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MRI-based brain tumour image detection using CNN based deep learning method

Arkapravo Chattopadhyay *, Mausumi Maitra

Department of Information Technology, Government College of Engineering and Ceramic Technology, Kolkata-700010, West Bengal, India

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ABSTRACT

Introduction: In modern days, checking the huge number of MRI (magnetic resonance imaging) images and finding a brain tumour manually by a human is a very tedious and inaccurate task. It can affect the proper medical treatment of the patient. Again, it can be a hugely time-consuming task as it involves a huge number of image datasets. There is a good similarity between normal tissue and brain tumour cells in appearance, so segmentation of tumour regions become a difficult task to do. So there is an essentiality for a highly accurate automatic tumour detection method.

Method: In this paper, we proposed an algorithm to segment brain tumours from 2D Magnetic Resonance brain Images (MRI) by a convolutional neural network which is followed by traditional classifiers and deep learning methods. We have taken various MRI images with diverse Tumour sizes, locations, shapes, and different image intensities to train the model well. Furthermore, we have applied SVM classifier and other activation algorithms (softmax, RMSProp, sigmoid, etc) to cross-check our work. We implement our proposed method using "TensorFlow" and "Keras" in "Python" as it is an efficient programming language to perform fast work.

Result: In our work, CNN gained an accuracy of 99.74%, which is better than the state of the result obtained so far.

Conclusion: Our CNN based model will help the doctors to detect brain tumours in MRI images accurately, so that the speed in treatment will increase a lot.

1. Introduction

Medical imaging refers to several techniques that can be used as non-invasive methods of looking inside the body [1]. The main use of medical image in the human body is for treatment and diagnostic purposes. So, it plays a significant role in the betterment of treatment and the health of the human.

Image segmentation is a crucial and essential step in image processing that determines the success of image processing at a higher level [2]. In this case we have mainly focused on the segmentation of the brain tumour from the MRI images. It helps the medical representatives to find the location of the tumour in the brain easily. Medical image processing encompasses the utilization and exploration of 3D image datasets of the physical body, obtained most typically from computed tomography (CT) or Magnetic Resonance Imaging (MRI) scanner to diagnose pathologies or guide medical interventions like surgical planning, or for research purposes. Medical image processing is applied by radiologists, engineers, and clinicians to understand the anatomy of either individual patients or population groups highly. Measurement, statistical analysis, and creation of simulation models which incorporate real anatomical geometries provide the chance for more complete understanding, as an example of interactions between patient anatomy and medical devices.

Tumour: The word "Tumour" is a synonym for the word "neoplasm" which is formed by an abnormal growth of cells. A tumour is significantly different from cancer [3].

1.1. Classification of tumour

There are three basic types of tumours: 1) Benign; 2) Pre-Malignant; 3) Malignant (cancer can only be malignant) [4].

1.1.1. Benign tumour

A Benign Tumour is not always Malignant or cancerous. It might not invade close tissue or unfold to alternative components of the body the way cancer can. In most cases, the outlook with

* Corresponding author.
E-mail addresses: arkapravo1998@gmail.com (A. Chattopadhyay), mou1232005@yahoo.com (M. Maitra).

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benign tumours is not at all serious but it can be serious if it presses on vital structures such as blood vessels or nerves.

1.1.2. Pre-Malignant tumour

In these tumours, the cells are not cancerous. However, they need the potential to become malignant. The cells will grow and unfold to alternative components of the body.

1.1.3. Malignant tumour

Malignancy (mal- = "bad" and ignis = "fire") Malignant tumours area are cancerous. They develop once cells grow uncontrollably. If the cells still grow and unfold, the malady will become dangerous. Malignant tumours will grow quickly and unfold to alternative components of the body during a method known as metastasis.

A latest research [5] in the year 2021 says that in United States among 24530 adults (13840 men & 10690 Women) will be identified with cancerous tumours of brain and in the spinal cord. A person's probability of developing this type of brain tumour in their lifespan is less than 1%. It causes 85% to 90% of all primary central nervous system (CNS) tumours. A number of 3,460 children under the age of 15 will also be identified with a brain or CNS tumour this year, other than this deals with adult primary brain tumours. Brain and alternative system nervous cancer is the tenth leading reason behind death for men and women. It is evaluated that 18,600 adults (10,500 men & 8,100 women) may die from primary cancerous brain and CNS tumours in the year 2021. Hence it's important to improve the accuracy of previously proposed methods for the betterment of medical image research. In our paper, our proposed 99.74% accurate CNN-based algorithm will help medical representatives in their treatment job without manually analyzing the MRI images so that the treatment speed can be enhanced.

2. Methods for brain tumour segmentation

Brain Tumour segmentation methods can be divided as three parts. Manual methods, Semi-automatic methods and Absolute automatic methods. We can determine it according to the level of user interaction required [6].

2.1. Manual segmentation methods

It needs a medical specialist to use the different information picturize by the MRI images along with anatomical and physiological knowledge achieve through training and experience. This procedure requires the medical specialist going through multiple slices of images part by part, analyzing the brain Tumour and manually cropping the tumour regions carefully. It's a time consuming task as manual segmentation is also doctor dependent and segmentation results are subject to large intra and inter ratter variability [7]. Although, this is widely applied to execute the results of semi-automatic and fully automatic techniques.

2.2. Semi-automatic segmentation methods

It needs the reaction of the user for three main purposes; initialization, intervention or feedback response and evaluation [8]. Initialization is mainly executed by defining a region of interest (ROI), restraining the estimated Tumour area, for the automatic algorithm to process. Parameters of pre-processing technique can also be balanced to fit the input images. In addition to initialization, automated algorithms can be directed towards a necessary result throughout the procedure by receiving feedbacks. This process also provides the adjustments in response. Again, user can estimate the results and change or repeat the procedure again if not satisfied. Hamamci et al. proposed the "Tumour Cut" method [9]. This method comprised applying the algorithm separately to each MRI modality (e.g. T1, T2, T1-Gd and FLAIR). Then we combine the outcome to obtain the final tumour volume. A current semi-automatic method applied to a novel classification approach [10]. In this technique segmentation problem was converted into a classification problem and a brain tumour is segmented by training and classifying within that same brain only. Commonly, a machine learning classification technique, for brain tumour segmentation, needs a large quantity of brain MRI scans images (with checked answers) from different cases to train. This outcome in a necessity handles intensity bias correction and other noises. Although in this approach, user initializes the procedure by sort out a subset of voxels linked with each tissue type, from a single case. For these subsets of voxels, algorithm extracts the intensity values along with spatial coordinates as features and trains a support vector machine (SVM) that is used to classify all the voxels of the same image to their corresponding tissue type. Semi-automatic brain tumour segmentation approach not only takes reduces time than manual method but also it can maintain efficient results but still prone to intra and inter-rater user variability. Therefore, recent brain tumour segmentation research is mainly focused on fully automatic methods.

2.3. Absolute automatic segmentation methods

In this approach user does not need any interaction. Most importantly, artificial intelligence and preparatory knowledge are merged to solve the segmentation problem.

2.3.1. Challenges

Automatic segmentation of gliomas (A type of tumour that occurs in the brain and spinal cord) is a very tuff and important problem. Brain tumour MRI data obtained from clinical scans or synthetic databases [11] are naturally complicated. The devices for MRI and protocols that are using for acquisition can vary significantly from scan to scan imposing intensity biases and other variations for each different part of image in the dataset. Several modalities need to significantly segment tumour sub-regions even adds to this complexity.

2.3.2. BRATS dataset

BRATS refer to "The Multimodal Brain Tumour Image Segmentation Benchmark". Objective assessment of the outcome of different brain tumour image segmentation approaches with the state-of-the-art is a difficult task. Moreover with the implement of a widely accepted benchmark, the BRATS benchmark [12], for automatic brain tumour segmentation, now it's reality to objectively comparison various glioma segmentation approaches using this common dataset. Latest version (2020) of the BRATS training dataset has 369 multi-modality MRI scans, out of which 293 have been acquired from glioblastoma (GBM/HGG) and 76 from lower grade glioma (LGG) of patients with gliomas (both high and low grades) along with their ground truth segmentations for assessment [13]. Assessment on the testing data is only possible with the online assessment tool. Outcomes are represented by the tool mainly in the form of popularly known Dice Score, Sensitivity (true positive rate) and Specificity (true negative rate) for three main tumour parts; whole tumour (all tumour components), core tumour (all tumour components except edema) and active tumour (only active cells). Dice scores are mainly used for performance measures. For each tumour region, P1 represents the segmented tumour area by the proposed method, and T1 is the actual tumour area in the ground truth. Then, dice score is calculated by the online tool for each region as

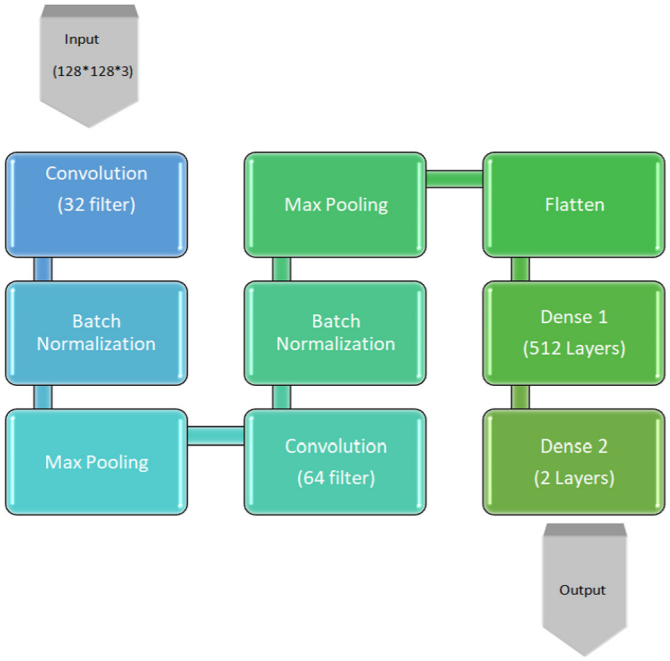

Fig. 1. Proposed methodology for tumour detection using 9-Layer Convolutional Neural Network.

$$Dice(P,T) = \frac{|P_1 \hat{} T_1|}{(|P_1| + |T_1|)/2}$$

3. Proposed methodology

Convolutional Neural Network is a well-ordered technique in the field of the medical image process. A convolutional neural network (CNN) could be a type of artificial neural network works in image recognition and process that's specifically designed for method component knowledge. CNN is a powerful image processing, computing method that use deep learning to perform each generative and descriptive tasks, typically exploitation machine vision that has image and video recognition, together with recommender systems and linguistic communication process (NLP). A neural network could be a combination of system of hardware and computer code similar to the operation of neurons within the human brain. Artificial neural networks are not ideal for the image process. A CNN uses a system very like a multilayer view-point that has been designed for reduced process necessities. The removal of limitations and increase in potency for image process ends up in a system which is way more effective, easier to train data for image process and linguistic communication process. We have changed the fundamental CNN model and projected a far better version of it. In our 9 layer CNN model, there are fourteen stages, as well as the hidden layers, which provide us with the foremost outstanding result for the apprehension of the tumour. The diagram presented in Fig. 1 is the projected methodology with a short narration.

In our proposed technique we have taken a complete variety of pictures as input and converted all the images into constant size 128*128*3 to form them unvaried dimensions. We tend to create a convolutional kernel that is convoluted with the input layer administering with thirty-two convolutional filters of size 2*2 every with the support of three channel tensors. We tend to used ReLU because of the activation function. The corrected linear activation function or ReLU could be a piecewise linear operate which will output the input directly if it is positive, otherwise, it will output zero. Next, we have applied batch normalization proposed by Sergey Ioffe et al. [14] in the year 2015. Batch normalization [15] (also referred to as the batch norm) could be a technique that not only creates neural networks quicker and additional stability through normalization of the layers' inputs by re-centering and re-scaling. We used it to form our algorithm quicker. See Fig. 2.

Next, the pooling operation implies sliding a 2D filter over each channel of the feature map and summarizing the features lying within the region covered by the filter. The dimensions of output obtained after a pooling layer for a feature map with dimensions n_h*n_w*n_c is

$$(n_h - f + 1)/s * (n_w - f + 1)/s * n_c$$

where,

-> n_h - height of feature map
-> n_w - width of feature map
-> n_c - no. of channels in the feature map
-> f - size of filter
-> s - stride length

A normal CNN model architecture is to have many convolutional and pooling layers piled up one after the other.

Pooling layers are used to decrease the dimensions of the feature maps. Thus, it decreases the number of parameters to learn the amount of computation performed in the network. The pooling layer summerise the features present in a range of the feature map generated by a convolutional layer. Therefore, further operations are performed on summarize features instead of accurately positioned features created by the convolutional layer. This makes the model more powerful to dissimilar in the position of the features in the input image.

Here, we have used a 2*2 Max pooling operation [16] that selects the maximum element from the range of the feature map covered by the filter. So, the output after the max-pooling layer would be a feature map containing the most important features of the previous feature map. See Fig. 3.

After this stage, we again used 64 filter convolutional, batch normalization, max-pooling methods before doing the flattening. We proposed two dense layers where the first dense layer has 512 hidden layers and 2nd dense layer has the final 2 layers. In the final layer, we used softmax as an activation function, as it is giving more accuracy than others. Again we used "categorical_crossentropy" as loss function and RMSProp (Root Mean Squared Propagation, or RMSProp, is an extension of gradient descent and Adaptive

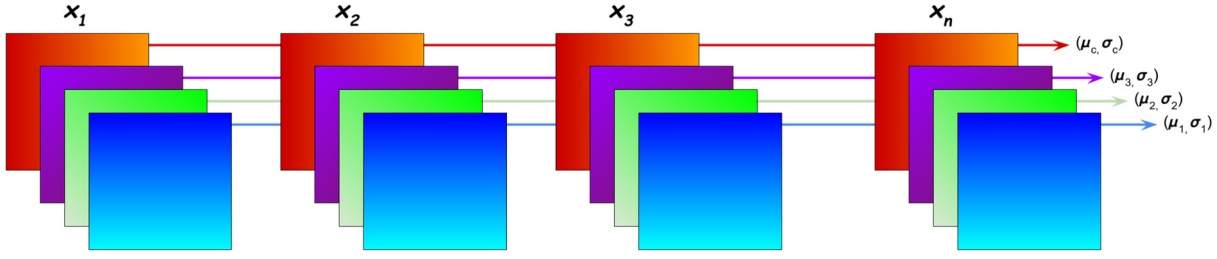

Fig. 2. Batch normalization.

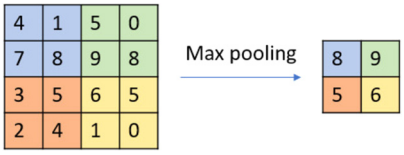

Fig. 3. 2*2 Maxpooling operation.

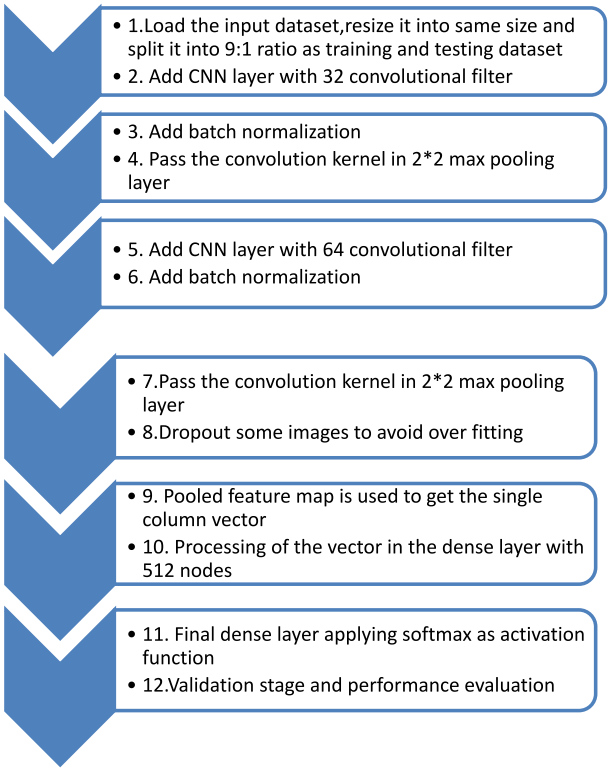

Fig. 4. Working flow of the proposed CNN model.

Gradient Algorithm version of gradient descent that uses a decaying average of partial gradients in the adaptation of the step size for each parameter.) as optimizer. Fig. 4 shows the working flow of the proposed CNN model.

Table 1
Comparison of different models.

Final Layer Activation Method	Optimizer	Accuracy (%)	Testing Accuracy (%)	Evaluation of the Model (%)
SVM	N/A	15.17	20.83	24.17
Sigmoid	RMSProp	97.63	58.33	68.72
Softmax	AdaMax	98.10	75	82.40
Softmax	RMSProp	**99.74**	93.78	97.71

4. Experimental results

4.1. Experimental dataset

We used the 2020 BraTS dataset for our experiment. We took a total of 2892 images with different types of tumours like T1, T2, and FLAIR. This dataset is consisting of two classes, where class 1 refers to tumour images and class 0 refers to non-tumour images. Some tumour datasets and non tumour dataset from our input images are shown in Fig. 5 and 6 respectively.

4.2. Results and discussion

Table 1 and Table 2 show our experimental results with different models, activation functions, optimizers of CNN. First we tried AdaMax (AdaMax algorithm is an extension to the Adaptive Movement Estimation (Adam) Optimization algorithm. More broadly, is an extension to the Gradient Descent Optimization algorithm) as optimizer then we found the accuracy of 99.74% using softmax in the final layer and RMSProp as optimizer, which is obtained for using 2473 number of training images, 273 number of testing images with 9:1 splitting ratio. Here we dropped out some images (around 5%) from the total 2892 image dataset to prevent over fitting.

Final output of the proposed method using 11 numbers of epoch has been shown in Fig. 7. Fig. 8 shows the training and validation accuracy with respect to the number of epochs and the corresponding loss is shown in Fig. 9.

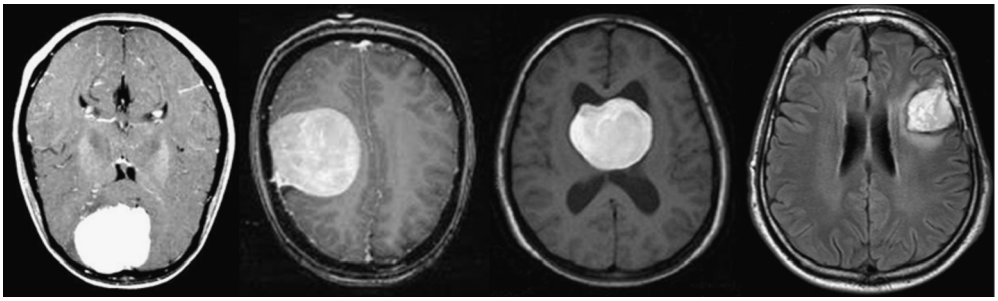

Fig. 5. Images with tumours.

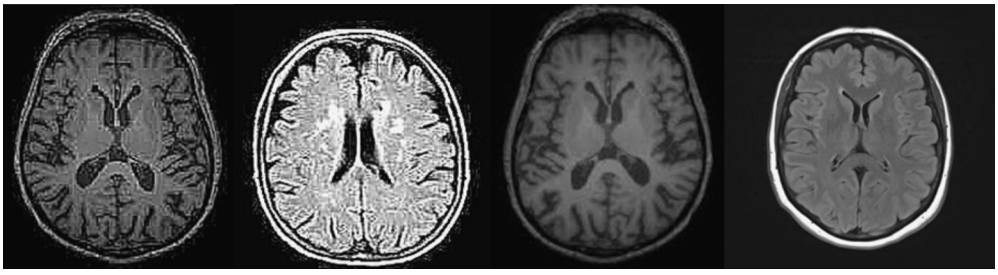

Fig. 6. Images with non-tumours.

```
Epoch 1/11
58/58 [==============================] - 80s 1s/step - loss: 13.7427 - accuracy: 0.7406 - val_loss: 1.8259 - val_accuracy: 0.6839
Epoch 2/11
58/58 [==============================] - 79s 1s/step - loss: 0.6205 - accuracy: 0.8180 - val_loss: 0.8964 - val_accuracy: 0.8256
Epoch 3/11
58/58 [==============================] - 79s 1s/step - loss: 0.2587 - accuracy: 0.9105 - val_loss: 1.3833 - val_accuracy: 0.8670
Epoch 4/11
58/58 [==============================] - 79s 1s/step - loss: 0.1062 - accuracy: 0.9680 - val_loss: 0.7154 - val_accuracy: 0.8929
Epoch 5/11
58/58 [==============================] - 79s 1s/step - loss: 0.1095 - accuracy: 0.9715 - val_loss: 0.1962 - val_accuracy: 0.9413
Epoch 6/11
58/58 [==============================] - 79s 1s/step - loss: 0.0536 - accuracy: 0.9849 - val_loss: 1.6301 - val_accuracy: 0.8549
Epoch 7/11
58/58 [==============================] - 79s 1s/step - loss: 0.0442 - accuracy: 0.9909 - val_loss: 0.5464 - val_accuracy: 0.9016
Epoch 8/11
58/58 [==============================] - 79s 1s/step - loss: 0.0688 - accuracy: 0.9862 - val_loss: 0.1340 - val_accuracy: 0.9706
Epoch 9/11
58/58 [==============================] - 82s 1s/step - loss: 0.0257 - accuracy: 0.9927 - val_loss: 0.4262 - val_accuracy: 0.9499
Epoch 10/11
58/58 [==============================] - 81s 1s/step - loss: 0.0072 - accuracy: 0.9974 - val_loss: 0.2805 - val_accuracy: 0.9706
Epoch 11/11
58/58 [==============================] - 75s 1s/step - loss: 0.0128 - accuracy: 0.9974 - val_loss: 0.4951 - val_accuracy: 0.9378
```

Fig. 7. Final output of our proposed method.

Table 2
Performance of the proposed CNN model.

No	Training Image	Testing Image	Splitting Ratio	Accuracy (%)
1	2199	543	8:2	99.73
2	2473	273	9:1	99.74

Fig. 8. Training and validation accuracy.

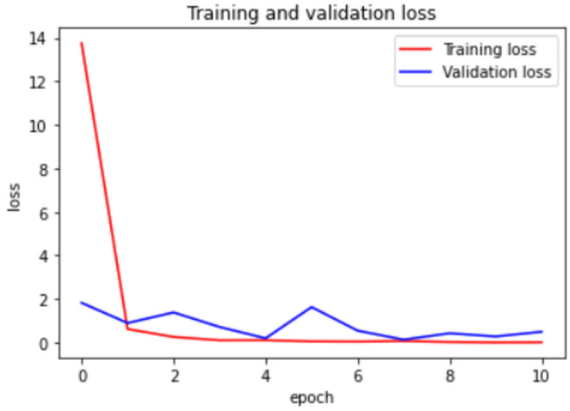

Fig. 9. Training and validation loss.

In this proposed model we got 99.74% accuracy that is higher than the state of the art results obtained by Seetha et al. [17] and Tonmoy Hossain et al. [18] as mentioned in the Table 3.

An example of predicted output image has been shown in Fig. 10.

Table 3
Performance comparison.

Methodology	Accuracy (%)
Seetha et al. [17]	97.50
Tonmoy Hossain et al. [18]	97.87
Proposed CNN model	**99.74**

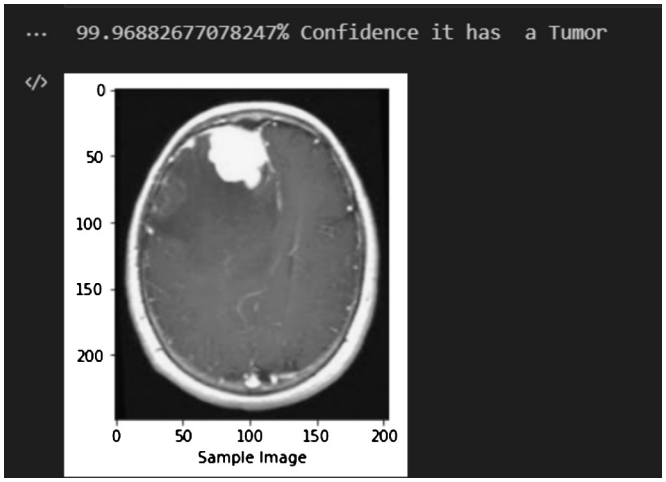

Fig. 10. Prediction by our proposed model.

5. Conclusion

MRI is most vastly used for tumour segmentation and classification. Although, convolutional neural networks (CNN) have the advantage of automatically learning representative complex features for both healthy brain tissues and tumour tissues directly from the multi-modal MRI images, so we decided to improve its accuracy. First we tried to implement SVM on CNN, but we got low accuracy of only 20.83%. Then we tried different parameters. We changed the final layer parameter to softmax and optimizer to AdaMax. Then we got 98.10% accuracy. But we need more, so we decided to change the optimizer to RMSProp, and finally we got the output accuracy to 99.74%. By using 2473 numbers of image as training data and 273 images for testing in 9:1 ratio with 11 epoch procedure we ultimately got our final result. Our model has 9 layer CNN model with 14 stages. Most importantly we also deleted some images to overcome overfitting.

Declaration of competing interest

We declare that we have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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