

AUTOMATIC CLASSIFICATION OF PREPROCESSED MRI BRAIN TUMORS IMAGES USING DEEP CONVOLUTIONAL NEURAL NETWORK

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Abstract- Brain tumors are one of the highest-risk diseases. Therefore, early diagnosis is essential to improving patients' healing rates. Brain tumors are diagnosed using medical imaging techniques including magnetic resonance imaging (MRI), positron emission tomography (PET), and computed tomography (CT). In our study, we exploited MRI images to diagnose several forms of brain tumors namely Glioma, Meningioma, and Pituitary. Because of the massive amount of data, manual examination of the patient's brain MRI images makes classification complex, time-consuming, and prone to mistakes, hence the interest in using the deep learning tool. The most potent deep learning method for automatically classifying medical images is the convolutional neural network (CNN). The subject of this paper is the classification of pre-processed MRI images of brain tumors. Different machine learning classifiers have been discussed and compared with the traditional classifier of our CNN model in order to get the greatest outcomes possible. The database used is unbalanced, so it is necessary to evaluate the performance of our systems with different metrics such as accuracy, recall, precision, and F1-Score. The implementation of the CNN architecture with its own classifier indicates its reliability, with an accuracy of 95.65%.

Keywords: MRI, Deep Learning, CNN, Tumors Classification.

1. INTRODUCTION

With billions of cells, the brain represents one of the most vital organs in the human body, uncontrolled cell division forms a group of abnormal cells, also called a tumor. The two primary forms of brain tumors are high-grade and low-grade ones; low-grade tumors are referred to as "benign," but high-grade tumors are also known as malignant. Benign tumors are different from cancerous tumors, this prevents it from spreading to other areas of the brain, on the other hand, malignant tumors are cancerous. As a result, it spreads rapidly and indefinitely to other parts of the body. Radiologists use neuroimaging (also called cerebral imaging) to help them diagnose and treat brain tumors, there are several imaging techniques

represented, such as magnetic resonance imaging (MRI), positron emission tomography (PET), and computed tomography (CT) [1]. These techniques can be used to assess tumor growth before and after treatment. In the detection and treatment phases, one of the greatest imaging modalities for detecting brain tumors and stimulating tumor growth is magnetic resonance imaging (MRI) of the brain. MRI scans may provide a plethora of details about brain anatomy and abnormalities inside brain tissue because of the high resolution of the images, which had a major impact on the field of automated medical image analysis. Since medical images can be scanned and loaded onto computers, researchers have come up with several automated algorithms for brain tumor diagnosis and type classification using brain MRI scans. However, because to their superior performance throughout the previous several decades, machine learning algorithms like Neural Networks (NNs) and Support Vector Machines (SVMs) have been the most extensively utilized.

On the other hand, recently, deep learning (DL) models have become an exciting trend in machine learning because, unlike flat designs like SVM and K-Nearest Neighbors (KNN), they can effectively express complicated connections without a huge number of nodes. As a result, they are quickly becoming the main reference in various fields of health domain, including medical image analysis and bioinformatics [2]. Among deep learning architectures, convolutional neural networks (CNN) are the most often employed, particularly in the classification of images, a CNN's basic architecture consists of a convolution layer that does feature extraction and produces feature maps, a pooling layer that subsamples these feature maps, and a fully connected layer that performs classification [2], [3].

A lot of research has been done on brain tumor classification in recent years, among these works, Damodaran and Raghavan [4], have used a neural network-based technique for detecting cerebral tumors on MRI images. The proposed method outperformed Bayesian and K-Nest Neighbors (K-NN) classification techniques in terms of accuracy. Support vector machines (SVM) were proposed as a tool for classifying brain MRI

images by Nandpuru, et al. [5]. G. Singh and Ansari [6], developed a brain tumor detection system using normalized histogram segmentation technique and K-Means algorithm. For the classification and accuracy of their system, they employed Naive Bayes and support vector machine (SVM) classifier. Halder and Dobe [7], proposed a brain tumor detection system for classifying MRI images based on SVM and rough K-means. Shil, et al. [8], converted MRI images to OtsuBinarization and then used K-means cluster segmentation to detect and classify brain tumors. Thara and Jasmine [9], used fuzzy k-means clustering and c-means clustering to perform segmentation and then neural networks to perform image classification. In their study, Anitha and Murugavalli [10], developed a classification method for detecting tumor cells in the brain based on the K-Nearest Neighbor (KNN) algorithm. Arunkumar, et al. [11], proposed a fully automatic and trainable model-based segmentation and classification system for MRI brain tumors using artificial neural networks (ANN).

Several studies have employed CNN for the classification of brain tumor on MRI images. Sarkar, et al. [12], presented an automated system to distinguish between normal and abnormal MRI images and to classify tumors as meningioma, glioma or pituitary tumors. AvSar and SalCin [13] used faster R-CNN approach to detect and locate tumors in MRI brain images. Das, et al. [14], developed a CNN model to classify MRI brain tumors in T1-weighted contrast-enhanced images. Sultan, et al. [15], used two datasets to propose a convolutional neural network (CNN) for the classification of brain tumors, the first classifying tumors into Three forms of brain tumors. The other makes a distinction between three glioma grades.

This study is different from the previous studies presented in [4-11], due to the role of convolutional neural networks (CNN) on automatic medical image classification. Moreover, the study aimed to investigate the classification of MRI images into 4 classes, normal and three different tumor types including glioma, meningioma and pituitary, as some previous studies did not look for the distinction between three different forms of brain tumors and the normal brain. The present study is also different from other studies presented in [12-15] in terms of image preprocessing techniques. Several important methods are used prior to the classification of MRI images using CNN with its own classifier and others Machine Learning Classifiers, including image resizing, image smoothing, grayscale conversion, and image enhancement, to reduce computation, smooth the images and improve their quality.

The proposed methodology is presented in Section 2, the experimental results are analyzed in Section 3, and the conclusion is provided in the last Section.

2. METHOD

The methodology for brain tumor classification is discussed in detail in this section. It consists of the following steps: dataset description and preprocessing, and CNN classification of brain tumors. The following is a list of each step in the proposed system.

2.1. Dataset Description and Preprocessing

Masoud Nickparvar [16] contributed to the dataset used in this paper. There are 7019 MRI RGB images in this dataset, separated into four classes as shown in Figure 1, 1620 images having Glioma, 1644 images containing Meningioma, 1756 images with Pituitary, and 1999 normal images.

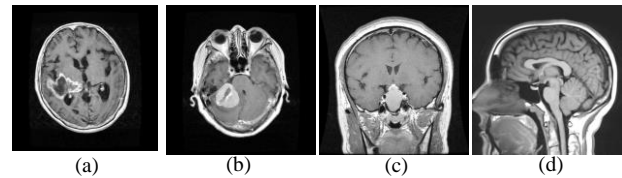


Figure 1. Dataset: (a) Glioma tumor, (b) Meningioma tumor, (c) Pituitary tumor, (d) Normal

Image preprocessing is a large field used in various domains such as medical imaging. In our human senses, the most powerful is our eye. Obtaining and exploring images is an essential part of the normal brain activity of human beings during their lifetime [17]. The image preprocessing of the proposed system consists of image resizing, image smoothing using a bilateral filter, grayscale conversion, image enhancement using histogram Equalization and gamma correction, and gray level Transform using quadratic function as mentioned in Figure 2.

The images are first resized to 128×128 to reduce the computations and then the bilateral filter is applied to smooth the images. A bilateral filter is a fundamental tool in image processing that consists of edge-preserving smoothing. It defines its filter weights from two laterals: the pixel position and the pixel intensity. This is a non-linear smoothing method that replaces the pixel value with the average of its neighbors which are determined as follows: Two-pixel values that are comparable to each other or close to each other [18].

Color to grayscale conversion is necessary for many image pre-processing applications to retain the principal characteristics of color images, such as contrast, brightness and structure. The grayscale image is a monochrome image that contains no color information. The values in the grayscale data matrix therefore represent intensities [19]. To improve the quality of images, one of the main methods of image pre-processing called "image enhancement" is to highlight certain important information in an image and to weaken or delete some secondary information. The basic purpose of image enhancement is to bring out hidden details or to improve low control-contrast changing the contrast improves the quality of the image. Histogram Equalization is a popular performance for contrast enhancement. Mapping the intensity values of the pixels in the input image so that the output image has a uniform intensity distribution, this technique increases the dynamic range of an image histogram. The histogram of an image mainly shows the comparative frequency of occurrence of different gray levels in the image [17].

Image enhancement techniques such as histogram equalization and homomorphic filtering are not appropriate for improving images with gamma distortion. For example, the principal objective of histogram equalization is to obtain a uniformly distributed histogram. This objective may not be adequate when the brightness of certain regions of the image is satisfied. It is primarily concerned with the histogram of the image and not the actual appearance of the image, as is the case with gamma correction. Therefore, traditional image enhancement techniques, such as histogram equalization and homomorphic filtering, cannot provide satisfactory results for images with gamma distortion. Therefore, gamma correction is a necessary preprocessing technique for such distortions [20].

After the previous pre-processing, the quadratic function is applied to transform the gray levels of the images. This function, presented in Equation (1), consists of decreasing the pixel values of the images [21].

$$f(x) = 255.0 \times (x / 255.0)^2 \tag{1}$$

The last step is to use the one-hot-encoding technique [22] for each pre-processed image by attributing the corresponding label as a binary array.

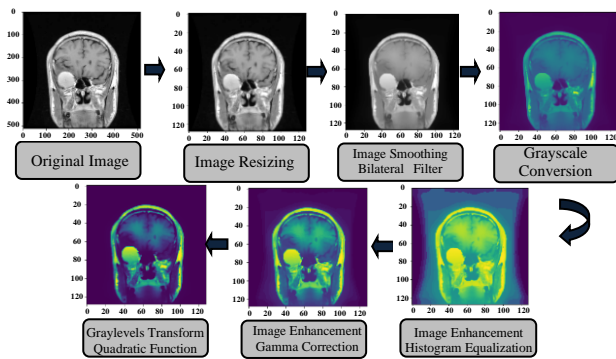


Figure 2. Dataset preprocessing

2.2. Brain Tumor Classification Using CNN

CNNs are multi-layer neural networks of unusual complexity. It's a good recognition algorithm for pattern recognition and image processing. It uses a weight-sharing network structure to simulate a biological neural network. In the field of computer vision problems, CNN is widely used. Compared to ANN (Artificial Neural Network), it has the property of sharing parameters, which reduces the number of parameters required for the model. In addition, the features extracted by CNN are of very high quality. A succession of convolution + pooling layers is used in the CNN model, succeeded by a fully connected layer. The final output layer is the Softmax activation function presented in Equation (2) as we use multiclass classification [14].

$$Softmax(x_i) = e^{x_i} / \sum_{k=1}^n e^{x_k} \tag{2}$$

where, x and n are input vector and the number of classes.

In this experiment, the dataset is split into 5612 images for the training phase (80%), and 1407 images for the validation phase (the remaining 20%). Each convolution layer is succeeded by a Maxpooling layer and

a dropout layer in our architecture. The dropout layer is a type of regularization used to reduce overfitting during the training phase. The activation function of each convolution layer is ReLU, which sets negative values to zero as shown in Equation (3) [23].

$$f(x) = \max(0, x) \tag{3}$$

The input image (128×128) was convolved with 64 filters of size 3×3, padding = "valid" (zero padding), and stride = 1, generating 32 features maps of size 126×126 in the first convolution layer. The first Maxpooling layer receives the features generated by the first convolution layer and reduces their size to 63×63 using a pooling size of 2×2. Then a Dropout layer is used. 128 filters with a kernel size of 3×3, padding = "valid", and stride = 1 is used in the second, third, and last convolution layers, producing 128 features maps of sizes 61×61, 28×28, and 12×12, respectively. Each of these layers is followed by a Maxpooling layer with a pooling size of 2×2, reducing the feature sizes to 3030, 14×14, and 6×6 pixels, respectively.

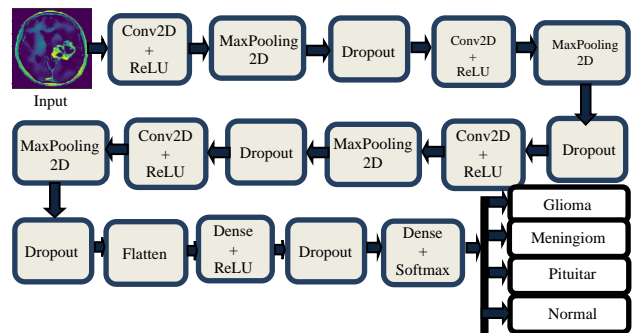


Figure 3. CNN model

Table 1. Model parameters

Layer	Output Shape	Parameters
Conv1	(None, 126, 126, 64)	640
Maxpooling1	(None, 63, 63, 64)	0
Dropout1	(None, 63, 63, 64)	0
Conv2	(None, 61, 61, 128)	73856
Maxpooling2	(None, 30, 30, 128)	0
Dropout2	(None, 30, 30, 128)	0
Conv3	(None, 28, 28, 128)	147584
Maxpooling3	(None, 14, 14, 128)	0
Dropout3	(None, 14, 14, 128)	0
Conv4	(None, 12, 12, 128)	147584
Maxpooling4	(None, 6, 6, 128)	0
Dropout4	(None, 6, 6, 128)	0
Flatten	(None, 4608)	0
Dense1	(None, 256)	1179904
Dropout5	(None, 256)	0
Dense2	(None, 4)	1028

After each Maxpooling layer, a dropout layer is applied. Then, to convert the matrices to vectors, a Flatten layer is used. The features are then fed into a dense layer of 256 nodes. After that, a dropout layer is applied. Finally, as we have four categories ('Glioma', 'Meningioma', 'Pituitary', and 'Normal'), another dense layer is used, which generates a vector with four nodes. The Softmax activation function [23] is used to convert a real vector into a categorical probability vector at the output of this layer. Figure 3 depicts the architecture, while Table 1 lists its parameters.

3. RESULTS AND DISCUSSION

The Adaptive Moment Estimation (Adam) optimizer [24] is employed to compile the CNN model after its construction. The training data is trained with the model using a batch size of 50 and 50 epochs. The model uses the optimizer to adjust its weight after each epoch, which minimizes the loss function and increases the final prediction. Figure 4 shows four parameter values, the loss, and the accuracy of the training and validation datasets generated by the model implementation. The loss is calculated using a loss function, which compares the loss to the target. Since only one class corresponds to each data point, categorical cross-entropy is used as the loss function. [25]. The loss and accuracy of training and validation datasets for 50 epochs are shown in Figure 4.

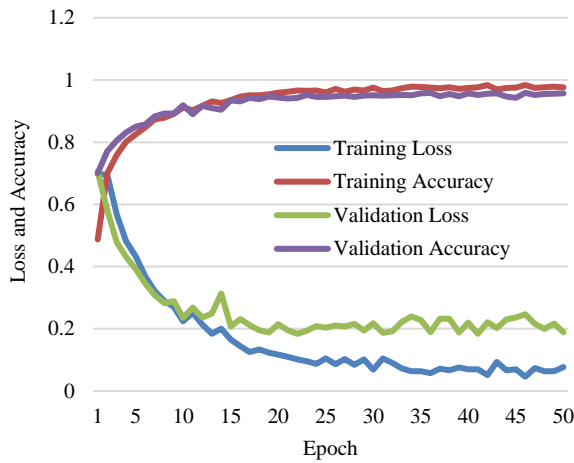


Figure 4. Loss and accuracy of our model for 50 epochs

A comparison of the traditional classifier Softmax of our model with other well-known machine learning classifiers was performed on our CNN model. These classifiers include XGBoost [26], Support Vector Machines (SVM) [27], Random Forest (RF) [28], K-Nearest Neighbors (k-NN) [29]. Features are extracted using most of the layers of our CNN model, i.e., from the first layer to the Flatten layer. These features are then used as input for machine learning classifiers to perform brain tumor classification.

A classifier's performance is measured using a variety of metrics. The most popular quality measure is accuracy. The ratio of correctly classified samples over all the data samples is known as classification accuracy. When there are an identical number of samples from each class in the test dataset, accuracy is a useful metric to measure performance. As a result, the dataset taken into account for the mentioned classification problem is unbalanced. Therefore, it is crucial to evaluate the proposed approach with other performance metrics. confusion matrices were employed to evaluate the efficacy of our tumor classification approach. The right and wrong classifications are given in a confusion matrix in tabular form. Table 2 provides an illustration of a confusion matrix for the outcome of our experiment using the conventional classifier Softmax.

Table 2. Confusion matrix of the proposed Model

Predicted / Actual	Glioma	Meningioma	Normal	Pituitary
Glioma	319	19	2	3
Meningioma	10	332	9	3
Normal	0	6	372	4
Pituitary	2	3	0	320

Various metrics may be obtained from a confusion matrix to show how effectively the classifier is performing. The most important metrics are accuracy, precision, recall, and F1-score and are calculated using the relations given in Equations (4)-(7) [30].

$$Accuracy = \frac{TN + TP}{TN + FP + FN + TP} \tag{4}$$

$$Precision = TP / (FP + TP) \tag{5}$$

$$Recall = TP / FN + TP \tag{6}$$

$$F1 - Score = \frac{2 \times Recall \times Precision}{Recall + Precision} \tag{7}$$

where, the number of cases classified as true negative, true positive, false negative, and false positive, respectively, is represented by *TN*, *TP*, *FN*, and *FP*. Table 3 shows the performance of the proposed system when the different classifiers were used.

Table 3. Results of our models

Metrics / Models	Accuracy	Precision	Recall	F1-Score
CNN	95.65%	95.67%	95.65%	95.65%
CNN + XGBoost	90.02%	90.04%	90.02%	89.88%
CNN + SVM	95.01%	95%	95.01%	95%
CNN + RF	92.45%	92.64%	92.45%	92.42%
CNN + K-NN	90.67%	91.41%	90.67%	90.27%

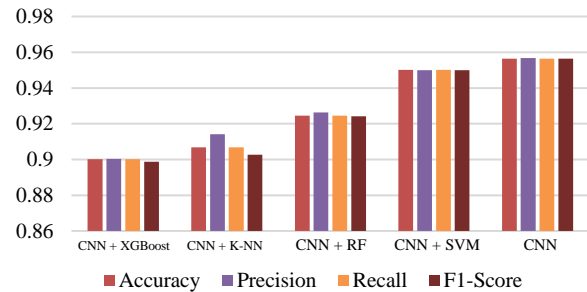


Figure 5. Performance metrics of the different classifiers

The results show that the CNN model with its traditional classifier Softmax performed best compared to other Machine Learning classifiers, as shown in Figure 5. We utilized our final model to make predictions on a new dataset that our model had never seen before. To fit our model, we loaded each of the images presented in Figure 6 and performed preprocessing on each of them. We then used our model to put the prediction into action. Above the images, the test results are mentioned.

The proposed model's accuracy is compared to other recently developed brain tumor classification models. Convolutional Neural Network (CNN) [12], [14], Faster Region-based CNN (R-CNN) [13], and Artificial Neural Network (ANN) [11] were utilized in these models. The accuracy of each model is shown in Table 4. These prediction accuracies are all lower than the accuracy achieved by our model.

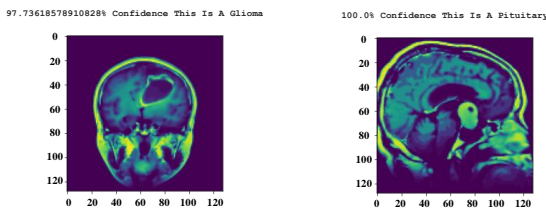


Figure 6. Results on Test Data

Table 4. The proposed model in comparison to other current models

Model	Technique	Accuracy
[12]	CNN	91.30%
[13]	R-CNN	91.66%
[11]	ANN	92.14%
[14]	CNN	94.39%
Our Model	CNN	95.65%

4. CONCLUSIONS

In the field of medicine, the classification of brain tumors is extremely essential. In this work, we focused on the creation of a CNN model that can distinguish between normal images and three common forms of tumors: Glioma, Meningioma, and Pituitary tumors. The proposed methodology starts by pre-processing the dataset by applying several popular methods including image resizing, image smoothing, grayscale conversion, and image enhancement. The CNN model is then used for feature extraction, and its own classifier Softmax is finally used to classify the images. This classifier proved to be the most accurate compared to other machine learning classifiers, as it provided the best possible results with an accuracy of 95.65%. Furthermore, our model outperformed most of previous work mentioned above. As a perspective, use of software optimization techniques could further improve the performance of our system.

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