# Measurement of Multimodal Brain Tumor Segmentation using Neural Network

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Abstract— The motive of this project is to come up with a fully automatic tumor segmentation approach using convolutional neural networks. Tumors can appear anywhere in the brain and have almost any kind of shape, size, and contrast. These reasons motivate the use of a flexible, high capacity deep neural network. This is a summary of the work done in this regard with an effort to describe in as much detail the methodology used. The BraTS Brain Tumor Segmentation challenge dataset that contains brain MRI scans for more than 200 patients is used in this study. A patch wise segmentation approach is used and will see 98% accuracy on the test set of patches. A variety of experiments are done around the depth of the neural network used different architectures etc to train the the hest architecture for this task. Convolutional neural network find the exact location of gliomas CNN & is used to Deep neural network are used to find the spectral location. Deep neural network is to find the hidden units in gliomas.Neural networks are predict the patient organs in future.

Keywords— Deep neural network, Convolutional neural network, Gliomas.

## INTRODUCTION

Gliomas are the brain tumors with the highest mortality rate and prevalence. These neo plasma can be graded into Low Grade Gliomas and High Grade Gliomas with the former being less aggressive and infiltrative than the latter Even under treatment, patients do not survive on average more than 14 months after diagnosis Current treatments include surgery, chemotherapy, radio therapy, 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.

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 on co logical patients. Magnetic resonance imaging 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. So, automatic and reliable segmentation methods are required however, the large spatial and structural variability among brain tumors make automatic segmentation a challenging problem. In this paper, we propose an automatic segmentation method based on Convolutional Neural Networks exploring small kernels. The use of small kernels allows designing a deeper architecture, besides having a positive effect against over fitting, 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 CNN based segmentation methods, proved together with data augmentation to be very effective for brain tumor segmentation in MRI images. Our proposal was validated in the Brain Tumor Segmentation Challenge database, obtaining simultaneously the first position for the complete, core, and enhancing regions in Dice Similarity Coefficient metric for the Challenge data set. Also, it obtained the overall first position by the online evaluation platform. We also participated in the on-site Challenge using the same model, obtaining the second place, with Dice Similarity Coefficient metric of and 0.75 for the complete, core, and enhancing regions, respectively up with a fully automatic image The existing approach used image segmentation techniques based on clustering to detect the brain tumor and calculating the tumor area. By developing a novel image segmentation approach, called K-means integrated with C-means for abnormal MRI images. The previous approach is done by integrated Kmeans clustering algorithm with the Fuzzy C-means algorithm to overcome the limitations and get benefits of them. After clustering stage, the extraction of the tumor is done automatically without user interaction by using thresholding and level set methods to contour the tumor area. The last stage of our proposed technique is calculating the tumor area in the processed image. Kmeans algorithm can detect a brain tumor faster than Fuzzy C-means. However, Fuzzy C-means predicted tumor cells that are not predicted by K-means algorithm. This technique gives an accurate result as compared to the Kmeans algorithm. Even though original Fuzzy C-means algorithm yields good results for segmenting noise free images, it fails to segment noisy images. Therefore, we get benefits from integrating these two algorithms to reduce the number of iterations, which affects execution time and gives an accurate result in tumor detection.

Gliomas are the brain tumors with the highest mortality rate and prevalence. This neoplasm with the former being less aggressive and infiltrative than the latter. Even under treatment, patients do not survive on average more than 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 changes 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, 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 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 as.

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 also used a MRF to segment brain tumors after a first over segmentation of the image into super voxels, with a histogram-based estimation of the likelihood function. As observed by 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.

Must predict the membership of the input to each of the clusters. In this paper, inspired by the groundbreaking work on deep CNNs, we investigate the potential of using deep architectures with small convolutional kernels for segmentation of gliomas in MRI images. Proposed the use of small 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 cascaded convolutional layers have the same effective receptive field. At the same time, it has the advantages of applying more processing step that aims to address data heterogeneity caused by acquisitions of MRI images.

## A. PRE PROCESSING

Pre-Processing MRI images are altered by the bias field distortion. This makes the intensity of the same tissues to vary across the image.

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 pathology. So, to make the contrast and intensity ranges more similar across patients and acquisitions, we apply the intensity normalization method proposed. On each sequence. In this intensity normalization method, a set of intensity landmarks are learned for each sequence from the training set. And are chosen for each MRI sequence as described in. Represents intensity at the percentile. After training, the intensity normalization is accomplished by linearly transforming the original intensities between two landmarks into the corresponding learned landmarks. In this way, the histogram of each sequence is more similar across subjects.

After normalizing the MRI images, we compute the mean intensity value and standard deviation across all training patches extracted for each sequence.

## CONVOLUTIONAL NEURAL NETWORKING

Convolutional Neural Network CNN was 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. By using kernels, information of the neighborhood is taken into account, which is a useful source of context information. Usually, a non-linear activation function is applied on the output of each neural unit. If we stack several convolutional layers, the extracted features become more abstract with the increasing depth. The first layers enhance features such as edges, which are aggregated in the following layers as motifs, parts, or objects. Use maxpooling or average-pooling it is used to reduce over fitting.

In each training step, it removes nodes rum the network with probability. In this way, it forces all nodes of the FC layers to learn better representations of the data, preventing nodes from co adapting to each other. At test time, all nodes are used. 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.

## C. POST PROCESSING

Post-Processing some small clusters may be erroneously classified as tumor. To deal with that, we impose volumetric constrains by removing clusters in the segmentation obtained by the CNN that are smaller than a predefined threshold gain.

In this section, we analyze the effect of key components and the choice of the plane over which we extract patches on the performance of the proposed method. Also, we compare our method with the state of the art using the same database, including also methods based on deep learning for brain tumor segmentation. We evaluate the effect of each component on the proposed approach by studying the improvement in performance. This increment in performance is evaluated as the mean gain in the metrics DSC, PPV and Sensitivity, which is obtained in the following way we compute all metrics using the proposed method for the data sets then we remove or substitute the component under study, and compute the metrics for this alternative method. Finally, we subtract each metric for the two systems and calculate the average across the subtractions, obtaining the mean gain.

The metric of each experiment is present the box plots in the Leader board and Challenge data set, respectively and we exemplify the effect of the experiments in the segmentation of tumor in two patients HGG and LGG. In the experiments, we maintained the hyper parameters presented as possible to preserve the same conditions. Also, only the images in the Training data set are used in the learning phase of the intensity normalization method. All tests in this section use patches extracted from planes perpendicular to the axial axis of the MRI image, where it is evaluated the choice of the best axis.

The effect of the pre-processing on the segmentation was evaluated by comparing with an alternative method described . We chose this method, because it is also utilized in a CNN-based brain tumor segmentation method . This alternative pre-processing starts by applying a 1% win sorizing over the intensities within the brain. Then, the N4ITK is used to correct the bias field in each MRI sequence and the intensities are linearly transformed to. Finally, we normalized each sequence to have zero mean and unit variance. During the training stage of the CNN with this pre-processing for LGG, we found to be necessary to decrease the initial and final learning rate to and, respectively, otherwise the optimization would diverge the pre-processing using the intensity normalization method improved most of the metrics, obtaining a mean gain of 4.6% Leader board: 4.2% Challenge: 4.9%. This improvement was specially larger for LGG, indicating that the proposed pre-processing increased the detection of the complete as well as the core of the tumor, which is considered a difficult task. Also, comparing the drop in performance, when removing our pre-processing and the one verified when removing any other component, we verify that this pre-processing was the key component for improving the segmentation in LGG. Grades is interesting, because we know that the features learned by the CNN are computed in local regions by a bank of band-pass filters at different scales, instead of point-wise properties as an intensity. Shah presented a study regarding the segmentation of multiple sclerosis based on MRI images, showing that classifiers based on point-wise features, as intensity, improved after normalization. This improvement was obtained by minimizing the data heterogeneity from multi-stimuliscanner MRI acquisitions.

It proposed the grid integration of medical image processing applications as grid workflows, where the workflow manager is responsible for the execution of all tasks related to grid communication and the developer is responsible for setting the access rights on his code and defining the workflow manager what to do with it. The processing steps can be applied in order to achieve runtime reduction. It presented a novel solution for reconstructing medical volumes proposing the web service implementation as an additional layer to a dataflow framework. It is used image-based analysis of brain MRI scan as a case study a centralized data are located in a centralized data repository and a disturbed one data are delivered directly from producing to consuming services, showing that in the disturbed data the flow model achieved a satisfying speed up of the workflow execution. The number of operators, enabling versatile image processing or classification functionalities, however, is exponentially growing in the recent years. It is expected that the incorporation of these operators, as well as the transition from closed systems with a fixed set of operators systems. The median filter is used to remove noise from the MRI report; segmentation is carried out by watershed algorithm through which one can identify the brain cancer in earlier manner. Convolutional neural networks CNNs consist of multiple layers of receptive fields. These are small neuron collections which process portions of the input image.

The outputs of these collections are then tiled so that their input regions overlap, to obtain a better representation of the original image; this is repeated for every such layer.

#### PROPOSED SYSTEM

## Image acquisition

Images are obtained using MRI scan and these scanned images are displayed in a two dimensional matrices having pixels as its elements. These matrices are dependent on matrix size and its field of view. Images are stored in MATLAB and displayed as a gray scale image of size 256\*256. The entries of a gray scale image are ranging from 0 to 255, where 0 shows total black color and 255 shows pure white color. Entries between this ranges vary in intensity from black to white. For experimental purpose 30 female and 30 male patients were examined, all patients have ages ranging from 20 to 60 years. Their MRI scans were stored in database of images in JPEG image formats. By the help of MRI, the brain tumor images are acquired and these scanned images are exhibited in 2D matrix where the pixels are considered to be the elements. Such matrices rely on field of view and size of the matrix. MATLAB is implemented to reserve the images and are exhibited in a gray scale with a dimension of 256\*256. The intensity of these gray scale images are represented as a number from decimal 0 to 255, where 0 resembles purely black color and 255 resembles purely white color. Any intermediate values within this range differ in ardency from black to white. The experiment was carried out on 20 female and 10 male patients, all of them lying between 20 to 60 years. The ulcer affected images procured from their tests were stored in JPEG image formats. .



## B.Noise Removal

Digital images always suffer from a number of noises. Noise is an outcome of faults in the image procurement phase which results in the pixel values thus affecting the true intensities of the real scenario. One can remove these noises using adaptive filtering, linear filtering or median filtering. In case of linear filtering, Gaussian or averaging filters are implemented to remove the unwanted presence of noises as the pixel &39;s value for this filter is substituted with its local values. Average filters are implemented for the removal of the pepper and salt noise present in the image. Median filtering is similar to an averaging filter, and can be easily utilized and produces better results. In this type of filtering, the pixel values are decided by the pixel values of neighborhood. Its sensitivity is less when compared to the outliers.

## C.Sharpening of Image

Image sharpening can be accomplished by the application of various high pass filters. As the noises are filtered by the application of various low pass filters, there is a need of image sharpening as the sharp edges are needed, which aids in detecting the boundary of the brain tumors. To increase the periphery of the objects present in the image, Gaussian high pass filter are implemented. Gaussian filters results in improved performances and is broadly implemented to increase the minute details about the object.

## D.Feature Extraction

The feature extraction is pulling out the come jointly which shows the forecast tumor at the median filter algorithm output. The pull out crowd together is given to the threw holding process. It applies twice over mask of the entire image. It makes the dark pixel turn out to be gloomy and white turn out to be brighter.

## E.EdgeDetection

In this phase, image is intensified in a way that minute details are ameliorated and noise is filtered.

Generally used noise filtering techniques are applied, which helps us to procure the feasible results. Enhancement leads to the procurement of more conspicuous edges, image sharpening, and noise reduction, thus reducing the obscuring impression of the image and the possible twisted results of the intervening system. Eventually image partitioning will also be implemented. This ameliorated and refined image aids in edge determination and improves the overall image quality. Edge detection procedure helps us to find the precise position of brain tumors.

Depth of the output volume controls the number of neurons in the layer that connect to the same region of the input volume. All of these neurons will learn to activate for different features in the input. For example, if the first Convolutional Layer takes the raw image as input, then different neurons along the depth dimension may activate in the presence of various oriented edges, or blobs of color.

Stride controls how depth columns around the spatial dimensions width and height are allocated. When the stride is 1, a new depth column of neurons is allocated to spatial positions only 1 spatial unit apart. This leads to heavily overlapping receptive fields between the columns, and also to large output volumes. Conversely, if higher strides are used then the receptive fields will overlap less and the resulting output volume will have smaller dimensions spatially.

Sometimes it is convenient to pad the input with zeros on the border of the input volume. The size of this zero-padding is a third hyper parameter. Zero padding provides control of the output volume spatial size. In particular, sometimes it is desirable to exactly preserve the spatial size of the input volume.



Figure 1.1: Deep Neural Network

#### Spatial arrangement

Three hyperparameters control the size of the output volume of the convolutional layer: the **depth**, **stride** and **zero-padding**.

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region of the input volume. All of these neurons will learn to activate for different features in the input. For example, if the first Convolutional Layer takes the raw image as input, then different neurons along the depth dimension may activate in the presence of various oriented edges, or blobs of color.

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Figure1.2 Fuzzy segmented

Convolutional neural networks (CNNs) consist of multiple layers of receptive fields. These are small neuron collections which process portions of the input image. The outputs of these collections are then tiled so that their input regions overlap, to obtain a better representation of the original image; this is repeated for every such layer.

Median filtering is implemented on the acquired images to get rid of the unwanted noises.

The features of the proposed work will make the detection processes more accurate and easier as there are some standard characteristics of each feature for a specific tumor.

Image-based tumor detection uses one or more algorithms as the primary modeling. Some can detect edges, some can detect shapes while others can detect other features.

## CONCULSION

intensity and patch normalization. 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.In designing our method, we address the heterogeneity caused by multi-site multi-scanner acquisitions of MRI images using intensity normalization. We show that this is important in achieving a good segmentation. 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, although not thoroughly explored in Deep Learning methods for brain tumor segmentation. Also, we investigated the potential of deep architectures through small kernels by comparing our deep CNN with shallow architectures with larger filters. We found that shallow architectures presented a lower performance, even when using a larger number of feature maps. Finally, we verified that the activation function.So we use the deep neural networking to rectify the glioma in brain in this paper deep neural to analyze the gliomas stages and find the affected organ in future.Using neural networking we will predict the future affected area and Comparing with the best generative model, we were able to reduce the computation time approximately by ten fold.Concerning the 2016 database, we obtained the second position among twelve contenders in the on-site challenge.



Figure 1.3 Deep Learning

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