(None, 4)	2052

Table II: Classification Report

	Precision	Recall	F1 Score	Images
Glima_tumor	0.97	0.84	0.90	82
Meningioma_tumor	0.99	1.00	1.00	398
N0_tumor	0.88	0.88	0.88	110
Pitutory_tumor	0.92	1.00	0.96	92

Table III: Evaluation of the proposed model against prior work

Authors	Classification Method	Accuracy
Abhiwinanda <i>et al.</i> ¹²	CNN	0.841
Pashaei <i>et al.</i> ²²	CNN & KELM	0.936
Anaraki <i>et al.</i> ²³	CNN & GA	0.942
Proposed method	CNN	0.961

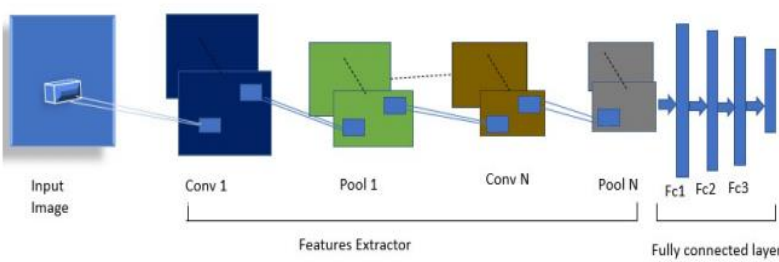


Figure 1: Architecture of CNN

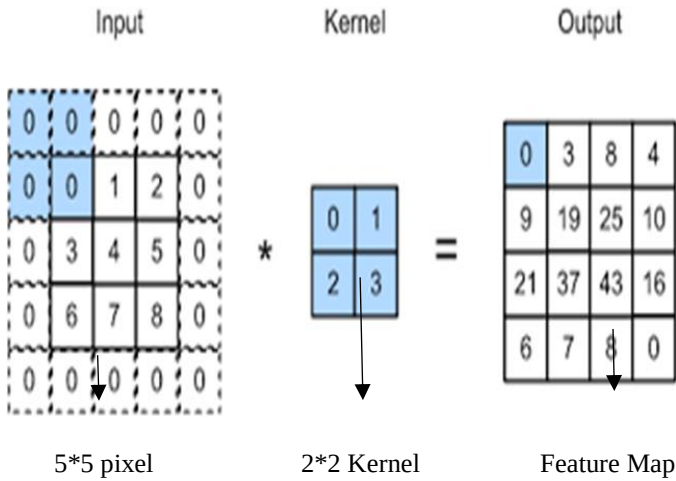


Figure 2: Illustration of the convolution process

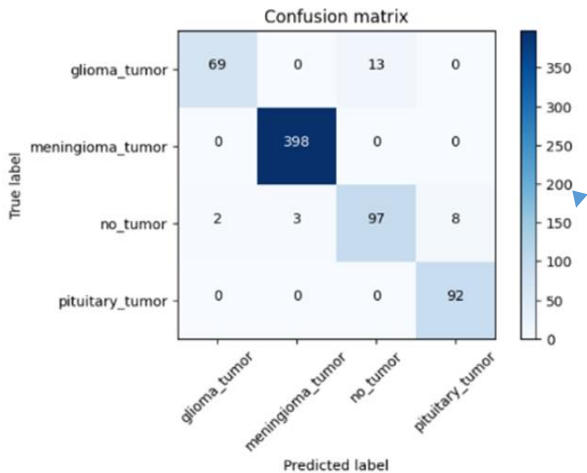


Figure 3: Confusion Matrix

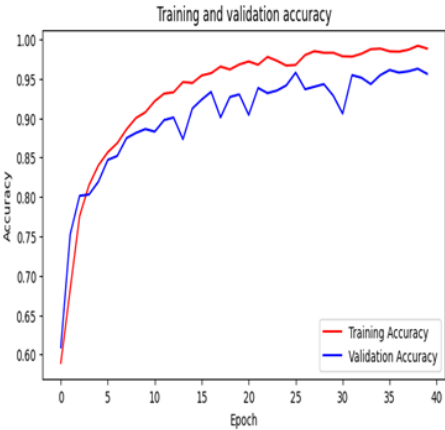


Figure 4(a)

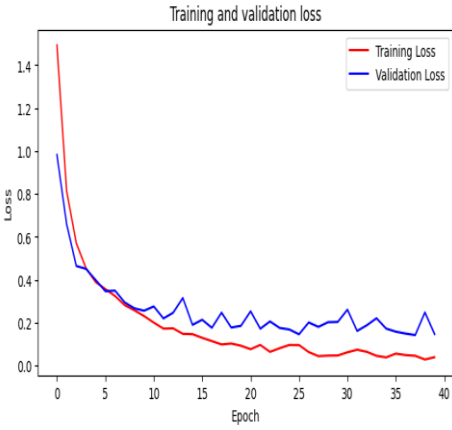


Figure 4(b)

Figure 4: (a) Accuracy (b) Loss Graphical representation per Epoch

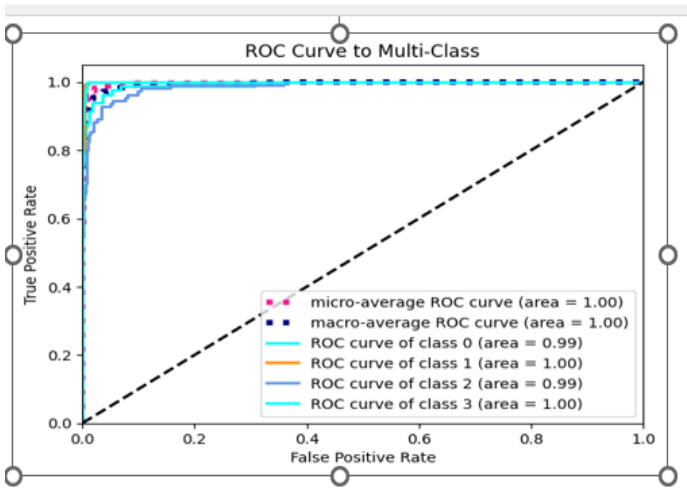


Figure 5: Represenataion of ROC Curve

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