

A CONVOLUTION NEURAL NETWORK ALGORITHM FOR BRAIN TUMOR IMAGE SEGMENTATION

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Abstract—Gliomas are the most common occurring condition in brain tumor. It is aggressive in nature leading to a very short life span and predicting the presence of high grade glioma has many real time difficulties. Even under treatment patients do not survive an average of more than 14 years, this situation requires a technique that can predict the presence of tumor at the early stage. For these reasons we propose an automatic segmentation method based on convolution neural network in MRI (Magnetic Resonance Imaging) images. Convolution Neural Network (CNN) is an artificial neural network in which several neurons are connected in the way of visual cortex. Convolution layers have fewer weights which make CNN easy to train. In this paper, a sequence of trained data is fed to the pre-processor which estimate the bias field correction. This image is normalized and standard deviation is calculated. Using fuzzy clustering the presence of tumor cell is determined by patch extraction from different patches.. In CNN, Back propagation is used to calculate the gradient of loss function with respect to all weights in the network. Pooling and data augmentation technique are used in CNN.

IndexTerms—Magnetic Resonance Imaging, Glioma,Brain

I. INTRODUCTION

Brain tumor or intracranial neoplasm occurs when abnormal cells form within the brain. There are two main types of tumors: malignant or cancerous tumors and benign tumors. Cancerous tumors can be divided into primary tumors that start within the brain, and secondary tumors that have spread from somewhere else, known as brain metastasis tumors. All types of brain tumors may produce symptoms that vary depending on the part of the brain involved. These symptoms may include headaches, seizures, problem with vision, vomiting, and mental changes. The headache is classically worse in the morning and goes away with vomiting. More specific problems may include difficulty in walking, speaking, and with sensation. As the disease progresses unconsciousness may occur. Even under treatment, patients do not survive on average more than 14 months after diagnosis [3]. Current treatments include surgery, chemotherapy, radiotherapy, or a combination of them [4].

Most automatic brain tumor segmentation methods use hand designed features. These methods implement a classical machine learning pipeline according to which features are first extracted and then given to a classifier whose training procedure does not affect the nature of those features. An alternative approach for designing task adapted feature representations is to learn a hierarchy of increasingly complex features directly from in-domain data. Deep neural networks have been shown to excel at learning such feature hierarchies [7]. In this work, convolution neural network approach is applied to learn the feature hierarchies adapted specifically to the task of brain tumor segmentation that combine information across MRI modalities. Gliomas consist of various parts, each of which shows a different imaging phenotype in multimodal magnetic resonance imaging (MRI). Typically, the core of HGGs consists of enhancing, non-enhancing and necrotic parts, whereas the core of LGGs does not necessarily include an enhancing part. Another critical feature, for both understanding and treating gliomas, is the peritumoral edematous region. Edema occurs from tumor cells, as well as a biological response to the angiogenic and vascular permeability factors released by the spatially adjacent tumor cells.

In this paper, a number of specific CNN architectures is proposed for tackling brain tumor segmentation. Our architectures exploit the most recent advances in CNN design and training techniques, such as Maxout hidden units and Dropout regularization. Several architectures are also investigated which take into account both the local shape of tumors as well as their context.

II. METHODS

A. PREPROCESSING

The image data from the CT and MRI devices usually needs preprocessing before the visualization. Preprocessing is useful because the quality of the input data is not satisfying some requirements. So it usually needs a pre-processing methodology. MRI images are altered by the bias field distortion. This makes the intensity of the same tissues to vary across the image. To remove the skull portion surrounding the brain tissue by using MRI pre-processing.

A sequence of trained data is fed to the pre-processor which estimate the bias field correction. 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. To make the contrast and intensity ranges more similar across

patients and acquisitions. The intensity normalization method is proposed for each sequence. Use of normalization technique, leads to changes in the range of pixel intensity values and these intensity values are determined. After normalization the MRI images, compute the mean intensity values and standard deviation across all training patches After normalizing the MRI images, the mean intensity value is computed and standard deviation across all training patches extracted for each sequence. Then, the patches are normalized on each sequence to have zero mean and unit variance.

B. CONVOLUTION NEURAL NETWORK

A Convolutional Neural Network (CNN) is comprised of one or more convolutional layers (often with a subsampling step) and then followed by one or more fully connected layers as in a standard multilayer neural network.

The architecture of a CNN is designed to take advantage of the 2D structure of an input image (or other 2D input such as a speech signal). This is achieved with local connections and tied weights followed by some form of pooling which results in translation invariant features. Another benefit of CNNs is that they are easier to train and have many fewer parameters than fully connected networks with the same number of hidden units. In this article the architecture of a CNN is discussed and the back propagation algorithm to compute the gradient with respect to the parameters of the model in order to use gradient base optimization. See the respective tutorials on convolution and pooling for more details on those specific operations. This practical explores the basics of learning (deep) CNN.

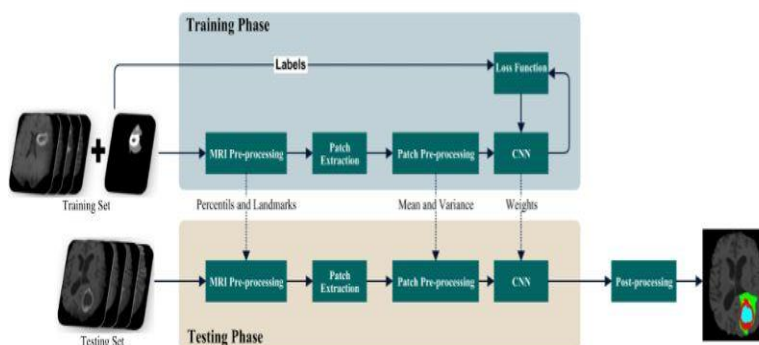


Fig.1 Overview of the proposed method

The first part introduces typical CNN building blocks, such as ReLU units and linear filters, with a particular emphasis on understanding back-propagation. The second part looks at learning two basic CNNs. The first one is a simple non-linear filter capturing particular image structures, while the second one is a network that recognises typewritten characters (using a variety of different fonts). These examples illustrate the use of stochastic gradient descent with momentum, the definition of an objective function, the construction of mini-batches of data, and data jittering.

Comparison of hyper parameter

Table 1

stage	Mean	Variance	Bias
Normal	0.1726 0.1728, 0.1632	0.0052, 0.0236, 0.0183	0.2250, 0.2243, 0.2231
Abnormal	-0.2705, -0.2730, -0.2694	0.0050, 0.0168, 0.0281	-0.2814, -0.2821, -0.2815

Initialization

Define It is important to achieve convergence. The activations and the gradients are maintained in controlled levels, otherwise back-propagated gradients could vanish or explode. Activation Function ReLU is the abbreviation of Rectified Linear Units. This is a layer of neurons that applies the non-saturating activation function $f(x)=\max(0,x)$. It increases the nonlinear properties of the decision function and of the overall network without affecting the receptive fields of the convolution layer. This method achieves better results than the more classical sigmoid, or hyperbolic tangent functions, and speed up training similar intensity scale across different subjects for the same MRI sequence, which is an explicit or implicit assumption in most segmentation methods. However,

imposing a constant 0 can impair the gradient flowing and consequent adjustment of the weights. These limitations are coped using a variant called leaky rectifier linear unit (LReLU) that introduces a small slope on the negative part of the function. This function is defined

$$f(x) = \max(0; x) + a \min(0; x)$$

Where, **a** is the leakyness parameter. In the last FC layer, soft max is used.

Pooling

Another important concept of CNNs is pooling, which is a form of non-linear down-sampling. There are several non-linear functions to implement pooling among which *max pooling* is the most common. It partitions the input image into a set of non-overlapping rectangles and, for each such sub-region, outputs the maximum. The intuition is that once a feature has been found, its exact location isn't as important as its rough location relative to other features.

The function of the pooling layer is to progressively reduce the spatial size of the representation to reduce the amount of parameters and computation in the network, and hence to also control over fitting. It is common to periodically insert a pooling layer in-between successive convolutions layers in a CNN architecture. The pooling operation provides a form of translation invariance. The pooling layer operates independently on every depth slice of the input and resizes it spatially. The most common form is a pooling layer with filters of size $s \times 2$ applied with a stride of 2 down samples at every depth slice in the input by 2 along both width and height, discarding 75% of the activations. Every MAX operation would in this case be taking a max over 4 numbers. The depth dimension remains unchanged. In addition to max pooling, the pooling units can also perform other functions, such as average pooling and even L2-norm pooling. Average pooling was often used historically but has recently fallen out of favour compared to the max pooling operation, which has been found to work better in practice.

Regularization

The most common form of regularization. It can be implemented by penalizing the squared magnitude of all parameters directly in the objective. The L2 regularization has the intuitive interpretation of heavily penalizing peaky weight vectors and preferring diffuse weight vectors. Due to multiplicative interactions between weights and inputs this has the appealing property of encouraging the network to use all of its inputs a little rather than some of its inputs a lot. Dropout can be seen as an ensemble of different networks and a form of bagging, since each network is trained with a portion of the training data.

Data Augmentation

Data augmentation is a common procedure in the context of CNN, when the data set is relatively small. In the case of MRI images, a large number of samples is present for healthy and tumorous tissue, which may be the reason why most recent studies on brain tumor segmentation based on Deep Learning did not explore data augmentation.

In this method two types of data augmentation investigated. In the first case, the effect of data augmentation by increasing the number of samples using rotations. In this study, two variants are evaluated. In the first, multiples of (90°, 180° and 270°) are used for rotations (corresponding to the Proposed method), while in the second, three rotation angles are sampled from an array using an uniform distribution, whose angles were equally spaced. Increased the data set during training by generating new patches through the rotation of the original patch. In the proposed method, angles multiple of 90 are used although another alternative will be evaluated.

LOSS FUNCTION

A loss function is used for parameter estimation, and the event in question is some function of the difference between estimated and true values for an instance of data. It is the function to be minimized during training. The Categorical Cross-entropy is used, where \hat{c} represents the probabilistic predictions (after the softmax) and c is the target. In the next subsections, the architecture and training of our CNN is discussed.

III Architecture

This paper is aimed at automatic segmentation metain tumor having large variability in intra-tumoral structures, which makes the segmentation a challenging problem. To overcome such complexity, a CNN is analysed and tuned the intensity normalization transformation for each tumor grade LGG and HGG

The architectures used for HGG is deeper than the one for LGG, because going deeper did not improve results in the latter. To go deeper, one must include more layers with the weights, which may increase over-fitting, given the smaller training set of LGG.

For doing segmentation, a precise sense of location is needed. pooling can be positive to achieve invariance and to eliminate irrelevant details. Overlapping pooling is applied with 3×3 receptive fields and 2×2 stride to keep more information of location. The feature maps are padded before convolution, so that resulting feature maps could maintain same dimension.

IV Training

Headings, CNN and the Loss function was train and it must be minimized, but it is highly non linear. stochastic gradient descent is used as an optimization algorithm, which takes steps proportionally to the negative of gradient in the direction of local minima.

nesterov's accelerated momentum is also used to accelerate the algorithm in those regions. The momentum V is kept constant, while the learning rate ϵ was linearly decreased after each epoch.

Post Processing

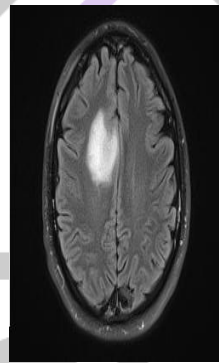
By taking the matching weights in between training phase and test phase. The resultant image is thresholded with the value less than 1 to detect the tumor area. This same procedure can be used to detect tumors from various MRI images.

V EXPERIMENTAL RESULTS AND DISCUSSION

In this section, the effect of key components is analyzed and the choice of the plane over which The patches are extracted for the analysis of the proposed method. Also comparing our method with the state of the art using the same database, including also methods based on deep learning for brain tumor segmentation.

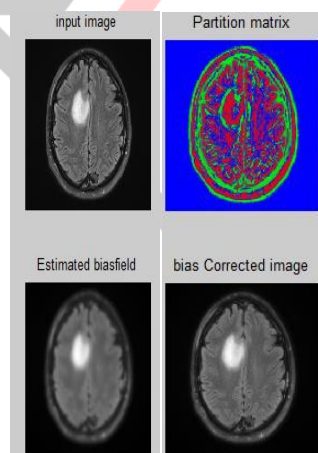
CNN-based method for segmentation of brain tumors in MRI images. A pre-processing stage consisting of bias field correction, intensity and patch normalization are obtained. After that, during training, the number of training patches is artificially augmented by rotating the training patches, By taking the matching weights in between training phase and test phase. The resultant image is thresholded with the value less than 1 to detect the tumor area. This same procedure can be used to detect tumors from various MRI images.

The input image is resized in (256 256). This image converted from rgb (red green blue) to gray and then bias field is estimated. This image is fed to the MRI pre- processor.

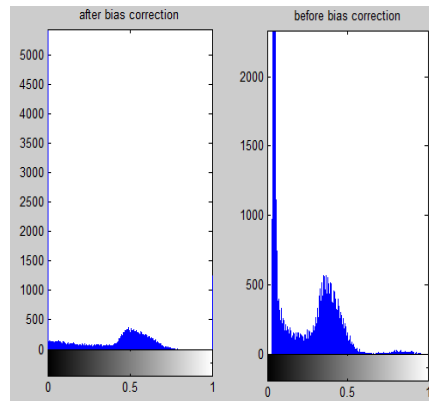


(A). Input Image

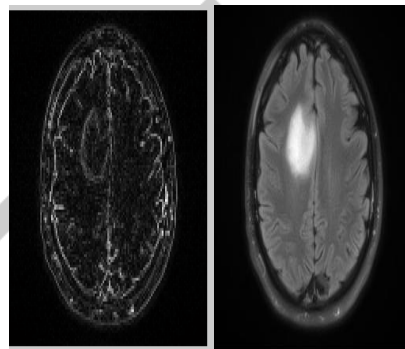
In MRI preprocessing step, the intensity normalization of each and every pixel values are calculated. After normalization the MRI images, compute the mean intensity values and standard deviation across all training patches are determined.



(B). INTENSITY NORMALIZATION AND BIAS CORRECTION

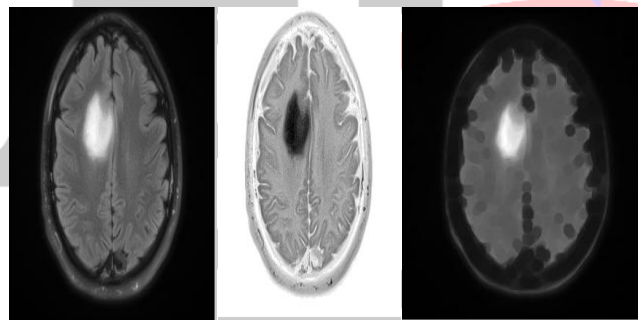


(C).HISTOGRAM OUTPUT FOR BEFORES BIAS CORRECTION AND AFTER BIAS CORRECTION

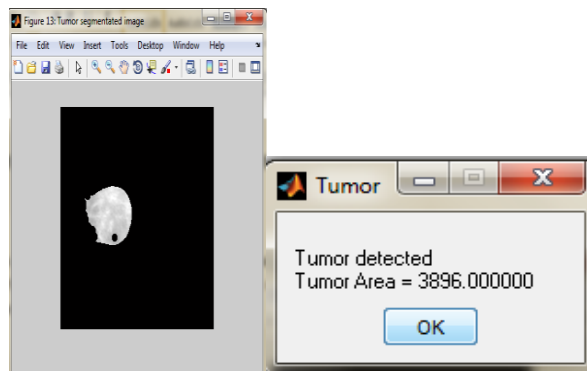


(D). PATCH EXTRACTION

Using fuzzy clustering the presence of tumor cell is determined by patch extraction from different patches. Fuzzy clustering (also referred to as soft clustering) is a form of clustering in which each data point can belong to more than one cluster.



(E).MAXPOOLIN (F).NONINEARITITY(G)CONVOLUTE IMAGE



(H)TUMOR SEGMENTED IMAGE

VI CONCLUSION

CNN-based method for segmentation of brain tumors in MRI images. A pre-processing stage consisting of bias field correction, intensity and patch normalization are done. After that, during training, the number of training patches is artificially augmented by rotating the training patches, and using samples of HGG to augment the number of rare LGG classes. The CNN is built over Convolutional layers with small 3_3 kernels to allow deeper architectures.

The potential of deep architectures through small kernels by comparing our deep CNN with shallow architectures with larger filters are investigated. Also the values are found that shallow architectures presented a lower performance, even when using a larger number of feature maps.

Finally, the activation function LReLU was more important than ReLU in effectively training our CNN is verified. By taking the matching weights in between training phase and test phase. The resultant image is thresholded with the value less than 1 to detect the tumor area. conclusion is that the contributions in this article are orthogonal to current state of the art, existing potential for further improvement brain tumor segmentation using MRI images by looking for synergies with the techniques studied by current works.

REFERENCES

- [1] B. H. Menze et al., "A generative model for brain tumor segmentation in multi-modal images," in Medical Image Computing and Computer-Assisted Intervention–MICCAI 2010. Springer, 2010, pp. 151–159.
- [2] A. Krizhevsky, I. Sutskever, and G. E. Hinton, "Imagenet classification with deep convolutional neural networks," in Advances in neural information processing systems, 2012, pp. 1097–1105.
- [3] G. E. Hinton et al., "Improving neural networks by preventing co-adaptation of feature detectors," arXiv preprint arXiv:1207.0580v1, 2012..
- [4] S. Bauer et al., "A survey of mri-based medical image analysis for brain tumor studies," Physics in medicine and biology, vol. 58, no. 13, pp. 97–129, 2013.
- [5] V. Rao, M. Sharifi, and A. Jaiswal, "Brain tumor segmentation with deep learning," MICCAI Multimodal Brain Tumor Segmentation Challenge (BraTS), pp. 56–59, 2015.
- [6] G. Urban et al., "Multi-modal brain tumor segmentation using deep convolutional neural networks," MICCAI Multimodal Brain Tumor Segmentation Challenge (BraTS), pp. 1–5, 2014.
- [7] D. Kwon et al., "Multimodal brain tumor image segmentation using glistr," in MICCAI Multimodal Brain Tumor Segmentation Challenge (BraTS) 2014, pp. 18–19.
- [8] D. Zikic et al., "Segmentation of brain tumor tissues with convolutional neural networks," MICCAI Multimodal Brain Tumor Segmentation Challenge (BraTS), pp. 36–39, 2014.
- [9] P. Dvořák and B. Menze, "Structured prediction with convolutional neural networks for multimodal brain tumor segmentation," MICCAI Multimodal Brain Tumor Segmentation Challenge (BraTS), pp. 13–24, 2015.
- [10] B. Menze et al., "The multimodal brain tumor image segmentation benchmark (brats)," IEEE Transactions on Medical Imaging, vol. 34, no. 10, pp. 1993–2024, 2015.