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A Review of Multimodal Brain Tumor Image Segmentation Using Convolutional Neural Networks

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Abstract: Brain tumor is a most dreadful and dangerous disease. Diagnosis of brain tumor is quite difficult. In this paper, we tend to propose automatic segmentation using convolutional neural network, exploring the small 3*3 kernel. Using small kernels provide deeper architecture and avoids overfitting. The intensity normalization is done using pre-processing step which is not common in CNN-based segmentation methods, which also proves data augmentation to be effective for brain tumour segmentation.

Keywords: Brain tumour segmentation, magnetic resonance imaging, convolutional neural networks, deeper architecture, machine learning

I. INTRODUCTION

Gliomas are the primary brain tumors in the glial cells. The patients suffering from high-grade glioma survived for a median survival rate whereas patients with low- grade glioma survived for several years so aggressive treatment is delayed as long as possible[1],[2]. For both the gliomas intensive neuroimaging protocols was chosen as best treatment strategy. In recent treatment techniques the images are evaluated based on qualitative or quantitative criteria. By replacing the current basic method with highly accurate image processing routines the diagnosis is being analyzed using automatic brain tumor segmentation.

The automatic or semi-automatic methods are required because the MRI images contain intensity inhomogeneities. Due to the abnormalities the tumor is segmented as abnormalities of normal tissue which is subjected to shape and connectivity constrains. Other approaches mostly rely on the probabilistic atlases. Moreover, the mass effect induced by the lesion or tumor may displace the normal tissues which will thereby limit the reliability of spatial prior knowledge for the healthy part of the brain. Twenty different segmentation algorithms were augmented by various developers as a part of a data and run on the manual images to test the performance against manual descriptions by expert raters. Each of these models will contain different biological information and has different processing tasks.

II. PRIOR WORK

Many prior work have been done using different algorithms to improve the accuracy and to overcome the constrains. In this paper we report the set-up and results of the Multimodal Brain Tumor Image Segmentation Benchmark(BRATS)[2]. A set of 65 multi-contrast MR scans of low and high- grade glioma patients were applied with segmentation technique known as twenty state-of-the-art segmentation algorithms and to 65 comparable scans generated using tumor image simulation software. Quantitative evaluations revealed considerable disagreement between the human raters in segmenting various tumor sub-regions (Dice scores in the range 74%-85%), illustrating the difficulty of this task. No single algorithm ranked in the top for all sub-regions simultaneously instead they worked best for different sub-regions.

In this existing method state-of-the-art algorithms for the tumor segmentation are based on techniques originally developed for other structures or pathologies, most notably for automated white matter lesion segmentation that has reached considerable accuracy, were other technologies have been tested for their applicability to brain tumor detection and segmentation.

We can categorize most current tumor segmentation methods into one of two broad families.

1. Generative probabilistic methods
2. Discriminative approaches

The generative models make use of detailed information about the appearance and spatial distribution of different tissue types. Its difficult to code the prior knowledge about the lesion. These models depend on the spatial priors and registration for aligning the images accurately[2]. In order to overcome these difficulties, joint registration, tumor segmentation and estimation of tumor displacement have been studied. The

drawback of generative model is the effort required for transforming an arbitrary semantic interpretation of the image.

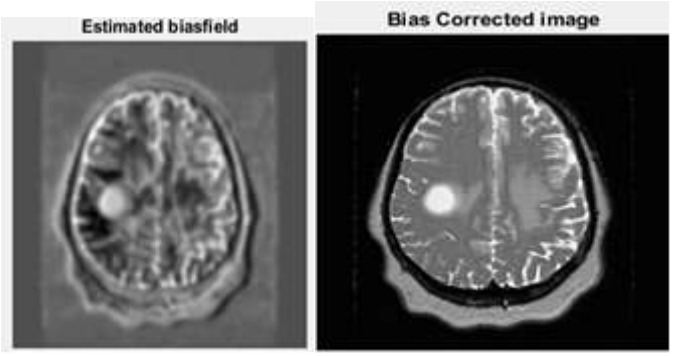
The discriminative models learn from the training images the characteristic differences between the lesions and the normal tissues[1]. To be robust against the artifacts such shape and intensity variations, they typically require the training data. These models involve two steps. In the first step it extracts the features and in the second step these features are fed into the classified algorithms and return the desired tumor classification maps when applied to new data. The major drawback of this approach is that it explicitly depends on the intensity features and the segmentation is restricted to images with the same imaging protocols as used in for training data. Thus, in order to overcome the disadvantages of the existing system, a new system was proposed.

III. PROPOSED SYSTEM

The proposed system involves automatic segmentation based on Convolutional Neural Network(CNN). CNN were used to achieve some breakthrough results and win well-known contests. The application of convolutional layers consists in convolving a signal or an image with kernels to obtain feature maps. So, a unit in a feature map is connected to the previous layer through the weights of the kernels. The weights of the kernels are adapted during the training phase by back propagation, in order to enhance certain characteristics of the input. Since the kernels are shared among all units of the same feature maps, convolutional layers have fewer weights to train dense FC layered, making CNN easier to train and less prone to overfitting. Here the MRI images are altered by bias field estimation. This makes the intensity of same tissues to vary across the image[14]. To correct it, we applied the N4ITK method. However, this is not enough to ensure that the intensity distribution of a tissue type is in a similar intensity scale across different subjects for the same MRI sequence, which is an explicit or implicit assumption in most segmentation methods. In fact, it can vary even if the image of the same patient is acquired in the same scanner in different time points, or in the presence of a pathology. So, to make the contrast and intensity ranges more similar across patients and acquisitions, we apply the intensity normalization method. After normalizing the MRI images, we compute the mean intensity value and standard deviation across all training patches extracted for each sequence.

3.1 Bias Estimation and Correction

It involves (i) RGB to grayscale conversion (if necessary) (ii) datatype conversion to Double (iii) contrast enhancement (iv) Bias field estimation and correction. Red, green and blue color, together are added in different ways to form an additive color model called RGB model. This model is generally used for sensing, representation and display of images in electronic systems. Whereas an image in which the value of each pixel is a single sample with only intensity information is a grayscale image. These images have many shades of gray in between white and black. Grayscale images are often the result of measuring the intensity of light at each pixel in a single band of the electromagnetic spectrum (e.g. infrared, visible light, ultraviolet, etc.), and in such cases they are monochromatic proper when only a given frequency is captured. But also, they can be synthesized from RGB model which involves RGB to grayscale conversion. the next step is to convert the datatype to double. The input image is represented in integer datatype by default but operation among integers requires large memory space. Thus, integer is converted to Double for convenient handling of data. Next step involves contrast enhancement. The difference in color and brightness of one object from the other creates contrast in an image. But we can perceive the image regardless of the change in illuminance through contrast enhancement. The final step in preprocessing is reduction of noise using Bias Field Corrected Fuzzy C-Means method[10]. Imperfections in the radio-frequency coils and problems associated with the acquisition sequences can be caused by MRI intensity inhomogeneities. The output is a slowly varying shading artifact over the image that can produce errors with the ordinary intensity-based classification. Thus, to compensate such inhomogeneities and to allow the labeling of a pixel to be influenced by the labels in its immediate neighborhood, an algorithm is formulated by modifying the objective function of the standard fuzzy c-means (FCM) algorithm. The neighborhood effect acts as a regularize and biases the solution toward piecewise-homogeneous labeling[1]. Such regularization is useful in segmenting scans corrupted by salt and pepper noise. After the pre-processing step the image is passed to the segmentation module for further processing. The output of this module is a bias corrected image.



a) Fig:3.11 b) *Fig:3.12*

3.2 Active Contour Segmentation

The output of the pre-processing module, i.e, the bias corrected image is the input for the segmentation module. The effective technique used for segmentation is active contour model, also called as snakes, is a framework in computer vision for describing an object outline from noisy 2D images[5]. The snake algorithm is more popular and is used in applications such as object tracking, edge detection and stereo matching. This algorithm is generally energy minimizing and resists deformation. A discrete version of this approach is represented in two dimensions by the active shape model, taking advantage of the point distribution model to restrict the shape range to an explicit domain learnt from a training set. Here a mask is being created and convoluted with the input image to get the enhanced portion of the lesion.

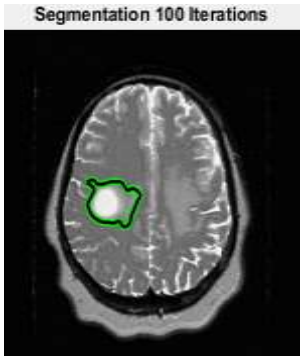


Fig:3.21

3.3 Feature Extraction(GLCM)

Next step is the extraction of image features. An image is defined by its texture. GLCM (Gray-Level Co-occurrence Matrix) is the commonly used tool for texture extraction. GLCM operates by extracting the texture of an image by detecting how often pairs of pixel with certain values and in a certain spatial relationship occur in an image, forming a GLCM and then calculating the spatial features from this matrix[3]. An image with the size of pixels and gray levels could illustrate the frequency of pixel (i.e) at the position of occurrence with gray level and in accordance with a distance d from a certain pixel at the position () with gray level. Frequency is denoted by (). The mathematical expression is

$$P_d(i,j) = \left|\left\{\left((r,s),(r+dx,s+dy)\right) : I(r,s) = i, I(r+dx,s+dy) = j\right\}\right|$$

As said earlier GLCM is the commonly used tool as it extracts second order statistics of an image. These statistics provide information about the contrast (measures the local variables in the matrix), correlation (measures the joint probability occurrence of the specified pixel pairs), Energy (provides the sum of squared elements in the GLCM) Homogeneity (measures the closeness of the distribution of elements in the GLCM to GLCM diagonal)

3.4 Convolutional Neural Network

This work is motivated by the recent success of CNN's object recognition of 2D images. CNN are currently primarily used for object recognition and is one of the deep learning methods[3]. CNN are used inside more complex framework in order to perform segmentation, the recent success in the domain of medical analysis was for mitosis detection including histology images[6]. CNN automatically learn representative complex features directly from the data itself. CNN take patches extracted from images as input and use trainable convolutional filters and local subsampling to extract complex features. CNN processes 4D images efficiently which comprises of 3D spatial intensity information along with a dimension for MRI modalities[1]. In CNN, there are small neuron collections which process input image, they are then tiled so that they overlap for a better representation and this is done for every such layer. Tiling permits CNNs to tolerate translation of the input image.

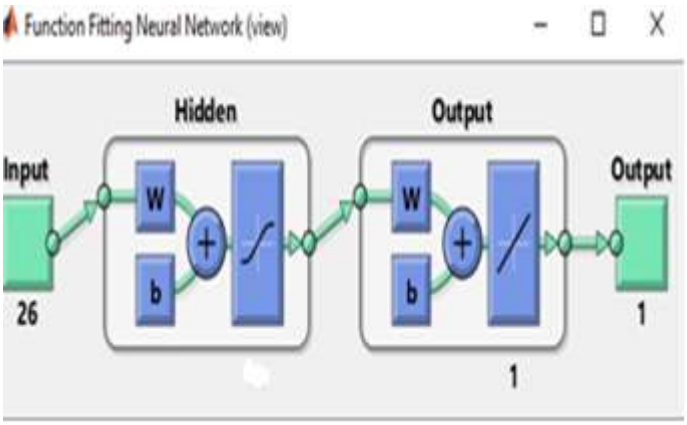


Fig:3.31

We use a standard CNN framework with the following, per layer
characteristics of the architecture:
–layer 0: input patch of size 19 ×19 ×4,
(i.e. we currently only use a single slice from each of the 4 channels)
–layer 1: 64 filters of size 5 ×5×4, (resulting in 15 ×15 ×64 nodes)
–layer 2: max-pooling with kernel size 3 and stride of 3, (resulting in 5 ×5×64 nodes)
–layer 3: 64 filters of size 3×3×64, (resulting in 3 ×3×64 nodes)

–layer 4: fully connected with 512 nodes
–layer 5: soft-max (fully-connected) with 5 output nodes (for the 5 classes)
All inner nodes in the network use a rectified linear unit (ReLU) as a non-linearity term. We use log-loss as the energy function for training, and optimization is performed with a stochastic gradient descent with momentum.

CNN is a machine learning technique in which the connectivity pattern between the is inspired by the organization of the animal visual cortex. The other name of CNN is shift invariant or space invariant artificial neural network. CNN consists of multiple layers of receptive fields and so it is used in image recognition[7]. Convolutional networks may include local or global pooling layers. The major advantage of CNN is that the lack of dependence on prior knowledge and human effort in designing features. The other advantage is that the memory footprint and performance is improved by using same filter for each and every pixel.

IV. CONCLUSION

In summary, we propose a CNN based method for brain tumor segmentation in MRI images. We start by preprocessing which involves RGB to grayscale, bias field estimation and correction using Fuzzy-C Means logic. The corrected image is segmented using active contour technique. This is followed by feature extraction using GLCM. The CNN is built over convolutional layers with small 3* 3 kernels to allow deeper architectures. The extracted features are given into the CNN module for further processing whose output will be the presence or absence of tumor.

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