Brain Tumor Classification Using Convolutional Neural Network and Feature Extraction

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Abstract

Convolutional Neural Networks (CNNs) are the most popular neural network model for the image classification problem, which has seen a surge in interest in recent years thanks to its potential to improve medical picture classification. CNN employs a number of building pieces, including convolution layers, pooling layers, and fully connected layers, to determine features in an adaptive manner via backpropagation. In this study, we aimed to create a CNN model that could identify and categorize brain cancers in T1-weighted contrast-enhanced MRI scans. There are two main phases to the proposed system. To identify images using CNN, first they must be preprocessed using a variety of image processing techniques. A total of 3064 photos of glioma, meningioma, and pituitary tumors are used in the investigation. Testing accuracy for our CNN model was 94.39%, precision was 93.33%, and recall was 93% on average. The suggested system outperformed numerous well-known current algorithms and demonstrated satisfactory accuracy on the dataset. We have performed several procedures on the data set to get it ready for usage, including standardizing the pixel sizes of the photos and dividing the dataset into 80% for train, 10% for test, and 10% for validation. The proposed classifier achieves a high level of accuracy of 95.3%.

Keywords: Brain Tumor; Convolutional Neural Networks; Kernel; Histogram Equalization; Feature Maps; Adam Optimization.

1. Introduction

A brain tumor develops from the uncontrolled proliferation of brain cells. Depending on the area of the brain affected, any unanticipated development may cause damage to human functions; furthermore, it may extend to other bodily organs, limiting human functions [1]. The human skull is a rigid and volume constrained body. According to the WHO's annual report on cancer, just 2% of all human cancers are brain cancers, yet it results in significant morbidity and damage [2]. Brain, other CNS, and intracranial cancers account for about 5,250 annual deaths in the UK, per data from Cancer Research UK [3]. The primary goal of this work is to speed up the process of classifying brain tumors using a deep learning-based system. When it comes to biomedical applications, detecting brain tumors is paramount. In recent years, the importance of early diagnosis of brain tumors has only increased. The purpose of the brain tumor classification system is to facilitate the diagnosis process for medical professionals. Preprocessing, feature extraction, and classification are only few of the procedures utilized during the classification procedure. Before using feature extraction to pinpoint an object's precise location, images must undergo preprocessing. This process filters, standardizes, and recognizes things before the extraction phase. Feature extraction is the technique of identifying distinguishing numerical characteristics in photographs [4].

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Doctors and other medical professionals would need computational aid to sift through these enormous data volumes, much alone conduct in-depth analyses. In addition, the inability to accurately categorize a life-threatening tumor may delay patients from receiving treatment. The detection of brain tumors and the inference of other concepts from data patterns have both seen widespread use of deep learning approaches over the ages. It is well-known that deep learning can be used to classify and model brain cancers. It's a strategy for finding hidden patterns and regularities in large data sets. It encompasses a wide variety of methods for uncovering hidden rules, paradigms, and relationships inside data sets, as well as for generating hypotheses about these connections. The most common uses of deep learning in the healthcare sector are shown in Figure 1.

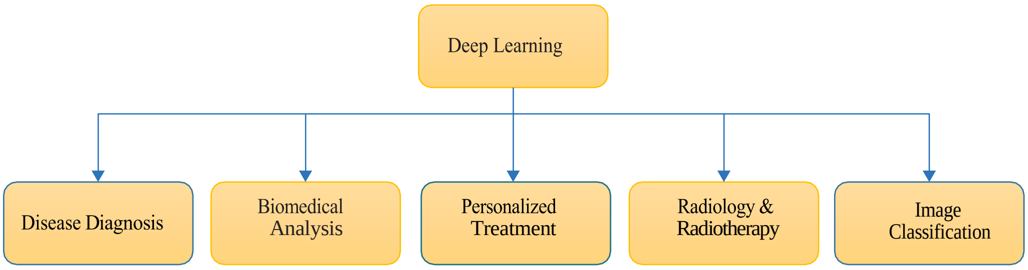

Figure 1: Primary applications of deep learning

2. Related Work

Due to its success in prediction and categorization, artificial intelligence (AI) tools are becoming increasingly popular in clinical research; this is especially true in clinical analysis to characterize brain tumors, and it is also used extensively in biomedical exploration and the construction of robust diagnostic systems for a wide range of diseases [5-7]. When it comes to data representation and hierarchical features, deep learning (DL) is a subfield of machine learning. In order to extract descriptors, DL algorithms employ a multi-layered structure of nonlinear processing methods. The output of one layer is used as the input for the next layer deeper in the network, which helps with data abstraction [8]. The purpose of convolutional neural networks (CNNs), a type of deep learning commonly used in visual image analysis, is to perform complex analyses with minimal human intervention [9]. It's used to arrange information in various tables [11] and is based on how the human brain works [10]. Lecun et al. [12] used a deep CNN resembling the modern one they created (called "LeNet") in document recognition applications in the late 20th century. The model "AlexNet" [13], which employs a deep CNN, garnered a lot of attention after it was used to classify images from (ImageNet LSVRC-2010). When compared to other popular network topologies at the time, AlexNet performed exceptionally well. Since then, CNNs have seen a great deal of success in the realm of deep learning. Increasing the number of training samples leads to a more accurate and robust model, which is why CNNs are preferable to traditional machine learning and vanilla neural networks [14]. In the CNN architecture, convolutional filters serve as feature extractors, and the more we delve, the more complex features (spatial and structural information) we extract. When training a classification network, the most distinguishing features are obtained through the convolution of small filters with the input patterns [11].

Different machine learning strategies have been used throughout the years to classify brain tumors. A hybrid of support vector machine (SVM) and k-nearest neighbor (KNN) was proposed for glioma classification in [15]. The best accuracy attained is 88% for binary classification and 85% for multiclassification. Wavelet Transform (DWT), principal component analysis (PCA), and artificial neural network (ANN) KNN are all used in [16] as part of a different method for detecting brain tumors in pictures. The success rate of the methods used is between 97% and 98%. Brain tumor categorization could be enhanced by expanding the tumor area via image dilation and partitioning it into subregions, as proposed by Cheng et al. [17]. Accuracy of 91.28% was achieved by using intensity histograms, GLCM, and BOW to extract features, followed by combining ring form segmentation and tumor region augmentation. To differentiate low- and high-grade Gliomas, Ertosun and Rubin [18] recommended using CNN. They had an accuracy of 71% and 96%, respectively. Paul et al. [19] used images of axial brain tumors to train and construct two separate classification methods (a fully linked CNN). The CNN architecture achieved 91.43 percent accuracy with its two convolutional layers and two fully connected layers. For the purpose of classifying brain malignancies, Afshar et al. [20] developed a capsule network (CapsNet) that takes into account both the MRI brain picture and the

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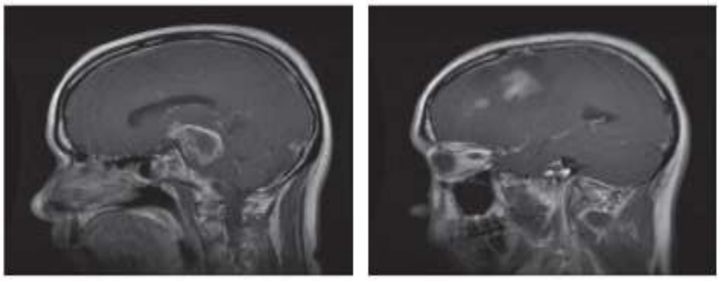
coarse tumor borders. This study had a reliability of 90.89 percent. Kabir Anaraki et al. [21] proposed two coupled regulatory models for classifying brain tumor pictures using CNN and genetic algorithms (GA-CNN). In the first case study, diagnostic accuracy for the three glioma grades was 90.9%, whereas in the second case study, diagnostic accuracy for glioma, meningioma, and pituitary tumors was 94.2%.

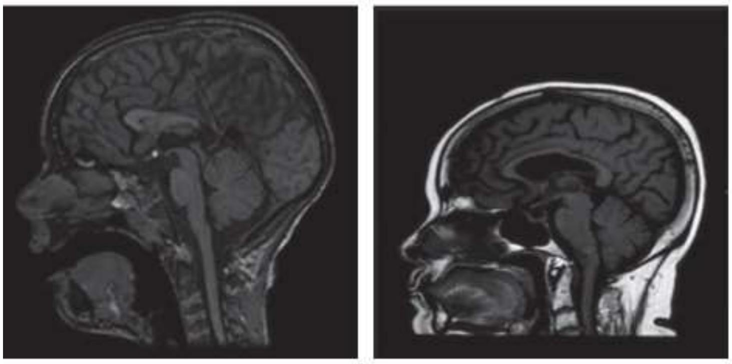
3. Method and Materials

A. Dataset

A publicly available brain tumor dataset [22] was used for this analysis. The X-ray images in this set were all taken of people who were diagnosed with brain tumors. This collection consists of 2,513 photographs of brain tumors and 2,087 images of healthy brain tissue. The X-ray images in Figure 2 are examples of both brain tumors and healthy people.



(a) Brain tumor images



(b) Healthy brain image

Figure 2: a) Brain tumor images. b) Healthy brain image.

B. Tools

When working with deep learning methods, Python is an ideal data processing tool. In this research, we look into different Python-based libraries that might be used to put our methods into action.

C. Proposed System

Figure 3 is a block diagram where the input is an X-ray image of a dataset split between people with brain tumors and those without them. First, we did some preprocessing, which included things like gathering photographs, splitting up the dataset, and exploring augmentation techniques before we began training the model. The results enhanced once the model was fitted and tweaked. Plotting the confusion matrix, the model loss, and the model accuracy reveals the path by which loss and accuracy change over time. Finally, the model's output may indicate whether or not an image representing a patient with a brain tumor was provided as input by the user. The simplest possible representation of the entire system is shown in the block diagram. The ability to make decisions is essential to the functioning of this system and is a major focus of the investigation.

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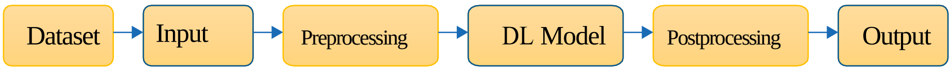

Figure 3: System block diagram

There is a preprocessing stage that occurs before the data is used for training and testing. Photos are scaled and redrawn as vectors. They are then normalized to a level that is manageable during the training phase. Reduce the image size to improve performance. In this study, the image was reduced in size to 256 pixels by 256 pixels. The subsequent action is to transform the entire set of photos into a matrix. There are three distinct uses for the dataset: training (80%), validation (10%), and testing (20%).

Using neural networks, CNNs introduce the concept of hidden layers. When a neural network is fed an image as input, the hidden layers perform a variety of modifications on that one vector. A large number of neurons populate each hidden layer, and connections are made between neurons in successive layers. Neurons in the same layer, however, do not communicate with one another. Different neurons perform various tasks and receive different amounts of information. The output of each neuron is biased in one direction or another depending on the functions and weights applied to it. This strategy involves going through multiple secret levels to get to the bottom of things. Finally, a completely linked layer combines the outputs of the preceding concealed layers. The inability to scale is a major drawback of conventional neural networks.

The convolutional layer is the foundation of deep transfer learning. The members of this team are in charge of settling on the aesthetic details. In effect, this layer acts as a filter on the original image. The input is multiplied by the weight ranges in a convolution process. Multiplying a 2D array of weights by an input data array yields a filter. Using a dot product on a region of the source and filter that is the same size yields a single value. This element serves as a buffer between the filter and the input's patchy signal. It is used here to multiple several inputs with the same filter, and it is smaller than the source. The filter is a novel approach to detecting particular types of characteristics; its comprehensive coverage of the entire frame makes it stand out.

The pooling layer allows for featured down sampling, which is used to synthesize a summary of the attributes. Two common pooling methods, average pooling and max pooling, are used to describe the typical and maximum occurrences of a function, respectively [23]. Indeed, the pooling layer strips the images of unnecessary details, making them legible. Each time average pooling is used, the layer takes the average of the value of its current view. When max pooling is activated, the layer always selects the greatest value in the current filter view. To reduce the number of output neurons required, the max pooling method selects only the highest value from each feature map according to the predetermined matrix size. This results in a significantly shrunken image of otherwise unaltered circumstances.

For usage in the fully linked layer, the flatten layer flattens the matrix data into a one-dimensional array. It is possible to flatten vectors. Finally, the classifier described in [24] is implemented. The final two steps of a convolutional neural network (CNN) are the flattening and fully connected layers. It is transformed into a one-dimensional array so that it can be used in the next fully connected stage of picture classification. Fully linked layers are widely employed in CNNs due to their shown usefulness in computer vision applications. The first steps of the CNN method, convolution and pooling, break the image into its individual features for analysis [25]. In a fully connected layer, all of the neurons are coupled to each input.

D.Performance Metrics for Image Classification

Accuracy, precision, recall, F1-score, and area under the curve (AUC) were just few of the metrics utilized to assess performance in this analysis. The following metrics were used to develop these standards: Number of images correctly identified as brain tumors (true positives, TP); number of normal cases correctly identified as normal (true negatives, TN); number of normal images incorrectly identified as tumors (false positives, FP); and number of normal tumor images (false negatives, FN). In Figure 7, we see a schematic representation of the confusion matrix.

From the value of the confusion matrix, the following equations can be derived:

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$$accuracy = \frac{TP+FN}{TP+TF+FP+FN'} \quad (1)$$

$$Precision = \frac{TP}{TP+FP'} \quad (2)$$

$$Recall = \frac{TP}{TP+FN'} \quad (3)$$

$$F1 - Score = \frac{2(Precision \times Recall)}{Precision+Recall} \quad (4)$$

4. Results

We employed various traditional metrics, such as accuracy, f-score, recall, accuracy, and confusion matrix, to assess the model's efficacy in determining if an MRI image of a brain tumor is indicative of a malignant tumor. In 35 epochs, the model trained with an accuracy of 97.47% and a loss of 0.402%. The results are graphically presented in Figures 4 and 5. Figure 4 demonstrates that the trained model outperforms the validation model. Figure 5 demonstrates the same thing, showing that validation loss is larger than training loss, ruling out overfitting as a problem in this model. Table 1 displays the CNN model's results.

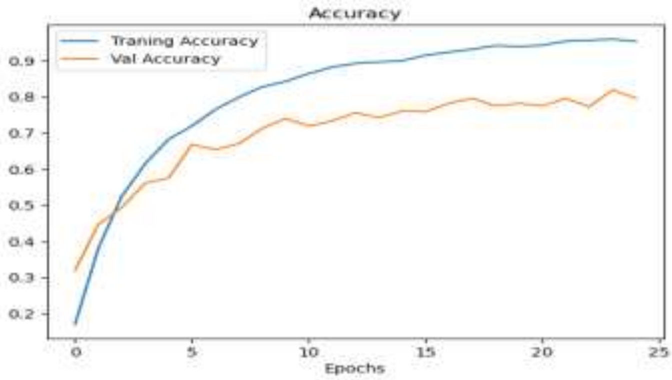

Figure 4: The training accuracy and the validation accuracy

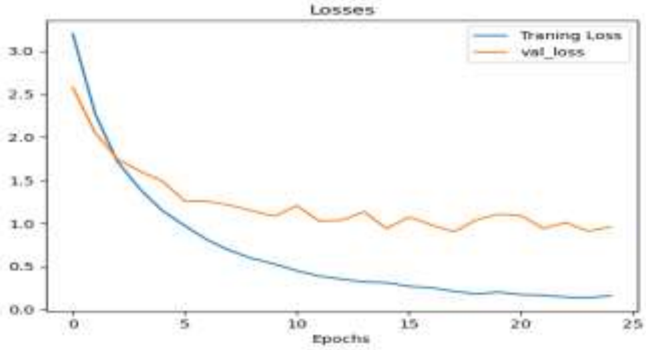

Figure 5: The training loss and the validation loss

Table 1: Performance of CNN model

	Accuracy	Loss	Val_loss	Val_accuracy
0	0.170033664	3.198289394	2.576953888	0.318604648
1	0.381313145	2.269231558	2.047766924	0.446511626
2	0.524130166	1.71208322	1.743744612	0.493023247
3	0.614197552	1.395517707	1.602933288	0.560465097
4	0.681818187	1.144699454	1.488075614	0.574418604
5	0.718855202	0.969701588	1.254717827	0.667441845
6	0.764309764	0.806428015	1.252981782	0.653488398
7	0.798260391	0.682261586	1.209767699	0.669767439
8	0.826879919	0.59039849	1.143775463	0.711627901
9	0.842031419	0.525008619	1.08087635	0.739534855

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10	0.863916934	0.44814828	1.203884244	0.718604624
11	0.882154882	0.386205852	1.02493751	0.732558131
12	0.891975284	0.349360436	1.034588575	0.755813956
13	0.896184087	0.318429798	1.132371306	0.741860449
14	0.899551094	0.309196472	0.936127365	0.760465145
15	0.914702594	0.266979158	1.071529984	0.758139551
16	0.9234007	0.250524998	0.981377184	0.781395376
17	0.931537569	0.20916155	0.90055877	0.795348823
18	0.941638589	0.177626193	1.038150549	0.774418592
19	0.93883276	0.199943826	1.105081797	0.781395376
20	0.942480385	0.171233356	1.089311838	0.774418592
21	0.953703701	0.16078265	0.937622488	0.795348823
22	0.956509531	0.142378956	1.008053184	0.772092998
23	0.959034801	0.132383794	0.906099498	0.818604648
24	0.953423142	0.158901662	0.956274271	0.795348823

It is quite evident from the confusion matrix shown in figure 6 that our model is, having 96.08 percent accuracy while error, can be given as 2.98 percent respectively. The summarization of cnn model is shown in figure 7.

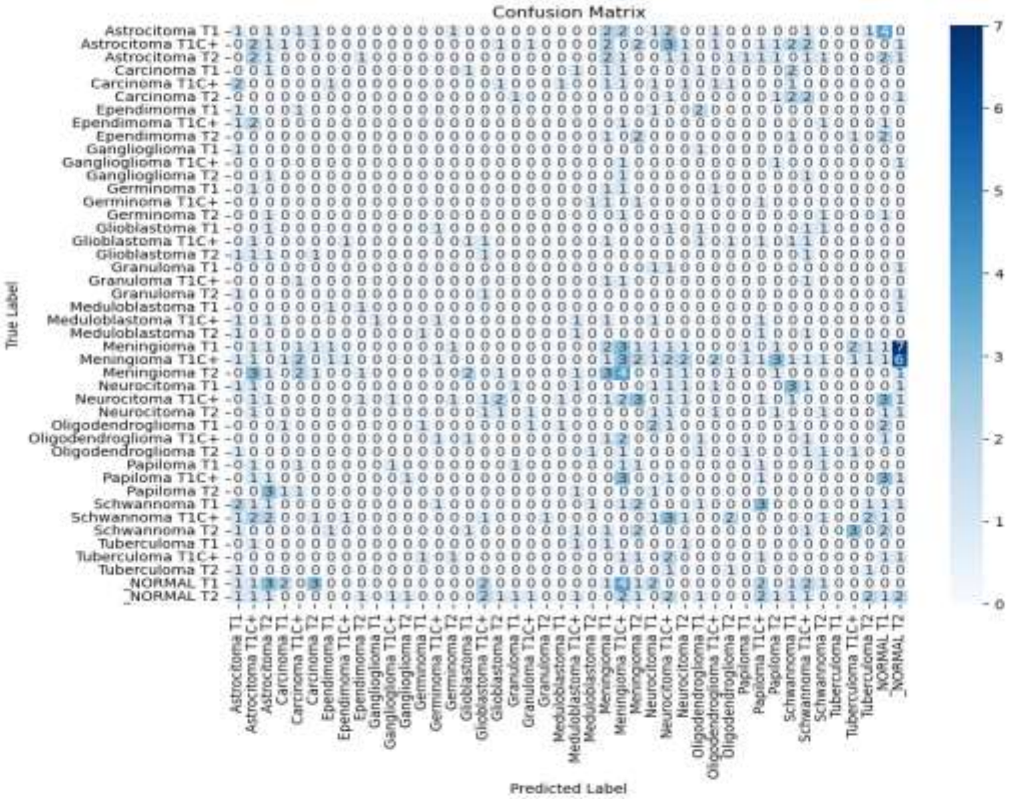

Figure 6: The confusion matrix of cnn model

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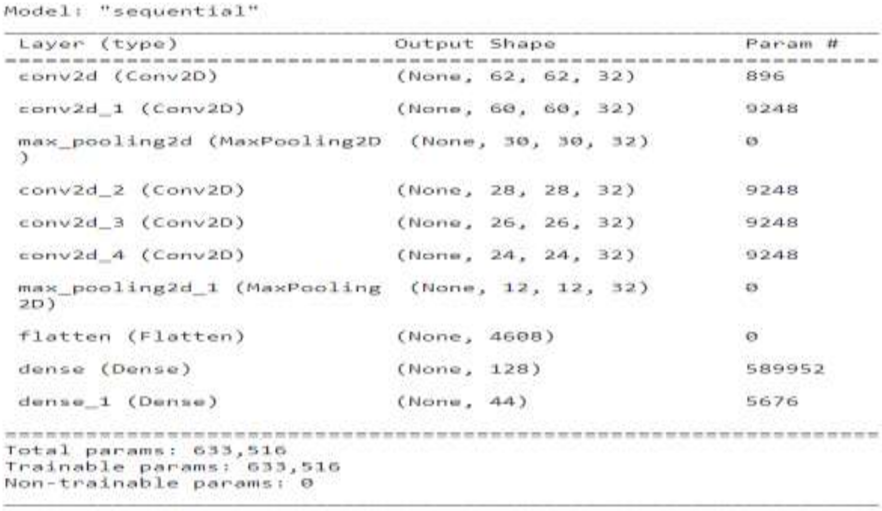

```
Model: "sequential"
_________________________________________________________________
 Layer (type)                Output Shape              Param #
=================================================================
 conv2d (Conv2D)             (None, 62, 62, 32)        896

 conv2d_1 (Conv2D)           (None, 60, 60, 32)        9248

 max_pooling2d (MaxPooling2D  (None, 30, 30, 32)       0
 )

 conv2d_2 (Conv2D)           (None, 28, 28, 32)        9248

 conv2d_3 (Conv2D)           (None, 26, 26, 32)        9248

 conv2d_4 (Conv2D)           (None, 24, 24, 32)        9248

 max_pooling2d_1 (MaxPooling  (None, 12, 12, 32)       0
 2D)

 flatten (Flatten)           (None, 4608)              0

 dense (Dense)               (None, 128)               589952

 dense_1 (Dense)             (None, 44)                5676

=================================================================
Total params: 633,516
Trainable params: 633,516
Non-trainable params: 0
_________________________________________________________________
```

Figure 7: The cnn model

6. Conclusion

In this study, we suggested a new CNN-based approach for automatically identifying tumors in Brain MRI scans. The f-score for the model is 97.3, and it has an accuracy of 96.08%. The model's findings can be obtained in 35 epochs because to its three-layer CNN and minimal preprocessing processes. The study's goal is to bring attention to the usefulness of machine learning in diagnostics and therapy planning. In the future, the Convolutional Neural Network will be used to identify brain tumors utilizing neutrosophic principles.

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