A Framework for Brain Tumor Image Analysis using Convolution with RELU

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Abstract: The most vital step in determining abnormal life-threatening tissues and creating an effective treatment plan for patients' recovery, is classifying a brain tumor. There are several different medical imaging modalities available to detect abnormal disorders in the brain. Due to its superior image quality and lack of ionizing radiation, magnetic resonance imaging (MRI) is widely employed in medical imaging. Segmentation, detection, and classification are known to be crucial phases in a digital imaging pathology lab for MRI brain tumor region analysis. In this study for the analysis and classification of medical images, a convolution+RELU algorithm is implemented, which is a combination of convolutional and RELU optimization approaches. This paper employs a robust and efficient convolution+RELU method utilizing the BraTS 2020 dataset. This approach significantly reduces the segmentation time compared to other optimization methods. Moreover, it achieves impressive performance metrics, including a precision of 99.8%, recall of 99%, and an f-measure of 99.3%. Convolutional neural networks (CNN) that use the convolution+RELU activation function effectively increase the learning speed and tumor analysis performance. The implemented convolution+RELU model attained 99.8% accuracy in the experimental phase, which is higher than the existing techniques.

Keywords: Brain tumor, BraTS 2020, Convolutional neural network, Convolution+RELU, Magnetic resonance imaging (MRI)

1. Introduction

Brain tumors are among the mental health conditions that cause the psychiatric symptoms, such as memory issues, panic attacks, anxiety disorders, or personality changes, and as a result, diminish the quality of life for an affected individual. Tumors are classified into two types: primary and secondary tumors. A primarily malignant tumor begins to grow within the brain itself. A secondary malignant tumor begins in another organ and travels to the brain by metastasis [1]. Amongst the different primary brain tumor forms, Glioma has the highest death rate. It typically develops from glial cells in the brain, and is categorized into two types: High Glioma (HG), and Low Glioma (LG) [2, 3]. Each year, France diagnoses close to 3000 new cases and men are more often impacted by

Gliomas. The majority of incidents are sporadic, but in rare instances, they are connected with specific family cancers [4]. To identify, monitor, and diagnose brain tumors, Magnetic Resonance Imaging (MRI) is a significant tool [5]. To help doctors and prevent risky histological operations, MRI is used to distinguish and classify distinct tumor types [6]. Brain tumors are frequently diagnosed and accessed using Computed Tomography (CT) and MRI [7]. MRI outperforms CT in the context of medical diagnostics. The contrast between the various soft tissues in the human body is improved through imaging [8]. Early detection of brain tumors saves lives and minimizes risk of difficulty in treatment, by avoiding surgical removal and manipulation of fragile brain tissues [9]. Radiologists frequently utilize MRI to examine brain tumors.

This analysis's outcome shows whether the brain is healthy or disordered, and the type of tumor is identified in the event of an irregularity. Since machine learning has become more prevalent, it is also important to consider its use in deciphering MR scans, to quickly and accurately identify brain tumors. Convolutional Neural Networks (CNN) are now used widely for features extracted from data in various researches, including the analysis of videos, natural language processing, and the analysis of medical imaging. CNN's key characteristic is its ability to extract the most significant patterns and information from training images [10]. The location of these tumors must be identified, in the resulting brain MRI image to diagnose and treat them. The computer-aided diagnosis (CAD)

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method of medical analysis has lately gained popularity among researchers [11]. Computer-aided systems are primarily used to diagnose brain tumors to gather comprehensive clinical data on the presence, type, and location of the tumor [12]. With its high-quality brain images, MRI is a widely used tool of analysis. Additionally, a deep learning technique known as CNN is now regarded as the main tool for medical picture analysis, due to its outstanding performance in computer vision applications [13]. The MRI technique is very important for brain imaging because it especially offers in a most suitable manner, the visualization of the maximum amount of both spatial and contrast determination [14]. Preprocessing, feature extraction, feature selection, dimension reduction, and categorization are typical phases in traditional machine learning algorithms for categorization [15]. The convolution+RELU method is used to segment the image of a brain tumor, and its contribution to this research is listed below,

- A convolution+RELU algorithm is a combination of convolutional and RELU optimization approaches and it is implemented, for classifying the brain tumor using medical images.

- This paper employs a robust and efficient convolution+RELU method utilizing the BraTS 2020 dataset.

- Convolutional neural networks that use the convolution+RELU activation function effectively increase the learning speed and tumor analysis performance.

- The implemented technique, according to experimental data, has a higher detection accuracy and a shorter execution time.

The overall structure of the paper is outlined as follows, the literature review is described in section 2, the implementation description of the methodology is in section 3, the result and discussion are described in section 4, and the conclusion is in section 5.

2. Literature Survey

Shivhare and Kumar [16] implemented the Tumor Bagging, which was a unique framework and its purpose was to improve the performance of brain tumor segmentation by merging multiple Multilayer Perceptron (MLP)-based segmentation approaches. By bagging the models, the proposed framework not only provided good segmentation performance, but also enhanced the learning of link weights and the basis of MLP. The simplicity of the implemented strategy was an advantage that made it perform significantly better than existing methods when applied to the benchmark BRATS dataset using the bagging approach. However, combined training features

led to longer training time of the model, for effective categorization of each tumor type.

Chattopadhyay and Maitra [17] implemented a CNN strategy to exclude brain tumors from 2D MRIs of the brain, followed by classic classifiers and methods of deep learning like LSTM and GAN. The implemented CNN-based model had learning representative complex features that automatically detected both tumor tissues and healthy tissues in the brain directly from multi-modal MRI images. However, the implemented CNN model needed a wide number of images for training, which is generally challenging to acquire in the medical field of imaging.

Naceur et al. [18] implemented the CNN's design that was inspired by the occipitotemporal pathway's selective attention strategy. The occipitotemporal pathway had a unique function termed selective attention that used various receptive field sizes in successive layers to identify the key elements in a scene. The accuracy of the implemented method's segmentation was increased by the use of overlapping patches, which allowed for a better representation of local picture information. However, the implemented model needed a lot of labeled data to train on, especially for challenging tasks like accurately segmenting brain tumors.

Metlek and Çetiner [19] implemented a ResUNet+ method, which was a convolution-based hybrid model, for the segmentation of brain tumors. BraTS 20, 2019, and 2018 datasets were utilized to evaluate the implemented ResUNet+ method. A hybrid method based on the residual block was implemented to address the semantic gap in UNet models and increase performance in fine-detail images. But the requirement of increased number of labeled data for training, made it more difficult to accurately segment the brain tumors.

Sahoo et al. [20] implemented Fast Fuzzy C-means (FFCM), which was a hybrid deep neural network method utilized for multimodal brain tumor segmentation. This method combined the benefits of inception v2 and the Fast fuzzy C-means models for edema, tumor core, and whole segmentation. The implemented method had the potential to improve patient outcomes while also lowering the likelihood of undesirable side effects. Meanwhile it was also challenging to train and verify the models due to limited quantity of currently accessible datasets.

Islam et al. [21] implemented superpixels, PCA, and TK-means clustering schemes that improved the detection of brain tumors to aid in the timely treatment. Brain tumors were detected accurately using image enhancement, graph-based, clustering, and region-growing methods. The extraction of features for detection and segmentation was done using both PCA, and TK-means. In the detection of brain tumors in MR images, the implemented superpixels,

PCA, and TK-means detection scheme achieved a higher accuracy and a shorter execution time (in seconds). However, PCA lowered the dimensionality of the data, hence, this resulted in the loss of delicate traits that were crucial for extraction and tumor detection.

Deepak and Ameer [22] implemented a fully automatic classifier for MRI scans of brain tumors. A combination of CNN with a support vector machine (SVM) was designed for medical image classification. Figshare open dataset, which included MRI images of the three different forms of brain tumors, was used to assess the completely automated system. Compared to CNN with a softmax classifier, the implemented CNN-SVM configuration yielded better classification results. However, the issue with CNN was the extensive training period that must be completed before feature extraction. Hence, the technique needed intense customization and strong memory.

These existing approaches have various applications and also suffer from some limitations that are mentioned above

such as the lengthy training procedure, the computationally expensive operations, and the need for a lot of labeled data. Concerns about privacy, accessibility, and expert inputs are also not addressed, making these approaches unsuitable for real-time applications. To overcome these issues, a combination of convolutional and RELU optimization approaches with deep learning models are implemented to detect brain tumors effectively using MRI images.

3. Methodology

The implemented method is utilized to solve the issue regarding large requirement of labeled data for the training, privacy issues. It was also difficult to compile a dataset having a significant range of MRI brain tumor images. Fig. 1 shows a CNN structure overview. Convolutional layers, pooling layers (such as max pooling), and fully connected (FC) layers are some of the building pieces that make up a CNN.
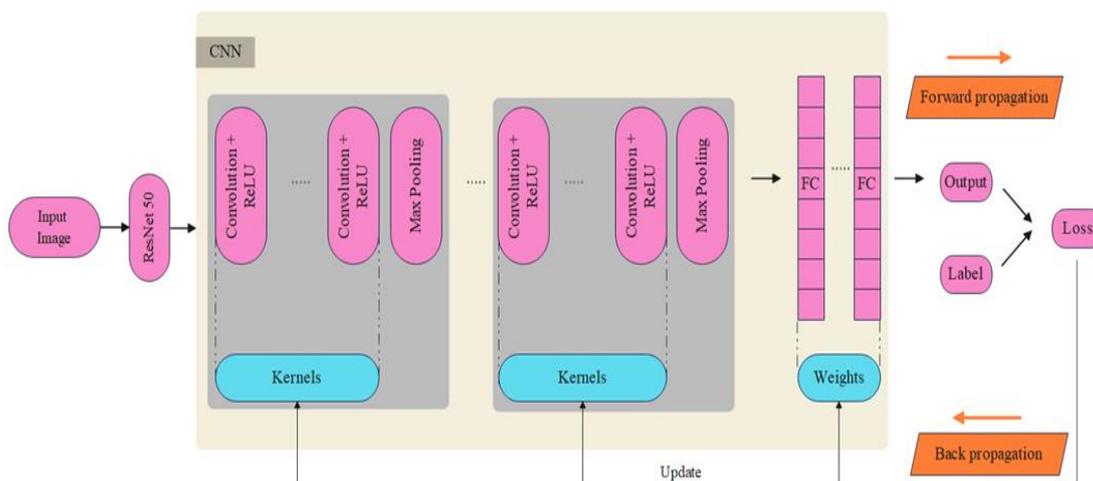

Fig. 1. CNN structure overview

Forward propagation on a training dataset is used to calculate a model's performance for specific kernels and weights. The backpropagation with the inclination drop enhancement method is used to update learnable parameters, such as kernels and weights, by the loss value of the rectified linear unit (ReLU). Layers for classification, convolutional, pooling, fully linked, and input are combined to form a CNN.

Pooling layers, convolutional layers, and fully linked layers are some of the structural components of CNN architecture. Through the process of forward propagation, data is transformed into output through these levels, and backpropagation is utilized to train neural networks using gradient descent optimization and the loss function as is seen in Fig. 1.

3.1. Dataset

This study evaluates the implemented network's

performance using the BraTS 2020 dataset [23]. Multi-modal brain MRI investigations consist of 369 training, 125 validation, and 169 test trials. Each research includes T1-weighted (T1), T2-weighted (T2), fluid-attenuated inversion recovery (Flair), and post-contrast T1-weighted (T1ce) sequences. Each MR image is the same size of $240 \times 240 \times 155$. Each study's necrotic and non-enhancing tumor core (NET), as well as the enhancing tumor (ET), and peritumoral edema (ED), were also explained by specialists. Although the annotations for validation and test trails are kept confidential, these are available for public use in online evaluation as well as for final segmentation competitions.

3.2. ResNet50

To help in the early diagnosis of tumors, it is advisable to utilize ResNet50 (residual CNN with 50 layers) to classify the tumor regions in the brain scans. In this regard, the effective ResNet50 CNN uses a learning technique to

adjust the network's parameters and hyperparameters. To perform this, a ResNet50 model is built using pre-set parameters using the collected dataset (pictures of brain tumors). This is carried out using MATLAB.

- The first layer uses convolution with a kernel size of 7x7 and 64 different kernels, each with a stride size of 2.

- Following that, there is max-pooling with a stride length of 2.

- The next convolution has three sizes: 1×1 with 64 kernels, 3×3 with 256 kernels, and finally 1×1 with 256 kernels. Nine layers are created in this stage by repeating these three layers three times.

- There are then 512 kernels of size 1×1, 128 kernels of size 3×3, and 128 kernels of size 1×1. To create 12 layers, this phase is completed throughout four epochs.

- 256 kernels of size 1×1, then 256 kernels of size 3×3, and 1024 kernels of size 1×1 are used in this following stage leading to 18 layers.

3.3. Convolutional Neural Network (CNN)

Convolutional or CNN-based deep neural networks contain some linear or mathematical processes known as "convolution." CNN often employs pooling layers that dynamically adjust to the size of features, facilitating better preservation of spatial information in brain tumor images, as compared to ResNet 50. An architecture of various levels, that include several pooling layers, hidden layers, output layers, and fully connected layers (FC), is a convolutional neural network (CNN). An array of these hidden layers with filter (kernels) of convolutional layers execute an image analysis operation aimed to determine the illnesses of patients. Spatial size representation and hyperparameters are decreased by the pooling layer. CNN is a type of artificial neural network that identifies MRI brain pictures without the need for manual feature extraction. ReLU is frequently used in CNNs instead of other activation functions like sigmoid and tanh, because of better performance and computational efficiency. ReLU regularly performs better than alternative means, in terms of training speed and model accuracy. The network also includes segments that have been activated by ReLU. The following (1) is the mathematical formula for ReLU,

$$f(y) = max(0, y) \qquad (1)$$

By accelerating the training period, the ReLU significantly contributes to the advancement of neural networks. Additionally, ReLU's computational procedures are easy and simple because the training dataset does not contain any division, multiplication, or exponential, and negative values are set to zero. To avoid overfitting, the input MRI pictures are downsized to 256×256. In CNN models, feature extraction and dimension reduction are carried out

via a sequence of layers with filters. The retrieved characteristics are subjected to a nonlinear transformation using the FC layer, which also functions as a classifier to analyze the image and provide the desired output of proper categorization of the required brain tumor regions. The fully connected layers of CNN are used to extract the feature vectors, and then for classification 1000 units of input softmax layer are supplied. The function of softmax activation is mathematically expressed in (2),

$$\sigma(z)_i = \frac{e^{z_i}}{\sum_{j=1}^{K} e^{z_j}} \qquad (2)$$

Where, a normalization term is applied to produce the proper probability distribution denoted as $\sum e^{z_j}$, z_i implies the function of standard exponential denoted as e^{z_i}, either $-$ negative or $+$ positive values taken for the input vector of ith term denoted as z_i, the input vector for the softmax function has n features of n target values denoted as z.

The following formula is used to calculate the proximity between the desired and actual output using Softmax's cross-entropy loss function, as represented in the below (3),

$$L = \sum_{j}^{J} y_j log\sigma(z)_i \qquad (3)$$

Where y_j denotes the real tag. The loss function for the classification shows the difference between the expected and actual results. The network's training procedure is considered as a parameter optimization procedure, which detects a set of ideal solutions in the parameter space to minimize L. A cross-entropy loss is used and the majority class is assessed, resulting in an imbalance of data.

3.4. Convolutional operation

Convolution is a particular type of linear operation used for feature extraction which applies a small array of numbers known as a kernel, across the input, which is an array of numbers known as a tensor. At each location of the input tensor, the element-wise product is computed between each element of the kernel and the corresponding element of the input tensor. This product is also known as the output value in the corresponding location of the output tensor. Multiple kernels are applied repeatedly during this process to create a feature map with arbitrary numbers that represent various properties of the input tensor; as a result, different kernels can be viewed as different feature extractions.

The kernel's number and size are two important hyperparameters that specify the convolution procedure. The former is typically 3×3, occasionally 5×5 or 7×7. The arbitrary is the latter and controls the depth of the feature maps that are the output. The implemented model's convolutional operation is in charge of extracting information from the MRI picture, which is a crucial

component. The anticipated features are sufficient to carry out a trustworthy training procedure. The input picture is used as the input vector for the first convolution layer, and the previous layers of the feature maps are used as the input vector for the remaining convolution layers. Equations (4) and (5) are used to perform convolution operations,

$$RELU(x) = \begin{cases} x, & if\ x > 0 \\ 0, & otherwise \end{cases}$$

(4)

Where the RELU's input is denoted as x, and the activation function of the rectified linear unit is denoted as $RELU$.

$$C_r^T = RELU\left(\sum_{y=1}^{N}\sum_{u=-x}^{X}\sum_{v=-x}^{X} P_y^{T-1}(i-u, j-v). K_{y,r}^T(u,v) + B_r^T\right)$$

(5)

Where the layer index is represented as T; the input vector of feature maps number is represented as N; the previous layer and the current layer of feature map indices are represented as y and r; at first the previous layer of T layer of feature maps vector is represented as P_y^{T-1}, and the image vector input is represented as P_y^0; the filter size and basis are represented as X and B; the kernel matrix is represented as K; and the kernel values indices are represented as u and v respectively.

3.5. Pooling layer

Translation invariance aims to introduce tiny shifting distortions and limit the number of future learnable parameters, while the pooling layer offers a convolutional operation of downsampling that lowers the dimensionality in the plane of the feature maps. Notably, it is important to understand that pooling layers do not possess any learnable parameters. However, pooling operations, akin to convolution processes, involve hyperparameters such as stride, filter size, and padding.

3.5.1. Max Pooling

The most popular kind of pooling operation is max pooling, wherein patches are taken from the input feature maps, and only the greatest value in each match is produced as output, with the remaining values being ignored. In practice, a max pooling with the size of the filter as 2×2 and a stride as 2 is usually utilized. Dimension of feature maps in-plane is downsampled by a 2-in factor, in this case. The dimension of feature maps' depth does not vary, unlike height and width.

3.6. Fully Connected layer

Usually, the output of the final convolutional or pooling feature map layers is flattened or transformed into a 1D (one-dimensional) list of numerals (or vectors), and linked to several dense layers, also called fully connected layers, in which every input and output are linked by an attainable weight. The characteristics produced by the convolution layers and the downsampling layers are then mapped to the network's final output, such as the probabilities for each class in a categorization job, by a subset of fully connected layers. The final full layers are connected with the number of outcome nodes that normally equals the number of classes. A nonlinear function, like RELU, is placed after each fully connected layer.

3.7. Training a network

The process of training a network involves fully connected layers and convolutional layers of the kernel that reduce discrepancies among the predictions and outputs, while also providing training dataset for ground truth labels. When training neural networks, the backpropagation algorithm is frequently employed, and the gradient descent optimization technique and loss function also play vital roles. In a training dataset, a loss function determines the level to which the model performs with particular kernels and weights. Learnable parameters, such as kernels and weights, are then updated by the loss value using an optimization algorithm like backpropagation or gradient descent, among others as seen in Fig. 1.

3.7.1. Loss function

The output predictions among the compatibility calculated by the network using forward propagation and the provided truth labels are measured by a function loss, also known as a function cost. Cross entropy is a frequently used function loss for multiclass categorization, although mean squared error is commonly used for continuous values of regression. One of the hyperparameters that must be selected by the tasks provided is the kind of loss function.

3.7.2. Gradient descent

The learnable network parameters, such as the weights and kernels, are iteratively updated by the optimization algorithm known as gradient descent, that aims to reduce loss. The direction in which the loss function's rate of rise is steepest is indicated by its gradient, and every parameter is updated with a step size arbitrary depending on a hyperparameter termed learning rate (Fig. 2), moving in the opposite direction of the gradient. Concerning each learnable parameter, formally the gradient is the loss partial derivative, and a parameter's single update is expressed in (6) as follows:

$$w := w - \alpha^* \frac{\partial L}{\partial w}$$

(6)

Where the loss function is represented as L; the learning rate is represented as α; and every learnable parameter is
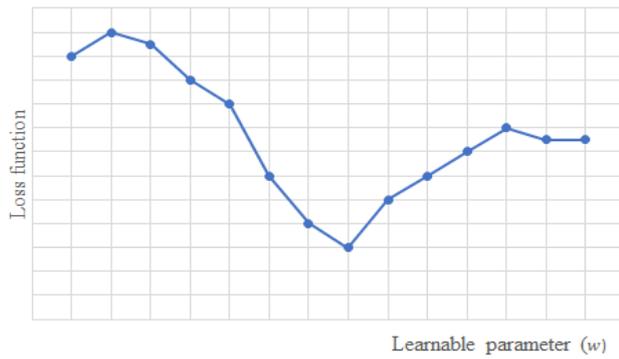
represented as w.

Fig. 2. Graphical representations of gradient descent

In Fig. 2, Gradient Descent is depicted as an optimization algorithm that efficiently minimizes the loss by iteratively adjusting the learnable parameters. The loss function quantifies the disparity between the predicted output and the true label. The direction in which the function increases at the sharpest rate is indicated by the loss function's gradient, and a learning rate-based step size is used to update all parameters in the gradient's negative direction.

4. Result

4.1. Experiment analysis

In this experiment, Anaconda Navigator 3.5.2.0 and Python 3.7 are used to simulate the CNN model of the RELU activation function. The following are the system requirements for the proposed research project: Intel Core i9 processor, 2 TB hard drive, Windows 10 (64-bit) operating system, and 16 GB of RAM. To be able to verify the usefulness of the implemented model on the dataset of BRATS 2020, the execution of the implemented CNN model of convolution+RELU activation function is related to MMRE and TL AI.

4.2. Evaluation parameters

The effectiveness of the implemented model is examined here in precision, recall f-measure, accuracy and dice are represented as follows in (7) to (11),

$$Precision = \frac{TP}{(TP+FP)} \qquad (7)$$

$$Recall = \frac{TP}{(TP+FN)} \qquad (8)$$

$$F-measure = \frac{(2*Precision*Recall)}{(Precisioon+Recall)} \qquad (9)$$

$$Accuracy = \frac{TP+TN}{(TP+TN+FP+FN)} \qquad (10)$$

$$Dice\ (P,T) = \frac{|P1^{\wedge}T1|}{(|P1|+|T1|)/2} \qquad (11)$$

Where, $P1$ refers to the segmented tumor area for each cancer location according to the implemented approach, and $T1$ refers to the real tumor area in the ground truth.

4.3. Quantitative investigation

This research uses BraTS 2020 dataset to validate the performance of the presented convolution+RELU activation, in terms of various training and testing combination ratios.

The implemented model achieved successful performance in the categorization of brain tumors in terms of precision as inferred from Table 1. In comparison to Recurrent Neural Network (RNN), the implemented convolution+RELU activation function CNN model gains a higher average precision of 99.8 %.

The implemented CNN model of the convolution+RELU activation function is examined with respect to recall in Table 2. The average value of recall for the 80:20 combination, attained by the proposed CNN model of the convolution+RELU activation function, is estimated at 99 %, which is much better than the average recalls achieved by the other comparable models. So, according to test results, utilizing the CNN model of the convolution+RELU activation function increases multiclass classification performance.

Table 1. The implemented model through precision performance analysis

Precision (%)							
Training and Testing ratio	Class	CNN			RNN		
		Sigmoid	tanh	Convolution+RELU	Sigmoid	tanh	Convolution+RELU
0.8888889	Glioma	93	94	95	94	93	95
	Meningioma	94	93	95	93	92	94
	Pituitary	94	94	94	93	94	95
	Mean	93.6	93.6	94.6	93.3	93	94.6
40:60	Glioma	96	95	97	95	96	96
	Meningioma	95	96	99	96	95	97
	Pituitary	95	94	97	95	96	97

Training and Testing ratio	Class	Sigmoid	tanh	Convolution+RELU	Sigmoid	tanh	Convolution+RELU
	Mean	95.3	95	97.6	95.3	95.6	96.6
60:40:00	Glioma	97	98	99.6	98	98	98.7
	Meningioma	96	98	99	98	98	98.7
	Pituitary	97	98	99	98	99	98.7
	Mean	96.6	98	99.2	98	98.3	98.7
	Glioma	98	99	99.8	99	98.5	98.3
80:20:00	Meningioma	99	99	100	98	97.4	99.8
	Pituitary	98	98	99.7	99	99	99
	Mean	98.3	98.6	99.8	98.6	98	99.1

Table 2. The implemented model employing recall performance analysis

Recall (%)

Training and Testing ratio	Class	CNN			RNN		
		Sigmoid	tanh	Convolution+RELU	Sigmoid	tanh	Convolution+RELU
20:80	Glioma	93	92	94	94	93	95
	Meningioma	94	93	95	95	94	95
	Pituitary	93	94	94	94	93	95
	Mean	93.3	93	94.3	94.3	93.3	95
40:60	Glioma	97	96	98	96	95	96
	Meningioma	96	95	98	97	94	97
	Pituitary	95	95	99	95	97	97
	Mean	96	95.3	98.3	96	95.3	96.6
60:40	Glioma	98	97	99	98	98	98.7
	Meningioma	95	98	97	98	98	98.7
	Pituitary	97	99	98	98	99	98.7
	Mean	96.6	98	99	98	98.3	98.7
80:20	Glioma	98	99	99	98.9	98.5	98.3
	Meningioma	99	99	99	98.6	99	98.3
	Pituitary	98	98	99	99.2	99	99.2
	Mean	98.3	98.6	99	98.9	98.3	98.6

When compared to alternative combinations, the implemented CNN model of convolution+RELU activation function with 80% and 20% of training and testing produced a better f-measure value of 99.3% as shown in Table 3. The implemented model achieved greater performances in the BRATS 2020 dataset, without the requirement of any manual segmentation, as opposed to the other models.

Table 3. The implemented model utilizing f-measure performance analysis

F-measure (%)

Training and Testing ratio	Class	CNN			RNN		
		Sigmoid	tanh	Convolution+RELU	Sigmoid	tanh	Convolution+RELU
0.8888889	Glioma	94	95	95	94	95	95
	Meningioma	93	94	93	93	92	93
	Pituitary	94	93	94	93	94	95
	Mean	93.6	94	94	93.3	93.6	94.3
40:60	Glioma	97	96	98	95	96	98
	Meningioma	96	96	97	96	95	95
	Pituitary	96	95	99	95	96	96
	Mean	96.3	95.6	98	95.3	95.6	96.3
60:40:00	Glioma	96	97	98	98	98	98

80:20:00	Class							
	Meningioma	98	99	96	98	98	96
	Pituitary	95	97	99	98	99	97
	Mean	96.3	97.9	97.6	98	98.3	97
	Glioma	96	99	99	99	98.5	98.5
	Meningioma	99.5	99	99.5	98	99	98.5
	Pituitary	99	98	99.5	99.2	99	99.2
	Mean	98.1	98.6	99.3	98.7	98.3	98.7

Table 4 analyses performance of the CNN model with convolution+RELU activation function in terms of classification accuracy using various testing and training percentages. By analyzing Table 4, the implemented model attained average classification accuracy of 99.8% in the 80:20 combination. The number of hidden neurons is carefully chosen by the CNN of the convolution+RELU activation function, which helps in the elimination of overfitting issues to produce better classification results and to speed up learning.

Table 4. The implemented model uses accuracy performance analysis

Accuracy (%)

Training and Testing ratio	Class	CNN			RNN		
		Sigmoid	tanh	Convolution+RELU	Sigmoid	tanh	Convolution+RELU
20:80	Glioma	93	94	95	94	95	95
	Meningioma	94	94	95	94	94	95
	Pituitary	93	93	94	95	94	94
	Mean	93.3	93.6	94.6	94.3	94.3	94.6
40:60	Glioma	97	97	99	97	98	99
	Meningioma	97	98	99.8	98	97	99.3
	Pituitary	98	97	99	98	98	98.6
	Mean	97.3	97.3	99.2	97.6	97.6	98.9
60:40	Glioma	98	99	99.7	99	99.3	99.4
	Meningioma	98	98	99	98	98.6	98
	Pituitary	97	98	99	99	98.8	99
	Mean	97.6	98.3	99.2	98.6	98.9	98.8
80:20	Glioma	98	99	99.8	99	98.3	99
	Meningioma	98	99	99.5	98	99	98.3
	Pituitary	99	98	99.7	99	98.3	98.3
	Mean	98.3	98.6	99.8	98.6	98.5	98.5

4.4. Comparative analysis

In this section, the existing and implemented models' comparative analysis is shown in Table 5. This framework for brain tumor image analysis using Convolution with RELU as the implemented method has proven to be significantly accurate gaining a high classification rate, making it a suitable choice for trustworthy classification, as it correctly detected the brain tumors using BraTS 2020 datasets. Compared with the other existing methods, the implemented method of Convolution+RELU using BraTS 2020 datasets achieves a higher classification accuracy at 99.8%.

Table 5. The existing and implemented models' comparative analysis

Study	Methodologies	Dataset	Classification accuracy
Chattopadhyay & Maitra [17]	CNN		99.74
Metlek & Çetiner [19]	ResUNet+	BraTS 2020	98.26
Sahoo et al. [20]	FFCM		99.63
Proposed method	Convolution+RELU		99.80%

5. Conclusion

This paper implements a Convolution+RELU deep learning-based methodology to enhance the categorization of brain tumor image analysis. In the beginning, the brain scans that are gathered from the BraTS 2020 dataset and are given a higher visibility level by using the normalization procedure. The fixed feature extractor is then used for the feature vectors extracted from the normalized pictures. CNN often employs pooling layers that dynamically adjust to the size of features, facilitating better preservation of spatial information in brain tumor images, as compared to ResNet 50. Meningiomas, pituitary, and glioma tumors are classified by a CNN classifier of convolution+RELU activation function utilizing the retrieved feature vectors. ReLU is known to be a successfully proven function that requires less computing power, and is lately being used as the standard activation function in CNN systems. The implemented model is examined in the experimental phase for precision, recall, f-measure, and accuracy. In comparison to the competing existing models, the implemented CNN model of convolution+RELU activation function delivered better performances in classifying brain tumors, by demonstrating a 99.8% accuracy rate. In the future, this research work may be extended to analyze high-dimension features extracted from real clinical MR images, to improve the detection system.

Author contributions

Pallavi Hallappanavar Basavaraja: Conceptualization, Methodology, Visualization, Software, Field study, Investigation **Nandeeswar Sampigehalli Basavaraju:** Data curation, Writing-Original draft preparation, Software, Validation, Field study, Writing-Reviewing and Editing.

Conflicts of interest

The authors declare no conflicts of interest.

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