
Segmentation and classification of specific pattern of Brain tumor using CNN

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ABSTRACT

A Brain tumor is a growth of cells in the brain or near it. Brain tumors can happen in the brain tissue close by locations include nerves, the pituitary gland, central nervous system, meninges and the membranes that cover the surface of the brain [1]. A glioma is a tumor that forms in the brain or spinal cord. A glioma is a tumor of the central nervous system that makes an appearance from glial stem or progenitor cells. Glial cells are a type of cell generally present in the nervous system. Gliomas predominantly occur in the brain and, rarely, in the spinal cord. They grow in approximately 6.6 per 100,000 individuals each year. They transpire at various ages, controlled by the subtype. Growing gliomas can compact areas of the brain where they occur and cause various symptoms including headaches, nausea, vomiting, cognitive impairment, seizures, gait imbalance, language impairment [2]. A meningioma is a tumor that makes an appearance from the meninges — the membranes that surround the brain and spinal cord. In spite of the fact that not technically a brain tumor, it is included in this category because it may compress or squeeze the adjacent brain, nerves and vessels. Meningiomas are tumors of the meninges, mostly benign and often managed by surgical resection, with radiation therapy and chemotherapy reserved for high-risk or refractory disease. [3]. Tumors can start nearly anywhere in the body. Tumors that start in the pituitary gland are called pituitary tumors. The anterior pituitary tumors start in the larger, front part of the pituitary gland known as the anterior pituitary. The posterior pituitary: The smaller, back part of the pituitary gland is an extension of brain tissue from the hypothalamus. The posterior pituitary stores and releases hormones made by the hypothalamus (vasopressin and oxytocin) into the bloodstream [4]. Machine learning applications in healthcare are already having a positive impact, and its potential is still in the early stages of being realized to deliver care [2]. In the future, machine learning in healthcare will become increasingly important as we strive to make sense of the ever-growing clinical data sets in healthcare. Heart disease, cancer, and brain tumors are diagnosed using medical imaging procedures such as MRI scans, CT scans, and ECG. As a result, deep learning assists doctors in better analyzing diseases and providing the best treatment to patients. In this paper, specific brain tumor segmentation and classification have been done using a Deep Convolutional Neural Network that incorporates a multiscale approach. The proposed neural model can look over MRI images containing three types of tumors: glioma, meningioma, and pituitary tumor. Data has been collected from <https://www.kaggle.com/datasets/masoudnickparvar/brain-tumor-mri-dataset?select=Training>. This dataset encompasses 7023 images of human brain MRI images which are classified into 4 classes: glioma - meningioma - no tumor and pituitary. no tumor class images were taken from the Br35H dataset. The goal of this work was to aid clinical researchers in gaining a clear and intuitive understanding of the application of data-mining technology on clinical data to promote the production of research results that are beneficial to doctors and patients.

Keywords: CNN, GLIOMA, MENINGIOMA, PITUITARY, MGMT, Br35H.

Introduction:

The brain is the most important organ in the human body which controls the entire functionality of other organs and helps in decision-making [10]. It controls the central nervous system and is responsible for performing the daily voluntary and involuntary activities in the human body. [1] A

tumor is an uncontrolled growth of tissues inside our brain that proliferates in an unconstrained way. The right way of understanding brain tumors and their stages is an important task for early detection and to prevent and carrying out the steps in curing the disease. In this case, magnetic resonance imaging (MRI) is widely used by radiologists to look over brain tumors[1]. The result of the analysis carried out in this paper reveals whether the brain is a normal or diseased one by applying deep learning techniques. In this article, CNN is used for the segmentation and classification of various types of tumours e.g. glioma, meningioma, and pituitary and no tumors. CNN has different layers of neurons which are connected. The neural network can acquire knowledge by [3] using a data set applied to the learning process. There will be one input and output layer whereas there may be any number of hidden layers. In the learning process, the weight and bias are added to neurons of each layer depending upon the input features and on the previous layers(for hidden layers and output layers). A model is trained based on the activation function applied to the input features and on the hidden layers where more learning happens to achieve the expected output. As CNN works with the fully connected layers, where it involves more processing. In this research paper, some parameters used in the CNN method have been tuned to improve the accuracy of this proposed model.

Literature review:

Several methods for detecting brain tumors in MRI images have been developed throughout the years. These technologies range from traditional image processing to neural network-based machine learning. Abiwinanda et al. [5] created a tumor classification system that is divided into two stages: offline database construction and online retrieval. The brain tumor photos are analyzed sequentially in the offline database phase. Tumor segmentation, feature extraction, and distance metric learning are the steps. The input brain picture will be processed similarly in online learning, and the extracted feature will be compared with the learned distanced metrics that are kept in the online database.

This technique, which does not involve a neural network, has a classification accuracy of 94.68%. Dong et al.[6], on the other hand, employed Deep Neural Networks using autoencoders to classify the brain tumor. Before the image was processed using DNN layers, it was subjected to image segmentation and feature extraction. The image's texture and intensity-based characteristics were recovered using the Gray Level Co-occurrence Matrix (GLCM) and DiscreteWavelet Transform (DWT). DNN layers consisting of two autoencoders and one softmax layer were used for classification in the final stage.

Additionally, Zhou et al. [7] are investigating the usage of Convolutional Neural Networks (CNN) with small 3 3 kernels to get to the deeper architecture and prevent overfitting. They also looked at using intensity normalization as a pre-processing step before entering the CNN layers. In this study, we analyze and explore the use of deep CNN on classifying numerous brain tumor-type diagnosis difficulties to get higher accuracy results.

Vaishnavee and Amshakala [8] addressed the problem of brain tumor segmentation utilizing SVM and self-organizing Map (SOM) strategies. Histogram equalization has been used in the pre-processing stage. Four characteristics were determined to be categorized, i.e. the mean, severity, amount of incidents, and variance. They used SOM clustering to identify the irregular brain clusters and segment them in the second stage. Also, brain MR photographs were categorized into different intra-tumor groups. To conduct this characterization of the gray level co-existing texture matrix (GLCMs) in sub-tumor levels, a Principle Component Analysis (PCA) was used to measure these texture characteristics as a step towards reducing dimensionally. however, the authors did not compare results in state of art and there was no justification for using SVM and SOM.

Nie et al. [9] reported a complete automatic 3D-CNN brain tumor segmentation system utilizing both T1, MR test (MRI), and Diffusion Tensor Imaging (DTI). Different pre-processing stages have been done using T1, DTI tensor, and fMRI-specific BLD (blood oxygen-dependent) variance rate for increasing MR modality i.e. strength standardization. The extractor function was 3D-CNN and the

final prediction was carried out by SVM with 89.9% (accuracy), 92.19% (sensitivity), and 88.22% (specificity). However, the proposed system is computationally expensive and unsuitable for large datasets.

Arikan et al. [10] proposed a semi-automated, collaborative seed selection-based SVM approach for the fragmentation of brain tumors. They used an anisotropic diffusion filter in the MR images during the pre-processing stage to eliminate noise. Random seeds would then be chosen for the SVM classification from the previously processed MR images

Convolution Neural network: A CNN consists of input, convolution, max pooling, fully connected (FC), and output layers stacked hierarchically. The convolution layer is the fundamental block of a CNN and contains kernels that are convolved over input images to detect features. A CNN kernel is a filter of different shapes such as 3×3 , 7×7 , and 13×13 , which is convolved over the input in a sliding window manner to generate a feature map. In this research, mostly 3×3 filter has been used at the first layer. A feature map is a group of features arranged in a topologically ordered manner, where each point in a map is connected to the previous layer's output via weights[21].

Pooling Layer: The (Max) Pooling Layer takes the 3×3 matrix of the convolution layer as input and tries to reduce the dimensionality further and additionally take the important features in the image. We want to generate a 2×2 matrix as the output of this layer, so we divide the input into all possible 2×2 partial matrices and search for the highest value in these fields. This will be the value in the field of the output matrix. If we were to use the average pooling layer instead of a max-pooling layer, we would calculate the average of the four fields instead. The pooling layer also filters out noise from the image, i.e. elements of the image that do not contribute to the classification. For example, whether the dog is standing in front of a house or front of a forest is not important at first[21].

Fully connected layer: These layers are an important aspect of CNNs, as they are responsible for determining the worth of individual features and their contribution to the final output. FC layers have a great effect on the output of the network, so using the low number of features in the FC layer can add both speed and precision to the network. The FC layer is connected to the output layer, which converts features into class probabilities using softmax [21] nonlinearity. Softmax function can be used more than one time in a fully connected layer to get more classification accuracy. The fully-connected layer now does exactly what we intended to do with the whole image at the beginning. In this layer, a neuron for each entry in the smaller 2×2 matrix connects to all neurons in the next layer. This gives us significantly fewer dimensions and requires fewer resources in training. This layer then finally learns which parts of the image are needed to make the classification of glioma, meningiomas, no tumor, and pituitary. If we have images that are much larger than our $5 \times 5 \times 3$ example, it is of course also possible to set the convolution layer and pooling layer several times in a row before going into the fully-connected layer.

Feature map: The feature map which is like an image is divided into several non-overlapping subsets and from each subset the relevant parameter is obtained. There are two types of pooling based on the parameter selected namely Max pooling and Average pooling. In Max pooling the maximum value from the subset is selected and in average pooling the average value of the subset is selected.

Dataset: Data has been collected from Kaggle website which consists of total 7023 MRI images, Out of 7023 images 5712 images categorized as training data and 1311 images categorized as test data. The dataset consists of for different types of MR images, including glioma, meningioma, no tumor and pituitary slices. Each type of tumor and no tumor proportion in the dataset is shown below fig.[1] and training and test dataset is shown below fig. [2]

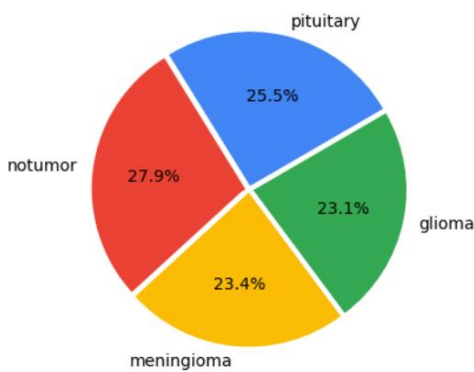
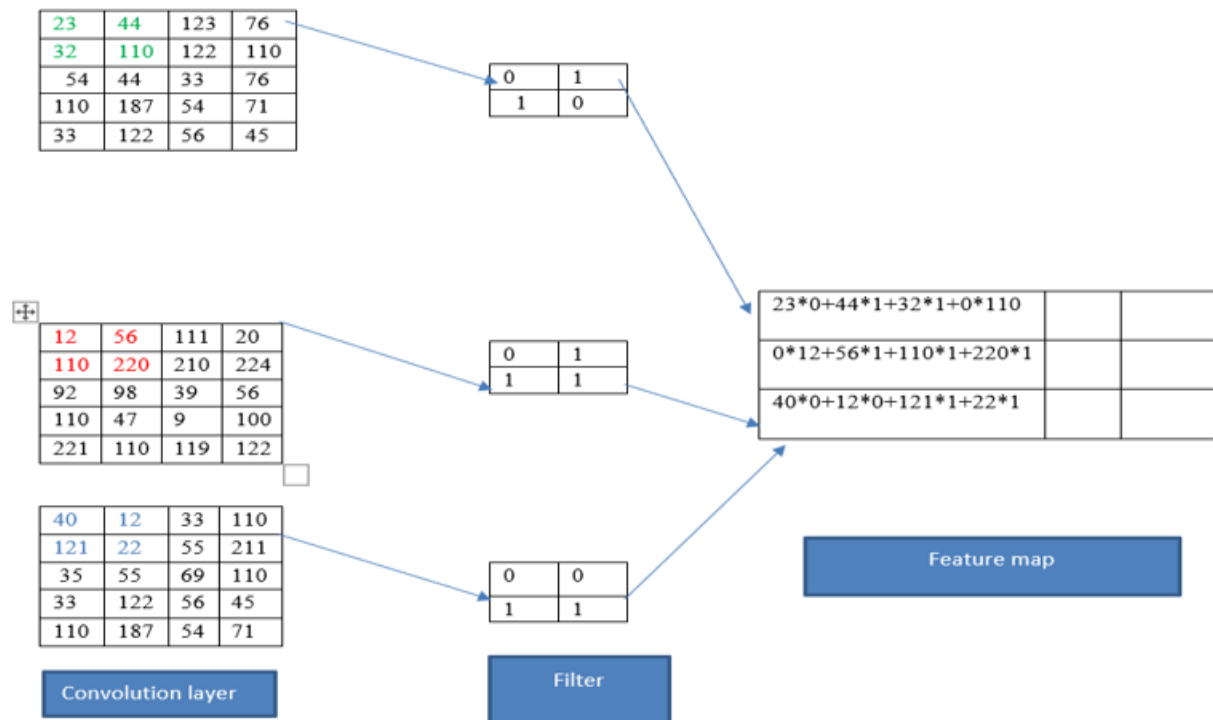


Fig. 1

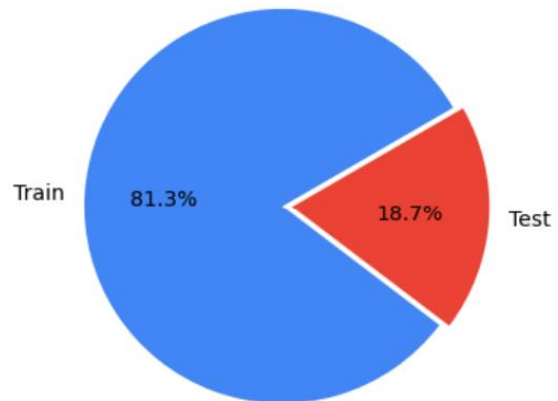
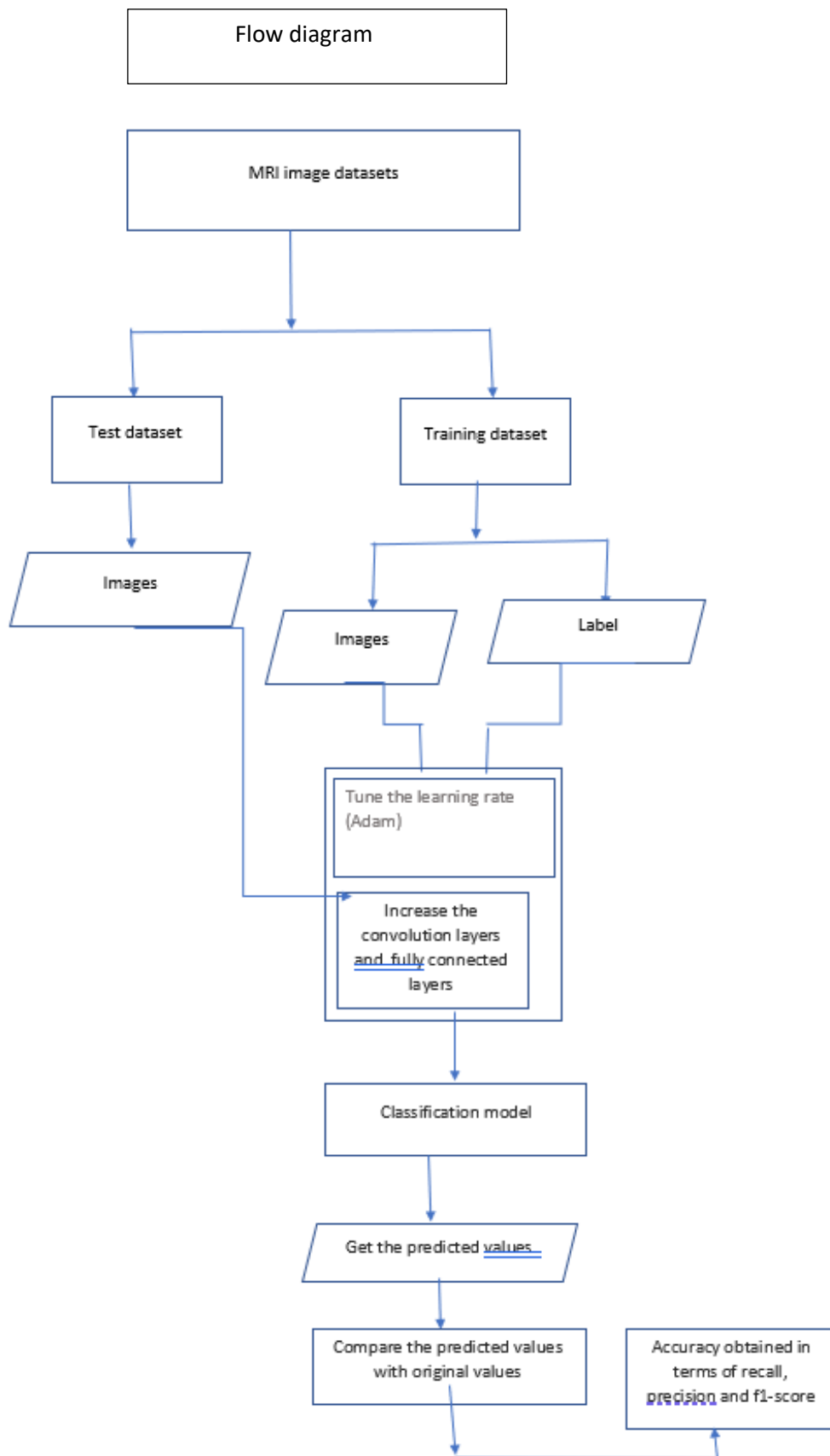


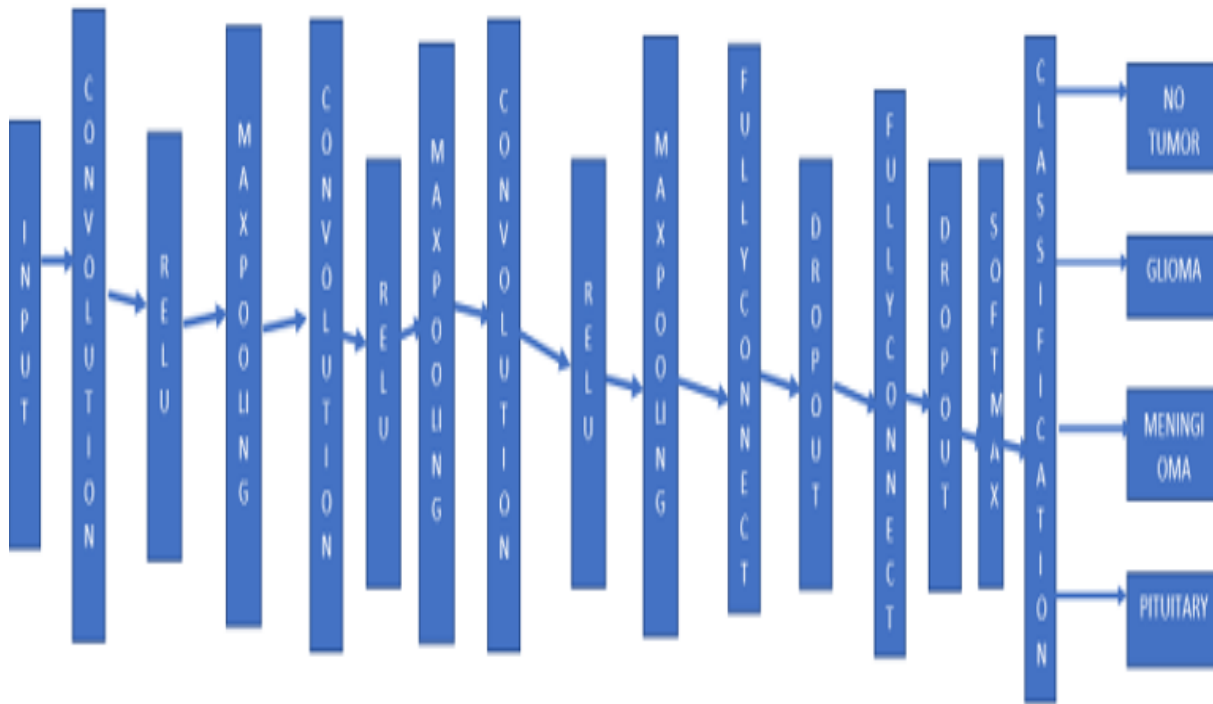
Fig.2

Methodology : The proposed CNN model classifies the brain tumor into four brain tumor types, i.e. glioma, meningioma, pituitary, and no tumor. The proposed CNN model for Classification has 16 weighted layers (1 input, 4 convolutions, 3 ReLU, 3 max pooling, 2 fully connected, 2 dropouts, 1 softmax, and 1 classification layer) which is shown in fig 4. The proposed CNN model is designed to classify a given image into 4 classes, the output layer has 4 neurons. The last fully connected layer, which is a four-dimensional feature vector, is given as an input to the softmax classifier, which makes the final prediction about the tumor type (glioma, meningioma, no tumor, pituitary). Refer to fig.4 for more information about the CNN architecture.



The architecture of proposed CNN model:

Fig. 3



Algorithm:

STEP1: Three hyperparameters to be optimized	Input Image size : Batch size : Learning rate : Dropout
STEP 2: Set the values for each of the parameters:	input image Size (256,128,64) : Batch size (256,64,16) : Learning rate (.0005,.0003,.0001) : Dropout(.3,.2,.1)
STEP3 : Overall accuracy obtained	: input image size -256,Batch size-256, Learning rate-.0005,Dropout-.3 low accuracy : input image size-64,Batch size-16,learning rate-.0001,dropout-.1 accuracy(97%)

The comparison of the framework with the previous work based on the different types of MRI image dataset:

Authors	Techniques used	Type of classification	Dataset used	Accuracy
[13]	SVM and KNN	Multi	T1-weighted CE-MRI, 708 meningiomas, 1426 gliomas, and 930 pituitary tumors	91.28%
[14]	CNN	Multi	T1-weighted CE-MRI, 208 meningioma, 492 glioma, and 289 pituitary tumor images	91.43%
[15]	CNN	Multi	T1-weighted CE-MRI, 708 meningiomas, 1426 gliomas, and 930 pituitary tumors	90.89%
[16]	GA-CNN	Multi	T1-weighted CE-MRI, 708 meningiomas, 1426 gliomas, and 930 pituitary tumors	94.20%
[17]	BWT-SVM	Binary	T2-weighted brain images, 67 normal and 134 abnormal	95%
[18]	CNN	Multi	T1-weighted CE-MRI, 708 meningiomas, 1426 gliomas, and 930 pituitary tumors	96.13%
[19]	CNN	Multi	T1-weighted CE-MRI, 248 meningiomas, 12 gliomas, and 55 pituitary tumors	95.23%
[20]	CNN	Multi	T1-weighted CE-MRI, 708 meningiomas, 1426 gliomas, and 930 pituitary tumors	84.19%
Our proposed system	CNN	Multi	T1-weighted CE-MRI gliomas (training--1320) (tesing-300), Meningiomas(training-1338)tesing(306),pituitary(training-1426)(testing-300) Notumor(training-1549)(testing-405)	97%

Results and discussion : A comparative analysis of glioma, meningioma, notumor, and the pituitary, was performed in the 3 accuracy metrics e.g. Precision, Recall, and F1-Score. The precision, recall, and f1-score values are provided in Table 1. The accuracy produced by the model is 97%. The sparse categorical accuracy is shown in figure # below which is much more significant than classification accuracy. The results of Precision, Recall, and F1-Score in Table 1 demonstrate the potential of the conceptual model in the classification of 4 classes. The proposed model generates a recall value of 98% or higher for all the classes as shown in Table 1. As can be seen from the comparative results, the proposed classification technique has the highest Precision, Recall, and F1-Score values (accuracy = 97%, sensitivity = 97%, precision = 97%, f1-score = 96%). Here the macro average represents the mean average of all classes (Precision, Recall, and F1-Score).

	Precision	Recall	F1-score	Support
Glioma	.22	.99	.37	300
Meningioma	.23	.98	.38	306
Notumor	.31	.98	.47	405
Pituitary	.22	.99	.37	300
Macro avg.	.24	.985	.40	1311

Table 1

Conclusion: In this research article, the authors have classified the brain tumor dataset using CNN to predict sparse categorical accuracy and classification accuracy. CNN model produces an accuracy of 97% in classification and 99.9% in categorical accuracy prediction. To reach that accuracy the authors have tuned some parameters in the optimizer and activation function. Increasing the hidden layers along with changes in activation function in some specific pattern elevates the accuracy which was the main contribution of this research paper.

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