Segmentation of Brain Tumors using SegNet in MR FLAIR Images

03CS7914 Project (Phase II)

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Praveena K M

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Abstract

Brain tumor detection and segmentation is a difficult and time-consuming task in medical image processing. Analysis of Magnetic Resonance Image (MRI) scans is a potent tool in contemporary technology that enables accurate detection of aberrant brain tissues. The size of a tumor and its minuscule details can be seen in the brain imaging for various patients. A difficult undertaking in daily clinical practice is still separating tumour boundaries from healthy cells. An MRI technique called fluid-attenuated inversion recovery (FLAIR) can tell a doctor how much of a tumor has infiltrated the body. For radiologists, it is challenging to identify and categorise the tumour from a variety of pictures. To solve these problems,proposed an automatic segmentation of brain tumor in MR Flair images using SegNet. Bias correction, intensity normalization algorithms are used for pre-processing the mri data.

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Chapter 1

Introduction

Medical image segmentation is similar to natural image segmentation, refers to the process of extracting the desired object (organ) from a medical image (2D or 3D), which can be done manually, semi-automatically or fully-automatically. Earlier approaches for medical image segmentation mostly depends on edge detection, template matching techniques, statistical shape models, active contours and machine learning, etc. Medical image segmentation can be a time-consuming task, and recent advances in Artificial Intelligence (AI) techniques are making it easier. Popular medical image segmentation tasks include liver and liver-tumor segmentation , brain and brain-tumor segmentation, optic disc segmentation , cell segmentation , lung segmentation and pulmonary nodules.

One of the primary tumours that develop in the brain the most frequently is a glioma. They fall into two categories: low- and high-grade gliomas. When compared to low grade gliomas, which can be either benign or malignant and grow more slowly in a patient, high grade gliomas (HGG) are more aggressive, highly malignant, and have a life expectancy of no more than two years. Accurate segmentation of the brain tumour and any surrounding tissues, such as edoema, enhancing tumours, non-enhancing tumours, and necrotic regions, is crucial for determining the course of the disease, the effectiveness of therapy, and the planning of a patient's course of treatment.
Magnetic resonance imaging (MRI) with many modalities is frequently used in clinical practise for tumour diagnosis and tracking. One of the most often used imaging methods is magnetic resonance imaging (MRI), which helps with tumour analysis by enabling the visualisation of its spread and provides more soft tissue contrast than other methods like computed tomography (CT) and positron emission tomography (PET). Additionally, multi-modal MRI protocols are frequently used to assess the tissues of brain tumours since they have the ability to differentiate various tissues using a particular sequence based on tissue characteristics. T1-weighted images, for instance, are good at differentiating healthy brain regions, whereas T1ce (contrast enhanced) images aid to distinguish tumour boundaries, which are brighter due to the contrast agent. Edema around tumors is detected well in T2-weighted images, while FLAIR images are best for differentiating edema regions from cerebrospinal fluid (CSF).

Gliomas have complex structure and appearance. Their borders are often fuzzy and hard to distinguish from healthy tissue (white matter, gray matter, and CSF), making them hard to segment.Manual segmentation of the brain tumor is a vital procedure and needs a group of clinical experts to accurately define the location and the type of the tumor. Moreover, the process of lesion

localization is very labor based and highly dependent on the physician's experience, skills, and their slice-by-slice decisions.Formerly, numerous machine learning algorithms were developed for the segmentation of normal and abnormal brain tissues using MRI images. Although malignant areas vary in shape, size, and placement, they can only be identified through intensity changes relative to the healthy cells around them, making the development of completely automated brain tumour approaches a difficult undertaking. These variables all contribute to laborious manual delineation that is costly and subject to operator bias. By offering a useful tool for accurate diagnosis and prognosis of brain cancers, automatic brain tumour segmentation using MRI would address these problems. Consequently, a lot of researchers have thought about automating the segmentation of brain tumours from MRI scans. Deep learning has recently emerged as a promising area of machine learning that outperforms conventional computer vision algorithms in a variety of applications, including semantic segmentation and object detection.

1.1 Proposed Project

1.1.1 Problem Statement

The project aims to develop a deep learning based method for the segmentation of brain tumors.

1.1.2 Proposed Solution

To develop a method for the segmentation of tumors in the brain lesion using FLAIR MRI data with a convolutional neural network SegNet is proposed. Bias correction, intensity normalization are used for pre-processing the mri data. After that MRI slices fed into the segmentation model for obtaining the segmented results.

Chapter 2

Report of Preparatory Work

2.1 Literature Survey Report

1. **Brain Tumor Segmentation Using Convolutional Neural Networks in MRI Images,**[1], Springer Journal of Medical Systems, 7 July 2019

   Enhanced Convolutional Neural Networks (ECNN) with loss function optimization by BAT algorithm is made used in-order to perform segmentation of a MRI image in an automated manner.Tiny kernels are used to achieve a deep architecture. It is having a positive effect against overfitting, given the fewer number of weights in the network. Skull stripping and image enhancement algorithms are used for pre-processing. After the process of skull stripping, the cortex of the brain can now be viewed as a unique dark ring which surrounds the brain in a MRI image. Image enhanced methods are used to remove those distinct dark ring surrounding the brain tissues. For example, key features are identified by using the noise removal process. Morphological operation 'thicken' is applied to the binary image. Mean intensity value and standard deviation of all training patches extracted for each sequence after normalization. Patches on each sequence are normalized to have zero mean and unit variance. Enhanced Convolutional Neural Network (ECNN) is used to segment the brain image after pre-processing. The experimental results show the better performance while comparing with the existing methods

2. **SegNet:A Deep Convolutional Encoder-Decoder Architecture for Image Segmentation,** [4] , IEEE Transactions on Pattern Analysis and Machine Intelligence , Volume: 39, Issue: 12, Dec. 1, 2017.

   In this work ,they presents a novel deep fully convolutional neural network architecture for semantic pixel-wise segmentation termed SegNet. This core trainable segmentation engine consists of an encoder network, a corresponding decoder network followed by a pixel-wise classification layer. The architecture of the encoder network is topologically identical to the 13 convolutional layers in the VGG16 network.The role of the decoder network is to map the low resolution encoder feature maps to full input resolution feature maps for pixel-wise classification. The novelty of SegNet lies is in the manner in which the decoder up-samples its

lower resolution input feature maps. Specifically, the decoder uses pooling indices computed in the max-pooling step of the corresponding encoder to perform non-linear upsampling. This eliminates the need for learning to upsample.The upsampled maps are sparse and are then convolved with trainable filters to produce dense feature maps.
Since all the fully connected layers are removed, the number of trainable parameters reduce from 134M to 17.4M .So it is computationally feasible.In SegNet only the pooling indices are transferred to the expansion path from the compression path, using less memory. Where as in UNet, entire feature maps are transferred from compression path to expansion path making, using a lot of memory.

3. **U-net: Convolutional networks for biomedical image segmentation.[9]** In International Conference on Medical Image Computing and Computer-assisted Intervention, pp. 234-241. Springer, Cham, 2015.

In this paper, presented a network and training strategy that relies on the strong use of data augmentation to use the available annotated samples more efficiently. The architecture consists of a contracting path to capture context and a symmetric expanding path that enables precise localization. The contracting path follows the typical architecture of a convolutional network. It consists of the repeated application of two 3x3 convolutions (unpadded convolutions), each followed by a rectified linear unit (ReLU) and a 2x2 max pooling operation with stride 2 for downsampling. At each downsampling step doubles the number of feature channels. Every step in the expansive path consists of an upsampling of the feature map followed by a 2x2 convolution (up-convolution) that halves the number of feature channels, a concatenation with the correspondingly cropped feature map from the contracting path, and two 3x3 convolutions, each followed by a ReLU. The cropping is necessary due to the loss of border pixels in every convolution. At the final layer a 1x1 convolution is used to map each 64- component feature vector to the desired number of classes. In total the network has 23 convolutional layers. To allow a seamless tiling of the output segmentation map , it is important to select the input tile size such that all 2x2 max-pooling operations are applied to a layer with an even x- and y-size.U-Net architecture is great for biomedical image segmentation, achieves very good performance despite using only using 50 images to train and has a very reasonable training time.

4. **Brain tumor segmentation using convolutional neural networks in MRI images,[3],** IEEE Transactions On Medical Imaging, Vol. 35, NO. 5, MAY 2016.

   Among brain tumors, gliomas are the most common and aggressive, leading to a very short life expectancy in their highest grade. In this paper, they propose an automatic segmentation method based on Convolutional Neural Networks (CNN), exploring small 3×3 kernels.The use of small kernels allows designing a deeper architecture, besides having a positive effect against overfitting, given the fewer number of weights in the network.The proposed CNN-based method for segmentation of brain tumors begin with a pre-processing stage consisting of bias field correction, intensity and patch normalization. After normalizing the MRI images, then computes the mean intensity value and standard deviation across all training patches extracted for each sequence. Then, normalize the patches on each sequence to have zero mean and unit variance.MRI images are altered by the bias field distortion. This makes the intensity of the same tissues to vary across the image.So intensity is normalized .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. In the CNN, Xavier initialization is used thus the activations and the gradients are maintained in controlled levels, Rectifier linear units (ReLU) is used as activation Function which responsible for non-linearly transforming the data. CNN with shallow architectures with larger filters gives a lower performance, even when using a larger number of feature map.

5. **Modality-Pairing Learning for Brain Tumor Segmentation ,[8]** ,arXiv preprint arXiv, 2020 - arxiv.org

   Automatic brain tumor segmentation from multi-modality Magnetic Resonance Images (MRI) using deep learning methods plays an important role in assisting the diagnosis and treatment of brain tumor. However, previous methods mostly ignore the latent relationship among different modalities. In this work, they proposed a novel end-to-end Modality-Pairing learning method for brain tumor segmentation. Modality-Pairing Network which consists of paralleled branches. Each branch focuses on specific modalities and all the branches are properly connected. The purpose of the pairing paths is to derive the features most relevant to each modality and obtain more abundant information among different modalities. The four modalities are divide into two groups and combine two modalities in each group. Experiments show a better choice to combine T1 and T1ce, T2 and Flair. These two groups are fed into the two branches separately Paralleled branches are designed to exploit different modality features and a series of layer connections are utilized to capture complex relationships and abundant information among modalities. They also used a consistency loss to minimize the prediction variance between two branches. Besides, learning rate warmup strategy is adopted to solve the problem of the training instability and early over-fitting. Lastly, uses average ensemble of multiple models and some post-processing techniques to get final results. This method is tested on the BraTS 2020 online testing dataset, obtaining promising segmentation performance, with average dice scores of 0 .891 , 0 .842 , 0 .816 for the whole tumor, tumor core and enhancing tumor, respectively.

6. **Brain tumor segmentation with deep neural networks, [10]** ,Medical Image Analysis, vol. 35, pp. 18–31, Jan. 2017

   In this paper, presented a fully automatic brain tumor segmentation method based on Deep Neural Networks (DNNs). The proposed networks are tailored to glioblastomas (both low and high grade) pictured in MR images. By their very nature, these tumors can appear anywhere in the brain and have almost any kind of shape, size, and contrast. They present a novel CNN architecture which differs from those traditionally used in computer vision, which can exploits local features and global contextual features simultaneously. Also, different from most traditional uses of CNNs, this networks use a final layer that is a convolutional implementation of a fully connected layer which allows a 40 fold speed up. The 2-phase training procedure allows us to tackle difficulties related to the imbalance of tumor labels. Finally, a cascade architecture in which the output of a basic CNN is treated as an additional source of information for a subsequent CNN.The time needed to segment an entire brain with the CNN architecture varies between 25 seconds and 3 minutes, making them practical segmentation methods.

7. **Automatic semantic segmentation of brain gliomas from MRI images using a deep cascaded neural network,[11]** Journal of Healthcare Engineering, vol. 2018, pp. 1–14, Mar. 2018

   Brain tumors can appear anywhere in the brain and have vastly different sizes and morphology. Consequently, the segmentation of brain tumor and intratumor subregions using magnetic resonance imaging (MRI) data with minimal human interventions remains a challenging task. In this paper, they present a novel fully automatic segmentation method from MRI data containing in vivo brain gliomas. This approach can not only localize the entire tumor region but can also accurately segment the intratumor structure. The proposed work was based on a cascaded deep learning convolutional neural network consisting of two subnetworks: (1) a tumor localization network (TLN) and (2) an intratumor classification network (ITCN). The TLN, a fully convolutional network (FCN) in conjunction with the transfer learning technology, was used to first process MRI data. The goal of the first subnetwork was to define the tumor region from an MRI slice. Then, the ITCN was used to label the defined tumor region into multiple subregions. Particularly, ITCN exploited a convolutional neural network (CNN) with deeper architecture and smaller kernel. The proposed approach was validated on multimodal brain tumor segmentation (BRATS 2015) datasets, which contain 220 high-grade glioma (HGG) and 54 low-grade glioma (LGG) cases. Dice similarity coefficient (DSC), positive predictive value (PPV), and sensitivity were used as evaluation metrics. Our experimental results indicated that our method could obtain the promising segmentation results and had a faster segmentation speed.

8. **Brain tumor classification from multi-modality MRI using wavelets and machine learning**",[6] Pattern Analysis and Appllications, vol. 20, no. 3, pp. 871-881, 2017.

In this paper, proposed a brain tumor segmentation and classification method for multi-modality magnetic resonance imaging scans. The data from multimodal brain tumor segmentation challenge (MICCAI BraTS 2013) are utilized which are co-registered and skull-stripped, and the histogram matching is performed with a reference volume of high contrast. All the images are visualized through ITK-Snap, while histogram matching is performed with Slicer3D to enhance the image contrast by choosing a high-contrast image as the reference. The next preprocessing step is to determine the bounding box around the tumor region.From the preprocessed images, the following features are then extracted: intensity, intensity differences, local neighborhood and wavelet texture. Random forest (RF) is a combination of decision trees. Each tree in ensemble is trained on randomly sampled data with replacement from training vector during the phase of training. Multiple trees are trained to increase the correlation and reduce the variance between trees.The integrated features are subsequently provided to the random forest classifier to predict five classes: background, necrosis, edema, enhancing tumor and non-enhancing tumor, and then these class labels are used to hierarchically compute three different regions (complete tumor, active tumor and enhancing tumor).

2.2 System Study Report

Past few years have witnessed the prevalence of deep learning in many application scenarios, among which is medical image processing. Brain tumor segmentation has been studied extensively over the past years. Diagnosis and treatment of brain tumors requires an accurate and reliable segmentation of brain tumors as a prerequisite. However, such work conventionally requires brain surgeons significant amount of time. Manual segmentation of the brain tumor is a vital procedure and needs a group of clinical experts to accurately define the location and the type of the tumor. Moreover, the process of lesion localization is very labor based and highly dependent on the physicians' experience, skills, and their slice-by-slice decisions. Alternatively, automated computer based segmentation methods present a good solution to save the surgeon's time and to provide reliable and accurate results, while reducing the exerted efforts of experienced physicians to accomplish the procedures of diagnosis or evaluation for every single patient .Formerly, numerous machine learning algorithms were developed for the segmentation of normal and abnormal brain tissues using MRI image.Computer vision techniques could provide surgeons a relief from the tedious marking procedure. Recently, deep learning-based methods such as convolutional neural networks (CNNs), have become increasingly popular and achieved significant progress in brain tumor segmentation tasks.

Chapter 3

Project Design

3.1 Resource Requirements

3.1.1 Hardware & Software Requirements

Operating System	: Any 64bit Operating System
Supporting softwares and libraries	: Python, Tensorflow, keras,nilearn,med2image,SimpleITK
Processor	: AMD Ryzen 7 4700U 2.00 GHz
RAM	: 8GB
Monitor	: Any colour monitor
Dataset	: Kaggle MRI LGG Segmentation Dataset
Supporting Enviornment	: Google Colab

3.1.2 Data Requirements

Brain MRI images together with manual FLAIR abnormality segmentation masks from kaggle LGG Segmentation Dataset is used. This dataset contains brain MR images together with manual FLAIR abnormality segmentation masks . The images were obtained from The Cancer Imaging Archive (TCIA). They correspond to 110 patients included in The Cancer Genome Atlas (TCGA) lower-grade glioma collection with at least fluid-attenuated inversion recovery (FLAIR) sequence and genomic cluster data available. Tumor genomic clusters and patient data is provided in data.csv file. The resolution of the images is 256x256 pixels. The images and its corresponding masks are stored in two separate folders with the same filename.

3.2 Proposed Method

The aim of the project is to develop a reliable segmentation method to locate the entire tumor volume and accurately segment the tumor part.The proposed system uses a CNN model segnet for solving the problem. The proposed method first preprocesses the mr flair data to remove artifacts and noises.Intensity normalisation and bais field corrections are used for preprocessing the image.Then the preprocessed image is fed into the SegNet ,which an encoder decoder FCN network for image segmentation to produce tumor segmented results.

Figure 3.1 shows the pipeline of the proposed system using SegNet networks.

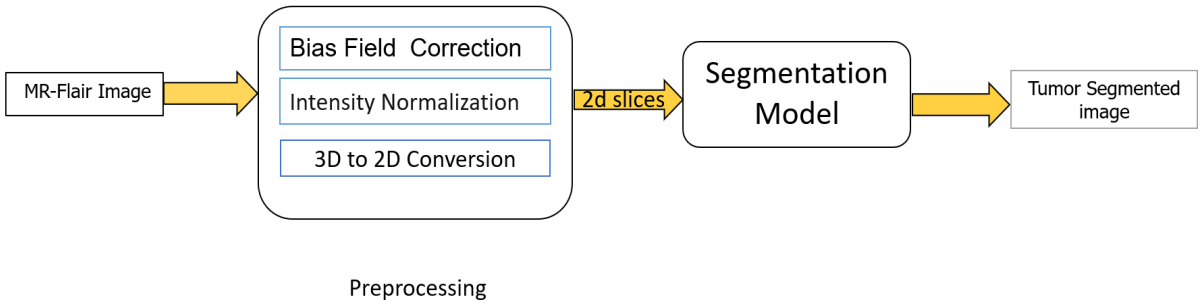

Figure 3.1: Block Diagram of the proposed system

3.2.1 Magnetic Resonance FLAIR Images

Magnetic resonance imaging (MRI) provides exquisite detail of brain, spinal cord and vascular anatomy, and has the advantage of being able to visualize anatomy in all three planes: axial, sagittal and coronal. It is based on the magnetization properties of atomic nuclei. A powerful, uniform, external magnetic field is employed to align the protons that are normally randomly oriented within the water nuclei of the tissue being examined. This alignment (or magnetization) is next perturbed or disrupted by introduction of an external Radio Frequency (RF) energy. The nuclei return to their resting alignment through various relaxation processes and in so doing emit RF energy. After a certain period following the initial RF, the emitted signals are measured. By varying the sequence of RF pulses applied collected, different types of images are created. Tissue can be characterized by two different relaxation times – T1 and T2. T1 (longitudinal relaxation time) is the time constant which determines the rate at which excited protons return to equilibrium. It is a measure of the time taken for spinning protons to realign with the external magnetic field. T2 (transverse relaxation time) is the time constant which determines the rate at which excited protons reach equilibrium or go out of phase with each other. It is a measure of the time taken for spinning protons to lose phase coherence among the nuclei spinning perpendicular to the main field.

The most common MRI sequences are T1-weighted and T2-weighted scans. T1-weighted images are produced by using short TE and TR times. Conversely, T2-weighted images are produced by using longer TE and TR times. CSF is dark on T1-weighted imaging and bright on T2-weighted imaging. A third commonly used sequence is the Fluid Attenuated Inversion Recovery (Flair). The Flair sequence is similar to a T2-weighted image with grey matter brighter than white matter but CSF is dark instead of bright and except that the TE and TR times are very long. By doing so, abnormalities remain bright but normal CSF fluid is attenuated and made dark. This sequence is very sensitive to pathology and makes the differentiation between CSF and an abnormality much easier.This removes signal from the cerebrospinal fluid in the resulting images. To null the signal from fluid, the inversion time (TI) of the FLAIR pulse sequence is adjusted such that at equilibrium

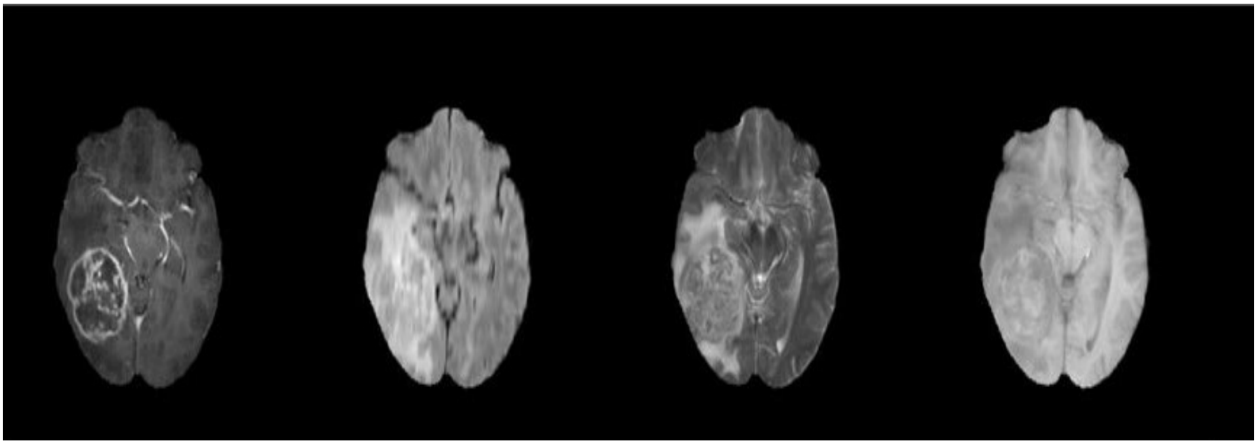

Figure 3.2: Example of brain MRI data from the BraTS2018 dataset. From left to right: FLAIR, T1, T1-c, and T2

there is no net transverse magnetisation of fluid. The FLAIR sequence is part of almost all protocols for imaging the brain, particularly useful in the detection of subtle changes at the periphery of the hemispheres and in the periventricular region close to CSF.

3.2.2 MRI Preprocessing

The intensity of brain tissue is one of the most important features for brain MRI segmentation. However, when intensity values are corrupted by MRI artifacts such as image noise, partial volume effect (PVE), and bias field effect, intensity-based segmentation algorithms will lead to wrong results. Thus, to obtain relevant and accurate segmentation results, very often several preprocessing steps are necessary to prepare MRI data.
Bias field signal is a low-frequency and very smooth signal that corrupts MRI images. To eliminate these unwanted artifacts, N4ITK bias field correction is applied for performing image-wise normalization and bias correction.The N4ITK bias field correction [12] is a variant of the popular nonparametric nonuniform intensity normalization (N3) algorithm for bias field correction .

Intensity values across MRI slices have been observed to vary greatly, so a normalization preprocessing step is also applied in addition to bias field correction so as to bring the mean intensity value and variance close to 0 and 1, respectively.So a data normalization for each slice of FLAIR MRI scans is applied by subtracting the mean of each slice and dividing by its standard deviation.Additionally removing the top and bottom 1% intensity values during the normalization process brings the intensity values within a coherent range across all images for the training phase. The widely used file formats in medical imaging are Neuroimaging Informatics Technology Initiative (Nifti), Minc, and Digital Imaging and Communications in Medicine (Dicom). So file format conversion is required.So the 3d mri files are converted to 2d image slices.

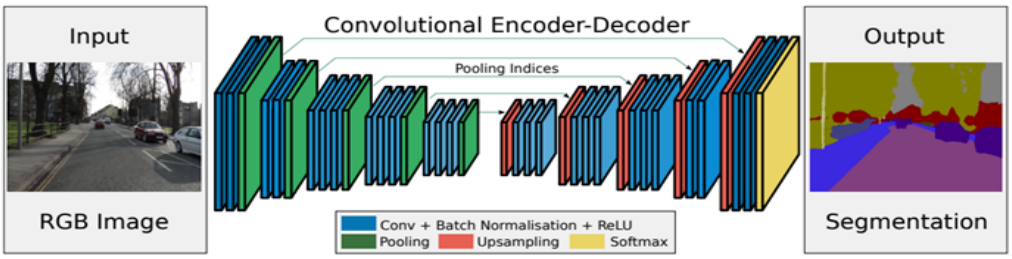

Figure 3.3: Illustration of SegNet for image Segmentation

3.2.3 Brain Tumor Segmentation with Segnet

SegNet [2]is a image segmentation architecture which uses an encoder-decoder type of architecture. It is a Fully Convolutional Network.The semantic segmentation model in Fig. 3.6 takes full-size images as input for feature extraction in an end-to-end manner. The motive for using SegNet networks instead of other deep learning networks is that SegNet has a small number of parameters and does not require high computational resources, and it is easier to train in end-to-end manner.

SegNet consists of an encoder network, a corresponding decoder network, followed by a pixel-wise classification layer at the bottom. Figure 4 provides an illustration of this architecture. 13 convolutional layers make up the encoder network, matching the first 13 convolutional layers of the VGG16 network used for object categorization. In instead of keeping better resolution feature maps at the deepest encoder output, they remove the completely connected layers. As compared to other contemporary architectures, this also drastically reduces the amount of parameters in the SegNet encoder network (from 134M to 14.7M). The decoder network contains 13 layers since there is a corresponding decoder layer for each encoder layer. A multi-class soft-max classifier is fed the final decoder output to generate class probabilities for each pixel separately.

Encoder network performs convolution with a filter bank to produce a set of feature maps.After that, these are batch normalised. Next, a max(0, x) element-wise rectified linear nonlinearity (ReLU) is used. The output is then subjected to max-pooling with a 2×2 window and stride 2 (non-overlapping window), and it is sub-sampled by a factor of 2. To provide translation invariance over minute spatial alterations in the input image, max-pooling is used. Each pixel in the feature map has a large input image context (spatial window) as a result of subsampling. It merely keeps track of the maximum feature values in each pooling window, which are stored in memory for each encoder feature map. In principle, this can be done using 2 bits for each 2×2 pooling window and is thus much more efficient to store as compared to memorizing feature map(s) in float precision.

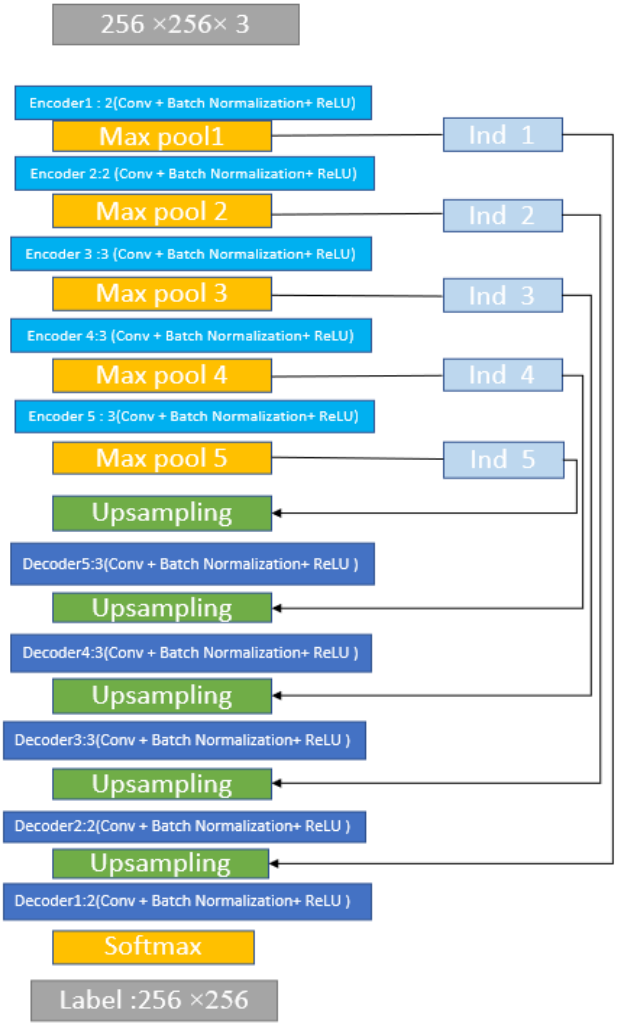

Figure 3.4: Architecture of SegNet

Decoder network up-samples its input feature map using the memorized max-pooling indices from the corresponding encoder feature maps. This step produces sparse feature maps. This SegNet decoding technique is illustrated in Fig 3.4 and upsampling in figure 3.5. These feature maps are then convolved with a trainable decoder filter bank to produce dense feature maps. A batch normalization step is then applied to each of these maps. It should be noted that despite having a 3-channel encoder input, the decoder corresponding to the first encoder (which is closest to the input image) outputs a multi-channel feature map (RGB). Contrary to other network decoders, this one creates feature maps with the same number of channels and sizes as the encoder inputs. A trainable soft-max classifier receives the high dimensional feature representation at the output

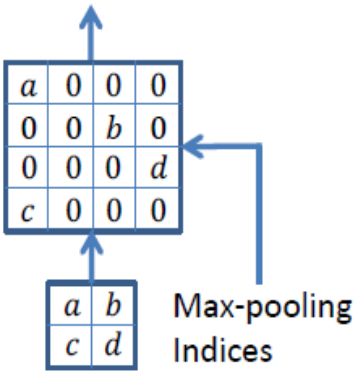

Figure 3.5: Upsampling using max-pooling indices

of the final decoder.Each pixel is classified by the soft-max classifier independently. The output of the soft-max classifier is a K channel image of probabilities where K is the number of classes. The predicted segmentation corresponds to the class with maximum probability at each pixel.

3.3 Training Phase

The proposed model must be trained with a dataset of images and their corresponding segmentation masks(ground truth). Providing a large neural networks training using limited training data, some precautions should be taken to prevent the problem of overfitting. Data augmentation, which is the

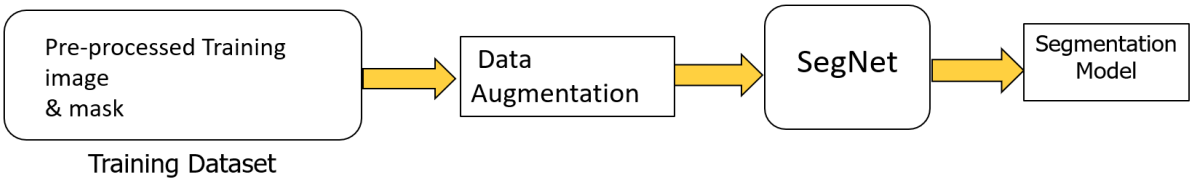

Figure 3.6: Training phase of the proposed system

process of creating new artificial training data from the original one in order to improve the model performance by making the model generalize well to the new testing data. So, a set of simple on the-fly data augmentation methods is applied by horizontal and vertical flipping, rotation, scaling, shearing, and shift.
Here publicly available LGG MRI FLAIR segmentation dataset is used for training the SegNet.

3.4 Tumor Segmentation Model

The figure 3.1 illustrates the proposed segmentation model for brain tumor segmentation. The input image is of nifti or DICOMM for as it is a medical image and perform bias field correction and intensity normalisation to the data and file format conversion is also performed in preprocessing stage. Here SegNet is trained with dataset and obtained a segnet Segmentation model for Brain MRI tumor segmentation. And when input a slice of MR FLAIR image to the model, the output will be a tumor segmented image.

Chapter 4

Implementation

The proposed model is implemented in keras tensorflow framework using Google Colab platform using NiBabel ,med2image,SimpleITK tools for nueroimage processing. The model is then trained with LGG Segmentation Dataset [13] with a batch size of 16 and image size of 256 × 256. Here uses SGD optimizer and the learning rate is 1e-4 with weight decay of 1e-4.
MRI images are usually stored using the NIfTi format. This is a very simple format that is typically a single file with extension .nii. If the file is compressed, it will end with .nii.gz instead. So NiBabel library is used for neuroimaging file formats. Figure 4.2 shows the plotted slices of MRI.

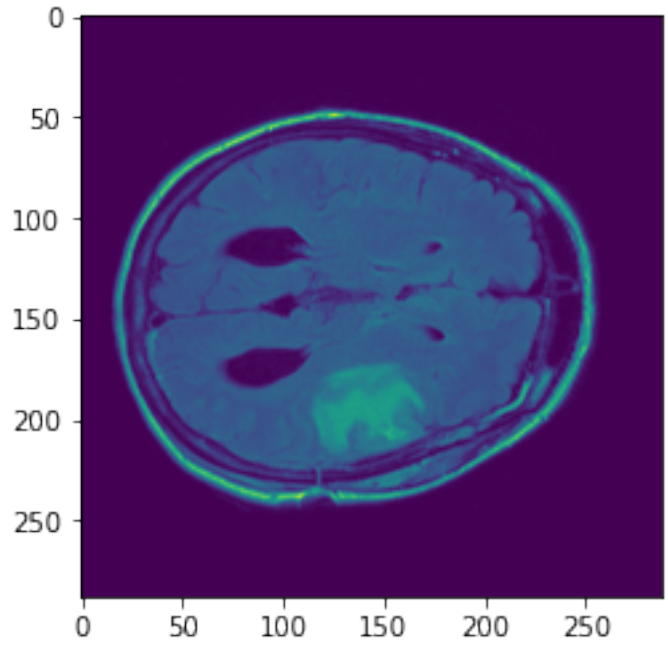

Figure 4.1: Single slice of input is plotted.

In preprocessing stage, the bias field correction and intensity normalization is performed and the corresponding outputs are shown in figure 4.3 and figure 4.4.

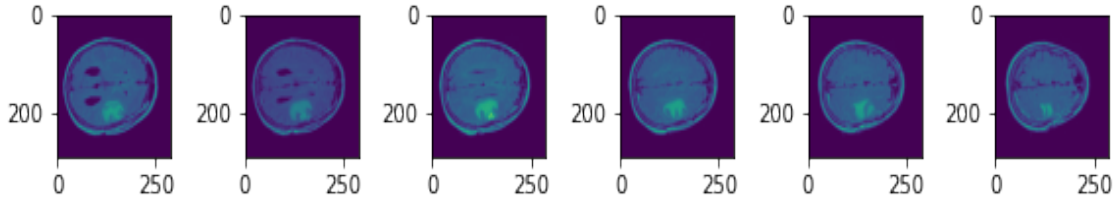

Figure 4.2: Plotting of 6 slices of nii file

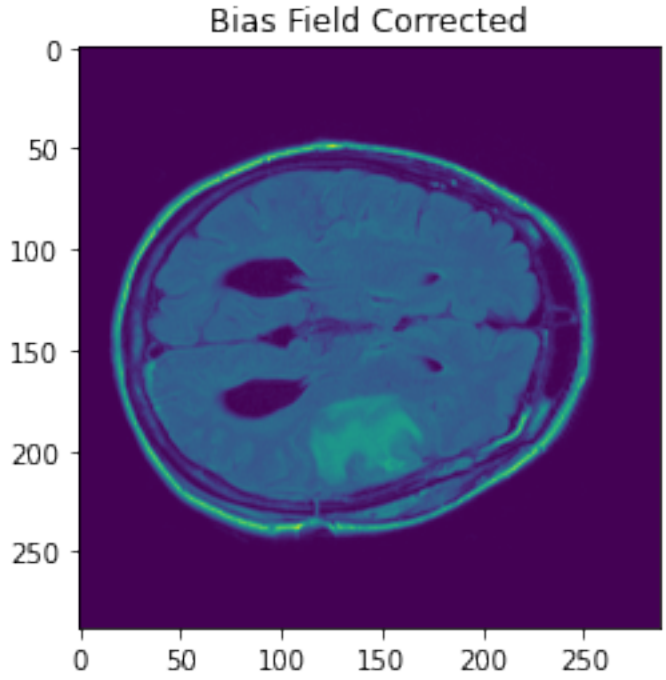

Figure 4.3: Bias Field Corrected Slice

Medical image format conversion is performed and a converted 2d slices is shown as in figure 4.5. .

For training 1 epoch it requires 33,393,669 parameters totally and in which there are 33,377,795 trainable parameters. It also supports the use of GPUs, which can greatly accelerate the execution of deep learning algorithms.

The final tumor segmented resultant image is shown in figure 4.6.

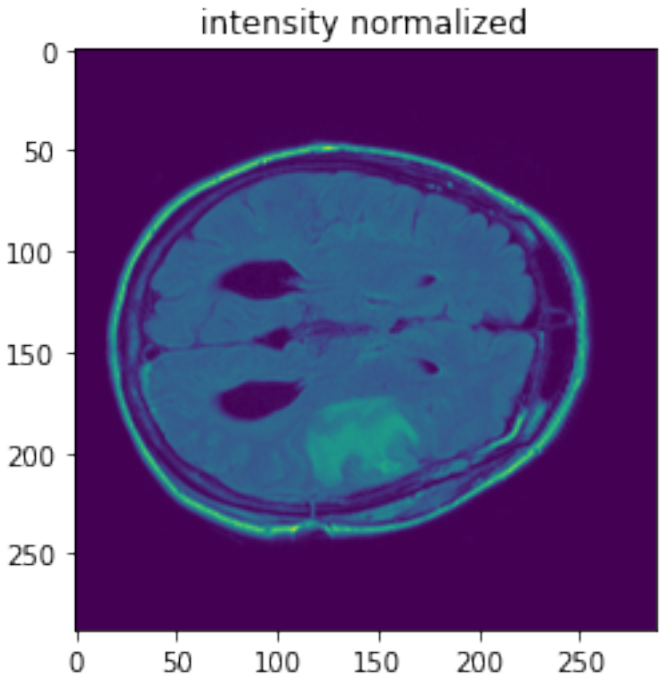

Figure 4.4: Result of Intensity Normalization

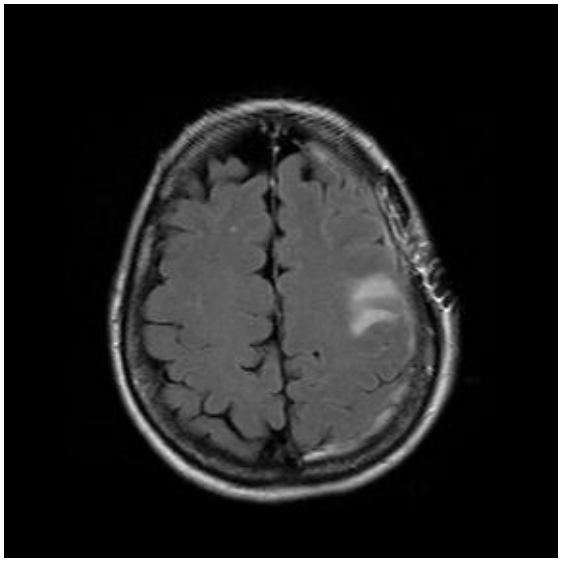

Figure 4.5: nii to jpg/png converted slices

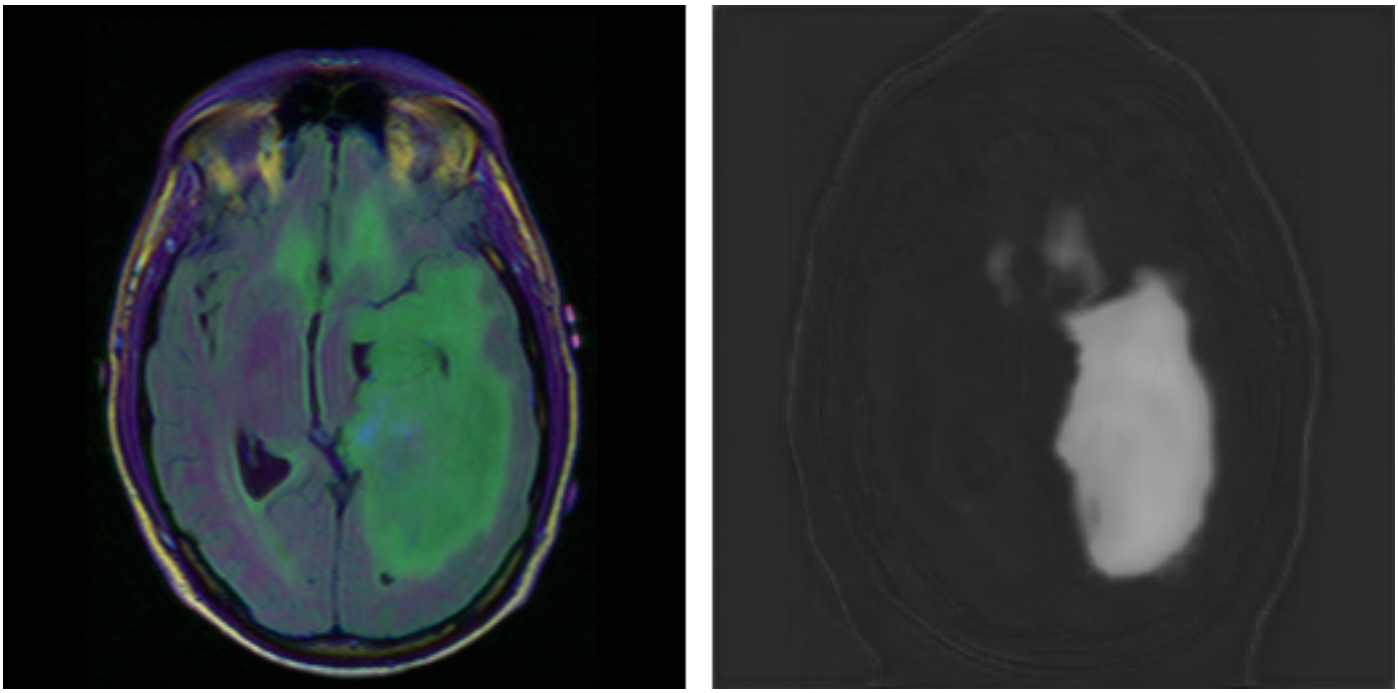

Figure 4.6: Input slice and its corresponding segmented output.

Chapter 5

Results & Conclusions

Medical image segmentation is an important image processing step in medical image analysis.Segmentation of tumors in brain MR images is to segment the normal brain tissue (unaffected) and abnormal tumor tissue (infected).

5.1 Performance Analysis

Most commonly used metrics for segmentation are the IoU , Dice Coefficient precision and recall is used to evaluate the model performances by testing the model .The Jaccard index, also known as Intersection over Union and the Jaccard similarity coefficient is a statistic used for gauging the similarity and diversity of sample sets. In 5.1 shows the result of performance evaluation.

IOU	96.01
Dice Coef	56.3
Precision	96.10
Accuracy:	97.4
Loss:	10.33

Figure 5.1: performance evaluation

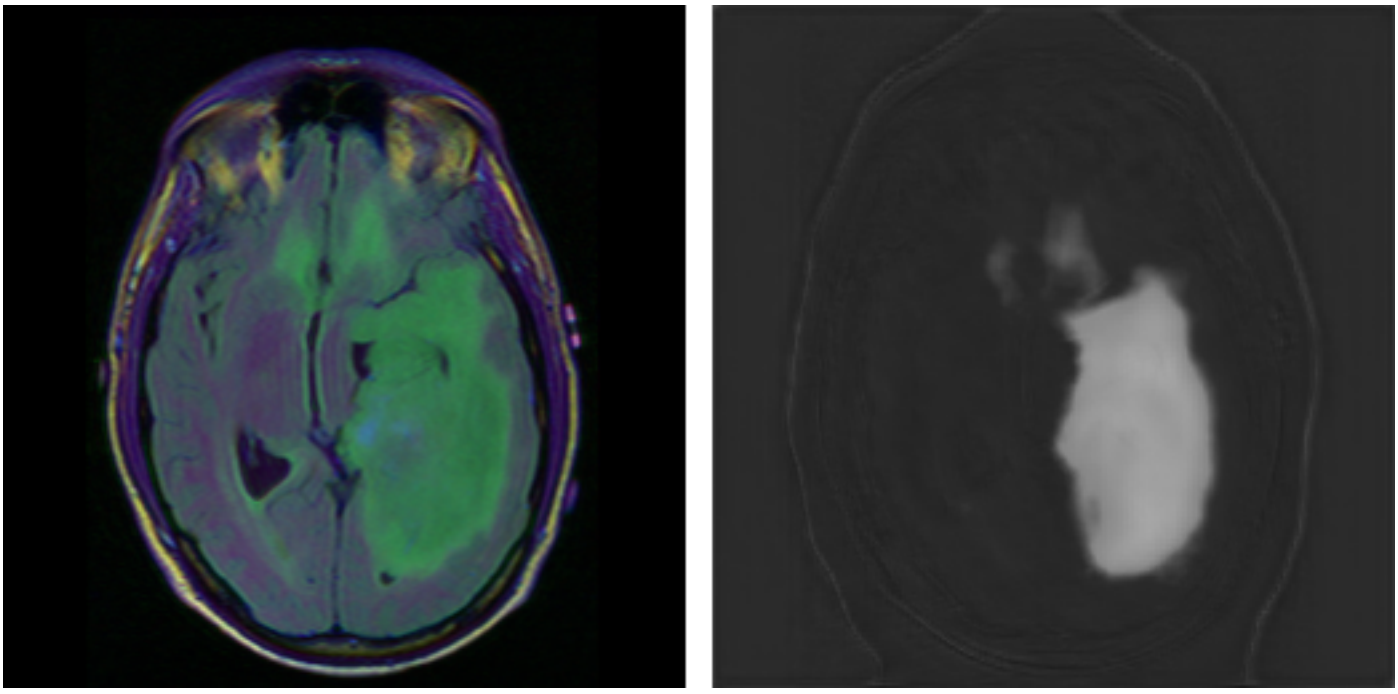

Figure 5.2: Predicted tumor segmented result

5.2 Conclusion

One of the most fatal forms of cancer worldwide is brain tumours. For proper treatment planning, surgery, and follow-up appointments, brain tumours must be diagnosed as soon as possible. However, it takes a lot of time and judgement to manually segregate brain tumours from MRI scans. Designing automatic and reliable brain tumour segmentation methods is therefore highly desirable. Using SegNet, a subset of CNN networks with MR FLAIR image data, this method suggests an accurate automatic segmentation method for the detection of brain cancers. When compared to manual brain tumour identification performed by clinical specialists, the results clearly show that the detection of brain tumours is quick and accurate. The evaluation matrices findings support the model's ability to produce accurate segmentation results. It implies that the model is extremely reliable and effective as well.

5.3 Future Scope

In this project, final predicted outputs are blurry, so in the future the post-processing and 3d visualisation of the output can be considered. Also from the segmented result, the class of tumor can be predicted with the help of classifiers.

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