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Deep Learning-Based Multi-Layers Brain Tumor Detection and Classification from MRI Images

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ABSTRACT

Background: According to American Cancer Society, brain tumor represents a highly feared disease in medical science, and it is among the most prevalent malignant tumors to be detected in people of different ages. Treatment of brain tumors requires early and accurate detection of the disease. Methodology: With using machine learning and deep features classifiers, this paper describes the classification of brain tumors. Using a set of pre-trained deep convolutional neural networks (DCNNs), deep features were extracted from a collection of brain magnetic resonance imaging (MR) images by incorporating the concept of translational learning (TL) into our proposed framework. After that, a number of machine learning (ML) classifiers assess the deep features that were recovered. Deep features are used for defining and sequencing several ML feature classifiers. For the prediction of final output, these are after that input into a number of ML classifiers. In this study, Three publicly available brain MRI datasets were used to evaluate the effectiveness of different types of pre-trained models, including machine learning classifiers and deep feature extractors, in classifying brain tumors.Results: The experimental results show that deep feature extractors significantly improved performance levels, and in most cases, a convolutional neural network (CNN) was used. This study achieved an accuracy of 0.98% and an accuracy of 0.99% for the valves.

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1. INTRODUCTION

The brain is one of the most vital organs in the body because it contains billions of cells. Uncontrolled cell division leads to the formation of an abnormal group of cells known as a tumor. Tumors are classified into two main categories: high-grade tumors (grades III and IV) and low-grade tumors (grades I and II).Brain tumors with a low grade are considered benign. The term "malignant" is used to describe high grade tumors. Non-malignant is a benign tumor. As a result, it stays in one area of the brain [1].On the other hand, the malignant tumor is cancerous. As a result, it easily and quickly spreads and without end to other bodily parts. It results in instantaneous death [2][3].

Medical specialists nowadays are presented with a plethora of diverse data. Their capability for gathering, processing, and analyzing such vast volumes of data is limited. They become easily fatigued, which hinders their capacity to assist patients in taking charge of their health. Ninety percent of data in the healthcare industry is images, which need to be analyzed to generate treatment plans and other purposes. Because of this, there is a growing market for medical image analysis, which presents many opportunities for developing cutting-edge IT-based healthcare solutions [4].Depending on how aggressive they are, brain tumours could be classified as non-cancerous or malignant. A secondary or primary tumor could be the brain tumor source. The etiology of tumor dictates this classification. Tumors of low grade are categorized as "Grades 1 and 2," while tumors of high grade are categorized as "Grades 3 and 4." [3]. These supplement the 120 distinct categories of brain tumors that the WHO has identified[4]. The imaging of brain tumors is an important topic of medical imaging research [5]. Metastatic brain tumors, which spread from other parts of the body to the brain, and primary brain tumors, which originate in the brain or brain tissue, are two types of brain cancer. The most common primary brain tumors in adults are central nervous system lymphomas and gliomas; the latter account for at least 80% of all malignant brain tumors. Magnetic resonance imaging (MRI) mimics the effects of a strong magnetic field by using radio waves and frequencies to create an internal image of the target tissue. Its advantages include soft tissue contrast and the absence of ionizing radiation exposure. Consequently, MRI is more effective at identifying brain lesions [6]. With promising outcomes, deep learning (DL) can significantly impact medical picture segmentation and classification. It boosts the automation of diagnosis based on non-invasive imaging. Interestingly, medical image processing advances have previously been effectively leveraged for computer-assisted brain tumor detection, opening up a wide range of potential research activities in DL to develop fully automated, accurate, and automatic diagnostic tools for clinicians [7]. One type of DL methods for classifying, identifying, and diagnosing brain cancers is the CNN-based models. Because CNN models are of a high accuracy rate, they are frequently utilized for image data. Comparable to a hierarchical model of various architecture kinds, a CNN architecture learns about images fundamentally through training [8]. CNN-based multiclassification as well as brain tumor detection have been the subject of numerous studies [5]. Meningioma, glioma, pituitary tumor, and no tumor have been the four brain tumor types classified in the presented work, and the sensitivity, accuracy, and precision values are excellent.

2. Related Work

The classification regarding a brain tumor has been the subject of several investigations. We examine the relevant studies in this part. An up to 95% success rate was attained in a study [9] that classified MRI images of pancreatic tumors using CNNs. CNN obtained effective results in recognizing various forms of high-grade tumors by utilizing the large dataset to train the model. Even with small amount of the training data, TL could increase the classification accuracy regarding MRI images of brain tumors, as demonstrated by the study [4]. 92% classification accuracy was achieved by using a pre-trained model on a small brain tumor data-set after it was updated for usage on a larger dataset. The DL methods for medical image segmentation, which include MRI images of brain tumors, were thoroughly examined in study [10]. According to the study, cutting-edge technologies like U-Net and SegNet perform exceptionally well at segmenting tumors with high cell accuracy, which makes treatment and diagnosis simpler. In this work [11], brain tumors were automatically detected and classified using ML techniques. 90% classification accuracy was attained by the employed algorithms, which included SVM and Random Forest (RF), which demonstrating the considerable promise of ML approaches for raising the accuracy of medical diagnosis. Classifying MRI images of brain tumors was one of the DL applications in medical imaging that were explored in a study [12]. The researcher discussed the drawbacks of applying DL in this domain, including the requirement for large amounts of training data and data processing, and illustrated the potential benefits of doing so, including increased efficiency and accuracy in medical diagnosis. In traditional machine learning methods, feature extraction is a critical step because classification accuracy depends on the retrieved features. Feature extraction falls into two primary types, which are Low-level (i.e., global) features, like intensity and features of texture, 1st-order statistics (like mean, skewness, and standard deviation), Examples of the first kind of feature extraction include 2nd-order statistics such as wavelet transform (WT), gray-level co-occurrence matrix (GLCM), Gabor features, and shape. Selvaraj et al. used these techniques to distinguish between normal and aberrant brain MRIs. [9] developed a binary classifier with the use of a least square SVM with first- and second-order statistics. John et al. [13] have utilized DWT and GLCM-based tumor detection as well as classification methods. While low-level features successfully capture the image, they are limited in their capability to do so because the majority of brain tumor types have similar boundaries, shapes, textures, and sizes. Ullah et al. [6] using DWT for extracting the approximation as well as detail coefficient regarding level-3 decomposition, lowered the coefficient through applying CM (i.e., color moments), and after that utilized a feed-forward ANN in order to discriminate between normal and aberrant brain MRIs. The second feature extraction type (BoW) consists of high-level (local) features, including scale-invariant feature transformation (SIFT), Fisher vector (FV), and bag-of-words. BoW has been used by numerous researchers in order to classify and retrieve medical images. Examples include the retrieval and classification of X-ray images according to organ levels and disease [8], the retrieval of brain tumor content [14], and breast tissue density classification in mammograms [15]. Cheng *etal*. [16] extracted the brain tumor using FV. Statistical features that have been obtained from SIFT, BoW, and FV are high-level features produced locally without considering spatial information. As a result, it is clear that the feature extraction phase of traditional ML has two primary problems. It just looks at traits that fall into one of two categories, which are: high- or low-level. Second, because the traditional approach of Machine Learning depends upon handcrafted features requiring significant prior knowledge—like tumor position or location in an image—there is a high chance of human error. Which is why, A method for developing a combination of low-level and high-level features that eliminates the need for manual feature development. After such tumors are segmented in an MRI, they must be rated differently. Previous research has employed binary classifiers to differentiate between malignant and benign classifications [6][17][18][19]. Ulah *etal.* [6]vv suggested a hybrid system that classifies brain MR images to normal and pathological categories using a feed-forward ANN, histogram equalization, and discrete wavelet transform. Kharrat et al. [17] identify brain tumors as abnormal or benign using a genetic algorithm and SVM. Additionally, Pappageorgiou *etal.* [19] Fuzzy knowledge maps were used to classify gliomas with an accuracy of 93.22% and 90.26% for high-grade and low-grade brain tumors, respectively Kumar and Shree [20][21] classified brain MRIs as pathological and normal. They utilized GLCM for the extraction of features and a probabilistic NN (PNN) classifier for the classification of brain MRIs to normal and pathological categories with 95% accuracy. Savarimuthu & Arunachalam [2] suggested a technique for using brain MR images to determine if brain tumors are abnormal or normal. They integrated feature extraction, classification, transformation, and augmentation in their proposed model. First, they used shift-invariant shearlet transform (SIST) to improve the brain MR image. The features were then obtained by using the DWT, Gabor, and grey level co-occurrence matrix (GLCM). Through feeding such collected properties into a feed-forward backpropagation NN, a high accuracy rate was achieved. A hybrid energy-efficient approach for the automated segmentation as well as identification of tumors was suggested by Sundar and Rajan [22][23]. Their suggested approach consists of seven drawn-out steps and has an accuracy rating of 98 percent. The primary issue of their proposed model is the long computation time that comes from using several techniques. Over the past decade, DL methods were widely utilized for the categorization of the brain MRI [24][25]. The DL approach incorporates steps of feature extraction and classification into self-learning, eliminating the requirement for manually created sensors (2021, 21, 2222, 5 of 21 extracted features). Before significant characteristics are found by self-learning, DL needs a data-set, for which there might often be a pre-processing step [26]. Reducing the semantic gap between high-level visual information seen by a human assessor and low-level visual information gathered by an MRI machine is one of the primary issues in MR imaging categorization. One popular DL technique for image data, CNNs, can be utilized as a tool for feature extraction to collect relevant characteristics that are needed for classification in order to close the semantic gap. Low-level features are extracted via feature maps found in the CNN model's bottom layers, whereas higher layers extract high-level features specific to the content (domain). Those low-level features are used by higher layers to create (encode) effective representations that combine global and local data. In the layer above, feature maps create basic structural elements like texturing, edges, and shape. A number of groups have lately validated their proposed techniques with CNNs for the brain classification MRIs and brain tumor datasets classification [27]. Ameer and Deepak used deep CNN and a pre-trained GoogLe-Net to extract characteristics from brain MR images [28] were able to classify 3 distinct brain tumour types with a 98% accuracy. Muhammad & Ahmet [29] have used a variety of CNN models, like Inception V3, AlexNet, DenseNet201, GoogLe-Net, and ResNet50, in order to correctly categorize brain MR pictures. They were able to attain the highest accuracy regarding any pre-trained model, 97.2%, by adding eight more layers and removing the final five levels of the pretrained ResNet50 CNN model. Khwaldeh *etal.* [30] The CNN model was introduced to classify brain MRI images into normal and pathological categories and high- and low-grade gliomas. By modifying the AlexNet CNN model and using it as the basis for their network model, they have been able to attain 91% accuracy. In spite of the significant research being conducted in this area, more work needs to be done for the purpose of developing a useful and reliable approach for classifying brain MR images. ResNet50, Beginning V3, and VGG16 models were employed to categorize the brain tumor data with the use of TL approaches through Saxena et al. [31]. ResNet50 model achieved the optimal rate with and accuracy of 95%. In the researches, brain cancers were categorized using CNN architectures [32][33]. These designs use a CNN to retrieve features from brain MRIs. Finding the best DL imaging model for accurately classifying brain MRI is the primary objective of these proposed models. Francisco et al. [34] reported on the automated segmentation regarding brain tumors, such as meningioma, pituitary, and glioma, using a multi-pathway CNN architecture. They have conducted an evaluation of their suggested model on public T1-weighted contrast-enhanced MRI data-set and were able to obtain an accuracy level of 97.30%. None-the-less, their program of training is highly expensive. Rajas *etal.* [35] To classify brain tumors using Bayesian fuzzy clustering (BFC), they therefore proposed a hybrid deep autocoding (DAE).

At first, to remove noise from the images, they tried using a non-local intermediate filter. Thereafter, the have utilized BFC approach in order to segment brain tumours. Furthermore, we have discovered a number of resilient properties (WPTE) by using information-theoretic metrics, wavelet packet Tsallis entropy, and scattering transform (ST). Cell tumors are ultimately classified using a hybrid DAE method, which has demonstrated exceptional accuracy. Because the complex model has become the primary problem, it necessitates a significant amount of computation time. The study results presented above demonstrate that DL methods produce significantly greater acquired accuracies for brain MRI classification compared to standard ML methods. DL models need large amounts of data for training for the purpose of outperforming traditional ML methods. The use of DL techniques in intelligent and expert systems as well as medical image analyses had been clearly clear in recent studies. It is essential to be aware of the limitations of the methods mentioned when working with brain tumor segmentation and classification. The primary shortcoming of previously proposed approaches is that they just consider binary classification (i.e., abnormal as well as normal) MRI datasets, ignoring multi-class data-set [29]. Throughout pre-screening phase of patient's care, radiologists and doctors must classify patients into binary groups (Sensors 2021, 21, 2222 6 of 21). The clinicians then base their subsequent decisions on this classification. The idea proposed by Aishwarya and Preethi [38] employs multiple phases for classification of brain tumor types. They have used wavelet-based GLCM to generate feature matrix. To further reduce obtained attributes, an oppositional flower pollination algorithm was applied (OFPA). A DNN finally classifies the MR brain image with 92% accuracy with the use of chosen parameters.

3. Methodology

The suggested system architecture is divided into multiple steps. This technique involves the following steps: gathering a data set in step one; pre-treatment in step two; model creation and training in step three; and model evaluation with the use of outcome measures in step four. The suggested method's structure has been depicted in Figure1.

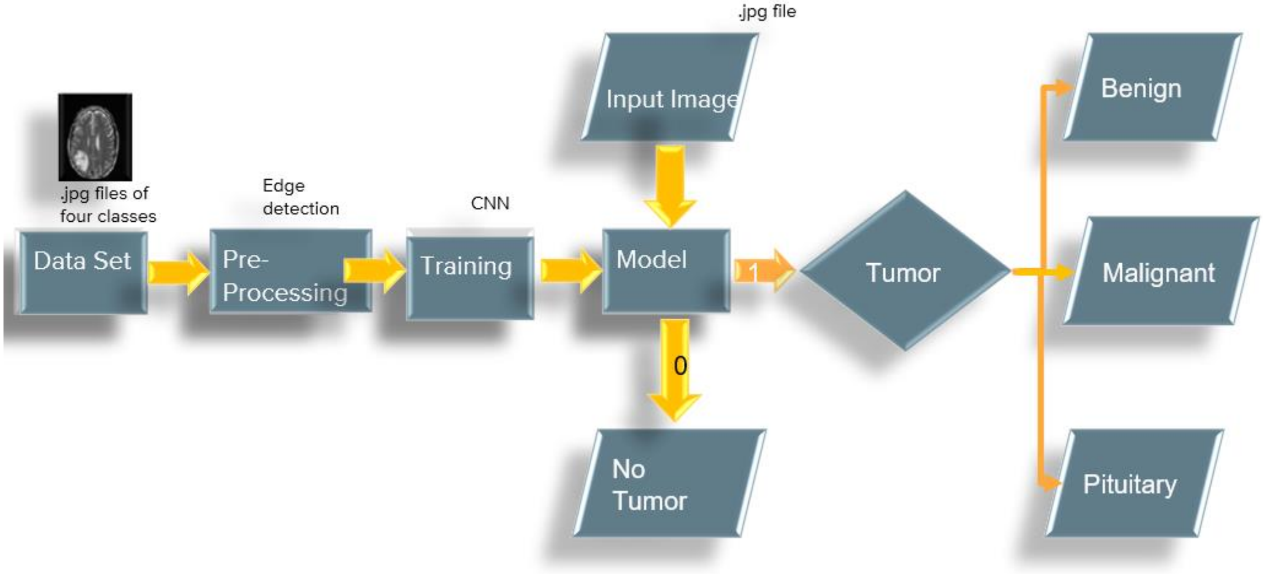

Figure1. Diagram of proposal method of brain tumor (MRI).

3.1Data Collection

Getting image dataset ready for network training is the first step in creating an image classification network. This stage is critical to the process as a whole. Using online resources is one way to collect data for picture classification. Kegel data set, which could be seen from this link: https://www.kaggle.com/datasets/sartajbhuvaji/brain-tumor-classification-mri, was used in this instance. The 7022 MRI images of human brain in the data-set have been categorized to four groups, These include pituitary (300 photos), glioma (300 images), meningioma (306 images), and no tumor (405 images). To enable the suggested model to function on any image and from any side, each patient was photographed from a variety of perspectives, including the sides, top, and back. Fig 2 displays data models together with the four different types of tumors.

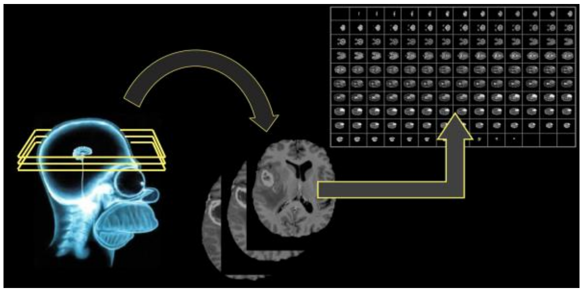

Figure2. Data Collection of Brain Tumor

3.2 Dataset Pre-processing

Data augmentation and pre-processing stages are very important before training operation. Augmented operation was done for expanding the sample size of the training using Keras data generator function by using horizontal flipping and rotating the image in 90 and 180 for augment the data and make normalization operation for images to adjust pixel values of an image in order to make it easier for a training model to learn from it.

3.3 Train Model

The presented work suggested pre-processing the data by training, classification of brain MRIs with using CNN for normalization and brightness enhancement. Fig2 depicts the proposed technique’s architecture.

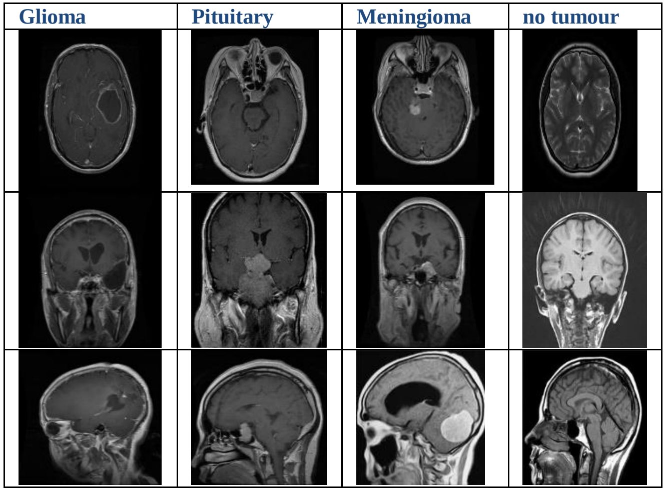

Figure 3. Sample of Dataset Brain Tumor

4. Experimental Results

The proposed method will be applied in several stages to detect diseases related to brain tumors; a detailed explanation will be provided later on. Brain Tumor classifier simulation in MATLAB offers a useful implementation guidance for development of a DL-based system for early brain tumor detection. It illustrates how CNN architecture could be trained and assessed on a large dataset and shows how efficient it is for classifying brain tumors. The simulation results indicate that DL-based algorithms for classifying brain tumors could detect the disease with a high degree of accuracy, which may find use in certain medical scenarios. An intriguing investigation into the potential uses of DL in biomedical applications is the Brain Tumor Classification Project. Utilizing the CNN architecture's capability and the dataset's abundance, the study offers a convincing illustration of how well DL works for classifying brain tumors. The project's outcomes show how effective is the CNN model performs in classification of brain tumor from images. High accuracy and efficiency are features of the system. The initiative also emphasizes the significance of thorough preprocessing of data as well as feature extraction in creating efficient algorithms for classifying brain tumors.

4.1. Evaluation Metrics

The metrics—like we use the accuracy, fine-tuning, F1 score, and reminders discussed in this section to evaluate the effectiveness of our rating grid. It is vital to assess the classification network's performance for the purpose of guaranteeing that the system correctly detects the disease in the image. Prior to listing the various assessment criteria, let us establish the following guidelines:

- TP: Images correctly categorized as normal are called true positivity.
- TN: Percentage of images that have been correctly identified as brain tumors is known as True Negative.
- FP: Images that are incorrectly classified as normal are known as the false positive rate.
- FN: The number of images that are misidentified as brain tumors is known as false negatives.

The following metrics could be utilized to assess this system's performance:

A. Accuracy

Accuracy is a common criterion for evaluating the performance of any classification network, so this is the percentage of images that the system successfully classifies. It is calculated by dividing the total number of samples by the number of correctly classified samples. The following formula can be used to determine accuracy: this system, encompassing:

$$Acc\% = \frac{TP+TN}{TP+TN+FP+FN} \times 100 \quad (5)$$

The rating system relies on accuracy to evaluate overall performance, but it can be misleading if there is an imbalance in the distribution of categories (for example, if one speaker's sample count is significantly higher than another's). Therefore, using other metrics, such as an F1 score, is more appropriate in this case.

B. Precision

The percentage of images represents the system's ability to identify them as normal, out of all the images that have been detected; it shows the accurate "positive" predictions. Any classification system's performance is measured using precision. We might use the next formula to get the precision:

$$Precision\% = \frac{TP}{TP+FP} \times 100 \quad (6)$$

Although precision is a valuable metric for assessing our classification network's overall performance, an unbalanced class distribution might cause precision to be misleading.

C. Recall

This shows what proportion of total number of images labeled as normal was correctly classified as normal, or the percentage of correctly identified images in the "positive" class. Any classification system's performance is measured using recall. We could use the next formula to determine recall:

$$Recall\% = \frac{TP}{TP+FN} \times 100 \quad (7)$$

Recall is a useful metric for the evaluation of performance of a classification system.

D. F1-score

The F1 score is a crucial indicator of model accuracy, as it combines the model's recall and accuracy rates. Accuracy is only reliable when classes are balanced—that is, when each class contains an equal number of samples. This metric is important because real-world datasets are often unbalanced, making its use essential. Ideally, there's a trade-off between accuracy and recall, so we need to maximize both recall and accuracy to classify images optimally. The F1 score is the score responsible for combining these two metrics. Maximizing the F1 score maximizes both recall and accuracy because it's the score that combines these two metrics. The harmonic means of the two metrics are used to compute the F1-score, and the next formula could be used to do so:

$$F1-score = \frac{2 \times Recall \times Precision}{Recall+Precision} \quad (8)$$

4.2. Train Model of CNN

CNN, which is explained below and contains eight important layers, will now extract the features. As shown in the tables below, each layer will be used once.

4.2.1. Convolution layer

The image size (padding) as well as filter size in this eight-filter layer are both 3 x 3. The default step value of 1 is appropriate as the filter action is 1 pixel. It is a component of the layer kernel, which is known as filter as well. Use a range of filters to extract distinct aspects from the source image and identify particular features or patterns. The filter is small enough to perform necessary calculations between filter and pixel values for extracting features while scanning the entire image. The layers that were initially hidden are used for the extraction of the simple as well as virtual attributes, includes edges that are oriented incorrectly. As we go further into the underlying levels of networks, attributes that need to be found and retrieved become increasingly complex, according to Table 1.

Table 4.1: Iteration of the Convolution layer

Iterations	Activation	Level of the Pyramid
1	13.240	1
2	19.465	1
3	30.248	1
4	86.844	1
5	138.573	1
6	144.125	1
7	177.693	1
8	196.736	1

4.2.2. Batch Normalization

Which refers to the Standardization of inputs to the layer for every one of the mini-batches. Table 2 shows that because of batch normalization, the process of learning is stabilized and the time of training for the deep network construction is significantly reduced.

Table 2: Iteration of the batch normalization

Iterations	Activation	Level of the Pyramid
1	0.001	1
2	0.456	1
3	0.764	1
4	0.922	1
5	0.987	1
6	1. 445	1
7	1. 095	1
8	1.134	1

4.2.3. ReLU layer

If the input value is not strictly proportionate to output value, the ReLU function has zero output. ReLU represents a linear function that has a number of the definitions. Due to its ease of training and often better output, it has become the standard activation function for a wide variety of NNs, as Table 3 illustrates.

Table 3: Iteration of ReLU

Iteration	Activation	Pyramid level
1	0.650	1
2	0.788	1
3	0.926	1
4	1.046	1
5	1.056	1
6	1.067	1
7	1.098	1
8	1.120	1

4.2.4. Max Pooling

While facilitating the use of several filters, pooling layer tries to decrease the size of the activation maps. Less time spent on calculations prevents models from becoming overweight. Use the two functions listed below to reduce the size of large arrays: The maximum value that may be calculated for each window should be found using the formula Max. Utilize the info from the solitary window to calculate an average. Medium: Max-pooling is still the most frequently utilized method. The main objective is to reduce the map's size by removing the activation map (or feature matrix) while maintaining larger values inside each window, as shown in Table 4.

Table4: Max-pooling Iteration

Iterations	Activation	Level of the Pyramid
1	0.846	1
2	1.370	1
3	1.551	1
4	1.548	1
5	1.693	1
6	1.067	1
7	1.891	1

8	1.843	1

4.2.5. Fully Connected

Table 5 shows that at the network layer, every one of the neurons in a layer is connected to every other neuron in the layer that is below it.

Table 5: Iteration of fully connected

Iteration	Activation	Pyramid level
1	0.35	1
2	2.25	1
3	3.69	1
4	5.08	1
5	6.18	1
6	7.32	1
7	8.92	1
8	9.29	1

4.2.6. Softmax layer

The SoftMax function increases a collection of K real values by 1, which can be used for the summation of a collection of real numbers. SoftMax might read negative, positive, 0, or more input data as probability values by converting it into values in the range of 0 to 1. SoftMax can handle little or negative inputs in 2 ways, which are: high probability or low probability. A probability between 0 and 1 will be produced by any negative or small input. The results are displayed in Table 6.

Table 6: Iteration of Softmax

Iteration	Activation	Pyramid level
1	0.25	1
2	0.67	1
3	0.95	1
4	0.97	1
5	0.99	1
6	1	1
7	1	1
8	1	1

4.2.7. Classification using CNN

The number of features will be lowered by computing the mean and standard deviation following extracting the features from CNN via a series of layers since they vary from one picture to the next. CNN and summarizing calculations of the traits to categorize whether or not a person has Brain Tumor illnesses are also used[9].

Table 7: Architecture Overview of the Deep Learning Model for Multi-Class Brain Tumor Classification

Layer (type)	Shape of the Output	Param #
2D-Convolutional-Layer-1	(C (None, 126, 126, 16) onv2D)	3525
2D-MaxPool-Layer-1(MaxPool ing2D)	(None, 63, 63, 16)	0
Dropout-Layer-1 (Dropout)	(None, 63, 63, 16)	0
2D-Convolutional-Layer-2 (C onv2D)	(None, 61, 61, 64)	9,280
2D-MaxPool-Layer-2 (MaxPool ing2D)	None, 30, 30, 64)	0
Dropout-Layer-2 (Dropout)	(None, 30, 30, 64)	0
2D-Convolutional-Layer-3 (C onv2D)	(None, 30, 30, 64)	36,928
2D-MaxPool-Layer-3 (MaxPool ing2D)	(None, 15, 15, 64)	0
Dropout-Layer-3 (Dropout)	(None, 15, 15, 64)	0
Flatten-Layer (Flatten)	(None,	0

	14400)	
Hidden-Layer-1 (Dense)	(None, 16)	230,416
Output-Layer (Dense)	(None, 4)	68

5. Results and Discussioin

The results from the trained model the study proposal was good, as we obtained an accuracy of val accuracy 99% an d a loss value of 0.0828. Figure 3 shows the curve of acc and loss during the training.

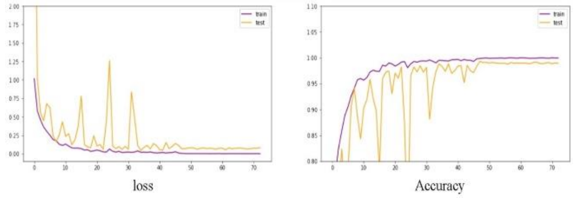

Figure 3: compression between loss and accuracy value (train, test) during training

In Table 8, the compression between the results of our suggested and related article

Table8: Comparative Performance Analysis of Brain Tumor Classification Methods

Ref	**Methodology**	**Dataset**	**Accuracy (%)**	**Specificity**	**Sensitivity**	**Precision**
[13]	CNN Model	RIDER REMBRANDT TCGA-LGG	98.14	0.9879	0.9701	0.9789
[17]	convolutional dictionary learning with local constraint (CDLLC)	REMBRANDT Three types astrocytoma (AST), oligodendroglioma (OLI), glioblastoma multiforme (GBM),	96.39	-	-	94.61
[18]	CNN Model Genetic Algorithm	Glioma, Meningioma and Pituitary	94.2%	-	-	-
[8]	(K-NN – SVM)	MIAS - Mammographic Image Analysis Society & DDSM -Digital Database of Screening Mammographies	98.24			-
Proposed	CNN Model	magnetic resonance (MR) images	0.99	0.97	0.98	0.98

6. Conclusions

The aim of this research is the enhancement of brain cancer detection method by using CNN and MRI images of brain tumors. A large dataset comprising three distinct tumor types, which are, meningioma (306 photos), pituitary gland (300 images), and glioma (300 images)—have been utilized in order to train the algorithm and increase accuracy. Before creating the artificial CNN, a comprehensive approach was followed to scale the training sample size, supplement the data, and carry out picture normalization using the data generator tool. We reported experimental findings of the proposed model on the used data set, where we achieved a loss value of 0.99 and a valve accuracy of 0.99 per cent. Our proposed methodology has tremendous potential benefits for improved patient identification of brain tumors.

REFERENCES

[1] S. E. Nassar, I. Yasser, H. M. Amer, and M. A. Mohamed, “A robust MRI-based brain tumor classification via a hybrid deep learning technique,” *J. Supercomput.*, vol. 80, no. 2, pp. 2403–2427, 2024.

[2] S. Das and R. S. Goswami, “Review, Limitations, and future prospects of neural network approaches for brain tumor classification,” *Multimed. Tools Appl.*, vol. 83, no. 15, pp. 45799–45841, 2024.

[3] A. A. Joshi and R. M. Aziz, “Deep learning approach for brain tumor classification using metaheuristic optimization with gene expression data,” *Int. J. Imaging Syst. Technol.*, vol. 34, no. 2, p. e23007, 2024.

[4] B. Kokila, M. S. Devadharshini, A. Anitha, and S. Abisheak Sankar, “Brain Tumor Detection and Classification Using Deep Learning Techniques based on MRI Images,” *J. Phys. Conf. Ser.*, vol. 1916, no. 1, 2021, doi: 10.1088/1742-6596/1916/1/012226.

[5] M. S. Ullah, M. A. Khan, N. A. Almujally, M. Alhaisoni, T. Akram, and M. Shabaz, “BrainNet: a fusion assisted novel optimal framework of residual blocks and stacked autoencoders for multimodal brain tumor classification,” *Sci. Rep.*, vol. 14, no. 1, p. 5895, 2024.

[6] A. Bunevicius, K. Schregel, R. Sinkus, A. Golby, and S. Patz, “REVIEW: MR elastography of brain tumors,” *NeuroImage. Clin.*, vol. 25, no. October 2019, p. 102109, 2020, doi: 10.1016/j.nicl.2019.102109.

[7] H. Sung *et al.*, “Global Cancer Statistics 2020: GLOBOCAN Estimates of Incidence and Mortality Worldwide for 36 Cancers in 185 Countries,” *CA. Cancer J. Clin.*, vol. 71, no. 3, pp. 209–249, 2021, doi: 10.3322/caac.21660.

[8] A. Bosch, X. Munoz, A. Oliver, and J. Marti, “Modeling and classifying breast tissue density in mammograms,” in *2006 IEEE computer society conference on computer vision and pattern recognition (CVPR’06)*, 2006, vol. 2, pp. 1552–1558.

[9] M. S. Ullah, M. A. Khan, A. Masood, O. Mzoughi, O. Saidani, and N. Alturki, “Brain tumor classification from MRI scans: a framework of hybrid deep learning model with Bayesian optimization and quantum theory-based marine predator algorithm,” *Front. Oncol.*, vol. 14, p. 1335740, 2024.

[10] R. Wang, T. Lei, R. Cui, B. Zhang, H. Meng, and A. K. Nandi, “Medical image segmentation using deep learning: A survey,” *IET Image Process.*, vol. 16, no. 5, pp. 1243–1267, 2022.

[11] A. Ghosh and A. Kole, “A comparative study of enhanced machine learning algorithms for brain tumor detection and classification,” *Authorea Prepr.*, 2023.

[12] S. Solanki, U. P. Singh, S. S. Chouhan, and S. Jain, “Brain tumor detection and classification using intelligence techniques: An overview,” *IEEE Access*, 2023.

[13] E. Irmak, “Multi-Classification of Brain Tumor MRI Images Using Deep Convolutional Neural Network with Fully Optimized Framework,” *Iran. J. Sci. Technol. - Trans. Electr. Eng.*, vol. 45, no. 3, pp. 1015–1036, 2021, doi: 10.1007/s40998-021-00426-9.

[14] U. Avni, H. Greenspan, E. Konen, M. Sharon, and J. Goldberger, “X-ray categorization and retrieval on the organ and pathology level, using patch-based visual words,” *IEEE Trans. Med. Imaging*, vol. 30, no. 3, pp. 733–746, 2010.

[15] A. Rehman, S. Naz, M. I. Razzak, F. Akram, and M. Imran, “A Deep Learning-Based Framework for Automatic Brain Tumors Classification Using Transfer Learning,” *Circuits, Syst. Signal Process.*, vol. 39, no. 2, pp. 757–775, 2020, doi: 10.1007/s00034-019-01246-3.

[16] W. Yang, Z. Lu, M. Yu, M. Huang, Q. Feng, and W. Chen, “Content-based retrieval of focal liver lesions using bag-of-visual-words representations of single-and multiphase contrast-enhanced CT images,” *J. Digit. Imaging*, vol. 25, pp. 708–719, 2012.

[17] M. Khosravi *et al.*, “Brain Tumor MR Image Classification Using Convolutional Dictionary Learning With Local Constraint,” 2021, doi: 10.3389/fnins.2021.679847.

[18] A. Kabir Anaraki, M. Ayati, and F. Kazemi, “Magnetic resonance imaging-based brain tumor grades classification and grading via convolutional neural networks and genetic algorithms,” *Biocybern. Biomed. Eng.*, vol. 39, no. 1, pp. 63–74, 2019, doi: 10.1016/j.bbe.2018.10.004.

[19] A. Kharrat, K. Gasmi, M. Ben Messaoud, N. Benamrane, and M. Abid, “A hybrid approach for automatic classification of brain MRI using genetic algorithm and support vector machine,” *Leonardo J. Sci.*, vol. 17, no. 1, pp. 71–82, 2010.

[20] S. E. Nassar, I. Yasser, H. M. Amer, and M. A. Mohamed, “A robust MRI-based brain tumor classification via a hybrid

deep learning technique," *J. Supercomput.*, vol. 80, no. 2, pp. 2403–2427, 2024.
[21] E. I. Papageorgiou *et al.*, "Brain tumor characterization using the soft computing technique of fuzzy cognitive maps," *Appl. Soft Comput.*, vol. 8, no. 1, pp. 820–828, 2008.
[22] M. Arunachalam and S. Royappan Savarimuthu, "An efficient and automatic glioblastoma brain tumor detection using shift-invariant shearlet transform and neural networks," *Int. J. Imaging Syst. Technol.*, vol. 27, no. 3, pp. 216–226, 2017.
[23] L. Huang, Y.-G. Zhao, and T.-J. Yang, "Skin lesion image segmentation by using backchannel filling CNN and level sets," *Biomed. Signal Process. Control*, vol. 87, p. 105417, 2024.
[24] A. M. G. Allah *et al.*, "Brain Tumor Detection and Classification Using Deep Learning Techniques based on MRI Images," *Complex Intell. Syst.*, vol. 11, no. 12, pp. 1–20, 2021, doi: 10.1007/s40998-021-00426-9.
[25] A. Rehman, M. A. Khan, T. Saba, Z. Mehmood, U. Tariq, and N. Ayesha, "Microscopic brain tumor detection and classification using 3D CNN and feature selection architecture," *Microsc. Res. Tech.*, vol. 84, no. 1, pp. 133–149, 2021, doi: 10.1002/jemt.23597.
[26] S. Arora and M. Sharma, "Deep learning for brain tumor classification from mri images," in *2021 Sixth International Conference on Image Information Processing (ICIIP)*, 2021, vol. 6, pp. 409–412.
[27] D. J. Hemanth, J. Anitha, A. Naaji, O. Geman, and D. E. Popescu, "A modified deep convolutional neural network for abnormal brain image classification," *IEEE Access*, vol. 7, pp. 4275–4283, 2018.
[28] N. M. Balasooriya and R. D. Nawarathna, "A sophisticated convolutional neural network model for brain tumor classification," in *2017 IEEE international conference on industrial and information systems (ICIIS)*, 2017, pp. 1–5.
[29] A. Çinar and M. Yildirim, "Detection of tumors on brain MRI images using the hybrid convolutional neural network architecture," *Med. Hypotheses*, vol. 139, p. 109684, 2020, doi: https://doi.org/10.1016/j.mehy.2020.109684.
[30] S. Khawaldeh, U. Pervaiz, A. Rafiq, and R. S. Alkhawaldeh, "Non-invasive grading of glioma tumor using magnetic resonance imaging with convolutional neural networks," *Appl. Sci.*, vol. 8, no. 1, p. 27, 2017.
[31] P. Saxena, A. Maheshwari, and S. Maheshwari, "Predictive modeling of brain tumor: a deep learning approach," in *Innovations in Computational Intelligence and Computer Vision: Proceedings of ICICV 2020*, Springer, 2020, pp. 275–285.
[32] X. Yang and Y. Fan, "Feature extraction using convolutional neural networks for multi-atlas based image segmentation," in *Medical Imaging 2018: Image Processing*, 2018, vol. 10574, pp. 866–873.
[33] B. Wicht, "Deep learning feature extraction for image processing." éditeur non identifié, 2017.
[34] F. J. Díaz-Pernas, M. Martínez-Zarzuela, M. Antón-Rodríguez, and D. González-Ortega, "A deep learning approach for brain tumor classification and segmentation using a multiscale convolutional neural network," in *Healthcare*, 2021, vol. 9, no. 2, p. 153.
[35] P. M. S. Raja, "Brain tumor classification using a hybrid deep autoencoder with Bayesian fuzzy clustering-based segmentation approach," *Biocybern. Biomed. Eng.*, vol. 40, no. 1, pp. 440–453, 2020.
[36] M. S. Ullah, M. A. Khan, A. Masood, O. Mzoughi, O. Saidani, and N. Alturki, "Brain tumor classification from MRI scans: a framework of hybrid deep learning model with Bayesian optimization and quantum theory-based marine predator algorithm," *Front. Oncol.*, vol. 14, p. 1335740, 2024.
[37] M. Khosravi *et al.*, "Brain Tumor MR Image Classification Using Convolutional Dictionary Learning With Local Constraint," 2021, doi: 10.3389/fnins.2021.679847.
[38] A. Kabir Anaraki, M. Ayati, and F. Kazemi, "Magnetic resonance imaging-based brain tumor grades classification and grading via convolutional neural networks and genetic algorithms," *Biocybern. Biomed. Eng.*, vol. 39, no. 1, pp. 63–74, 2019, doi: 10.1016/j.bbe.2018.10.004.

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