Acta Scientific COMPUTER SCIENCES

Volume 4 Issue 12 December 2022

Research Article

Brain Tumour Detection Using Convolutional Neural Network-XGBoost

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Received: October 30, 2022
Published: November 15, 2022

Abstract

Brain Tumour Detection is one of the most significant and essential task in the field of medical science. Brain tumours are of two types; malignant (cancerous) and benign (non-cancerous). Early detection followed by appropriate treatment is instrumental in increasing the probability of the patient getting cured. Manual methods are mostly time consuming, inaccurate leading to incorrect diagnosis. The main aim of this paper is to develop an automated system which can accurately detect the brain tumor with the help of a modified convolutional neural network algorithm called the CNN-XGBoost, which is an integrated and XGBoost, where CNN takes care of extracting training feature and XGBoost being used as the last level detector. The proposed method extracts the brain tumor from 2D Magnetic Resonance Images (MRI) of brain by using different algorithms like clustering, feature extraction, feature selection followed by CNN-XGBoost. Generally, this work is supposed to act as an assistive technology for doctors in order to make their work smoother and accurate. CNN is being implemented through Keras and TensorFlow. The most important task of this analysis is to distinguish between normal (without tumour) and abnormal (with tumour) images based on features, textures and image abnormalities. The proposed solution achieved high accuracy of identification at low computational cost.

Keywords: Convolutional Neural Network (CNN); XGBoost; Tumor Analysis; Feature Selection; Feature Extraction; Pattern Recognition; Magnetic Resource Image; Deep Learning

Abbreviations

ADAME: Adaptive Moment Estimation; CNN: Convolutional Neural Network; CNS: Central Nervous System; HSOM: Hierarchical Self Organizing Map; KNN: K-Nearest Neighbour; MLP: Multilayer Perceptron; MRI: Magnetic Resonance brain Images; SVM: Support Vector Machine; WHO: World Health Organisation; XGBoost: eXtreme Gradient Boosting

Introduction

The process of manipulating digital images using computer algorithms is primarily called as Digital Image processing. It is an essential preprocessing step in many applications, such as face recognition, object detection, and image compression. Medical image processing is useful in the analysis of different parts of the body. The two processes of Image segmentation and image feature extraction play a key role in the diagnosis of various types of anomalies in the body [18]. It plays a key role in the diagnosis and treatment of diseases. Image segmentation is a crucial and essential step in image processing that determines the success of a higher level of image processing [25].

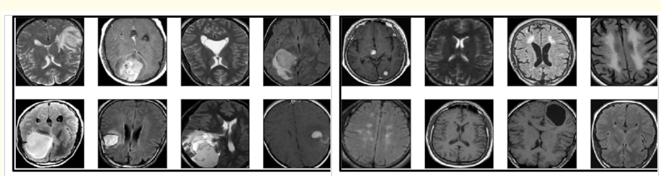
Brain tumors occur mostly due to the development of irregular cells within various parts of the brain. The pace at which malignant tumours spread and affect the main central nervous system is too fast. Cancer tumours may be classified into two categories;

primary tumours are those, which begin within the brain, secondary tumours, also known as brain metastasis tumours are those which spread to brain from somewhere else. On the other hand, a benign brain tumour is a mass of cells developing very slowly in the brain. Therefore, early detection of brain tumours can play an indispensable role in improving care choices, and end in a higher probability of survival. But, manual segmentation of MRI images of tumours or lesions is a time-consuming, demanding and burdensome task as it involves considerable amount of data.

Artificial Neural Networks (ANN) is one of the earliest and an efficient model to capture uncertainty in data [32]. After the addition of Deep Learning (DL) ([3], [1]) concept into ANN the Deep Neural Networks (DNN) models have been proposed ([8], [4]). DL has a dense network of layers where raw inputs are processed linearly and nonlinearly layer after layer in a hierarchical order. Representational learning is the general branch under which DL comes as a subfield. Several variants of DNN are available at present. Among these Convolutional Neural Networks (CNN) has been used as a very efficient model for image classification [22]. CNN works on data that is structured in a grid like manner. An image can be described as a $m \times n -$ dimensional matrix which is represented in a two dimensional grid. Thus, an image is considered as all the raw pixels which are features of the image. At a basic level a CNN may be described as a ANN which uses convolution in place of matrix multiplication, which is generally used in case of ANNs to compute the total input in at least one of the layers., It has been applied in several real life problems with success; like text based image retrieval [31], audio signal classification [9], study of gene characteristics [16], Computational Biology [7], Brain MRI segmentation [33], Diabetic retinopathy [26], Covid-19 detection [30], Confidence measure [29], There is a version of DNN called the Recurrent Neural Networks (RNN), which is suitable for temporal data analysis ([13], [2]). Deep learning has been useful health care [19] RNNs use sequential data or time series data and are commonly used for ordinal or temporal problems, such as language translation, natural language processing (NLP), speech recognition, and image captioning. Data Driven machine learning algorithms like Support Vector machines (SVM), Nearest Neighbour, Gradient Boosting and CNN are reliable and valid to classify tumours efficiently. However, most of the current methods applied for brain tumour classification do not make adequate use of image information and create robust features for identification. This leaves room for improved recognition through the provision of accurate high-level features.

Brain and other cancers of the nervous system are the 10th leading cause of death and the 5-year survival rate for people with cancers of the brain is 34% for men and 36% for women [36]. In addition, the WHO reports that about 400,000 people worldwide have been affected by brain tumours and 120,000 have died in the previous year [27]. In addition, an estimated 86,970 new cases of primary malignant and non-malignant brain and other CNS tumours are expected to be diagnosed in the United States in 2019[37].

Encephalon tumour is a very mundane and truculent disease, but surgery is a very important aspect for medics, and it is mandatory to abstract the tumour. This proposed study deals with the segmentation of Encephalon tumours and their relegation using CNN. Before performing the segmentation phase of the given MRI images, we must classify whether or not the tumour is present and then we will perform segmentation and area measurement on the segmented image below the images display regular and pathological (tumour) brain MRI. In our research work, we have used a Deep Convolutional Neural Network (Deep CNN or CNN) for classification where the last two layers give us the classification in 2 cases that the tumour is or is not present and in this sense the shape of the tumour can also be differentiated (Figure 1 (a) and 1(b)).



(a) Brain MRI Images with Tumor | (b) Brain MRI Images without Tumor

Figure 1

Literature Survey

Segmenting volumes of 3D MRI images manually and thus measuring the size of the tumour is a tedious affair and requires enough time. The efficiency of the process is also dependent upon the knowledge of the experts involved. Thus, development of accurate and fully automated systems for segmentation to measure the size of the brain tumour is of utmost necessity and highly suggestive.

Analysis of the segmented images helps in finding the exact size and the accurate location of the tumour. One of the effective approaches in tumour identification depends upon segmentation and using morphological operators. The first step is to improve the accuracy of the scanned image. Next, morphological operators are used over the scanned images to detect the tumours [23].

In this study we propose a fully automated method for the segmentation of brain tumours that is integrated into deep convolutional networks. Our approach was tested in the Multimodal Brain Tumor Image Segmentation (BRATS 2015) datasets comprising 220 high-grade brain tumours and 54 low-grade tumours. Cross-validation (Figure 4) has shown that our strategy can effectively achieve promising segmentation [14].

The approach used to remove brain tumour from 2D MRI is a Fuzzy C-Means clustering algorithm accompanied by conventional classifiers and a convolutional neural network. The experimental research was performed on a real-time dataset with a variety of tumour sizes, positions, shapes and different image strength. The traditional classifier component, we used six traditional classifiers, namely SVM, KNN, MLP, Logistic Regression, Naïve Bayes and Random Forest, which were implemented in scikit-learn [17].

The treatment is very consequential way to boost up the life of expectancy. More than one convolution layers with deep neural network is utilized for finding feature in neoplasm image. The utilization of diminutive kernels (3*3 or 5*5 size) sanctions by designing a deeper design, besides having a positive impact against over fitting. The goal is classification with segmentation of tumor part with the help of convolutional neural network and Watershed Algorithm. The input to the system is considered as brain scanned MRI image [24].

The K-means clustering technique to track tumor objects in MRIs of brain. The key concept in this color-based segmentation algorithm with K-means is to convert a given gray-level MR image into a color space image and then separate the position of tumor objects from other items of an MR image by using K-means clustering and histogram-clustering. Experiments demonstrate that the method can successfully achieve segmentation for MR brain images to help pathologists distinguish exactly lesion size and region [34].

Image segmentation is an important and challenging factor in the medical image segmentation. This segmentation method consists of two phases. In the first phase, the MRI brain image is acquired from patients' database, In that film, artifact and noise are removed after that HSOM is applied for image segmentation. The HSOM is the extension of the conventional self-organizing map used to classify the image row by row. In this lowest level of weight vector, a higher value of tumor pixels, computation speed is achieved by the HSOM with vector quantization [21].

A glioma is a tumor formed due to out of control cell growth of glial cells. Gliomas are categorized by subtypes and by a 1-4 grading system. Low-Grade Glioma (LGG) and High-Grade Glioma (HGG) are the two subtypes of glioma. Grade of a tumor is decided by the appearance of its cells under a microscope. LGG (Grades I and II) tumors are less aggressive, with low growth rate and are responsive to therapy. HGG (Grades III and IV) are highly malignant, more aggressive with high growth rate and are less responsive to therapy.

Proposed methodology

We suggest a novel method of classifying tumours using the CNN-XGBoost model to increase the efficiency of classification. By incorporating CNN as a Trainable Feature Extractor to automatically obtain features from the input and XGBoost as a Receiver at the top level of the network to produce performance, our method can ensure high reliability of the Extraction and Classification feature. In the following section, we will briefly clarify the two revolutionary classifiers and finally present the novel CNN-XGBoost model.

Deep learning

Deep learning is one of the most recent and useful methods of machine learning. In other words, it is said that DL learning is based on a deep-seated architecture. In fact, these architectures are the same old nerve networks that have become CNN's. These networks are data driven and feature engineering is carried out automatically, and we do not communicate with them, and that is precisely what makes these networks' accuracy and excellent performance in different areas. It is, in fact, a deep learning of a set of nerve-based techniques that automatically learn features from input data [35].

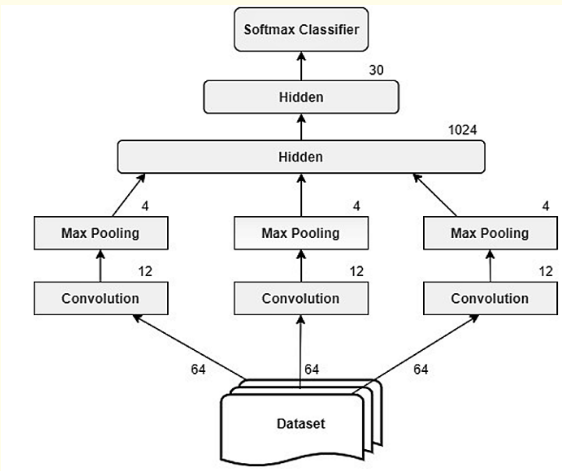


Figure 2: Convolutional Neural Network.

CNN (Figure 2) is a special type of DNN whose structure is influenced by the biology of the vision cortex of the cat [11]. CNN has a hierarchical structure that consists of several layers. CNN also features input layers, output layers, convolution layers, pooling layers, normalisation layers, and completely linked layers. CNN is different in terms of the number of layers used for the size and number of images, as well as the type of activation functions used. In CNNs, the parameters are chosen experimentally, based on trial and error [5]. In other words, each CNN consists of several layers, the main layers of which are the deep convolution layer and the Sub-Sampling layer.

Convolution layer

The fully-connected layer is similar to the way neurons are arranged in a traditional neural network. As a result, each node in a fully connected layer is directly connected to each node in both the previous and the next layers. Any node in the last frames of the pooling layer is connected as a vector to the first layer of the fully connected layer. These are the most common criteria used by CNN within these layers, which take a long time to practise. It takes a lot of time on the network. The performance of the network also depends on the number of levels in the network. After the features have been acquired, the features of the Convolution Layer are used to categorise images [12].

Sub-Sampling layer

The operation of this layer is done to reduce the size of the input image. By this layer, we're getting a point vector at the end of CNN. The aggregation or sub-sampling operation is used as a mean pooling or max pooling operation [15].

Feature extraction

Features are created from the initial data set for machine learning and image processing. This supports the learning process. If the input data of an algorithm is too large, it can be converted into a smaller set of features. The method of extracting a subset from the primary function set is called the extraction function. The selected features include information on the input data, so that the reduced representation of the agent can be performed instead of the full initial data. One of the important applications of the extraction function is the image processing, which is used to discern the desired segments or the shape (features) of the digital image or video stream (Figure 3).

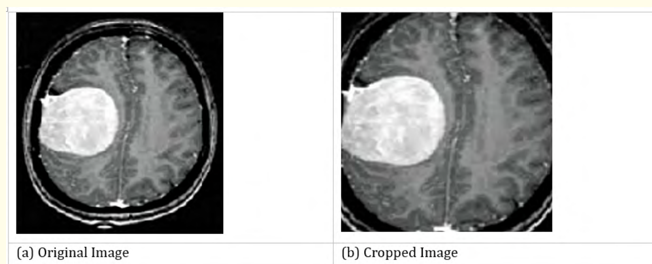


Figure 3

Methodology

The basic structure of the XGBoost Tumor Classification Model is shown in the figure 6. Next, the input image data is normalised and transferred to the CNN input layer. After training CNN with a BP algorithm for several epochs to get a proper image classification structure, XGBoost replaces CNN's output layer, a soft-max classifier, and uses CNN's training features. The CNN-XGBoost model is finally getting the results of the test images for a new classification. Our CNN-XGBoost model automatically obtains input features and generates more accurate classification results combining the two outstanding classifiers.

Simulation

In a few cases, certain parts of the pictures are mistakenly diagnosed as tumours, or the tumours cannot be seen by the physician; the most reliable diagnosis depends entirely on the ability of the physicians. CNN was used in this paper to detect tumours by brain images. Additional margins of the images were collected from the imaging centres. These margins have been clipped to prevent picture noise. One of the key reasons for using and incorporating the extraction function technique with CNN is to restore the image extraction feature in order to enhance the accuracy of the network. According to CNN's findings on the initial photos, a new method is proposed in this study to improve the accuracy of the network, combining the Clustering algorithm for feature extraction and CNN with XGBoost.

Feature extraction method

The central clustering approach is a clustering approach. This algorithm has a repeat procedure that iteratively attempts to obtain points as cluster centres for a constant number of clusters, which are basically the same mean points belonging to each cluster. And assign each sample data to a cluster that gives the data a minimum distance to the centre of the cluster. In the simple form of this method, the cluster centres are chosen at random first. Points are assigned to cluster centres according to the degree of similarity, and thus new clusters are obtained. In this paper, the first-order clustering algorithm was used to extract a function, an image obtained by applying the clustering algorithm to the image.

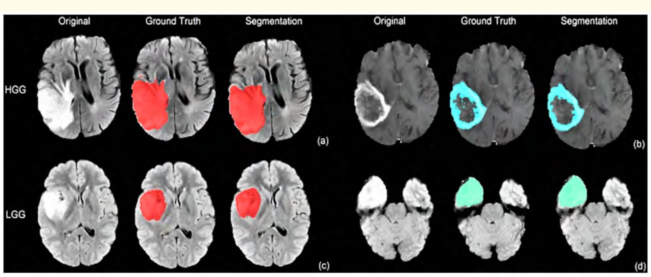


Figure 4: Detection and classification of HGG and LGG brain tumor.

Convolutional neural method

Initially, the images were applied to CNN without any form of character extraction. The initial dimension of the input image is 227×227. The architecture used to recognize and classify images, consisting of 5 Convolution layers and 3 layers of Sub-Sampling layers, Normalization layers, Normalization layers, Completely Connected layers and, finally, Classification layer [20]. There are 4096 neurons in the completely interconnected layers. There are two classes in this layer: a patient with a brain tumour and a normal patient. CNN uses the concepts of responsive fields, weight sharing and pooling to reduce the complexity of the network structure and the number of parameters. "Receptive field" is the same as constructing a series of spatially localized filters that can be used to obtain some of the key features of the input. While "weight sharing" decreases the number of parameters that need to be trained. 'Pooling' would simplify the model and keep it from being over-fitted (Figure 5).

Max pooling layer

When a feature is defined in a convolutional layer, the exact position of the feature becomes less important only if its approximate location is preserved relative to the other features. Therefore in response to the sensitivity of the output, an extra layer known as the max pooling layer is added to the existing convolution layers. Another key function of this max pooling layer is the protection of the scale invariant feature, which is an important and critical feature of CNN. In this layer, the features of the convolution layers are further divided into different partitions and max operation is applied to the output values of each partition. The formula activation function can be calculated in the max pooling layer. The formula is:

$$x_i^{l,j} = max_{k=1}^{r}\left(x_{(i-1)\times s+k}^{l-1,j}\right) \text{------------- (1)}$$

Owing to the partial structure of weight sharing in the max layer the local filters are close together and share their weights. The pooling function is fraction- ally distinct from the original one as the maximum operation and the shared weights take place in almost the same section.

$$x_i^{l,j} = max_{k=1}^{r}\left(x_k^{l-1,j}\right) \quad \text{-------------- (2)}$$

Forward and backward propagation

Forward propagation

It is mentioned that the forward spread is carried out in a convolution network with N nodes. If the m filters of w are used in the part of the convolution layer, the output size is (N-m+1). The output of each convolution layer is moved to the next layer, which is the max pooling layer. Equation 6 indicates the maximum pooling layer, e.g. a k large window size is taken and the output of each layer is a single value, which is the maximum of the window size output. If the input layer size is N node, then the total number of outputs from all max pooling layers is N/k node, as each k window is reduced to a single value via the max pooling layer.

Backward propagation

After the forward propagation iteration is completed, the error value is determined along with the loss function L (using the L2-norm here when the forward propagation edge in the CNN model is modified backwards using various gradient descent algorithms.

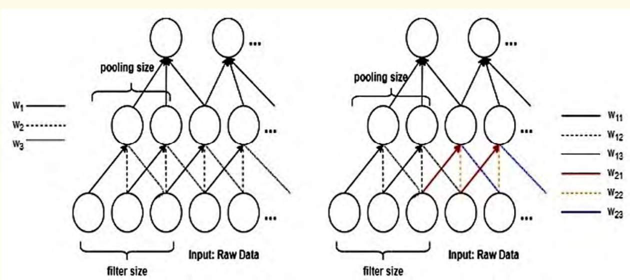


Figure 5: Weight sharing CNN.

Learning phase (backpropagation) is slower than the inference phase (forward propagation). This is even more pronounced by the fact that gradient descent often has to be repeated many times. In fact, gradient descent has a convergence rate of $O(1/\in)$ for a convex function where ϵ is the error of the final hypothesis. Thus the computational cost is less as compared to other algorithms.

eXtreme gradient boosting (XGBoost)

XGBoost has been commonly used in many fields to produce effective results and performance on many data problems, and is a highly powerful scalable tree-based machine learning framework. Scalability in all XGBoost scenarios is due to many significant systems and algorithmic optimizations, including a novel tree learning algorithm, a technically justified weighted quantum sketch procedure, as well as parallel and distributed computing [11].

Tree boosting is a very effective ensemble learning algorithm, which can transform several weak classifiers into a strong classifier for better classification performance. Let represents a database with n examples and m features. A tree boosting model output with K trees is defined as follows:

$$\hat{y}_i = \sum_{k=1}^{K} f_k(x_i), \ \ f_k \in F \quad \text{---------} \ (3)$$

Where K is the number of trees, f_k is $k-th$ tree model. $f_k(x_i)$ is the score of the $i-th$ observation obtained from $k-th$ tree. $F = \{f(x) = \omega_q(x)\}(q: R^m \to T, \omega \epsilon R^T)$ is the space of regression or classification trees (also known as CART). Each

f_k divides a tree into structure part q and leaf weights part ω. Here T denotes the number of leaves in the tree. The set of function

f_k in the tree model can be learned by minimizing the following objective function:

$$O = \sum_i l(y_i, \hat{y}_i) + \sum_k \Omega(f_k) \quad \text{------------} \ (4)$$

$l(y_i, \hat{y}_i)$ is a differentiable convex loss function which measures the distance between the prediction and the object . The second term $\Omega(f_k)$ represents the penalty term of the tree model complexity for the $k-th$ tree.

Tree boosting model whose objective function in above equation cannot be optimized through traditional optimization methods in Euclidean space. Gradient Tree Boosting is an improved version of tree boosting by training tree model in an additive manner, which means the prediction of the t-th iteration $\hat{y}_i^{(t)} = \hat{y}_i^{(t-1)} + f_t(x)$. The objective function in t-th iteration is changed as:

$$O^{(t)} = \sum_{i=1}^{n} l\left(y_i, \hat{y}_i^{t-1} + f_t(x_i)\right) + \Omega(f_t) \quad \text{----------} \ (5)$$

Where f_t is the $t-th$ tree and n is the number of observations.

XGBoost approximates above equation by utilizing the second order Taylor expansion and the final objective function at step t can be rewritten as:

$$O^{(t)} \simeq \tilde{O}^{(t)} = \sum_{i=1}^{n}\left[l\left((y_i, \hat{y}_i^{t-1} \right) + g_i f_t(x_i) + \tfrac{1}{2} h_i f_t^2(x_i) \right] \text{---------(6)}$$

Where g_i and h_i are first and second order gradient statistics on the loss function, and $\Omega(f) = \gamma T + \frac{1}{2}\lambda\|\Omega\|^2$ in XGBoost [28].

XGBoost is a fast implementation of GB algorithm, which has the advantages of fast speed and high accuracy. This XGBoost classifier (Figure 6) is added to the top level of the CNN to produce results for image classification in our paper.

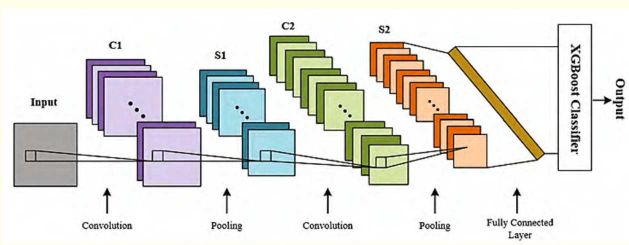


Figure 6: XGBoost Classifier.

Random forest

Random forest is a robust algorithm that can be used for remotely sensed data classification and regression. Random forest efficiency is on par with other machine learning algorithms, but it is much easier to use and more tolerant when it comes to over-fitting and outliers than other algorithms. Some common applications of random forest classification include land cover and land cover mapping and cloud and shadow detection. Random Forest developed by Leo Breiman [10] is a group of unpainted tree classifications or regressions made from random samples of training data. Random features are selected during the induction process. Prediction is made by aggregating (majority vote for classification or regression average) the ensemble predictions [6]. Random forest is also applied in classification of brain tumor detection. In this paper a comparison of random forest is done with proposed methodology of CNN and xGBoost.

SVM

The support vector machine is a novel small sample learning method, because it is based on the principle of structural risk minimisation rather than the traditional empiric risk minimisation principle, and is superior to existing methods for many performances. It has a good generalisation capability. Using the kernel function method, when samples are mapped with high-dimensional space, the method does not increase computational complexity thus effectively overcoming the curse of dimensionality.

Experimental Results

Dataset

The dataset consists of MR scans of LGG and HGG patients with repeat manual tumour definitions by a number of human experts, as well as realistic brain tumour datasets. The data collection consists of two categories of Clinical Image Data and Synthetic Image Data images. Clinical image data consists of 65 multi-contrast MR scans from Glioma patients, of which 14 were obtained from low-grade (histological diagnosis: Astrocytoma or Oligoastrocytomas) and 51 from high-grade (Anaplastic Astrocytoma and Glioblastoma multiform tumour) Glioma patients. The images represent a mixture of pre-and post-therapy brain scans, with two volumes showing resections. Over the course of several years, they have been acquired in four separate centres – Bern University, Debrecen University, Heidelberg University and Massachusetts General Hospital – using MR scanners from different suppliers and with different field strengths (1.5T and 3T) and imaging sequences (e.g. 2D or 3D). Synthetic evidence for BRATS 2015 consisted of simulated images for 35 high-grade and 30 low-grade Glioma with identical properties of tissue contrast and segmentation.

Data augmentation

The performance of deep neural learning networks also increases the amount of data available. Data increase is a tool used to artificially create new training data from existing training data. This is accomplished by applying field-specific techniques to training data examples that produce new and distinct training examples (Table 1). Image data increase is possibly the most common type of data increase and involves the development of transformed copies of images in a training dataset that belongs to the same class as the original image. Transforms provide a variety of image processing operations, such as shifts, flips, zooms, and more.

Dataset processing

The network architecture of the framework used to classify CNN-based tumours has been shown to have been implemented

	Number of examples	Percentage of positive examples	Number of positive examples	Percentage of negative examples	Number of negative examples
Training Data	1442	52.871	764	47.128	681
Validation Data	310	54.838	170	45.161	140
Testing Data	310	48.709	151	51.290	189

Table 1: Data augmentation.

with the aid of open source software, namely TensorFlow. The neural network has been trained and tested in the Python environment. The hyper parameter values for the experimental setup were selected as follows: number of convolution filter = 60 (first convolution layer), 6 (second convolution layer), window size = 1; convolution window size = 60; training batch size = 16; pooling window size = 21, window size = 2; number of hidden neurons = 1000 and training epoch size = 100. The ADAME optimization approach was used to measure and optimize the loss function of the CNN model built along with the minimum negative log-likelihood cost function. Adam is a method of optimization that can be used to change the weights in the network iteratively based on the training samples instead of the classical stochastic gradient descent method. The hyper-parameters in the current CNN model are explained as follows:

- **Training Epoch Size:** The epochs for training were set to 100.
- **Training Batch Size:** It was set to 16 as in CNN small batch size not only helps to avoid falling to local minimum value but also enhance the network's generalization ability.
- **Weight Initialisation:** Small random numbers are used to initialise the weight of the convolution kernels in the convolution layers. This includes the dataset following the Gaussian distribution (mean value = 0 and standard deviation = 0.1). However any dataset following the Gaussian distribution cannot be used for weight initialization as it may result in zero gradient networks. Thus in order to address this problem, two functions, namely the truncated Gaussian distribution function and the optimised Gaussian function, were used where small data values outside the range ($\mu - 2\sigma$, $\mu + 2\sigma$) were given up.

Parameters of analysis

All activities are summarized for dataset and presented using confusion matrix based on True Positive (TP), True Negative (TN), False Positive (FP), False Negative (FN), False Positive Rate (FPR) and False Negative rate (FNR) The expressions for these measures are provided in (6) and (7).

$$Recall = \frac{TP}{TP+FN}, Accuracy = \frac{TP}{TP+TN+FP+FN}, Precision = \frac{TP}{TP+FP} \quad \text{-------- (7)}$$

$$FPR = 1 - Specificity,\ FNR = 1 - Sensitivity \quad \text{----------- (8)}$$

Specificity is described as True positive rate and Sensitivity is described as True negative rate in an experiment. Sensitivity is the probability of a positive test given that the patient has that disease. Specificity is the probability of a negative test given that the patient does not have the disease.

Result analysis

CNN was able to clearly categorize the images of patients with tumours and normal patient tumours with a precision of 91.67%. According to CNN's findings on the initial images, a combination of a feature extraction clustering algorithm and CNN is used to improve network performance. Other classifiers such as the Softmax Fully Connected Layer Classifier in the CNN architecture, along with the XGBoost, were used to test the efficiency of the proposed technique. The results of the classification show that Random Forest produces better results or the same number of attributes and parameters, but not as good as the proposed algorithm. Random forest has achieved an accuracy of 87.63% and precision of 85.19% which is less than compared to proposed algorithm. For further analysis compared to proposed algorithm SVM and random forest is also implemented. The results of the entire algorithm are in the table 2. SVM has shown an accuracy of 89.16% and precision of 89.69% which is better than random forest but our proposed algorithm outcast SVM.

The parameters for accuracy, sensitivity, specificity and precision have also been used to verify the function of the classifier. The precision of CNN is achieved by the Softmax classifier used to classify images collected by 91.67%. The suggested solution (combination of XGBoost and CNN) increased the accuracy of the test data to 93.12 per cent. For further analysis compared to proposed algorithm SVM and random forest is also implemented. The results of the entire algorithm are in table 2. The reasoning is that we are using CNN to automatically extract high-quality features with less loss of image information and high-speed XGBoost to achieve an accurate classification (Figure 7). These findings demonstrate impressively the feasibility and reality of the proposed new image classification method with the CNN-XGBoost model.

	Recall	Precision	FPR	FNR	Accuracy
Random Forest	88.06%	85.19%	5.97%	7.812%	87.63%
SVM	90.16%	89.69%	5.71%	6.89%	89.16%
CNN	92.16	91.189	5.1%	6.7%	91.67%
CNN+ XGboost	93.012	95.16	4.57%	5.31%	93.12%

Table 2: Results.

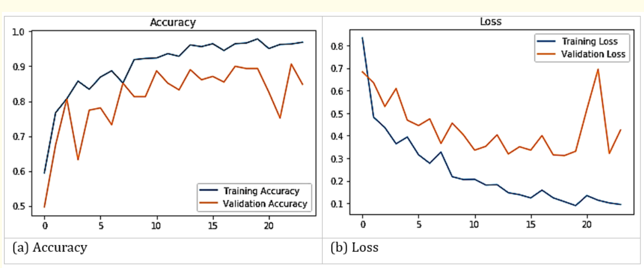


Figure 7: Accuracy and loss during training and validation.

Conclusions

In this paper, we presented a fully developed CNN with XG-Boost for brain tumour detection and segmentation using deep convolution networks. Based on the experiments on well-established benchmarking (BRATS 2015) datasets, which include both normal and brain tumour images for patients, we have shown that our approach can provide both effective and robust segmentation compared to manually-delineated ground reality. In addition, compared to other machine learning approaches, our CNN-XG Boost can also provide comparable results for the complete tumour regions and superior results for the core tumour regions. In our current research, the validation was carried out using a five-fold cross-validation scheme. The proposed method makes it possible to produce a patient-specific brain tumour segmentation model without manual intervention, potentially allowing for objective evaluation of lesions for clinical tasks such as diagnosis, treatment planning and patient monitoring.

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