Brain Tumor Segmentation using Deep Belief Neural Networks in MRI Images

Ms.S.Banupriya[1]
Department Of Ece,
T.S.M Jain College Of Technology

Ms.S.Pushkala[2]
Department Of Ece,
T.S.M Jain College Of Technology

Mrs.C.Rajeshwari[3]
Department Of Ece,
T.S.Mjain College Of Technology

Abstract- *Among brain tumors, gliomas are the most common and aggressive, leading to a very short life expectancy in their highest grade. Thus, treatment planning is a key stage to improve the quality of life of oncological patients. Magnetic resonance imaging (MRI) is a widely used imaging technique to assess these tumors, 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. The large spatial and structural variability among brain tumors make automatic segmentation a challenging problem. The proposed system an automatic segmentation method based on Deep Belief Neural Networks (DBN), exploring small 3 × 3 kernels. The use of small kernels allows designing a deeper archi-tecture, besides having a positive effect against overfitting, given the fewer number of weights in the network. We also investigated the use of intensity normalization as a pre-processing step, which though not common in DBN-based segmentation methods, proved together with data augmentation to be very effective for brain tumor segmentation in MRI images.*

Index Terms—*Brain tumor, deep learning, glioma, magnetic resonance imaging.*

I. INTRODUCTION

Gliomas are the brain tumors with the highest mortality rate and prevalence. These neoplasms can be graded into Low Grade Gliomas (LGG) and High Grade Gliomas (HGG), with the former being less aggressive and infiltrative . Even under treatment, patients do not survive on average more than 14 months after diagnosis.Current treatments include surgery, chemotherapy, radiotherapy, or a combination of them . MRI is especially useful to assess gliomas in clinical practice, since it is possible to acquire MRI sequences providing complementary information.

The accurate segmentation of gliomas and its intra-tumoral structures is important not only for treatment planning, but also for follow-up evaluations. However, manual segmentation is time-consuming and subjected to inter- and intra-rater errors difficult to characterize. Thus, physicians usually use rough measures for evaluation . For these reasons, accurate semi-automatic or automatic methods are required. However, it is a challenging task, since the shape, structure, and location of these abnormalities are highly variable.additionally, the tumor mass effect change the arrangement of the surrounding normal tissues. Also, MRI images may present some problems, such as intensity in homogeneity , or different intensity ranges among the same sequences and acquisition scanners .

In brain tumor segmentation, 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 a prior 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 neoplasm. Tumor growth models can be used as estimates of its mass effect, being useful to improve the atlases The neighborhood of the voxels provides useful information for achieving smoother segmentations through Markov Random Fields (MRF) .

Another class of methods learns a distribution directly from the data. Although a training stagecan be a disadvantage.
This methods can learn brain tumor patterns that do not follow a specific model. This kind of approaches commonly consider 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 neighborhood by embedding the probabilistic predictions of the classifier into a Conditional Random Field. 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.

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 hand-crafted features, which may require specialized knowledge . DBN have been used to win several object recognition and biological image segmentation challenges. Since a DBN 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
Built a cascade of two networks and performed a two-stage training, by training with balanced classes and then refining it with proportions near the originals. use a binary CNN to identify the complete tumor. Then, a cellular automata smooths the segmentation, before a multi-class CNN discriminates the sub regions of tumor. 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. 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.

A. MAGNETIC RESONANCE IMAGING

Magnetic resonance imaging, nuclear magnetic resonance imaging, or magnetic resonance tomography is a medical imaging technique used in radiology to visualize internal structures of the body in detail.

MRI is also a topographic imaging modality, in that it produces two-dimensional images that consist of individual slices of the brain. Protons placed in a magnetic field have the interesting property that they will absorb energy at specific frequencies, and then re-emit the energy at the same frequency. To measure the net magnetization, a coil placed around the head is used to both, generate electromagnetic waves and measure the electromagnetic waves that are emitted from the head in response. This causes the nuclei to produce a rotating magnetic field detectable by the scanner and this information is recorded to construct an image of the scanned area of the body. Magnetic field gradients cause nuclei at different locations to process at different speeds, which allow spatial information to be recovered using Fourier analysis of the measured signal. By using gradients in different directions, 2D images or 3D volumes can be obtained in any arbitrary orientation.

Image intensity in MRI depends upon several parameters. These are proton density, which is determined by the relative concentration of water molecules, and T1, T2, and T2* relaxation, which reflect different features of the local environment of individual protons. The degree to which these parameters contribute to overall image intensity is controlled by the application and timing of radiofrequency energy through different pulse sequences.

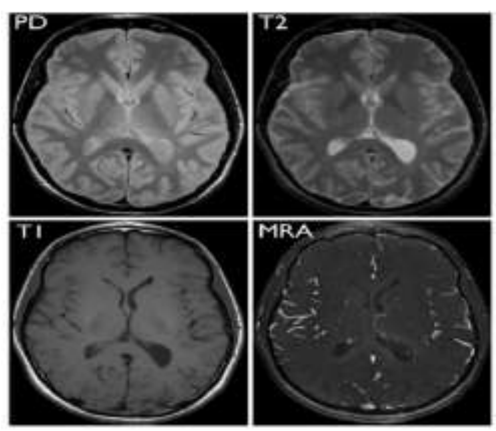

Fig 1: SELECTED IMAGES FROM A BRAIN MRI : Proton density (PD, top left), T1-weighted (T1, bottom left), T2 weighted (T2, top right), and MR angiography (MRA, bottom right)

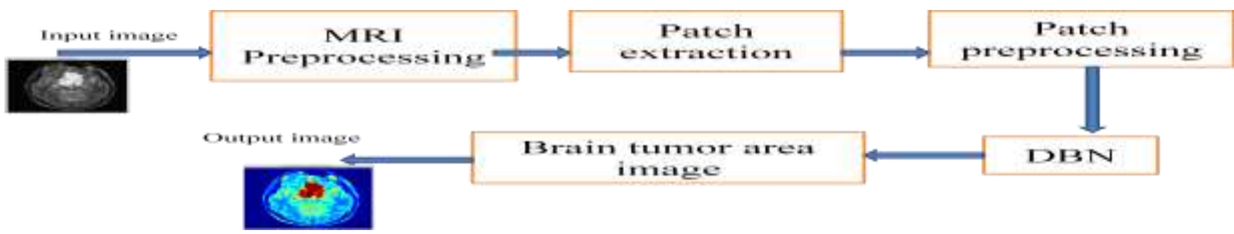

Fig. 2. Overview of the proposed method.

IMAGE DENOISING

Denoising is the process of reducing noise while retaining the signal features as much as possible. Furthermore, noise can be in the process of acquisition and Compression.

Image denoising is an important image processing task, both as a process itself, and as a component in other processes. Very many ways to denoise an image or a set of data exists. The main properties of a good denoising model are that it will remove noise while preserving edges. Traditionally, linear models have been used. One common approach is to use a Gaussian filter, or equivalently solving the heat-equation with the noisy image as input-data, i.e. a linear, 2nd order PDE-model. For some purposes this kind of denoising is adequate.

B. IMAGE SEGMENTATION

Segmentation partitions an image into distinct regions containing each pixel with similar attributes. To be meaningful and useful for image analysis and interpretation, the regions should strongly relate to depicted objects or features of interest. Meaningful segmentation is the first step from low-level image processing transforming a grey scale or colour image into one or more other images to high-level image description in terms of features, objects, and scenes. The success of image analysis depends on reliability of segmentation, but an accurate partitioning of an image is generally a very challenging problem. Segmentation techniques are either contextual or non contextual. The latter take no account of spatial relationships between features in an image and group pixels together on the basis of some global attribute, e.g. grey level or colour. Contextual techniques additionally exploit these relationships, e.g. group together pixels with similar grey levels and close spatial.

II. PROPOSED SYSTEM

Deep belief Neural Networks are very similar to ordinary Neural Networks. They are made up of neurons that have learnable weights and biases. Each neuron receives some inputs, performs a dot product and optionally follows it with a non-linearity.

Deep belief Neural Networks take advantage of the fact that the input consists of images. In particular, unlike a regular Neural Network, the layers of a Deep belief Neural network have neurons arranged in 3 dimensions width, height, and depth. The input images in CIFAR-1 are an input volume of activations, and the volume has dimensions 32x32x3. As we will soon see, the neurons in a layer will only be connected to a small region of the layer before it, instead of all of the neurons in a fully-connected manner.
Neural Network architecture we will reduce the full image into a single vector of class scores, arranged along the depth dimension.

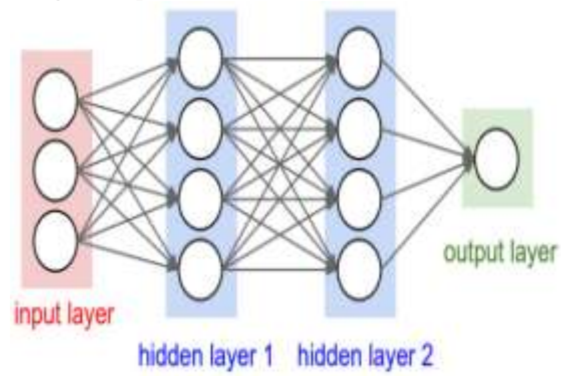

Fig 3 DBN Architecture

A. Architectures

INPUT [32x32x3] will hold the raw pixel values of the image, in this case an image of width 32, height 32, and with three color channels R, G, B. Deep belief layer will compute the output of neurons that are connected to local regions in the input, each computing a dot product between their weights and a small region they are connected to in the input volume. This may result in volume such as [32x32x12] if we decided to use 12 filters.

Pooling Layer:

It is common to periodically insert a Pooling layer in-between successive layers in Deep belief Network architecture. Its function 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 overfitting. The Pooling Layer operates independently on every depth slice of the input and resizes it spatially, using the MAX operation. The most common form is a pooling layer with filters of size 2x2 applied with a stride of 2 downsamples 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 (little 2x 2 regions in some depth slice). The depth dimension remains unchanged.

Layer Patterns

The most common form of DBN Network architecture stacks a few CONV-RELU layers, follows them with POOL layers, and repeats this pattern until the image has been merged spatially to a small size. At some point, it is common to transition to fully-connected layers.

Layer Sizing Patterns

The input layer (that contains the image) should be divisible by 2 many times. The convolution layers should be using small filters (e.g. 3x3 or at most 5x5), using a stride of S=1S=1, and crucially, padding the input volume with zeros in such way that the DBN layer does not alter the spatial dimensions of the input.

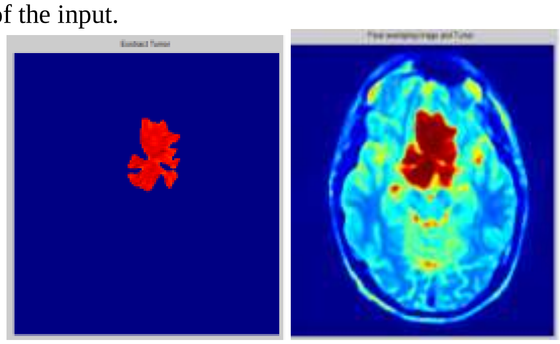

Fig 4. Final extracted tumor image

III. CONCLUSIONS

A novel CNN-based method for segmentation of brain tumors in MRI images. We start by a preprocessing stage consisting of bias field correction, intensity and patch normalization. Brain tumors are highly variable in their spatial localization and structural composition, so we have investigated the use of data augmentation to cope with such variability. We studied augmenting our training data set by rotating the patches as well as by sampling from classes of HGG that were underrepresented in LGG. We found that data augmentation was also quite effective, al-though not thoroughly explored in Deep Learning methods for brain tumor segmentation. The DBN will exactly extract the tumor cells of the image. The process analyzes the pixels of the input image layer by layer to detect the affected parts of the brain.

REFERENCES

[1] S. Bauer *et al.*, "A survey of MRI-based medical image analysis for brain tumor studies," *Phys. Med. Biol.*, vol. 58, no. 13, pp. 97–129, 2013.

[2] D. N. Louis *et al.*, "The 2007 who classification of tumours of the central nervous system," *Acta Neuropathologica*, vol. 114, no. 2, pp. 97–109, 2007.

[3] E. G. Van Meir *et al.*, "Exciting new advances in neuro-oncology: The avenue to a cure for malignant glioma," *CA, Cancer J. Clinicians*, vol. 60, no. 3, pp. 166–193, 2010.

[4] G. Tabatabai *et al.*, "Molecular diagnostics of gliomas: The clinical perspective," *Acta Neuropathologica*, vol. 120, no. 5, pp. 585–592, 2010.

[5] B. Menze *et al.*, "The multimodal brain tumor image segmentation benchmark (BRATS)," *IEEE Trans. Med. Imag.*, vol. 34, no. 10, pp. 1993–2024, Oct. 2015.

[6] N. J. Tustison *et al.*, "N4ITK: Improved n3 bias correction," *IEEE Trans. Med. Imag.*, vol. 29, no. 6, pp. 1310–1320, Jun. 2010.

[7] L. G. Nyúl, J. K. Udupa, and X. Zhang, "New variants of a method of MRI scale standardization," *IEEE Trans. Med. Imag.*, vol. 19, no. 2, pp. 143–150, Feb. 2000.

[8] M. Prastawa *et al.*, "A brain tumor segmentation framework based on outlier detection," *Med. Image Anal.*, vol. 8, no. 3, pp. 275–283, 2004.

[9] B. H. Menze *et al.*, "A generative model for brain tumor segmentation in multi-modal images," in *Medical Image Computing and Comput.-Assisted Intervention-MICCAI 2010*. New York: Springer, 2010, pp. 151–159.

[10] A. Gooya *et al.*, "GLISTR: Glioma image segmentation and registra-tion," *IEEE Trans. Med. Imag.*, vol. 31, no. 10, pp. 1941–1954, Oct. 2012.

[11] D. Kwon *et al.*, "Combining generative models for multifocal glioma segmentation and registration," in *Medical Image Computing and Comput.-Assisted Intervention-MICCAI 2014*. New York: Springer, 2014, pp. 763–770.

[12] S. Bauer, L.-P. Nolte, and M. Reyes, "Fully automatic segmentation of brain tumor images using support vector machine classification in combination with hierarchical conditional random field regu-larization," in *Medical Image Computing and Comput.-Assisted Intervention-MICCAI 2011*. New York: Springer, 2011, pp. 354–361.

[13] C.-H. Lee *et al.*, "Segmenting brain tumors using pseudo-condi-tional random fields," in *Medical Image Computing and Comput.-As-sisted Intervention-MICCAI 2008*. New York: Springer, 2008, pp. 359–366.