BRAIN TUMOR SEGMENTATION

A MINI PROJECT REPORT

submitted by

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RET19CSCY05

to
The APJ Abdul Kalam Technological University in partial fulfillment of the requirements for the award of the Degree

of

Master of Technology

in

Computer Science & Engineering with Specialization in Information Systems

Department of Computer Science and Engineering

Rajagiri School of Engineering and Technology
Rajagiri Valley, Kakkanad, Kochi, 682039
April 2020

DECLARATION

I undersigned hereby declare that the miniproject work **Brain Tumor Segmentation** , submitted for partial fulfillment of the requirements for the award of degree of Master of Technology of the APJ Abdul Kalam Technological University, Kerala is a bonafide work done by me under supervision of **Mrs. Dincy Paul** . This submission represents my ideas in my own words and where ideas or words of others have been included, I have adequately and accurately cited and referenced the original sources. I also declare that I have adhered to ethics of academic honesty and integrity and have not misrepresented or fabricated any data or idea or fact or source in my submission. I understand that any violation of the above will be a cause for disciplinary action by the institute and/or the University and can also evoke penal action from the sources which have thus not been properly cited or from whom proper permission has not been obtained. This report has not been previously formed the basis for the award of any degree, diploma or similar title of any other University.

Place
Date

Dhanya Paulose

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CERTIFICATE

This is to certify that the report entitled **Brain Tumor Segmentation** submitted by **Dhanya Paulose** to the APJ Abdul Kalam Technological University in partial fulfillment of the requirements for the award of the Degree of Master of Technology in Computer Science & Engineering with Specialization in Information Systems is a bonafide record of the miniproject work carried out by her under our guidance and supervision. This report in any form has not been submitted to any other University or Institute for any purpose.

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ABSTRACT

Brain tumor segmentation is the process of separating the tumor from normal brain tissues in clinical routine, it provides useful information for diagnosis and treatment planning. However, it is still a challenging task due to the irregular form and confusing boundaries of tumors. Tumor cells thermally represent a heat source their temperature is high compared to normal brain cells. Automatic segmentation of brain tumor is the process of separating abnormal tissues from normal tissues, such as white matter (WM), gray matter (GM), and cerebrospinal fluid (CSF). The process of segmentation is still challenging due to the diversity of shape, location, and size of the tumor segmentation The main objective of this project is to develop a new deep learning model for the segmentation of brain tumors from MRI images.

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Chapter 1

INTRODUCTION

1.0.1 General Background

Brain tumor segmentation is the process of separating the tumor from normal brain tissues in clinical routine, it provides useful information for diagnosis and treatment planning. However, it is still a challenging task due to the irregular form and confusing boundaries of tumors. Tumor cells thermally represent a heat source their temperature is high compared to normal brain cells. Automatic segmentation of brain tumor is the process of separating abnormal tissues from normal tissues, such as white matter (WM), gray matter (GM), and cerebrospinal fluid (CSF). The process of segmentation is still challenging due to the diversity of shape, location, and size of the tumor segmentation. The metabolic process, psychological process, and detailed information of the images, are obtained using positron emission tomography (PET) image, Computer Tomography (CT) image and Magnetic Resonance Image (MRI). Here we are developing a new deep learning model for the segmentation of brain tumors.

1.0.2 Objective

By using Fully Automatic Brain tumor Segmentation method we can reduce the time of manual diagnosis by experts. Also it is very much efficient for detecting "glioblastomas" which is one of the most dangerous tumor tissue. The process of segmentation is still challenging due to the diversity of shape, location, and size of the tumor segmentation. Here we separate abnormal tissues from normal tissues,

such as white matter (WM), gray matter (GM), and cerebrospinal fluid.(CSF).

1.0.3 Scheme

This project can be extended using more efficient model for detecting brain tumors. It will be much easier,faster, and convenient than conventional manual brain tumor segmentataion.

1.0.4 Chapter Outline

Chapter one introduces about the project, motivation, major project area and scope of application. Chapter two deals with literature survey which consist of theoretical background and existing system. Chapter three defines the basic system architecture which consist of system design and module overview . In the project there are five modules, namely pre-processing, segmentation, feature extraction, and identification. The fourth chapter, pre-processing is a series of operations performed on the input image. The fifth chapter, segmentation identify coconut in the input image. The feature extraction is the process of extracting the most important data from identified coconut this is deals in chapter six. The seventh chapter, identification , here identifying the ripeness of coconut. Chapter nine deals with the tools and languages used in the project. Chapter ten deals with the results and observations. Chapter eleven concludes the project and specifies the future work

Chapter 2

LITERATURE SURVEY

2.1 Fully Automatic Brain Tumor Segmentation using End-to-End Incremental Deep Neural Networks in MRI Images

Brain tumor is a growing abnormal cell in the brain or central spin canal. In USA, National Brain Tumor Society estimates that every year 13,0 0 0 patients die, and 29,0 0 0 patients suffer from primary brain tumors (i.e., primary tumor is a tumor starts in the brain). In 2007, they expected in UK , more than 4,200 patients have a brain tumor each year. Thus, the number of experts is insufficient compared to the number of patients in the world. In addition, if we count also the potentiality of medical mistakes (i.e., false negatives: diagnostic result indicates that a person does not have a disease, but in fact he has) besides low survival rates of patients with life-threatening diseases such as Glioblastomas. Glioblastomas affect children between 5 and 10 years old, and adults between 30 and 40 years old. Moreover, Glioblastomas are the most frequent primary brain tumors in adults . MRI is the investigation tool of choice for the segmentation of brain tumors such as Glioblastomas and for the evaluation of treatment response . Usually, an expert radiologist uses MRI technique to generate a sequence of images (Flair, T1, T1 contrast, T2, ...etc) to identify different regions of tumor. This variety of images helps radiologists and experts to extract different types of information about the tumor (shape, volume ...etc). In general, the manual segmentation in MRI is a time-consuming

procedure and depends on skills of each expert . During the last three decades, the problem of brain tumor segmentation has attracted many researchers, in which the number of huge published papers as noted by Menzeet al. involving brain tumor segmentation increased exponentially. In this case, the creating of a smart brain tumor segmentation system has always been a highly needed option. In addition, instead of wasting time with manual diagnosis by the experts, this smart segmentation system decreases the needed time for the diagnosis process. This way gives to doctors more time with their patients in the process of treatment and follow-up. There are many researches that have been carried out for automating this task of radiologist (i.e. localization and segmentation of the whole tumor and its sub-regions), these algorithms are classified into two categories : Generative models , these models need a prior knowledge about tumor and its tissue and its appearance, but these models require recording several parameters about tumor's features. However, Discriminative models directly learn the characteristics of tumor and how to segment it from manually annotated data (created by radiologists).

Nowadays, getting an efficient Brain Tumor Segmentation in Multi-Sequence MR images as soon as possible, gives an early clinical diagnosis, treatment and follow-up. The aim of this study is to develop a new deep learning model for the segmentation of brain tumors. The proposed models are used to segment any type of the brain tumors such as Glioblastomas etc.. (with both high and low grade).Brain tumors have four properties: different sizes, shapes, contrasts, in addition, it appears anywhere in the brain.In this, it using three end-to-end Incremental Deep Convolutional Neural Networks models for fully automatic Brain Tumor Segmentation. This model is different from the other CNNs-based models that follow the technique of trial and error process which does not use any guided approach to get the suitable hyper-parameters. Moreover, we adopt the technique of Ensemble Learning to design a more efficient model. For solving the problem of training CNNs model, it adopts a new training strategy which takes into account the most influencing hyper-parameters by bounding and setting a roof to these hyper-parameters to accelerate the training.

This method consists of two phases.In first phase there is an Incremental XCNet algorithm which generates CNNs models,that is from a base model (a limited number of layers).Then obtain deeper and scalable model through our technique of Incremental XCNet.Second phase consists of a new strategy called $ELOBA\_\lambda$ to train the CNNs models, in which it takes into account the most in uencing hyper-parameters (Epochs, Learning rate, Optimizer, Batch size).The training strategy $ELOBA\_\lambda$ bounds and sets a roof to these hyper-parameters to fast the training of the generated CNNs models.Then using an end to end incremental deep neural networks called EnsembleNet which combines on parallel the instances of Incremental XCNet to get the benefits of each model based on a new non-parametric fusion technique.

In this section, it evaluate the models on a public dataset 2017 of BraTS. It show the results of our 3 models with the state-of-the-art models measuring both the segmentation performance and the inference time using three described metrics. Unlike other CNNsbased models, our sequential architectures 2CNet, 3CNet have deep architectures which help to extract relevant and very highlevel features. Moreover, EnsembleNet also takes the advantage of these deep architectures to build a parallel architecture that brings together the most important features of the same subject. Thanks to the $ELOBA\_\lambda$ training strategy that uses a simple and practical idea based on the use of many optimizers over a bounded range of training space instead of using one optimizer as used in the conventional CNNs models.

In addition, we developed a new training strategy $ELOBA\_\lambda$. First, In addition, we developed a new training strategy $ELOBA\_\lambda$. First, $ELOBA_\lambda$proved itself as an effective strategy and a simple method, in which it is the first strategy to our knowledge, shows how to train a CNNs model. Second, our training strategy $ELOBA\_\lambda$ is created for giving us the exact time when we should change the model's architecture. Finally, $ELOBA_\lambda$is a dynamicand adaptable method, in which we can change all the hyper-parameters (i.e., the number of epochs, learning rate, batch size, optimizers) based on the workstation computing power and the architecture's size.proved itself as an effective strategy and a simple method, in which it is the first strategy to our knowledge, shows how to train a CNNs model. Second, our training

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2.2 Machine learning based brain tumour segmentation on limited data using local texture and abnormality

Primary brain tumours are a diverse group of neoplasm originating within the central nervous system. For procedures such as biopsy and advanced image analysis techniques such as radiomics , tumour segmentation in medical images is an important step. In clinical practice, segmentation is mostly performed manually, where an experienced radiologist delineates the tumour on several slices of a 3D brain scan. This scan typically originates from Magnetic Resonance Imaging (MRI), Computed Tomography (CT) or Positron Emission Tomography (PET). Apart from being time and labour intensive, manual delineation is prone to inter and intra-observer variability. In this work, four manual performers segmented scans from 10 low-grade and 20 high-grade glioma patients.

Brain tumour segmentation in medical images is a very challenging task due to the large variety in tumour shape, position, appearance, scanning modalities and scanning parameters. Most existing segmentation algorithms use information from four different MRI-sequences, but since this is often not available, there is need for a method able to delineate the different tumour tissues based on a minimal amount of data. Here present a novel approach using a Random Forests model combining voxelwise texture and abnormality features on a contrast-enhanced T1 and FLAIR MRI. It transform the two scans into 275 feature maps. A random forest model next calculates the probability to belong to 4 tumour classes or 5 normal classes. Afterwards, a dedicated voxel clustering algorithm provides the final tumour seg-

mentation.

1. **Materials and Methods**

   - BraTS 2013 training set

     The BraTS 2013 dataset is used for optimising and training our model. This dataset consists of 10 low-grade and 20 high-grade glioma patients.For every patient, a T1, T2, T1 contrast and FLAIR preoperative scan is available. These scans are already coregistered using trilinear interpolation and have a $1mm1mm1mm$ voxel size. Moreover, for every patient gold-standard labels for the different tumour tissues (being necrosis,oedema, non-enhancing and contrast enhancing tissue) are included.

   - BraTS 2017 validation set

     The larger BraTS 2017 dataset is used for validating the method. In this collection, 75 low-grade and 210 high-grade patients are included.Both the scan types and preprocessing steps are similar to the BraTS 2013 dataset. However, in this edition, there is no separate label for non-enhancing tumour tissue, as this is combined with the necrotic voxels.

Methodology:

1. Preprocessing

   The BraTS images are already coregistered and resliced. To mimic these preprocessing steps for the scans acquired in our centre, SPM12 (version 6906, Wellcome Trust Centre for Neuroimaging, University College London) running on MATLAB R2017b (The MathWorks, Inc., Natick, MA) is used for co-registering the FLAIR image to the T1ce scan of the same patient. Next, the scans are spatially normalised to MNI space (Montreal Neurological Institute [14]) and trilinearly interpolated to a $1mm \cdot 1mm \cdot 1mm$ voxel size. Furthermore, for both the BraTS and Ghent University Hospital scans, the segmentation module in SPM12 is applied to the T1ce scan to calculate tissue

probability maps (TPMs) for five healthy tissues (grey matter (GM), white matter (WM), cerebrospinal fluid (CSF), skull and soft tissue. This technique is based on a Gaussian mixture model and prior spatial probabilities. These TPMs will later on be used as normality features. During the SPM segmentation, bias field correction is applied to correct for magnetic field inhomogeneities, and the corrected images are also saved and used for all following analyses.

2. Feature Extraction

For every patient, 275 feature maps are calculated based on the T1ce and coregistered FLAIR scans. To capture the local texture, 30 features are calculated on both the T1ce and the FLAIR scan and on four different spatial scales, contributing a total of 240 features. Next, there are 5 normality features capturing the healthy region of the brain, and 30 abnormality features showing the deviation from normality.

- Texture Feautures

  Here calculate three types of texture parameters for a total of 30 different features. Every feature contains for a certain voxel information from the $3 * 3 * 3$ voxels environment surrounding this voxel. To account for distant interactions, the scans are also downsized with a factor 2, 4 or 8 using MATLAB's imresize3 function. The same texture features are again calculated on the smaller images, followed by upscaling with cubic interpolation to the original matrix size.

- Grey-level co-occurence features

  The grey-level co-occurence matrix (GLCM) describes the occurence of pairs of voxel intensities.We only consider distance of 1 voxel to determine a voxel pair. More distant interactions are accounted for using the downsizing step. In 3D,voxel pairs can be determined in 13 directions.Thus determine 9 GLCM-based features, which are the averages over these 13

directions

- Grey-level run-length features

  The grey level run length matrix (GLRLM) quantifies one-dimensional runs, being a set of consecutive, collinear voxels having the same grey level, in the image . Again,these runs can be calculated in 13 different directions, such that the GLRLM-based features are the averages over these 13 directions. We calculate 10 features: short/long run emphasis, grey level non-uniformity, run length non-uniformity, low/high level run emphasis and short/long run with low/high grey levels emphasis.

- Grey-level size-zone features

  The grey-level size-zone matrix(GLSZM) quantifies zones or clusters of a certain grey level in the image,and is therefore independent of direction. Again, calculate 10 features: small/large zone emphasis, grey-level non-uniformity, size-zone non-uniformity, low/high grey-level emphasis and small/large zones with low/high grey-levels emphasis.

- Normality and abnormality features

  Next to the texture features, where only local information is included,we also include normality and abnormality features. In this way anatomical information can be incorporated in the model.

- Tissue probability maps

  The five TPMs calculated during the segmentation step in SPM12 give the probability for every voxel to belong to GM, WM, CSF, skull or soft tissue using prior anatomical probabilities and assuming a healthy intensity distribution. These TPMs can therefore identify normal appearing regions in the brain.

- Abnormality features

  An MRI scan presenting a brain tumour will in general show strong devi-

ations from the normal appearing intensities. Therefore, we also calculate abnormality maps starting from the TPMs. These include five probability maps for GM, WM, CSF, non-brain regions and tumour using outlier detection.

3. Random Forest Classification

The goal of the random forests classification algorithm is to estimate the probability of a voxel belonging to a tissue type based on the calculated features in that voxel. Here consider 9 different classes, divided into 5 normal and 4 tumour types: GM, WM, CSF, non-brain, background, necrosis, oedema, non-enhancing tumour and enhancing tumour. During the training phase, 1000 voxels per tissue are randomly selected per patient in the training set, and the feature values are stored together with the corresponding tissue class. The training matrix is balanced since there is an equal amount of training samples for every class, which implies that there is no bias towards a certain class when predicting an unknown voxel.

Since calculating and storing 275 feature maps is both time and memory consuming, and to reduce overfitting, we try to find an optimal subset of features. For this, we apply sequential forward selection using three-fold cross-validation on the training set. This algorithm starts from an empty feature set, and predictors are sequentially added to the model until no further improvement is obtained. As indicator for the model performance, we apply two criteria: total accuracy over all classes, and accuracy of the tumour classes. Finally, we combine these two feature sets in the final model. Next to feature selection, the number of trees and tree depth influence the model performance.

4. Post Processing

After estimating the tissue probabilities using the Random Forests model, voxels are assigned to the tissue with highest probability. Morphological op-

erations yield the tumour region. In this step, the mask of all voxels having a tumour label is eroded with 5 voxels and again dilated with 5 voxels. This should remove loosely connected regions, such as small enhancing blood vessels. Now, the largest disconnected part is chosen as the tumour region. Since there can still be isolated voxels, the final tumour mask is obtained using voxel clustering in an iterative way, assuming a Gaussian mixture model and taking into account the local neighbourhood.

In each iteration four steps are performed:

- For every tissue γ_i, we calculate the mean $\overrightarrow{\mu}_i$ covariance-matrix $\overrightarrow{\Sigma}_i$
- Compute the probability density function for each class in each voxel at location $\overrightarrow{\mathrm{X}}$ with intensity vector $\overrightarrow{\mathrm{I}}$

  $pdf(\overrightarrow{\iota}(\overrightarrow{\chi})|\gamma_i) = (2\pi)^{N/2}(\overrightarrow{\Sigma}_i)^{-1/2}\exp(\text{-}1/2(\overrightarrow{\mathrm{I}}(\overrightarrow{\mathrm{X}}\text{-}\overrightarrow{\mu}_i) - (\overrightarrow{\Sigma}_i)^{-1}(\overrightarrow{\mathrm{I}}(\overrightarrow{\mathrm{X}} - \overrightarrow{\mu}_i))$

- we incorporate the prior information using the neighbourhood for every voxel. For every class γ_i and voxel at position $\overrightarrow{\mathrm{X}}$, we calculate the linear neighbourhood function $Nb(\gamma_i, \overrightarrow{\mathrm{X}})$
- In the last step, the posterior probability is calculated:

The performance of the Random Forests model is graphically illustrated using a confusion matrix, obtained using three-fold crossvalidation. It is clear that for healthy tissues, there is a high probability of being correctly classified, with a minimal accuracy of 90.0

2.3 Brain tumor detection based on Convolutional Neural Network with neutrosophic expert maximum fuzzy sure entropy

Brain tumor studies are one of the most popular topics in the academic community today. In general, the cancer tumor classification is the segmentation of tumor regions and the classification of the tumor.The NS approach has recently been used to perform segmentation successfully in the field of biomedicine and other related fields.Here,developed the neutrosophic expert maximum fuzzy-sure entropy (NS-EMFSE) segmentation method.The present study proposing the Neutrosophic Expert Maximum Fuzzy-Sure Entropy Set Convolutional Neural Network (NS-EMFSE- CNN) hybrid classification method by combining neutrosophic expert maximum fuzzy-sure entropy (NSEMFSE) segmentation and Convolutional Neural Network approaches. In the proposed NS-EMFSE-CNN, the MRI image in DICOM format is initially preprocessed and segmented using NS-EMFSE[4]. The features obtained following the convolution layers of CNN were given to the inputs of classifiers such as SVM and KNN. Next, using the CNN method,the tumor in these segmented MRI images is classified as malignant or benign.

Brain tumor classification is a challenging task in the field of medical image processing. The present study proposes a hybrid method using Neutrosophy and Convolutional Neural Network (NS-CNN). It aims to classify tumor region areas that are segmented from brain images as benign and malignant. In the first stage, MRI images were segmented using the neutrosophic set expert maximum fuzzy-sure entropy (NS-EMFSE) approach. The features of the segmented brain images in the classification stage were obtained by CNN and classified using SVM and KNN classifiers. Experimental evaluation was carried out based on 5-fold cross-validation on 80 of benign tumors and 80 of malign tumors. The findings demonstrated that the CNN features displayed

a high classification performance with different classifiers.

The main contributions of the present study can be summarized as follows:

(a) CNN architecture is used as a feature extractor to avoid manual feature extraction.

(b) These features are used in various classification (SVM-KNN) algorithms.

(c) The CNN structure was used with Neutrosophy for image processing for the first time.

(d) A new hybrid method called NS-EMFSE-CNN using segmentation and classification is proposed.

(e) The Classification performance of Brain Tumor images with NS- EMFSE-CNN method was higher compared to conventional CNN classifcation.

Neutrosophic Image:

Neutrosophy (NS) is a useful and successful approach in analyzing uncertain situations compared to other methods. In NS theory, events are analyzed by dividing them into three categories as true (T), indeterminacy (I) and falsity (F) subsets. In image processing applications such as segmentation and edge detection, all pixels of the image is subdivided into T, I and F subsets. Then, the edge detection/segmentation process of the image is performed through necessary operations on these subsets. In this study, the tumor/tumors is kept in the T subset, the edges are in the I subset, and the background is kept in the F subset. It is necessary to convert the image to the neutrosophic domain in order to implement Neutrosophy in the field of image processing. To this aim, P(i, j) pixel in the image domain is named as $P\_neutrosophic$ in the neutrosophic domain for conversion.

The main purpose of the present paper is to design an efficient automatic brain tumor segmentation system by classifying brain tumors as benign and malig-

nant. Brain tumors were segmented using NS-EMFSE method. The features of the segmented images were extracted from CNN architectures by Alexnet and then were classified with SVM and KNN classifier. CNN is one of the deep learning methods consisting of feed-forward layers. MatConvnet library was used with Matlab 2017b version for the application. The highest performance was yielded by SVM classifier by 95.62 perecentage. This accuracy rate is expected to increase if a higher number of images are used in the database. Segmentation and classification studies are one of the most popular topics in image processing. The use of Neutrosophy and CNN approaches, which are popular and successful segmentation and classification methods, will make a significant contribution to image processing. The results obtained using the NS-EMFSE-CNN method are given in . It was observed that the brain images segmented using the proposed NS-EMFSE-CNN method yielded successful results in finding benign and malignant tumors.

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Chapter 3

BASIC ARCHITECTURE

3.1 System design

The outline of project is given below

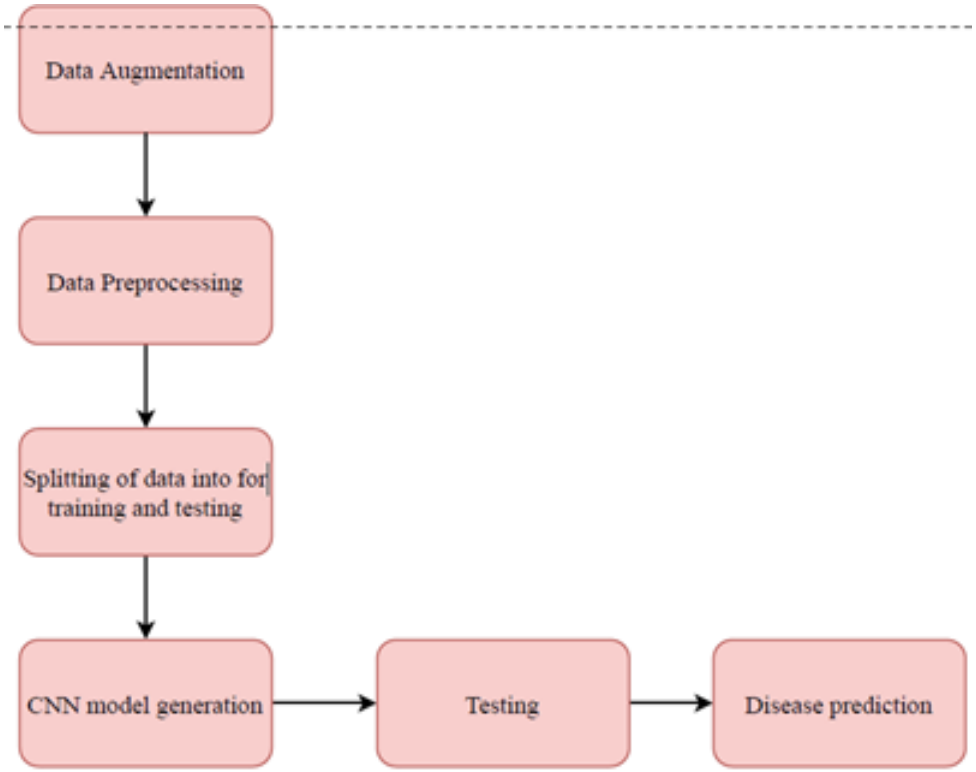


Figure 3.1: Sytem Design

3.2 Module Overview

- DATA AUGMENTATION AND DATA PREPROCESSING MODULE
  The different steps done in Preprocessing module are:
  - Read the input image and augment to increase the size of data set size.
  - Preprocess the image using cropping.
  - Splitting of data for testing and training

- MODEL CREATION MODULE
  First we create a basic model with minimum number of layers. Then we can improve the accuracy by Increasing number of layers.

- TESTING AND PREDICTION MODULE
  Model generates an ouput.It is compared with actual output.If it matches that image will take into account else it will backpropagate the error and go for next iteration.Finally after the specified number of epochs it shows whether an image is tumor effected or not.

Chapter 4

DATA AUGMENTATION AND DATA PREPROCESSING MODULE

4.1 Read the Raw input

Here the raw input is the MRI images. In Data Augmentation, it expands the size of training set by creating the modified versions of images in dataset. For Preprocessing, cropping is used to remove irrelevant details in image.

4.2 Median Blur

The image will be polluted by gaussian noise,salt-pepper noise and mixed noise in the process of acquisition and transmission, which affects seriously the effect of image.In this project i am using Median bluring for image smoothing in RGB color space.

Median filtering is a nonlinear process useful in reducing impulsive, or salt-and-pepper noise. It is also useful in preserving edges in an image while reducing random noise. Impulsive or salt-and pepper noise can occur due to a random bit error in a communication channel. In a median filter, a window slides along the image, and the median intensity value of the pixels within the window becomes the output intensity of the pixel being processed.For example, suppose the pixel values within a window are 5,6, 55, 10 and 15, and the pixel being processed has a value of 55. The output of the median filter an the current

pixel location is 10, which is the median of the five values.

Like low pass filtering, median filtering smoothes the image and is thus useful in reducing noise. Unlike lowpass filtering, median filtering can preserve discontinuities in a step function and can smooth a few pixels whose values differ significantly from their surroundings without affecting the other pixels. If the two impulsive values are due to noise, the result of using a median filter will be the reduce the noise.

Chapter 5

MODEL CREATION MODULE

First we create a basic model with minimum number of layers. Then we can improve the accuracy by Increasing number of layers.

5.1 Creation of model

(a) Incremental XCNet:

Data: X: the number of convolution layers,$S\epsilon\{0,1\}$: the number of pooling layers, F: the number of filters, FC: the number of fully connected layers

Result: M: a CNNs trained model

- Create a bloc (X,S) and FC : $M_o \leftarrow (X,S) + FC\triangleright$ Creating the first bloc

- $M_o = ELOBA\_\lambda(M_o)$ Run the training using $ELOBA\_\lambda$ to Adjust the Network's weights.

- **while**(The new added bloc is not null) do
  i. Remove FC and freeze all layers of$M_{i-1(i\epsilon N)} \leftarrow (X,S)$
  ii. Double the number of filters

iii. Adding a new bloc (X, S) and FC:

$M_{i(i\epsilon N)} \leftarrow M_{i-1(i\epsilon N)} + (X, S) + FC$

iv. $M_{i(i\epsilon N)} = ELOBA\_\lambda M_{i(i\epsilon N)}$

- **end while**

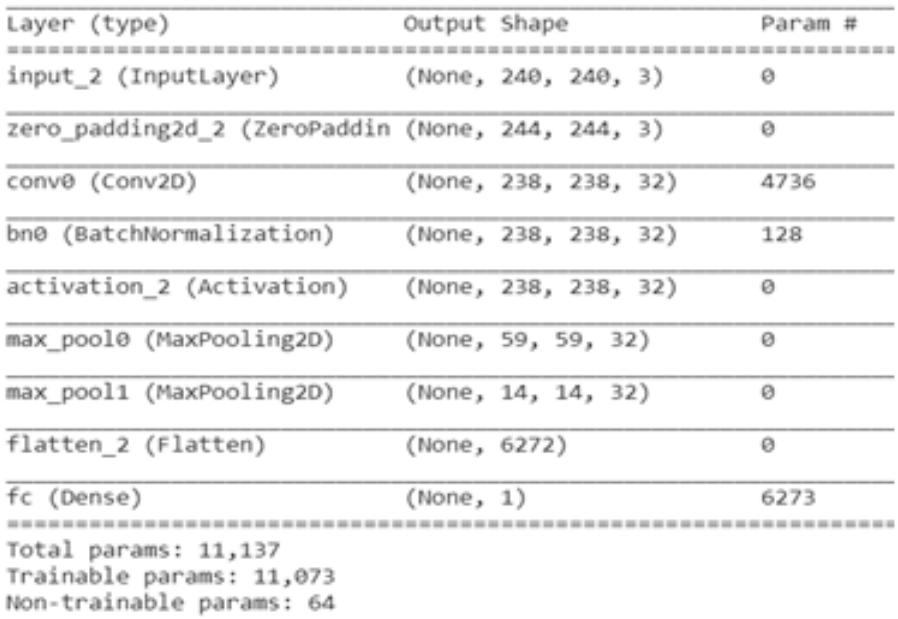
5.2 Edge Detection

(b) $ELOBA\_\lambda$

Data: M: an untrained CNNs base model, λ: Epochs, Bs :Batch size ϵ [bs _ min , bs _ max], K : *apositiveinteger*, Lr: Learning rate ϵ[r _ min , r _max], R : *apositivenumber*,Op: ϵOptimizer = {Adam, RMSprop, SGD} **Result**: M: a trained CNNs base model

- for (j = 1 : j← j+1 : j = 3) do
  - i. op=optimiser(j)
  - ii. for ($Bs = bs\_min$: Bs ←Bs + K : Bs = bs_max) do
    - A. for($Lr = r\_max$: Lr←Lr—R : Lr = r_min) do
      - Training(M,λ, Bs, Lr, Op) →Run the back-propagation with the hyper-parameters (λ, Bs, Lr, Op)
      - $Dice_t(M)$ → Compute the Dice coefficient
      - while ($Dice_t(M) > Dice_{t1}(M)$),Where $Dice_{t1}(M)$ is the Dice coefficient of the last iteration, in the first execution ($Dice_0(M)$) is equal to 0
      - do
        - Save the model M and its weights
        - Training(M,λ, Bs, Lr, Op)
        - $Dice_t(M)$
      - end while
    - B. end for
  - iii. end for

- end for

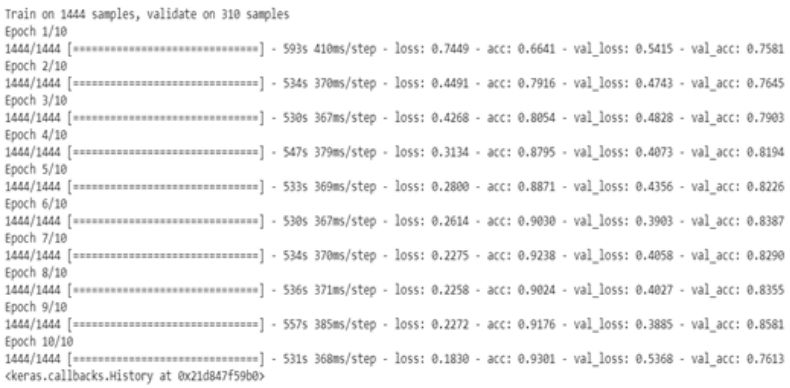


Layer (type)	Output Shape	Param #
input_2 (InputLayer)	(None, 240, 240, 3)	0
zero_padding2d_2 (ZeroPaddin	(None, 244, 244, 3)	0
conv0 (Conv2D)	(None, 238, 238, 32)	4736
bn0 (BatchNormalization)	(None, 238, 238, 32)	128
activation_2 (Activation)	(None, 238, 238, 32)	0
max_pool0 (MaxPooling2D)	(None, 59, 59, 32)	0
max_pool1 (MaxPooling2D)	(None, 14, 14, 32)	0
flatten_2 (Flatten)	(None, 6272)	0
fc (Dense)	(None, 1)	6273

Total params: 11,137
Trainable params: 11,073
Non-trainable params: 64

Figure 5.1: Basic Model

Figure 5.2 shows the number of epochs used for correct prediction.That is actual class is compared with class predicted by the model. If mismatch found and we back propagate it and go for next epoch until the prediction become accurate.



```
Train on 1444 samples, validate on 310 samples
Epoch 1/10
1444/1444 [==============================] - 593s 410ms/step - loss: 0.7449 - acc: 0.6641 - val_loss: 0.5415 - val_acc: 0.7581
Epoch 2/10
1444/1444 [==============================] - 534s 370ms/step - loss: 0.4491 - acc: 0.7916 - val_loss: 0.4743 - val_acc: 0.7645
Epoch 3/10
1444/1444 [==============================] - 530s 367ms/step - loss: 0.4268 - acc: 0.8054 - val_loss: 0.4828 - val_acc: 0.7903
Epoch 4/10
1444/1444 [==============================] - 547s 379ms/step - loss: 0.3134 - acc: 0.8795 - val_loss: 0.4073 - val_acc: 0.8194
Epoch 5/10
1444/1444 [==============================] - 533s 369ms/step - loss: 0.2800 - acc: 0.8871 - val_loss: 0.4356 - val_acc: 0.8226
Epoch 6/10
1444/1444 [==============================] - 530s 367ms/step - loss: 0.2614 - acc: 0.9030 - val_loss: 0.3903 - val_acc: 0.8387
Epoch 7/10
1444/1444 [==============================] - 534s 370ms/step - loss: 0.2275 - acc: 0.9238 - val_loss: 0.4058 - val_acc: 0.8290
Epoch 8/10
1444/1444 [==============================] - 536s 371ms/step - loss: 0.2258 - acc: 0.9024 - val_loss: 0.4027 - val_acc: 0.8355
Epoch 9/10
1444/1444 [==============================] - 557s 385ms/step - loss: 0.2272 - acc: 0.9176 - val_loss: 0.3885 - val_acc: 0.8581
Epoch 10/10
1444/1444 [==============================] - 531s 368ms/step - loss: 0.1830 - acc: 0.9301 - val_loss: 0.5368 - val_acc: 0.7613
<keras.callbacks.History at 0x21d847f59b0>
```

Figure 5.2: Epochs

Chapter 6

TESTING AND PREDICTION MODULE

To obtain better and more efficient CNNs models, we put our models under a serie of different tests and different scenarios: im- age patch size, different pre-processing, and the number of patches used for training. For the evaluation of our models tumor segmen- tation performance, we use the evaluation metrics that used in BraTS:

6.1 Confusion matrix

It is often used to describe the performance of a classification model (or "classifier") on a set of test data for which the true values are known. It allows the visualization of the performance of an algorithm. It allows easy identification of confusion between classes. It shows the number of images correctly predicted.

```
confusion_matrix
```

```
array([[151,   0],
       [159,   0]], dtype=int64)
```

Figure 6.1: Performance matrix

Chapter 7

SYSTEM REQUIREMENT

7.1 Software Requirements

7.1.1 Language

Python

Python is a widely used high-level programming language for general-purpose programming. Python has a design philosophy which emphasizes code readability (notably using white space indentation to delimit code blocks rather than curly braces or keywords), and a syntax which allows programmers to express concepts in fewer lines of code than possible in languages such as C++ or Java. Python is an easy to learn, powerful programming language. It has efficient high-level data structures and a simple but effective approach to object-oriented programming. Python's elegant syntax and dynamic typing, together with its interpreted nature, make it an ideal language for scripting and rapid application development in many areas on most platforms. The Python interpreter and the extensive standard library are freely available in source or binary form for all major platforms from the Python Website.

7.1.2 Tools

OpenCV

OpenCV is the leading open source library for computer vision, image processing and machine learning, and now features GPU acceleration for real-time operation.

OpenCV is released under a BSD license and hence it's free for both academic and commercial use. It has C++, C, Python and Java interfaces and supports Windows, Linux, Mac OS, iOS and Android. OpenCV was designed for computational efficiency and with a strong focus on real-time applications. Written in optimized C/C++, the library can take advantage of multi-core processing. Adopted all around the world, OpenCV has more than 47 thousand people of user community and estimated number of downloads exceeding 6 million. Usage ranges from interactive art, to mines inspection, stitching maps on the web or through advanced robotics.

OpenCV Functionality are

- Image/video I/O, processing, display (core, imgproc, highgui)
- Object/feature detection (objdetect, features2d, nonfree)
- Geometry-based monocular or stereo computer vision (calib3d, stitching, videostab)
- Computational photography (photo, video, superres)
- Machine learning clustering (ml, flann)
- CUDA acceleration (gpu)

7.1.3 Pip

Pip is a package management system used to install and manage software packages written in Python. Many packages can be found in the Python Package Index.pip is a recursive acronym that can stand for either "Pip

Installs Packages" or "Pip Installs Python". One major advantage of pip is the ease of its command-line interface, which makes installing Python software packages as easy as issuing one command. Most importantly pip has a feature to manage full lists of packages and corresponding version numbers, possible through a "requirements" file. This permits the efficient re-creation of an entire group of packages in a separate environment (e.g. another computer) or virtual environment.

7.1.4 Numpy

NumPy is the fundamental package for scientific computing with Python. It contains among other things:

- A powerful N-dimensional array object
- Sophisticated (broadcasting) functions
- Tools for integrating C/C++ and Fortran code
- Useful linear algebra, Fourier transform, and random number capabilities

Chapter 8

Result and Discussion

In the fully automatic Brain Tumor segmentation, when we give the name of our MRI image it will say whether the image is a tumor effected one or not."True" or "False" is used for this.

```
result = processImage('/content/gdrive/My Drive/Braint/yes/Y157.JPG')
print(f"Is tumorous MRI : {result}")
```

```
Is tumorous MRI : True
```

```
result = processImage('/content/gdrive/My Drive/Braint/no/No22.jpg')
print(f"Is tumorous MRI : {result}")
```

```
Is tumorous MRI : False
```

Figure 8.1: Final Output

Here I got an accuracy of around 87 percent.Also we can increase the accuracy by adding more number of layers in our convolutional neural network.

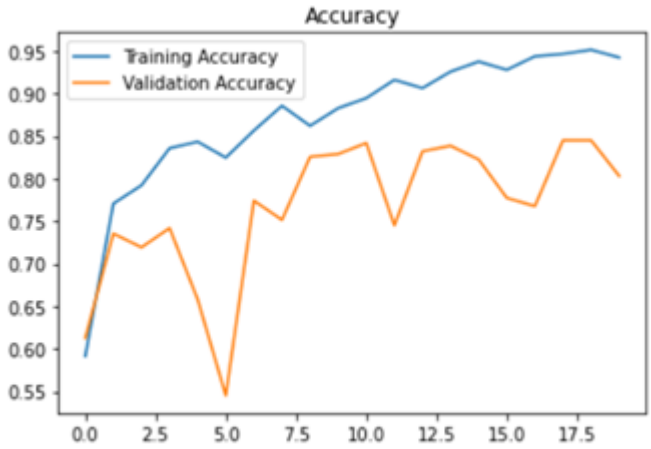


Figure 8.2: Evaluation plot

Chapter 9

Conclusion and Future Work

Early detection of tumor effected cells are necessary to reduce the drastic death rate due to brain tumor among adults as well as children.Nonetheless owing to many limitations such as lack of experts, lack of proper methodology and other speciality of tumor cells such as its high temperature compared to normal cells, early prediction and detection becomes very challenging. We can avoid the wasting time of manual diagnosis by the experts and this smart segmentation system decreases the needed time for the diagnosis process. This way gives to doctors more time with their patients in the process of treatment and follow-up.

This project is possible to do Brain Tumor Segmentation by using videos of brain tissues instead of MRI images.

Bibliography

[1] A. Singh, S. Bajpai, S. Karanam, A. Choubey, T. Raviteja, Malignant brain tumor detection, Int. J. Comput. Theory Eng. 4 (6) (2012) 1002.

[2] T. Logeswari, M. Karnan, An improved implementation of brain tumor detection using segmentation based on soft computing, J. Cancer Res. Exp. Oncol. 2 (1) (2009) 006–014

[3] E.C. Holland, Progenitor cells and glioma formation, Curr. Opin. Neurol. 14 (6) (2001) 683–688.

[4] E.C. Holland, Progenitor cells and glioma formation, Curr. Opin. Neurol. 14 (6) (2001) 683–688.

[5] S.J. Chiu, X.T. Li, P. Nicholas, C.A. Toth, J.A. Izatt, S. Farsiu, Automatic segmen- tation of seven retinal layers in SDOCT images congruent with expert manual segmentation, Opt. Express 18 (18) (2010) 19413–19428

[6] V. Dill, A.R. Franco, M.S. Pinho, Automated methods for hippocampus segmen- tation: the evolution and a review of the state of the art, Neuroinformatics 13 (2) (2015) 133–150.

[7]] L. Shen, H.A. Firpi, A.J. Saykin, J.D. West, Parametric surface modeling and reg- istration for comparison of manual and automated segmentation of the hippocampus, Hippocampus 19 (6) (2009) 588–595.

[8] H. Kutlu, E. Avcı, A novel method for classifying liver and brain tumors using convolutional neural networks, discrete wavelet trans-

form and long shortterm memory networks, Sensors 19 (9) (2019) 1992.

[9] K. Usman, K. Rajpoot, Brain tumor classification from multimodality MRI using wavelets and machine learning, Pattern Anal. Appl. 20 (3) (2017) 871– 881.

[10] P. Afshar, A. Mohammadi, K.N. Plataniotis, Brain tumor type classification via capsule networks, in: 2018 25th IEEE International Conference on Image Processing (ICIP), IEEE, 2018, pp. 3129–3133.