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ILLUMINATING BRAIN TUMOR IN MRI METAPHORS BY USING A HYBRID MODEL OF FASTER R-CNN AND CNN

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Abstract:
In this study the problem of fully computerized brain tumor classification and segmentation, in Magnetic resonance imaging (MRI) containing both Glioma and Meningioma types of brain tumors are considered. This paper proposes a Convolutional Neural Network (CNN), for classification problem and Faster Region based Convolutional Neural Network (Faster R-CNN) for segmentation problem with reduced number of computations with a higher accuracy level. This research has used 218 images as training set and the systems shows an accuracy of 100% in Meningioma and 87.5% in Glioma classifications and an average confidence level of 94.6% in segmentation of Meningioma tumors. The segmented tumor regions are validated through ground truth analysis and manual analysis by a Neurologist.

Keywords:
Convolutional Neural Networks, Brain Tumor, Magnetic resonance imaging, Segmentation, Classification, Computer Vision

INTRODUCTION

Brain tumor is the advancement of unusual tissues in the cerebrum and distinguishing something very similar at a beginning phase can be dealt with appropriately. By and large, brain tumor can be delegated in excess of hundred kinds in light of the area and development of growth. Specialists have named mind tumor in stages as Grade I, II, III and IV as per the development and side effects of cerebrum growth. The significant brain growths are harmless and Threatening where harmless have some consistency in shape and non-dynamic, yet dangerous doesn't have consistency in shape and dynamic. The image processing techniques used to identify the brain tumor are Magnetic Resonance Imaging (MRI), Positron Emission Tomography (PET) and Computed Tomography (CT). By comparing all these three imaging techniques, MRI is good quality medical imaging for detecting brain tumor. In this study, four types of brain tumor are used namely benign- slow growing tumor, malignant, which are most commonly seen in infants and children called PNE, glial-astrocytic tumor and astrocytoma-low grade tumor.

LITERATURE REVIEW

In previous works segmentation techniques are used to detect brain tumor by segmenting the tumor area. Faster R-CNN algorithms are mainly used for object detection in natural images by creating bounding box with class names and score. In this system object detection algorithm Faster R-CNN are used to detect the tumor in brain and created bounding box on tumor with tumor name.
Brain Tumor is an abnormality growth arising from the brain tissues, which could be life threatening if not detected and appropriately treated at an early stage. Typically, Magnetic resonance imaging (MRI) and Computer Tomography (CT) scans are used by medical staff to obtain detailed images of the brain for initial analysis, over invasive procedures such as tissue biopsies. Further, use of computer-based image analysis in collaboration with medical knowledge, can contribute significantly to aid the early diagnosis [2]. Hence, increasing number of existing and new computer-based image classification and segmentation algorithms are applied and validated in this line of study by many researchers [1-3, 5-7].
Image classification and segmentation has been studied for many years with several different types

of algorithms, in image processing and computer vision, for supervised, unsupervised feature extractions. Recently, CNN has become the most popular approach for image segmentation and classification in different areas of research, such as medical imaging, video surveillance, factory automation, etc.[2] to achieve automation. The foremost appeal of CNN is its ability to learn increasingly complicated features from the input for the classification task. For instances, architectures of CNN such as, Alex Krizhevsky network (AlexNet) is a popular choice in medical image segmentation [3], whereas GoogLeNet and ImageNet are extensively used in visual recognition, and computer vision[4].However, applications of CNN was restricted in the past decade due to the computational cost and the training time associated with the system architecture. But recently, with the advancements of modern computing technologies, specifically Graphics Processing Unit (GPU), the performance of CNN has improved drastically with significant reduction in processing time.

Recently, Deep learning techniques are extensively used in medical imaging to, identify local anatomical characters, detect organs and body parts, and identify cells of different shapes and sizes. According to literature, normal and abnormal classes of brain MRI can be easily distinguished using machine learning algorithms, classifiers, and neural networks.[5–7].Yet, at present the prospective of CNN for tumor detection and segmentation is at preliminary investigation stage and poorly studied. One of the key challenges faced by researchers is accurate tumor identification with low complex networks. A recent study [8], showed a high accuracy in classification of meningioma, glioma and pituitary tumors, but their approach requires higher number of convolution layers, and kernels resulting in a high computational cost.

In this research, CNN based system for tumor classification and segmentation is proposed. With the method presented, it was possible to gain similar level of classification accuracy as in [8], with a relatively simple architecture using only two convolutional layers and less number of kernels. Further, the initial model was extended to identify the bounding box of the meningioma tumor with an average confidence level of 94.6%.Moreover, the proposed method is able to extract tumor mask with a high accuracy. Since, most of the Faster-R CNN based segmentation focus on non-medical applications [9], [10], this paper provides an insight into the possibility of using Faster-R CNN in medical imaging as well. The segmented tumor regions are validated through ground truth analysis and nasalization process was done by different Neurologists.

CONVOLUTIONAL NEURAL NETWORK

CNN is a layered engineering which performs convolution, initiation, pooling, and completely connectedness to break down visual symbolism. The fundamental improvement of CNN from the conventional fake brain organization (ANN) is the convolution layer. The main role of convolution is to extricate highlights from the info pictures. In the convolutional layer, the model purposes various types of channels of various sizes to assemble different element maps. By presenting this layer, the model will radically lessen the quantity of weighted boundaries. Additionally by convolutional procedure, the organization can gain proficiency with the connections between's the adjoining pixels [11]. As the initial step, input pictures are taken care of to the model and the speck item is applied to the info picture and boundary vectors of every neuron. Then convolution administrator is applied to each contribution at each convolutional layer. The principal distinction between R-CNN and Quicker R-CNN is that R-CNN utilizes the district proposition at pixel level as information, while Quicker R-CNN utilizes the area recommendations at highlight map level as information. Further, to work on the presentation in Quicker R-CNN, particular pursuit at RPN is supplanted by CNN.

METHODOLOGY

Data Preparation: In this research, T1-weighed MRI brain tumor dataset presented at [14], [15] is used. These MRI images were collected from Nanfang Hospital, Guangzhou, China, and General Hospital, Tianjing Medical University, China, from 2005 to 2010.This particular dataset consists of labels, patient IDs, image data and tumor boarder coordinates along with T1- weighted axial, sagittal

and coronal planes. It consists of 3064 MRIs from 233 patients with 3 kinds of brain tumors; namely meningioma (708 slices), glioma (1426 slices) and pituitary tumor (930 slices) with coronal, sagittal and axial planes MRI.
Since T1-weighted MRI is popular imaging modality acquired for treatment planning [16], in our study it focuses only on contrast enhanced T1 MRI. These T1 type images have a contrast agent (gadolinium) to improve the contrast of the areas affected by the tumor. For the experiments presented in this paper, only axial MRI of two types of tumors, that is meningioma (119 slices) and glioma (138 slices) is used. Since the pituitary tumor only occurs in pituitary gland, it is not hard to classify this type of tumors, but classification of meningioma and glioma is not that straightforward. Initially, experiment dataset is split into three; for training, testing and validation.

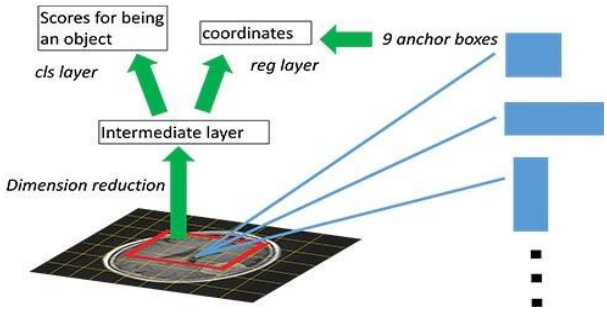


Fig 1: A region proposal network

Proposed System Architecture: The CNN model employed is based on [13] and only minimal preprocessing is used to avoid information loss and to retain the useful features of the MRI dataset. At the preprocessing stage, the input image is down sampled to 128x128 image and fed into the CNN model as shown in the Fig.2.It must be noted that due to down sampling the sensitivity of the output could be reduced by a small fraction, as some features of the input could be lost during the process, Since the input images are in uint8 format, pixel values of all the images are divided by 255 to normalize. Therefore the pixel values of normalize images are in the range of 0-1.
The proposed system consists of two stages; training and testing. The model is trained using 218 images of two tumor types, meningioma and glioma, and tested with another dataset which is independent from training dataset. The proposed architecture of the working model is shown in Fig.2. This architecture comprise of pre-processing for dimension reduction, CNN model for feature extraction and tumor classification, and finally faster R-CNN model for tumor extraction. In mathematics the convolutional procedure can be expressed as (2), As shown in Fig 2, first the normalized dataset is fed to the1st convolutional layer. The over-fitting was reduced, with the normalization techniques employed in the system architecture, at the 1st convolutional layer, the input images are convolved with 20 filters each with 3×3 size kernels, and creates 20 different feature vectors. In general, 20 feature maps were sufficient at the first layer, to gain a sufficient accuracy. Then the output of this layer is fed to ReLU and maxpool layers with 2×2 window size.
The 2nd Convolutional layer also consists of 10 filters having 3×3 kernel size. As in the previous layer, the output of the convolution layer is fed to activation function (ReLU) and maxpool with 2×2 window size. The output at this stage will have 10 feature vectors. It was observed that, 10 feature vectors are sufficient at this stage to achieve a good level of overall performance. The purpose of using max pooling layer is to reduce the dimension by interpreting the maximum value of the window.
Proposed model for tumor segmentation: After CNN classify the tumor as meningioma or glioma, faster R-CNN is used for tumor segmentation and localization. In our system, only the meningioma dataset is used for the dataset was split into two; 110 images for training and 9 images for the validation. Here each region proposal consists of an “object ness” score for that particular region, and coordinates for the bounding box representing the region proposals. At the last layer of the CNN, a 3×3 sliding window moves across the feature map and it maps to a lower dimension. The basic objective is to search each location in the last feature map, with search boxes of varying sizes and

centered on the region of interest. Each region box gives the coordinates of the box and whether an object is present within it. As in Fig.2, each

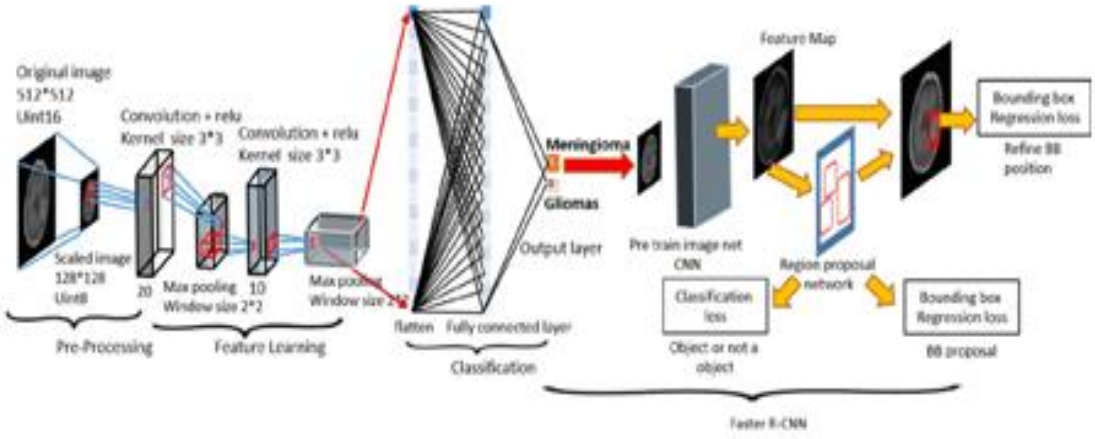


Figure 2: Proposed architecture

If an anchor has an object score above a certain threshold, the anchor coordinates get forwarded as a region proposal. Thus before proposing regions for the feature extraction, the system runs one full CNN over the full image and extends the neural network for prediction by soft ax layer. The significance of this is, instead of training many different models to classify each object class; it outputs the class probabilities directly. Therefore it has only one neural network to train. Henceforth, the proposed architecture performs much better in terms of speed, since it only needs to locate the tumor area bounding box rather than classifying. Thus, the final output of the proposed model is the bounding box and the confidence level indicating the probability of the region box being a meningioma.

Exact tumor Boundary detection: The normalized coordinates of the bounding box are given as the output of the faster R-CNN model and these coordinates are with reference to the low resolution images (128×128).After detecting the coordinates of the bounding box, it is mapped to the image with original resolution (512×512) and obtain the estimated area of meningioma tumor.

Although the system architecture so far was able to identify a box region of the tumor with a high confident level, still this model fails to give an idea about the exact location and the area of the invasive tumor. To identify the spread of the exact tumor, it was necessary to have a tumor mask with a high accuracy level. Several edge detection algorithms such as Prewitt and Sobel are applied to the bounding box which is obtained from Faster R-CNN, to identify the tumor edges. Prewitt and Sobel operators calculate the gradient of the image intensities at each pixel point and give the direction of intensity changes. Fig. 3 presents the binary images with tumor boundaries for different gray scale threshold values. Then, using an average filter, the output of the edge detection stage is smoothened. Later an appropriate grayscale threshold level was used to generate a binary masked image to filter out the tumor cells from the original MRI as seen in the fourth row. The final row of the table shows the generated tumor mask against rest of the image. The accuracy of the segmented outcome is confirmed by analyzing them against the ground truth demarcations presented by a Neurologist. Table III shows result of a special case. As this particular MRI consists of artifacts due to bone structures, it is very difficult to identify the malignant tumor region with the naked eye. The significance of the proposed model is, it was trained using a limited data set which covers all the axial levels of the brain including the level of the pons, midbrain and lateral ventricles etc. Hence as show in Table III, this system is able to segment tumors, which not clearly visible to naked eye, with a confidence level of 99%.

EXPERIMENTAL RESULTS

This section presents the results obtained by the proposed brain tumor classification and segmentation method. The proposed method was implemented using python tensor flow and keres

libraries, and validated using more than 200 image sets of both healthy and diseased patients. The results are analyzed in two folds: first with the accuracy of the classification data and then with the accuracy of the extracted tumor mask. The tests were performed on a computer with Intel(R) 8 Series Chip set processor, 4.00GB RAM and 64-bit operating system, ×64-based processor. In this work presented, only T1 MRI was used, with the objective of fine tuning the proposed system to be able to classify the tumors with highest possible performance for a single type of imaging modality, which is T1 MR Images.

Further, this experiment proceeds only using axial plane slices, as they have higher resolution and less noise compared to coronal and sagittal plane slices. Once the tumor is detected in axial plane slices at initial stage of detection, the Radiologists could proceed with further analysis using both coronal and sagittal plane slices. Initially the accuracy of the proposed system was analyzed for the classification of meningioma and glioma tumors as shown in Table I. The two-layered CNN used for feature extraction and classification demonstrates a very accurate result in identifying the tumor type and extracting the tumor regions. According to the results presented in Table I, the proposed model was able to classify the two tumor types with a nearly 94% accuracy. Further, the detection accuracy of meningioma is 100%. These results were generated after running our proposed network on a data set of 218 images.

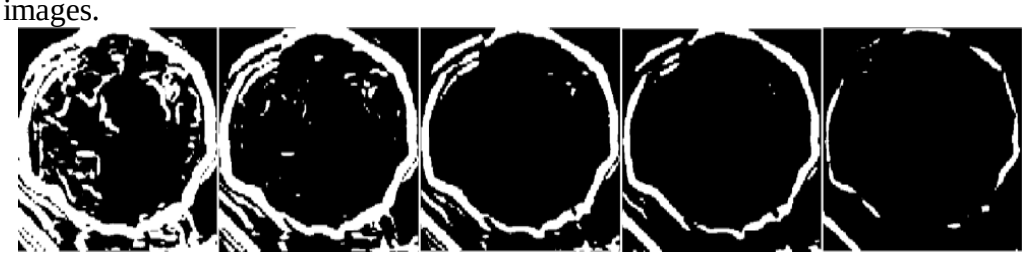


Fig 3: Binary images (extracted tumor) for different threshold levels

Moreover, the classification task is improved by segmenting the tumor regions from classified images. Table II presents the segmentation outputs of our system for selected images. The results were checked against ground truth pixel level labels generated by Neurologists. The original T1 images of the meningioma tumors are shown in Table II under first row 'T1 images'. These images were selected randomly from the validation dataset of meningioma tumors. These original images, which are of size 512×512, are down sampled to 128×128 to gain a high speed training process as well as to reduce the computational cost. Here it is noticed that none of the significant features are lost due to down sampling to this dimension. The second row of table shows the resultant images for the validation dataset after feeding them to the pre-trained model. The bounding boxes and confidence levels for each tumor are labeled in the images itself using our system.

Next, it maps the low resolution output of the system to original resolution (512×512) to improve the clarity of the detection process. The Original resolution images with the bounding boxes are shown in the third row of Table II. Then it extracts the approximated tumor boundary within the relevant bounding boxes. For this purpose, Prewitt edge detection operator was applied only to the bounding box region.

TABLE I: RESULT OF THE CLASSIFICATION PROCESS

Classes	**Meningioma**	**Glioma**
Total number of images in data base	119	138
Number of images used for train CNN	104	114
Training accuracy	100%	88.5%
Number images used for testing	15	24
Number of images classified successfully	15	21
Testing accuracy	100%	87.5%

TABLE II: SEGMENTATION RESULTS

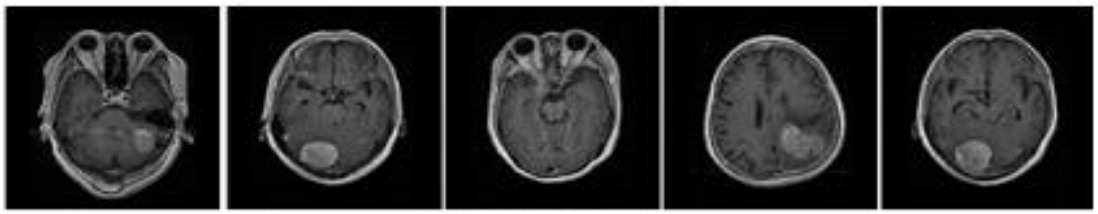
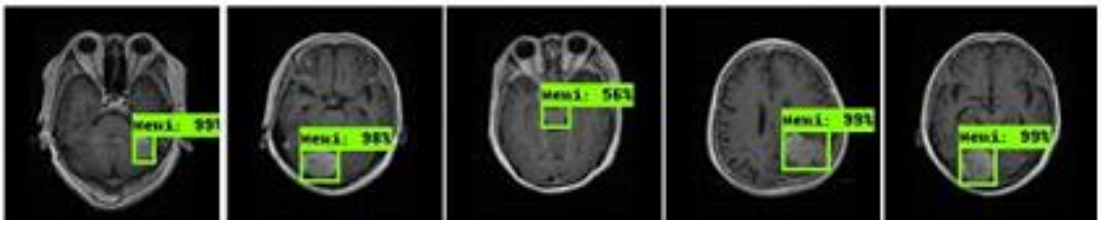
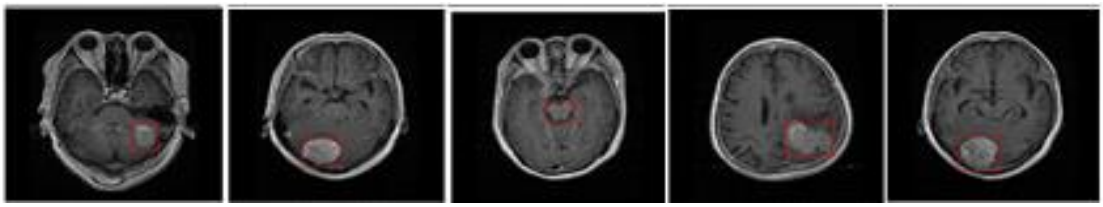
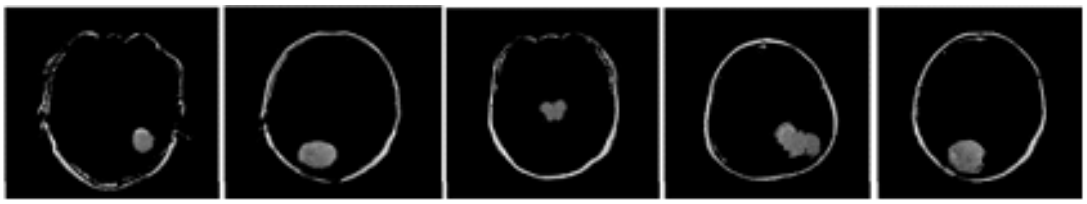
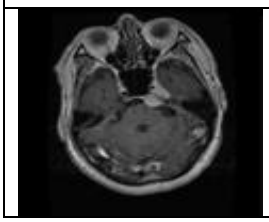
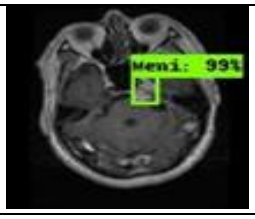
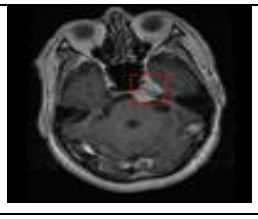
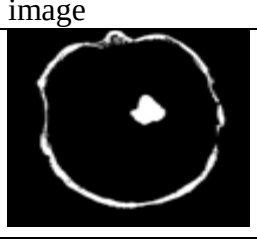
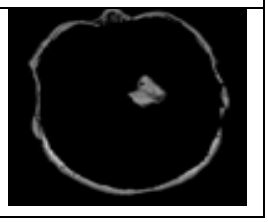
T1 Image 512 x 512	
Bounding box of Tumor with Confident levels 128 x 128	
Original Resolution Images with Bounding box 512 x512	
Binary image of Tumor masks against rest of the image	
Extracted tumor region against rest of the image	

TABLE III: RESULTS FOR SPECIAL CASE

T1 Image 512 x 512	Bounding box of Tumor with Confident levels 128 x 128	Original Resolution Images with Bounding box 512 x512	Binary image of Tumor masks against rest of the image	Extracted tumor region against rest of the image
				

CONCLUSIONS

This paper presents a CNN based unique mechanism to automate the brain tumor classification and segmentation process of T1 weighted MR images. The system presented has an average accuracy of 94% for all the classifiers. Further, the segmentation process is validated as accurate through ground truth demarcations presented by a Neurologist. The average confidence interval for the tumor region extraction is 94.6%, which is a significant performance level. Possible future direction is to generalize the automation process for T2- weighted and Flair-weighted MR images of different planes, such as sagittal and coronal plane slices. Hence, the proposed system would provide an additional diagnostic support to healthcare centers with limited trained staff and resources.

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