

Brain Tumor Detection and Classification in MRI Images

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ABSTRACT: Early and precise detection of tumors improve the quality of life of oncological patients. Keeping this in mind, in this paper we propose an effective method of brain tumor detection and classification. Simply, brain tumor is an abnormal growth caused by cells reproducing themselves in an uncontrolled manner. Brain tumors are having large variability in their characteristics compared to other cancer tissue. So that for effective classification the deep learning technique convolutional neural network (CNN) is used. This method pre-processes MRI image classifies and extracts tumors using MATLAB.

KEYWORDS: Brain Tumor, MRI images, Deep Learning, Convolutional Neural Network, MATLAB

I. INTRODUCTION

Tumor is a deathly disease. According to certain surveys there were an estimate around 14.1 million cancer cases are reported in the world in 2012, of thee 7.4 million cases were in men and 6.7 million in women. This number is expected to increase to 24 million by 2035. Among different cancers brain tumor is most aggressive. The average survival rate of brain tumour is only 34.4%.The prognosis and early cure of brain tumour depends on the early detection and treatment. For early detection and effective treatment of the brain tumour a precise and reliable method for cancer detection is needed. So, in this paper we use an automatic segmentation method. In this method we are using convolutional neural network for the classification of tumor.

Tumors can be benign or malignant, can occur in different parts of the brain, and may be primary or secondary. A primary tumor is one that has started in the brain, as opposed to a metastatic tumor, which is something that has spread to the brain from another part of the body. The incidence of metastatic tumors is more prevalent than primary tumors by 4:1 ratio. Tumors may or may not be symptomatic: some tumors are discovered because the patient has symptoms, others show up incidentally on an imaging scan, or at an autopsy. A glioma is a type of tumor that starts in the brain or spine. It is called a glioma because it arises from glial cells. The most common site of gliomas is the brain Gliomas [1] make up about 30% of all brain and central nervous system tumors and 80% of all malignant brain tumors.

Magnetic Resonance Imaging (MRI) is a widely used imaging technique to assess these tumors. MRI is preferred because of its higher resolution than CT and also no known harmful effects from the strong magnetic field used for MRI. But the large amount of data produced by MRI prevents manual segmentation in a reasonable time, limiting the use of precise quantitative measurements in the clinical practice. MRI images [1] may present some problems, such as intensity inhomogeneity, or different intensity ranges among the same sequences and acquisition scanners. To remove these disadvantages in the MRI images we are using pre-processing techniques such as bias field

and intensity normalization. Magnetic Resonance Imaging (MRI) is one of the power full visualization techniques [1], which is mainly used for the treatment of cancer. Using MRI image technology, the internal structure of the body can be acquired in a safe and invasive way. Magnetic Resonance Imaging is a radiation-based technique; it represents the internal structure of the body in terms of intensity variation of radiated wave generated by the biological system, when it is exposed to radio frequency pulses. Magnetic Resonance Imaging is a very useful medical modality for the detection of brain abnormalities and tumor. It does not produce any damage to healthy tissue with its radiation, it provides high tissue information. Brain imaging allows a look into the brain and providing a detailed map of brain connectivity

II. LITERATURE SURVEY

The classification of Brain tumor segmentation methods can be made depending on the degree of human interaction as:

Manual segmentation involves delineation of the boundaries of tumor manually and representing region of anatomic structures with various labels. Manual segmentation requires software tools for the ease of drawing regions of interest (ROI), is a tedious and exhausting task. MRI scanners produce multiple 2-D slices and the human expert has to mark tumor regions carefully, otherwise it will generate jaggy images that lead to poor segmentation results.

In semi-automatic brain tumor segmentation, human interaction is least as possible. According to Olabarriaga, the semiautomatic or interactive brain tumor segmentation components consist of computational part, interactive part and the user interface. Since it involves both computer and humans' expertise, result depends on both the combination. Efficient segmentation of brain tumor is possible through this strategy but it is also subjected to variations between expert users and within same user.

In Fully automatic segmentation method, there is no intervention of human and segmentation of tumor is determined with the help of computer. It involves the human intelligence and is developed with soft computing techniques, which is a difficult task. Brain tumor segmentation has various properties which reduce the advantage of humans over machines. These methods are likely to be used for large batch of images in research environment. However; these methods have not gained popularity for clinical practice, due to lack of transparency and interpretability. In brain tumor segmentation, we find several methods that explicitly develop a parametric or non-parametric probabilistic model for the underlying data. These models usually include a likelihood function corresponding to the observations and aprior model. Being abnormalities, tumors can be segmented as outliers of normal tissue, subjected to shape and connectivity constrains. Other approaches rely on probabilistic atlases. In the case of brain tumors, the atlas must be estimated at segmentation time, because of the variable shape and location of the neoplasms. Tumor growth models can be used as estimates of its mass effect, being useful to improve the atlases. The neighbourhood of the voxels provides useful information for achieving smoother segmentations through Markov Random Fields (MRF). Zhao [5] also used a MRF to segment brain tumors after a first overs segmentation of the image into super voxels, with a histogram-based estimation of the likelihood function. As observed by Menze et, generative models generalize well in unseen data, but it may be difficult to explicitly translate prior knowledge into an appropriate probabilistic model.

Another class of methods learns a distribution directly from the data. Although a training stage can be a disadvantage, these methods can learn brain tumor patterns that do not follow a specific model. This kind of approaches commonly considers voxels as independent and identically distributed, although context information may be introduced through the features. Because of this, some isolated voxels or small clusters may be mistakenly classified with the wrong class, sometimes in physiological and anatomically unlikely locations. To overcome this problem, some authors include information of the neighbourhood by embedding the probabilistic predictions of the classifier into a Conditional Random Field [10] Classifiers such as Support Vector Machines and more recently, Random Forests (RF) were successfully applied in brain tumor segmentation. The RF became very used due to its natural capability in handling multi-class problems and large feature vectors. A variety of features were proposed in the literature: encoding context, first-order and fractals-based texture, gradients, brain symmetry, and physical properties. Using supervised classifiers, some authors developed other ways of applying them.

Tustison developed a two-stage segmentation framework based on RFs, using the output of the first classifier to improve a second stage of segmentation. Geremia proposed a Spatially Adaptive RF for hierarchical segmentation, going from coarser to finer scales. Meier used a semi-supervised RF to train a subject-specific classifier for post-operative brain tumor segmentation.

Other methods known as Deep Learning deal with representation learning by automatically learning an hierarchy of increasingly complex features directly from data. So, the focus is on designing architectures instead of developing handcrafted features, which may require specialized knowledge. CNNs have been used to win several object recognition and biological image segmentation challenges. Since a CNN operates over patches using kernels, it

has the advantages of taking context into account and being used with raw data. In the field of brain tumor segmentation, recent proposals also investigate the use of CNNs. Zikic [9] used a shallow CNN with two convolutional layers separated by max-pooling with stride 3, followed by one fully-connected (FC) layer and a softmax layer. Urban et al., evaluated the use of 3D filters, although the majority of authors opted for 2D filters [11]. 3D filters can take advantage of the 3D nature of the images, but it increases the computational load. Some proposals evaluated two-pathway networks to allow one of the branches to receive bigger patches than the other, thus having a larger context view over the image. In addition to their two-pathway network, Havaei built a cascade of two networks and performed two-stage training, by training with balanced classes and then refining it with proportions near the originals. Lyksborg et al. use a binary CNN to identify the complete tumor. Then, a cellular automata smooths the segmentation, before a multiclass CNN discriminates the sub-regions of tumor. Rao, extracted patches in each plane of each voxel and trained a CNN in each MRI sequence, the outputs of the last FC layer with softmax of each CNN are concatenated and used to train a RF classifier. Dvořák and Menze divided the brain tumor regions segmentation tasks into binary sub-tasks and proposed structured predictions using a CNN as learning method. Patches of labels are clustered into a dictionary of label patches, and the CNN must predict the membership of the input to each of the clusters.

In this project, inspired by the ground-breaking work of Simonyan and Zisserman [12] on deep CNNs, we investigate the potential of using deep architectures with small convolutional kernels for segmentation of gliomas in MRI images. Simonyan and Zisserman proposed the use of small 3×3 kernels to obtain deeper CNNs. With smaller kernels we can stack more, convolutional layers, while having the same receptive field of bigger kernels. For instance, two 3×3 cascaded convolutional layers have the same effective receptive field of one 5×5 layer, but fewer weights. At the same time, it has the advantages of applying more non-linearities and being less prone to overfitting because small kernels have fewer weights than bigger kernels. We also investigate the use of the intensity normalization method proposed by Nyul as a pre-processing step that aims to address data heterogeneity caused by multi-site multi-scanner acquisitions of MRI images. The large spatial and structural variability in brain tumors are also an important concern that we study using two kinds of data augmentation.

In this project we are using the method proposed by the Sérgio Pereira, Adriano Pinto, Victor Alves and Carlos A. Silva in which brain tumor segmentation is done by using convolutional neural networks

III. PROPOSED METHOD

This method has three main stages: pre-processing, classification of tumor and post-processing

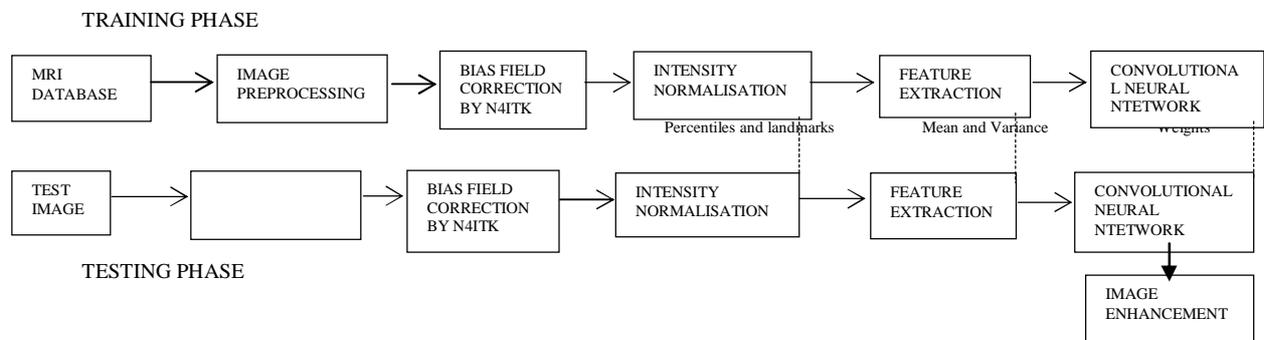


Fig 1. Block diagram of brain tumor detection and classification system

A. PREPROCESSING

MRI images are suffered of bias field distortion and intensity inhomogeneity. There already exist several algorithms for correcting non uniform intensity in the magnetic resonance images, due to field in homogeneities. To correct bias field distortion N4ITK method [2] adopted. This is not enough to ensure the intensity distribution of the tissue. Because there will be variation in intensity even if MRI of same patient is acquired in same scanner at different time slots. So we are using intensity normalisation method in this system. It makes the contrast and intensity ranges more similar across patients and acquisition.

Popular intensity inhomogeneity correction method, N3 (nonparametric non uniformity normalisation) is used in the N4ITK algorithm[2]. It is iterative and seek smooth multiplicative field that maximizes high frequency content of distribution contents of tissue intensity. This is fully automatic method. And it is having an advantage that it doesn't require a prior tissue model for its application. It can apply to almost any MRI images.

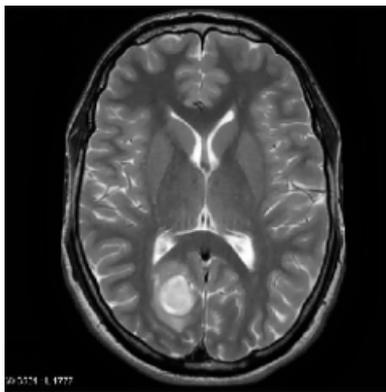


Fig 2. Original image

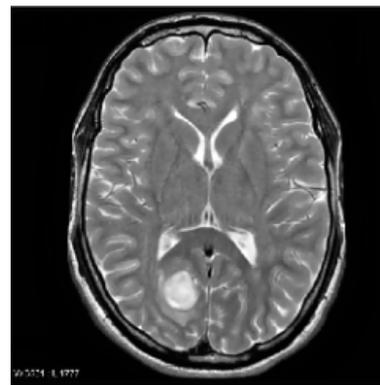


Fig 3. Bias corrected image

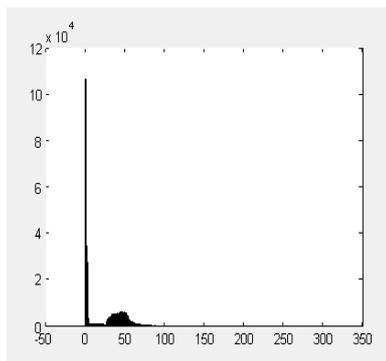


Fig 4. Histogram of original image

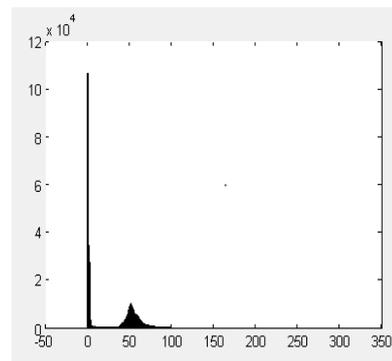


Fig 5. Histogram of bias corrected image

Intensity normalization standardizes the intensity scales in MRI. Without standardized intensity scale, it will be difficult to generalize the relative behaviour of various tissue types across different volumes in the presence of tumor. The intensity normalization consisting of 2-stage method, proposed by Ny'ul [4] et al is used here for evaluation. The two stages are training stage and transformation stage. The main purpose of training stage is to find the parameters of the standard scale and in transformation stage the histograms of candidate volume are mapped to a standard histogram scale. By this for each sequence more similar histogram is obtained. The mean intensity value and standard deviation are computed during the training stage. These values are used to normalize the testing patches. Intensity normalisation consists of training stage and transformation stage. In training stage, we find the parameters of standard scale and in transformation stage histogram of input image is mapped to a standard scale (intensity of interest (IOI)).

The 2 stage intensity normalisation algorithm [4] can be summarised as below. As first step determine the histogram of each image in the training set of images. Form this histogram determine the range of intensity value of interest. P_{low} and P_{high} denotes the minimum and maximum percentile value of the overall intensity range that defines the boundaries of this IOI. The value lies outside this range are discarding as outliers. The minimum and maximum intensity value of the image, i_{low} and i_{high} are mapped to corresponding minimum and maximum intensity value i'_{low} and i'_{high} of standard intensity scale. User can choose the value of i'_{low} and i'_{high} according to their requirement from the learning algorithm. After mapping new landmark are calculated from the rounded mean of each of the landmark from the mapped image from the training set of images

At the end of training phase standard scale landmark are obtained. It I used to perform transformation of test image. For transformation of image compute the histogram of the test image. Then find out the minimum and maximum intensity values corresponding to P_{low} and P_{high} . From this determine the intensity values corresponding to each decile of histogram respect to P_{low} and P_{high} . Now the each decile is intensity normalization for the new image. These values enable segmenting the image in ten segments. Each segments is then linearity mapped to the corresponding segments of the standard image intensity scale.

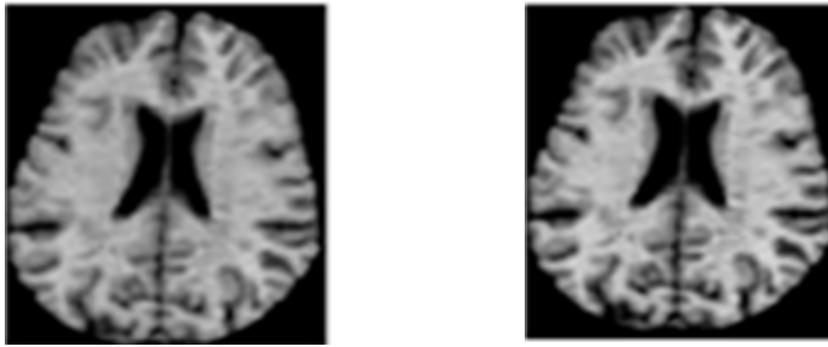


Fig 6. Input image and intensity normalized image

B. CLASSIFICATION

In this approach, classification is done by using convolutional neural network (CNN) [7]. Convolutional neural networks are deep learning techniques mainly for image recognition. The segmentation is done by exploring small 3x3 kernels. Feature maps are obtained by convolving an image with these small kernels. Each unit in feature map is connected to previous layer by weights of kernels. These weights are obtained by back propagation during training phase. This network has fewer weights to train which makes training easier and reduces over fitting, since the kernels are shared among all units of feature maps. The same feature is detected independently of the location, because the same kernel is convolved over the entire image. A non-linear activation function is applied on the output of each neural unit.

The convolutional layers are stacked to increase the depth, by which the extracted features become more abstract.

The important concepts are:

- i Initialization
Initialization is to achieve convergence. This maintains the back-propagated gradients.
- ii Activation function
For non-linear transformation of data, Rectifier linear units (ReLU), is defined as

$$f(x) = \max(0, x)$$
 Activation functions helps in fast learning and speed up training. The limitations due to imposing constant 0 are eliminated by using a variant called leaky rectifier linear unit (LReLU). This functions is defined as

$$f(x) = \max(0, x) | \alpha \min(0, x)$$
 Where α is the leakiness parameter. In last FC layer softmax is used.
- iii Pooling
In feature maps, spatially nearby features are combined by pooling. This makes the representation more compact, reduces computational load and invariant to small changes in the images. Max-pooling is used to join the features.
- iv Regularization
Regularization reduces over fitting. Drop out used in each fully connected layer, removes nodes from the network with probability p . This prevents the nodes from co-adapting to each other. But all the nodes are used during testing phase.
- v Data Augmentation
Data Augmentation increases the size of the training sets and reduce over fitting. Data set is increased by generating new patches through the rotation of the original patch. In this approach, angles multiple of 90° are evaluated.
- vi Loss Function
This function should be minimized during training.

C. POST-PROCESSING

There is a chance to recognize small clusters as tumor. Post processing done to avoid these kinds of errors. In this stage small clusters in the segmentation, obtained by the CNN are removed which are smaller than a predefined threshold value τ .

IV. RESULTS AND DISCUSSION

The pre-processing methods made segmentation more effective and accurate. N4ITK algorithm is used to correct bias field distortion in MRI images. In intensity normalization intensities of images are transformed to [0, 1].

Then we normalized each sequence to have zero mean and unit variance. CNN based classification also improve after intensity normalization. Since we used convolutional neural network for the classification brain tumor variabilities segmented more accurately. CNN classifies mainly four tumor classes- Edema, Necrosis, Non enhancing and enhancing tumor.

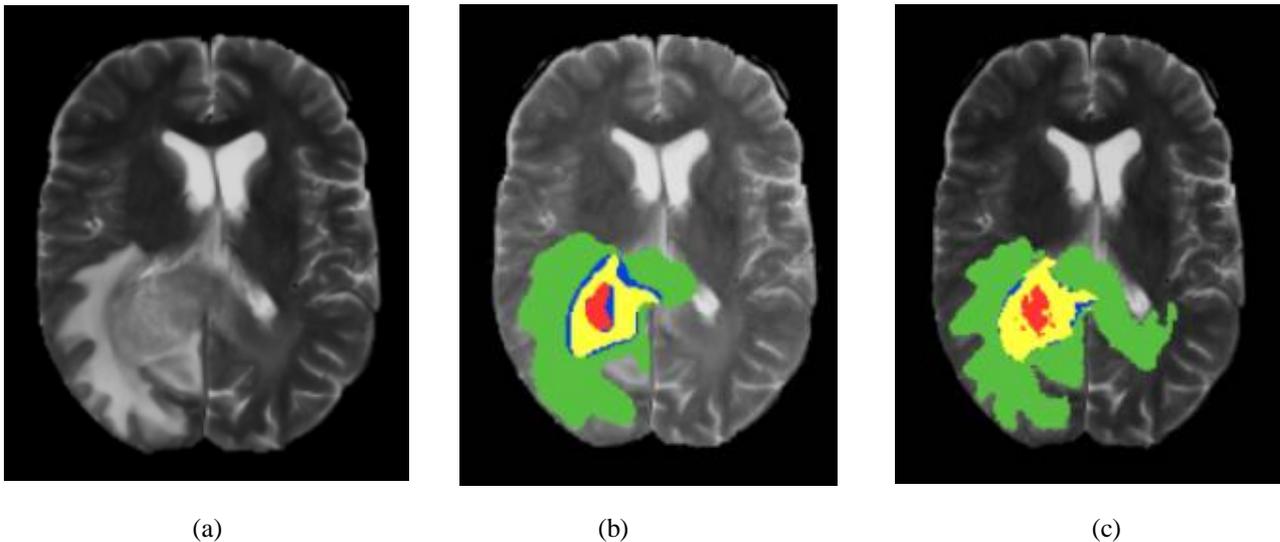


Fig 7. (a) input MRI, (b) output segmented image of proposed method, (c) manually segmented image. Each colour represents a tumor class: Green-Edema, Blue-Necrosis, Yellow-Non enhancing tumor, Red-enhancing tumor

V. CONCLUSION

We presented a method for segmentation of brain tumors in MRI images based on convolutional neural networks. This method consists of mainly, pre-processing stage, classification stage and post processing stage. Bias field correction, patch and intensity normalization are done in the pre-processing stage. In our method the distortion caused by multi-site multi-scanner acquisition of MRI images is removed by intensity normalisation method proposed by Nyul et al. intensity normalisation is help to improve the effectiveness of the classification. For classification CNN found to be effective due to the use of deal with variability in brain tumor. On comparing this method with conventional methods it takes only less computational time. This method has higher potential in tumor detection and classification.

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