Brain Tumor Segmentation Using Deep Learning by Type Specific Sorting of Images

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Problem Statement

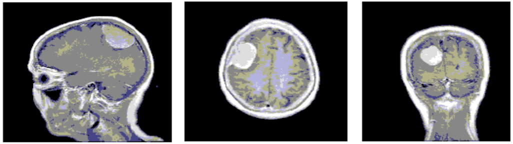
Deep learning has been playing a major role in the field of computer vision. One of its applications is the reduction of human judgment in the diagnosis of diseases. Especially, brain tumor diagnosis requires high accuracy, where minute errors in judgment may lead to disaster. For this reason, brain tumor segmentation is an important challenge for medical purposes. Currently several methods exist for tumor segmentation but they all lack high accuracy.

Here, we present a solution for brain tumor segmentation by using deep learning. In this work, we studied different angles of brain MR images and applied different networks for segmentation. The effect of using separate networks for segmentation of MR images is evaluated by comparing the results with a single network. Experimental evaluations of the networks show that Dice score of 0.73 is achieved for a single network and 0.79 in obtained for multiple networks.

Introduction

Brain tumors are the consequence of abnormal growths and uncontrolled cells division in the brain. They can lead to death if they are not detected early and accurately. Some types of brain tumor such as Meningioma, Glioma, and Pituitary tumors are more common than the others.

Magnetic Resonance Imaging (MRI) is a medical imaging technique, which is extensively used for diagnosis and treatment of brain tumors in clinical practice. The MR images are taken from three different directions. These views are called sagittal, axial and coronal. These three types of brain MR images are shown below.



Sagittal view Axial view Coronal view

Figure 1: Brain MRI slices captured from different directions.

Introduction (cont.,)

Brain Tumor segmentation techniques are a critical component in tumor detection. Using machine learning techniques that learn the pattern of brain tumor is useful because manual segmentation is time-consuming and being susceptible to human errors or mistakes.

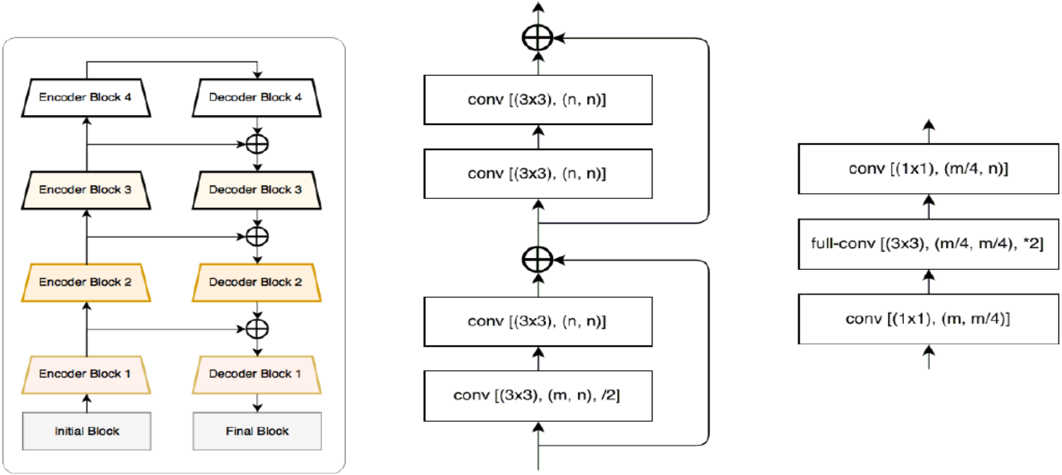
Usually, healthy brain tissue consists of three parts: gray matter, white matter, and cerebrospinal fluid. The segmentation is used to identify areas surrounded by a tumor. The segmentation should separate the active tumorous tissue from the necrotic tissue, and also the edema should be identified. This is done by identifying abnormal areas when compared to normal tissue.

Methodology

In this work, we present an automatic brain tumor segmentation technique based on Convolutional Neural Network. Convolutional neural networks (CNNs) do not use hand-crafted features. The network used is LinkNet. We have used three MRI views of human brain. The main contribution of our paper is the partitioning of the images based on the direction of captured MR images. Hence, three networks are trained separately to achieve better segmentation results.

LinkNet is a light deep neural network architecture designed for performing semantic segmentation. This network is 10 times faster than SegNet and more accurate. The LinkNet Network consists of encoder and decoder blocks that arrange to break down the image and build it back up before passing it through a few final convolutional layers. The architecture of LinkNet is presented in next slide.

Methodology (cont.,)



a. LinkNet Architecture

b. Encoder Block

c. Decoder Block

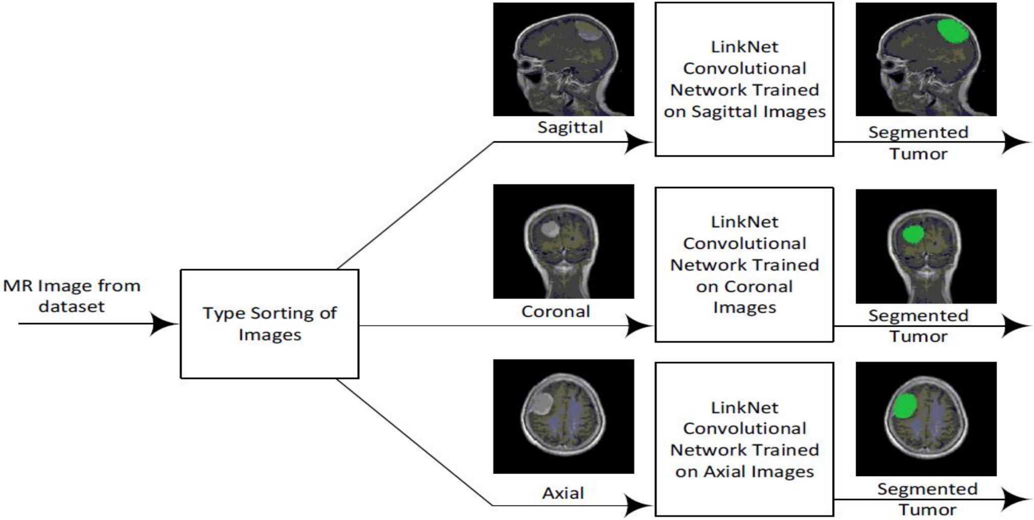
Figure 2. (a) LinkNet architecture, (b) convolutional modules in encoder-block, (c) convolutional modules in decoder-block

Methodology (cont.,)

At first, we did not consider the view angle of the images. We initially used a single Linknet network and sent all training dataset to that network for segmentation. All dataset images are grayscale and the foreground of the images are located at the center. Images are captured from different views of the skull; hence the size and position of the tumors vary in different angles. These differences in the size of the tumors make the diagnosis of the tumor hard.

We found out using a single network for identification of tumors in all images does not produce accurate results. We considered the difference network to be trained on separate MR images according to their angles. Hence, sagittal, coronal and axial images are sorted and each group is used to train one of the three networks. We used an individual LinkNet network for each of the three mentioned groups of images. Figure 3 shows our proposed method.

Methodology (cont.,)



MR Image from dataset

Type Sorting of Images

Sagittal

LinkNet Convolutional Network Trained on Sagittal Images

Segmented Tumor

Coronal

LinkNet Convolutional Network Trained on Coronal Images

Segmented Tumor

Axial

LinkNet Convolutional Network Trained on Axial Images

Segmented Tumor

Figure 3: Overview of the proposed method.

Methodology (cont.,)

This brain tumor T1-weighted CE-MRI image-dataset consists of 3064 slices. There are 1047 coronal images. Coronal images are captured from the back of the head. Axial images that are taken from above are 990 images. Also, there are 1027 sagittal images that are captured from the side of the skull. This dataset has a label for each image, identifying the type of the tumor. These 3064 images belong to 233 patients. The dataset includes 708 Meningiomas, 1426 Gliomas, and 930 Pituitary tumors.

For the single LinkNet network, we used 2100 of images for network training that 20% of these images are considered as validation and the rest of the data is used for the test purpose. Also for the training of the three LinkNet networks, we separate all images into three groups. Each group contains one type of MR image based on the image view. In each group, about 900 images are used for the training procedure and about 200 images are used as test images. Our network uses binary cross-entropy as the loss function and the network is tuned using this parameter.

Experimental Results

For comparison purposes, we used a simple network which has a probability map concatenation. The probability map is obtained from the ground truth binary maps of the training images to show probability of a pixel being tumor. We evaluate the segmentation results using Dice criterion. The Dice coefficient, also called the overlap index, is a metric for validation of medical image segmentation. The pair-wise overlap of the repeated segmentations is calculated using the DICE, which is defined by:

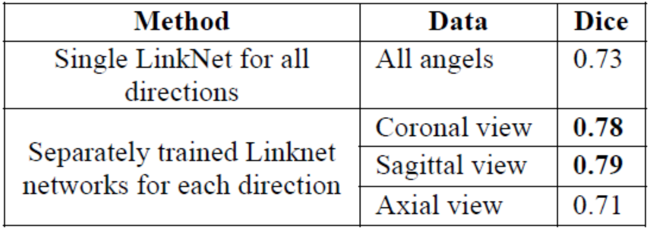
$$DICE = \frac{2TP}{2TP + FP + FN}$$

where TP is true positive results or correctly segmented tumor pixels, FP is false positive, and FN is the false negative results of the segmentation. False positive results are obtained when a pixel which is not tumor is classified as tumor. Also, FN is referred to the number of pixels that are tumor and are falsely labeled as non-tumor.

Experimental Results (cont.,)

As shown in Table 1, the results for LinkNet networks that are trained individually by different angles are better than single LinkNet network that is trained by all dataset without separating which shows the importance of detaching the dataset.

Table 1: Results of different approaches



Method	**Data**	**Dice**
Single LinkNet for all directions	All angels	0.73
Separately trained Linknet networks for each direction	Coronal view	**0.78**
	Sagittal view	**0.79**
	Axial view	0.71

Conclusion

In this paper, we introduced a new method for CNN to automatically segmenting the most common types of brain tumor, i.e. the Glioma, Meningioma, and Pituitary. This technique does not require preprocessing steps. The results show that the separation of images based on angles improves segmentation accuracy. The best Dice score that was obtained is 0.79 was obtained from segmentation of tumors in sagittal view images. Sagittal images do not contain details of other organs and tumor is more prominent than other images. The lowest Dice score in our experiments was 0.71 which is related to the images from the axial view of the head.

As compared to other images, axial view contains fewer details. It is expected that by performing preprocessing on this group of images better classification of tumor pixels could be obtained and the Dice score will increase. Our proposed method may be implemented as a simple and useful tool for doctors in segmenting of brain tumor in MR images.

Thank you!