Computer Assisted Methods in Engineering and Science
30(3): 305–321, 2023, doi: 10.24423/cames.649

This article belongs to the *Special Issue on Digital Twin Empowered Internet of Intelligent Things for Engineering Cyber-Physical Human Systems* edited by C. Venkatesan, Y.-D. Zhang, Q. Xin

Brain Tumor Classification in MRI Images Using Genetic Algorithm Appended CNN

T. BALAMURUGAN1)*, E. GNANAMANOHARAN2)

1) *Department of Electronics and Communication Engineering, Government College of Engineering, Dharmapuri, Tamilnadu, India*

2) *Department of Electronics and Communication Engineering, Annamalai University, Chidambaram, Tamilnadu, India; e-mail: gnanamanohar@gmail.com*

* *Corresponding Author e-mail: balamurugan.thiyagu@gcedpi.edu.in*

Brain tumors are fatal for majority of the patients, the different nature of the tumor cells requires the use of combined medical measures, and categorizing such tumors is a difficult task for radiologists. The diagnostic structures based on PCs have been offered as an aid in diagnosing a brain tumor using magnetic resonance imaging (MRI). General functions are retrieved from the lowest layers of the neural network, and these lowest layers are responsible for capturing low-level features and patterns in the raw input data, which can be particularly unique to the raw image. To validate this, the EfficientNetB3 pre-trained model is utilized to classify three types of brain tumors: glioma, meningioma, and pituitary tumor. Initially, the characteristics of several EfficientNet modules are taken from the pre-trained EfficientNetB3 version to locate the brain tumor. Three types of brain tumor datasets are used to assess each approach. Compared to the existing deep learning models, the concatenated functions of EfficientNetB3 and genetic algorithms give better accuracy. Tensor flow 2 and Nesterov-accelerated adaptive moment estimation (Nadam) are also employed to improve the model training process by making it quicker and better. The proposed technique using CNN attains an accuracy of 99.56%, a sensitivity of 98.9%, a specificity of 98.6%, an F-score of 98.9%, a precision of 98.9%, and a recall of 99.54%.

Keywords: deep learning, convolutional neural networks, EfficientNetB3, genetic algorithm, brain tumor classification.

1. INTRODUCTION

In the disciplines of biomedicine and artificial intelligence, progress is being made at unprecedentent rate. Many individuals are affected by cancer. Because of its unpredictability, it poses a severe threat to their livelihood. A brain tumor is one of the most severe and life-threatening diseases. Nearly 23 000 people were diagnosed with brain tumors in 2015 [1–3]. The use of MRI in detecting and treating brain tumors is critical. It generates diagnostic images of the brain free of tissue damage or skull anomalies, and it provides clinicians with critical information for identifying brain tumors and other brain diseases [4, 5]. Irmak [6] used CNN models to classify brain tumor MRI images. The proposed framework correctly identified three types of brain tumors, grades II, III and IV with an accuracy of 98.14%. The suggested CNN models can be used to help radiologists and doctors in confirming their first screening.

Diaz-Pernas *et al.* [7] presented a fully automatic brain tumor identification and image segmentation using the multiscale technique. This technique does not need the use of image preparation software. As a result, the deep learning model achieves a 97.3% accuracy, and this is higher than the other approaches using the same database. Mohan ans Subashini [8] surveyed brain tumor grade categorization. The primary goal of their work was to identify medical images in the early stages of brain tumors and clarify diagnostic images for cancer therapy, both before and after surgery, by bridging the gap between the radiologist and the computer. The difficulty of recognizing a brain tumor early was confirmed by evaluating image segmentation and classification algorithms on brain MRI images.

Pei *et al.* [9] performed deep learning-based brain tumor segmentation, subtype classification, and survival prediction using radiographs. They also looked at indicators including Dice score coefficient, Hausdorff distance at percentile 95 (HD95), classification accuracy, and mean square error (MSE). The suggested technique provides reliable tumor segmentation and survival prediction. Khan *et al.* [10] used a CNN-based strategy and data augmentation and image processing techniques to categorize tumorous and non-tumorous brain MRI scan pictures. The suggested model employs ResNet 50 and Inception V3 to achieve 89% and 75% accuracy, respectively, and this approach demands relatively little processing resources while achieving the highest accuracy and efficiency.

Ismael *et al.* [11] developed an improved method for categorizing brain tumor types based on the residual network and tested their findings using a standard dataset of 3064 MRI images. The suggested approach correctly diagnoses three forms of brain tumors: meningioma, glioma, and pituitary tumors, with a 99% accuracy rate. The proposed residual-based network outperforms comparable types of brain tumor classification systems in the same dataset.

Özyurt *et al.* [12] classified brain tumors as well. The proposed method identifies tumor areas segregated from MRI images as benign or malignant using a hybrid method using neutrosophy and CNN. The characteristics of the phases of classification were obtained using CNN. They were classified using SVM and KNN classifiers. Experimental validation based on a five-fold categorization of 80 benign and malignant tumors was carried out with an accuracy of 95.62%.

On MRI scans, Anaraki *et al.* [13] used a CNN-based learning model and a genetic algorithm-based classification model to identify brain tumors. The suggested approach classifies the different stages of glioma and achieves a classification accuracy of 90.9%. Physicians may be able to identify brain tumors in their early stages because of the suggested CNN model's flexible methodology.

Kumar and Mankame [14] optimized a convolutional neural network to identify brain tumors. Because of the various sizes of the images and enormous datasets, segmenting MRI images is a complex process. Different techniques were developed in the literature for brain tumor classification but due to accuracy and ineffective decision making, the existing techniques failed to provide improved classification. In [14], a deep CNN was applied based on a unique dolphin echolocation based sine cosine algorithm (Dolphin-SCA). The suggested method achieved a maximum accuracy of 96.3%. Deepak and Ameer [15] used transfer learning to create a brain tumor classification utilizing deep CNN characteristics. Their study focused on a 3-class classification problem to differentiate between meningioma, glioma, and pituitary tumors, and the proposed classification adopted the concept of deep transfer learning and used a pre-trained GoogLeNet to extract features from brain MRI image. The selected deep learning strategy has a 98% accuracy rate and outperforms similar brain tumor classification schemes in the literature.

A deep multiscale 3D CNN model for grading brain tumors from volumetric 3D MRI images was proposed by Mzoughi *et al.* [24]. When classifying brain tumor images into low-grade and high-grade gliomas, the suggested method has a classification accuracy of 96.49%. A computer-aided diagnosis (CAD) system based on CNN was proposed by Ayadi *et al.* [25] to classify brain tumors. The accuracy of classifying the tumor type was 94.74% in experiments using an 18-weighted hierarchical CNN model on three different datasets, and the accuracy of classifying the tumor grade was 90.35%.

In 2018, Pereira *et al.* [26] succeeded in overcaming the requirement for expert annotation of regions of interest (ROI) by using CNN to predict tumor grade directly from image data. Two prediction techniques using whole-brain imaging and automatically-identified tumor regions were assessed. They made predictions with an accuracy of 89.5% for whole-brain grade and 92.98% for tumor ROI.

In our study, the categorization of brain tumors from MRI images is based on a unique CNN approach. Using the EfficientNetB3 and genetic algorithms, the suggested scheme extracts features from MRI brain images. The evolutionary algorithm and EfficientNetB3 features are then used in the CNN to evaluate the test MRI images. In this study, MRI images are used to classify three different types of brain tumors using a CNN-based approach. It can be challenging to select the best deep neural network architecture for a given task, but this can be done using trial and error or a standard architecture. The proposed method, in contrast to conventional approaches, uses genetic algorithms (GAs) to create the architecture of convolutional neural networks. The network that performs the best on the dataset is chosen for further processing after GA examines networks with various numbers of layers and parameters. Bagging is an ensemble technique for lowering final diagnostic variance.

1.1. Problem statement

This study examines recent research on the early detection of brain tumors and demonstrates that there is still room for development. MRI image acquisition produces noise, and removing this noise is a challenging task. Brain tumors have tentacles and diffuse structures, making accurate segmentation a problematic task. Another crucial task is choosing and extracting the best features and the correct quantity of training and testing samples to improve the classification. Because feature learning occurs automatically, deep learning models have received much attention. However, this necessitates a large amount of computing power and memory. As a result, lightweight models capable of providing high accuracy with minimal computation time are developed. Some existing methods work well on the entire tumor but not on other areas (enhanced, non-enhanced).

1.2. Major contribution

This research presents a CNN-based technique for classifying brain tumors in MRI images. CNN structures that provide the best results using a GA were located. The suggested method is very effective at classifying images of various types of brain tumors and accurately classifying glioma tumors. The proposed algorithm accurately classified two additional tumor types that are widely dispersed as well as different grades of gliomas. Making decisions solely based on the raw data of the MRI images eliminates the need for laborious processes such as segmenting or stripping the skull.

Furthermore, the time required for classification is much shorter than the time needed for analysis. As a result, depending on the severity of the tumor, appropriate action can be taken at the proper time. This paper demonstrates that the proposed method outperforms similar methods in the literature.

2. PROPOSED METHODOLOGY

2.1. Preprocessing

Unclean data is converted into clean data collection through data preparation. In other words, when data is received from many sources, it is always in a raw format, making analysis difficult. To get better results from the models used in machine learning, applications need to prepare data correctly. Some machine learning algorithms require data in the specified format. Another factor to consider is how the dataset is organized. Preprocessing allows running many deep learning algorithms and machine learning parallel to choosing the best algorithm. The batch sequence generator is shown in Fig. 1.

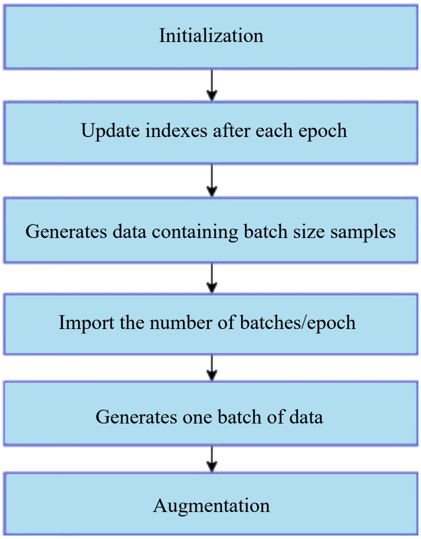

Fig. 1. Batch sequence generator.

2.1.1. Data augmentation. Image classification datasets are often more significant. Consequently, data augmentation is often used to improve the generalization characteristics of models. Random horizontal flipping, shift scale rotation, Gaussian noise, and random RGB color and brightness changes are prominent techniques for rescaling photographs. There are numerous methods for rescaling and cropping images, including single-scale and multiscale training. Multi-crop assessment throughout the test period is also popular, although it is more computationally intensive and yields lower results. In data augmentation, random rescaling and cropping are to learn the essential attributes of each item at numerous sizes and locations. It does not support any of these data augmentation techniques.

Augmentations are a versatile and straightforward Python tool for augmenting images. This method is a simple yet effective approach for incorporating images into computer vision applications such as object categorization, segmentation, and detection. It can process a wide variety of image changes in a short amount of time, and can be used for various computer vision applications such as classification, semantic segmentation, instance segmentation, object recognition, and location estimation. Augmentations work well in imagery, medical imagery, satellite imagery, manufacturing and industrial applications, and power generation networks.

2.2. Feature extraction

In recent years, the researcherers have increasingly been working with datasets containing hundreds, if not thousands, of attributes. Machine learning tends to overfit as the number of features in the dataset approaches the number of observations contained in the dataset. Regularization or dimensionality reduction methods are used (feature extraction) to prevent such problems. This might help reduce the danger of overfitting while also maximizing the advantages of feature extraction approaches, such as increased accuracy and data visualization, quicker training, and model explainability. Feature extraction is a technique to reduce the number of features in a dataset by creating new features from existing ones.

Most of the original feature set information should be generalized by these new compressed features. Another way to reduce the number of functions in a data set is to use function selection. The difference between function selection and function extraction is that the former prioritizes the relevance of existing processes in the dataset and excludes the latter. Instead, we prioritize the importance of current features and try to eliminate unwanted elements. Next, the transformation or change of images into its unique cluster is performed based on their similarity. Feature extraction methods include texture features, co-occurrence matrix, Gabor features, wavelet-based total features, choice boundary characteristic extraction, least noise fraction transform, nonparametric weighted characteristic extraction, and spectral aggregate assessment. The most important parts of the characteristic discount model are evaluated using linear discriminant evaluation and impartial element evaluation.

2.2.1. EfficientNetB3 model. This paper presents an efficient method based on the EfficientNetB3 CNN model. The variant of the EfficientNet family is chosen because it provides a good balance of computational resources and accuracy. The concepts presented here can be applied to more powerful variants. The EfficientNet family of models is built around mobile inverse bottleneck convolution (MBConv). MB Conv is based on ideas from the MobileNet model. The concept is to employ deep separable convolutions. It comprises deep convolutional layers that alternate with pointwise convolutional layers. As shown in Fig. 2, the EfficientNetB3 convolutional network is a network architecture that provides a new scaling method that uniformly scales all network depth, width, and resolution dimensions. The architecture employs a grid search strategy to discover relationships between different underlying networks. Dimension scaling is with limited resources. Using this strategy, appropriate scaling factors for each dimension can

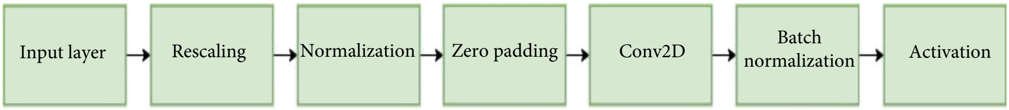

Fig. 2. Stages of EfficientNetB3 model.

be found that need to be scaled. These parameters are used to mount the underlying network to the desired size. Growing the overall performance of the neural network by growing it deeper or broader is a novel technique to enhance it. However, it has a higher computational cost [16]. To overcome this, researchers offer a novel scaling strategy that scales up CNNs in a well-established way using simple multiple coefficients. Figure 2 depicts the stages of the EfficientNetB3 model.

Unlike most approaches, this method does not arbitrarily scale network dimensions along with width, intensity, and resolution. Each measurement is evenly scaled using a set of scaling factors in the proposed technique [17–19]. While scaling individual dimensions improves version performance, it also stabilizes all network dimensions, such as width, intensity, and image resolution. In this scenario, the one-cycle strategy is applied to achieve optimal learning. In most cases, one-cycle policies have two phases. Phase 1 involves gradually increasing the learning rate to the maximum while gradually decreasing the momentum to the minimum. The second phase is the reverse of the first. The proposed model with multiple layers and predetermined models is explained in the following subsections.

2.3. Feature selection by enetic algorithm

This research uses a GA to evolve the CNN's ideal structure by selecting suitable network parameters. Among these parameters are the number of fully connected layers, the size of the filters, the number of convolutional and maximum pooling layers, the activation function, the dropout probability, the optimization method, and the learning rate. Unlike most approaches, this method does not erratically scale network dimensions along with width, intensity, and resolution. Each measurement is evenly scaled using a set of scaling factors in the proposed technique. To investigate the impact of the scaling technique, we performed a procedural analysis of the effect of scaling in multiple dimensions of the version. In this scenario, the one-cycle strategy is applied to achieve optimal learning.

In most cases, one-cycle policies have two phases. Phase 1 involves gradually increasing the learning rate to the maximum while gradually decreasing the momentum to the minimum. The second phase is the reverse of the first [20–23]. The proposed model with multiple layers and predetermined models is explained in the following subsections. The suggested deep learning model overview is shown in Fig. 3.

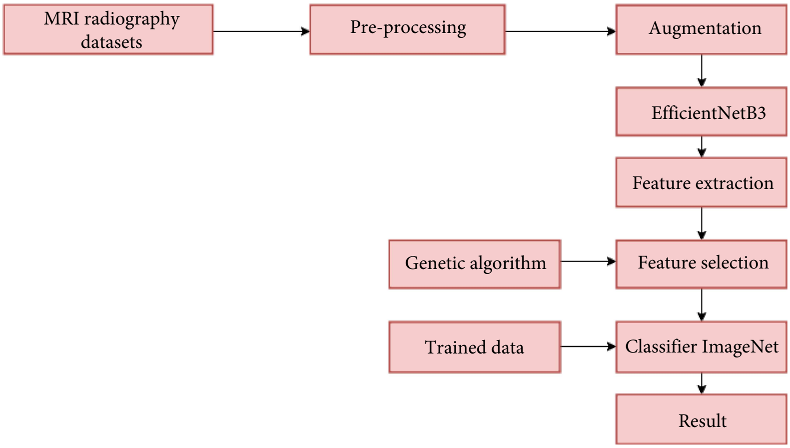

FIG. 3. Overview of the proposed deep learning model.

The flowchart of the genetic algorithm is presented in Fig. 4.

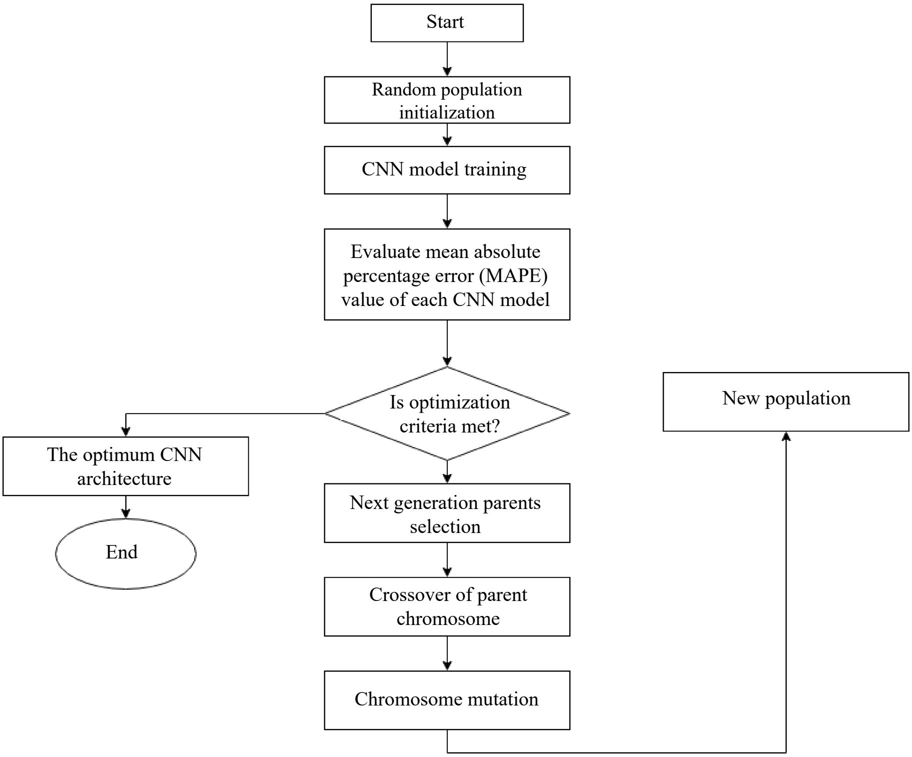

FIG. 4. Flowchart of the genetic algorithm.

3. RESULTS AND DISCUSSION

Unlike most approaches, this method does not erratically scale network dimensions along with width, intensity, and resolution. Each measurement is evenly scaled using a set of scaling factors in the proposed technique. To investigate the impact of the scaling technique, we performed a procedural analysis of the effect of scaling in multiple dimensions of the version. While scaling individual dimensions improves version performance, it also stabilizes all network dimensions, such as width, intensity, and image resolution. The suggested system's strength is validated using a variety of statistical studies. The percentiles of sensitivity (SN), specificity (SF), and accuracy (AC) are calculated.

3.1. Sensitivity

The ability of the test to correctly identify patients with a disease. It is expressed as SN:

$$\mathrm{SN} = \mathrm{TP}/(\mathrm{TP} + \mathrm{FN}). \tag{1}$$

3.2. Specificity

The ability of the test to correctly identify people without the disease is expressed as SP:

$$\mathrm{SP} = \mathrm{TN}/(\mathrm{TN} + \mathrm{FN}). \tag{2}$$

3.3. Accuracy

The percentage of correct predictions in the test data is calculated by dividing the total number of predictions by the number of accurate predictions. It is expressed as AC:

$$\mathrm{AC} = \mathrm{TP} + \mathrm{TN}/(\mathrm{P} + \mathrm{N}), \tag{3}$$

where true positives (TP) represent the expected number of positive cases that were positive; true negative (TN) indicates the expected number of negatives and whether they were negatives; false-negative (FN) represents the number of negative predicted cases that were positive. This is also known as a type 2 error; false positives (FP) represent the number of cases that are negative but predicted to be positive. This is also known as a type 1 error.

In this scenario, the one-cycle strategy is applied to achieve optimal learning. In the following subsections, the proposed model with multiple layers and predetermined models is explained.

Figure 5 depicts the projected outcomes of the selected deep learning models.

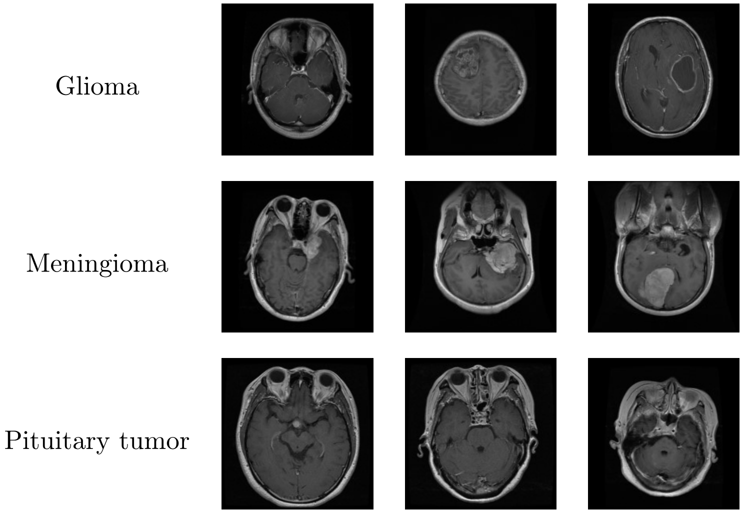

Fig. 5. Sample test images from the radiography dataset.

Figure 6 presents the outcomes with respect to the classification of images.

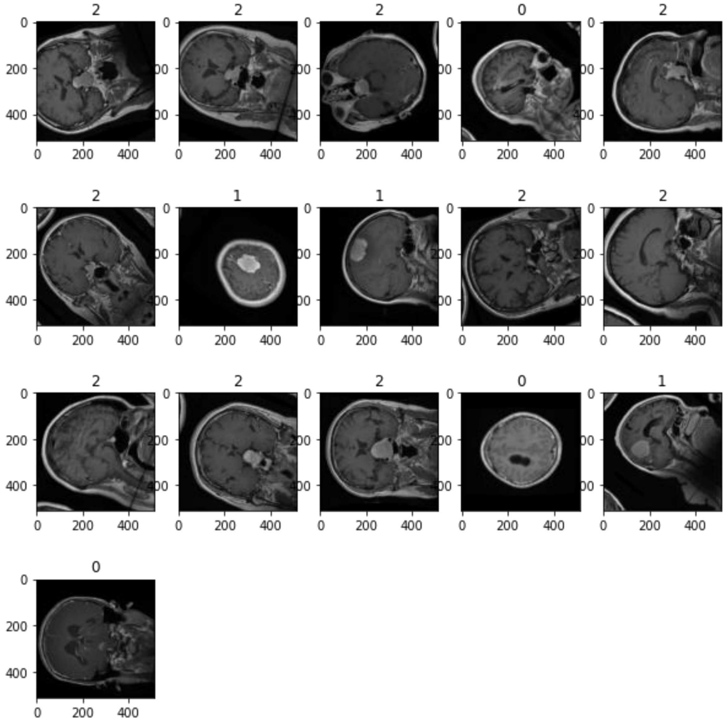

Fig. 6. Classified images (0 – glioma, 1 – meningioma, and 2 – pituitary tumor).

The suggested brain tumor classification strategy was implemented in Python, and classification, validation training, and testing were carried out using the accessible brain tumor datasets [27]. A confusion matrix is a commonly used table to describe the performance of a classification model on a set of test samples where the correct value was found. Table 1 summarizes the proposed brain tumor classification tasks.

TABLE 1. Model summary.

Layer(type)	Output shape	Value
Input	(none, 512, 512, 3)	0
Rescaling	(none, 512, 512, 3)	0
Normalization	(none, 512, 512, 3)	7
Zero padding	(none, 512, 512, 3)	0
Conv2D	(none, 256, 256, 40)	1080
Batch normalization	(none, 256, 256, 40)	160
Activation	(none, 256, 256, 40)	0
Depthwise Conv2D	(none, 256, 256, 40)	360
Batch normalization	(none, 256, 256, 40)	160
Activation	(none, 256, 256, 40)	0
Global average	(none, 40)	0

Figures 7a and 7b illustrate the comprehensive information obtained layer by layer of the EfficientNetB3. Figure 7c shows the test confusion matrix derived from EfficientNetB3. Table 2 summarizes the performance metrics. The accuracy of the suggested scheme was compared to the accuracy of previous brain tumor classification systems, and it surpasses them all, as shown in Fig. 8.

TABLE 2. The parameters used to find the optimum CNN structure.

Parameters	Value
Number of convolutional + max pooling layers	2, 3, 4, 5, 6
Number of fully connected + dropout layers	1, 2, 3
Activation functions	Elu, softmax
Feedforward optimizer	Nadam
Learning rate	$1e^{-4}$, $1e^{-5}$, $1e^{-8}$, $3e^{-4}$, $5e^{-5}$
Dropout rate	0.2, 0.3, 0.4, 0.5

Figures 8a and 8b depict the freezing of the lower layers, but in the higher layers of the model, those weights are retrained. Figures 8c and 8d depict the unfreezing of all layers and training of the whole model, and Figs. 8e and 8f

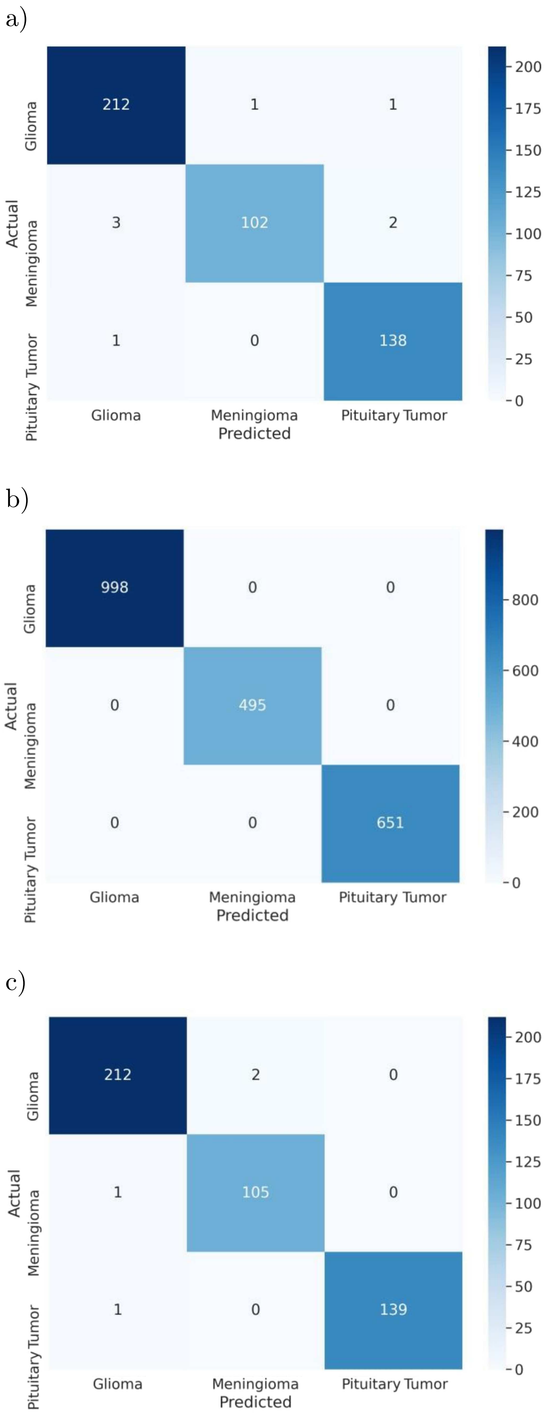

Fig. 7. a) Actual value comparison using a confusion matrix, b) trained confusion matrix, c) test confusion matrix.

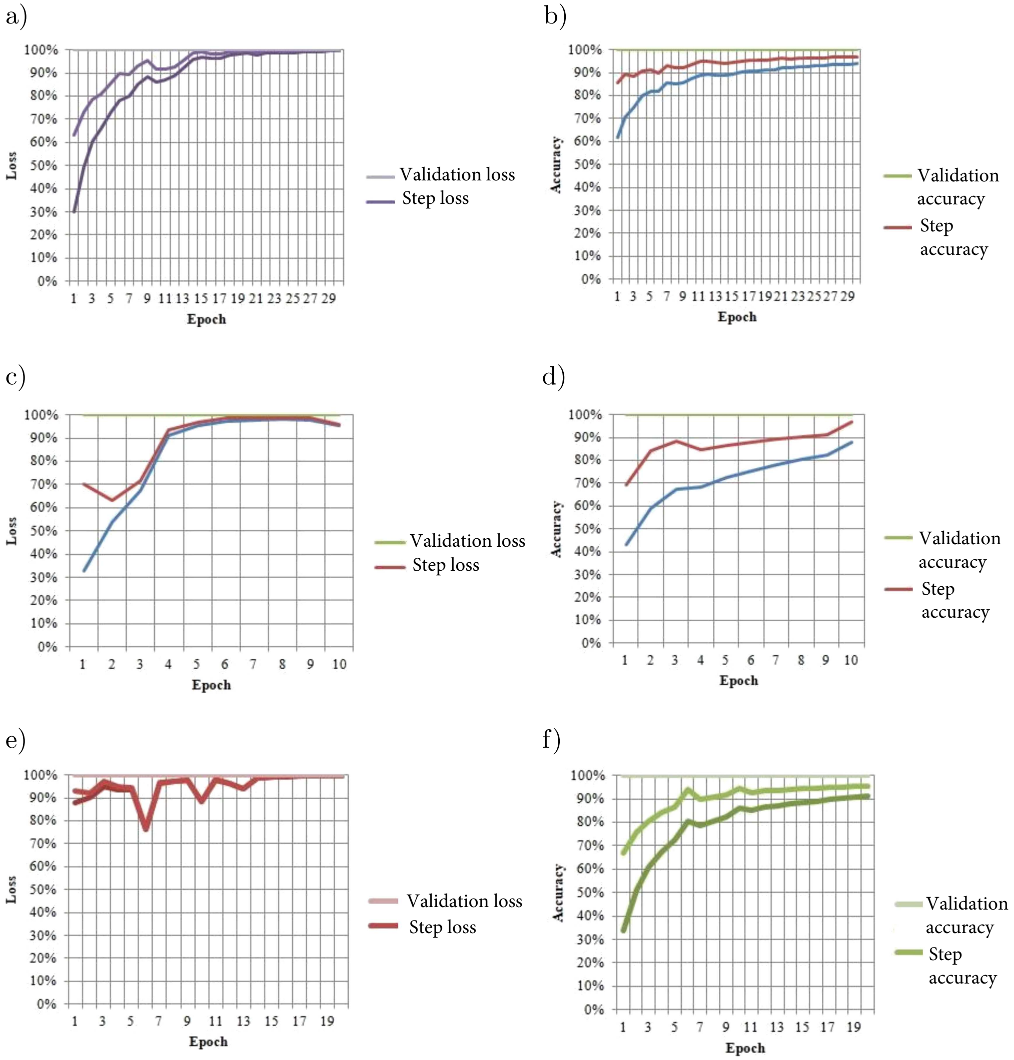

FIG. 8. a, c and e) epoch vs. loss; b, d and f) epoch vs. accuracy (the bottom line represents training loss).

imply the graph plotted between the epoch vs. loss and epoch vs. accuracy. The sensitivity and specificity of the proposed protocol were compared to similar protocols reported in the literature. The proposed scheme is superior to the other schemes, as shown in Table 3. Various parameters used for this research are given below:

- total parameters: 12 360 498,
- trainable parameters: 12 273 195,
- non-trainable parameters: 87 303.

Table 3. Evaluation of performance for classification of brain tumors.

Tumor stage	Proposed EfficientNetB3 performance analysis			
	Accuracy [%]	Sensitivity [%]	Specificity [%]	Precision [%]
Glioma	98.52	96.43	98.95	98.99
Meningioma	99.23	98.67	98.66	99.40
Pituitary	99.16	98.69	98.37	97.78

Table 4 shows the performance evaluation of the proposed technique compared with other conventional algorithms. The proposed classifier outperforms them.

Table 4. Performance evaluation of the proposed technique vs. existing methods.

Algorithm	Recall	Precision	F-score	Accuracy	Sensitivity	Specificity
SVM	87.5	91.4	91.2	95.2	94.5	95.7
ELM	90.92	95.5	93.5	92.9	96.7	94.5
GA	95.98	94.1	94.2	95.9	96.6	94.9
Fuzzy C Means	97.69	95.96	94.9	95.9	95.7	95.1
KNN	96.43	93.17	92.4	93.9	92.5	95.2
CNN	95.01	92.5	93.3	93.4	93.3	97.5
Proposed CNN	99.54	98.9	98.9	99.56	98.9	98.6

The proposed CNN algorithm can be used to segment MRI brain images. The algorithm was introduced to classify abnormal brain images in meningiomas, gliomas, and pituitary glands to assess the accuracy of the proposed classification. The results show better predictive performance. The algorithm is more accurate in detecting and classifying abnormal brain tumors than existing methods. The proposed EfficientNetB3 algorithm provides an accuracy of 99.56%, which is higher than that of the conventional brain tumor detection algorithm.

4. CONCLUSION

Due to deep learning's state-of-the-art results, machine learning studies and research have expanded beyond feature engineering to architectural engineering. The suggested approach increases the accuracy to 99.56% by combining the EfficientNetB3 model with a GA deployed in the softmax layers of the CNN. Meningioma, glioma, and pituitary tumor are the three types of brain tumors classified by the selected system. The process is made more accurate and effective by using a GA. A sufficient number of medical images are used to train and test the proposed CNN model. The effectiveness of the CNN model produced by the suggested optimization method is demonstrated by the results obtained using the proposed CNN model and by comparing it to state-of-the-art techniques. The CNN model developed in this work may help physicians and radiologists to validate initial screening for multiple brain tumor classifications. The proposed technique is superior to comparable CNN-based tumor classification models.

REFERENCES

1. H.N.T.K. Kaldera, S.R. Gunasekara, M.B. Dissanayake, Brain tumor classification and segmentation using faster R-CNN, [in:] *2019 Advances in Science and Engineering Technology International Conferences (ASET)*, Dubai, United Arab Emirates, pp. 1–6, 2019, doi: 10.1109/ICASET.2019.8714263.

2. S. Iqbal, M.U. Ghani, T. Saba, A. Rehman, Brain tumor segmentation in multi-spectral MRI using convolutional neural networks (CNN), *Microscopy Research and Technique*, **81**(4): 419–427, 2018, doi: 10.1002/jemt.22994.

3. S. Das, O.F.M.R.R. Aranya, N.N. Labiba, Brain tumor classification using convolutional neural network, [in:] *2019 1st International Conference on Advances in Science, Engineering and Robotics Technology (ICASERT)*, Dhaka, Bangladesh, pp. 1–5, 2019, doi: 10.1109/ICASERT.2019.8934603.

4. W. Zhang, Y. Wu, B. Yang, S. Hu, L. Wu, S. Dhelimd, Overview of multi-modal brain tumor MR image segmentation, *Healthcare*, **9**(8): 1051, 2021, doi: 10.3390/healthcare9081051.

5. S. Abbasi, F. Tajeripour, Detection of brain tumor in 3D MRI images using local binary patterns and histogram orientation gradient, *Neurocomputing*, **219**: 526–535, 2017, doi: 10.1016/j.neucom.2016.09.051.

6. E. Irmak, Multi-classification of brain tumor MRI images using deep convolutional neural network with fully optimized framework, *Iranian Journal of Science and Technology-Transactions of Electrical Engineering*, **45**(3): 1015–1036, 2021, doi: 10.1007/s40998-021-00426-9.

7. F.J. Díaz-Pernas, M. Martínez-Zarzuela, M. Antón-Rodríguez, D. González-Ortega, A deep learning approach for brain tumor classification and segmentation using a multiscale convolutional neural network, *Healthcare*, **9**(2): 153, 2021, doi: 10.3390/healthcare9020153.

8. G. Mohan, M.M. Subashini, MRI based medical image analysis: Survey on brain tumor grade classification, *Biomedical Signal Processing and Control*, **39**: 139–161, 2018, doi: 10.1016/j.bspc.2017.07.007.

9. L. Pei, L. Vidyaratne, M. Rahman, K.M. Iftekharuddin, Context aware deep learning for brain tumor segmentation, subtype classification, and survival prediction using radiology images, *Scientific Reports*, **10**: 19726, 2020, doi: 10.1038/s41598-020-74419-9.

10. H.A. Khan, W. Jue, M. Mushtaq, M.U. Mushtaq, Brain tumor classification in MRI image using convolutional neural network, *Mathematical Biosciences and Engineering*, **17**(5): 6203–6216, 2020, doi: 10.3934/mbe.2020328.

11. S.A. Abdelaziz Ismael, A. Mohammed, H. Hefny, An enhanced deep learning approach for brain cancer MRI images classification using residual networks, *Artificial Intelligence in Medicine*, **102**: 101779, 2020, doi: 10.1016/j.artmed.2019.101779.

12. F. Özyurt, E. Sert, E. Avci, E. Dogantekin, Brain tumor detection based on convolutional neural network with neutrosophic expert maximum fuzzy sure entropy, *Measurement*, **147**: 106830, 2019, doi: 10.1016/j.measurement.2019.07.058.

13. A.K. Anaraki, M. Ayati, F. Kazemi, Magnetic resonance imaging-based brain tumor grades classification and grading via convolutional neural networks and genetic algorithms, *Biocybernetics and Biomedical Engineering*, **39**(1): 63–74, 2019, doi: 10.1016/j.bbe. 2018.10.004.

14. S. Kumar, D.P. Mankame, Optimization driven deep convolution neural network for brain tumor classification, *Biocybernetics and Biomedical Engineering*, **40**(3): 1190–1204, 2020, doi: 10.1016/j.bbe.2020.05.009.

15. S. Deepak, P.M. Ameer, Brain tumor classification using deep CNN features via transfer learning, *Computers in Biology and Medicine*, **111**: 103345, 2019, doi: 10.1016/j.compbiomed.2019.103345.

16. A.M. Sarhan, Brain tumor classification in magnetic resonance images using deep learning and wavelet transform, *Journal of Biomedical Science and Engineering*, **13**(6): 102–112, 2020, doi: 10.4236/jbise.2020.136010.

17. R. Karakış, M. Tez, Y.A. Kılıç, Y. Kuru, İ. Güler, A genetic algorithm model based on artificial neural network for prediction of the axillary lymph node status in breast cancer, *Engineering Applications of Artificial Intelligence*, **26**(3): 945–950, 2013, doi: 10.1016/j.engappai.2012.10.013.

18. G.R. Chandra, K.R.H. Rao, Tumor detection in brain using genetic algorithm, *Procedia Computer Science*, **79**: 449–457, 2016, doi: 10.1016/j.procs.2016.03.058.

19. Z.N.K. Swati *et al.*, Brain tumor classification for MR images using transfer learning and fine-tuning, *Computerized Medical Imaging and Graphics*, **75**: 34–46, 2019, doi: 10.1016/j.compmedimag.2019.05.001.

20. N. Abiwinanda, M. Hanif, S.T. Hesaputra, A. Handayani, T.R. Mengko, Brain tumor classification using convolutional neural network, [in:] *2018 World Congress on Medical Physics and Biomedical Engineering*, *FMBE Proceedings*, L. Lhotska, L. Sukupova, I. Lacković, G.S. Ibbott [Eds], vol. 68/1, pp. 183–189, Springer, Singapore, 2018, doi: 10.1007/978-981-10-9035-6_33.

21. M.R. Ismael, I. Abdel-Qader, Brain tumor classification via statistical features and back-propagation neural network, [in:] *2018 IEEE International Conference on Electro/Information Technology (EIT)*, Rochester, MI, USA, pp. 0252–0257, 2018, doi: 10.1109/EIT.2018.8500308.

22. A. Pashaei, H. Sajedi, N. Jazayeri, Brain tumor classification via convolutional neural network and extreme learning machines, [in:] *2018 8th International Conference on Computer and Knowledge Engineering (ICCKE)*, pp. 314–319, 2018, doi: 10.1109/ICCKE. 2018.8566571.

23. N. Noreen, S. Palaniappan, A. Qayyum, I. Ahmad, M. Imran, M. Shoaib, A deep learning model based on concatenation approach for the diagnosis of brain tumor, *IEEE Access*, **8**: 55135–55144, 2020, doi: 10.1109/ACCESS.2020.2978629.

24. H. Mzoughi *et al.*, Deep multi-scale 3D convolutional neural network (CNN) for MRI gliomas brain tumor classification, *Journal of Digital Imaging*, **33**: 903–915, 2020, doi: 10.1007/s10278-020-00347-9.

25. W. Ayadi, W. Elhamzi, I. Charfi, M. Atri, Deep CNN for brain tumor classification, *Neural Processing Letters*, **53**: 671–700, 2021, doi: 10.1007/s11063-020-10398-2.

26. S. Pereira, R. Meier, V. Alves, M. Reyes, C.A. Silva, Automatic brain tumor grading from MRI data using convolutional neural networks and quality assessment, [in:] *Understanding and Interpreting Machine Learning in Medical Image Computing Applications: First International Workshops*, MLCN DLF IMIMIC 2018, Lecture Notes in Computer Science, Vol. 11038, pp. 16–20, Springer, Cham, 2018, doi: 10.1007/978-3-030-02628-8_12.

27. Brain tumor dataset, 2017, https://figshare.com/articles/dataset/brain_tumor_dataset/1512427.

Received June 14, 2022; revised version August 16, 2022;
accepted September 6, 2022.