

Brain Tumor Segmentation Using Convolutional Neural Network

MSc. Data Analytics Research Project

Smit Jagdish Chheda Student ID: x18186319

School of Computing National College of Ireland

Supervisor: Mr. Hicham Rifai



National College of Ireland

Project Submission Sheet - 2019/2020

School of Computing

Chudent News	Cruit le adiate Chile ada	
Student Name:	Smit Jagdish Chneda	
Student ID:	x18186319	
_		
Programme:	MSc. Data Analytics	Year: Sept 19-20
Module:	Research Project	
Lecturer:	Prof. Hicham Rifai	
Submission Due		
Date:	17 th August 2020	
Project Title:	Brain Tumor Segmentation using Conv	olutional Neural Network
Word Count:	6115 words	

I hereby certify that the information contained in this (my submission) is information pertaining to research I conducted for this project. All information other than my own contribution will be fully referenced and listed in the relevant bibliography section at the rear of the project.

<u>ALL</u> internet material must be referenced in the bibliography section. Students are encouraged to use the Harvard Referencing Standard supplied by the Library. To use other author's written or electronic work is illegal (plagiarism) and may result in disciplinary action. Students may be required to undergo a viva (oral examination) if there is suspicion about the validity of their submitted work.

Signature:	Smit Jagdish Chheda
Date:	17 th August, 2020

PLEASE READ THE FOLLOWING INSTRUCTIONS:

Attach a completed copy of this sheet to each project (including multiple copies)	
Attach a Moodle submission receipt of the online project submission, to each project (including multiple copies).	
You must ensure that you retain a HARD COPY of the project, both for your own reference and in case a project is lost or mislaid. It is not sufficient to keep a copy on computer.	

Office Use Only	
Signature:	
Date:	
Penalty Applied (if applicable):	

Brain Tumor Segmentation Using Convolutional Neural Network Smit Jagdish Chheda X18186319

Abstract

Segmentation of the brain tumors is an essential function in the production of clinical data. Early care plays an important part in enhancing patient safety and increasing patient sustenance rates. The purpose of this implementation is to find out how does Neural network models results out when trained on large data set of MRIs. A novel method to image segmentation was applied to separate tumor from magnetic resonance (MRI) images by testing Neural network models- UNet, Feature Pyramid Network and ResNet50.Data set contained a total of 3886 MRI that were used to implement the approach where at first, augmentation was done and then the models were trained on large data sets after which tumor were segmented. For evaluating which model performed better, Dice co-efficient and IoU were used and the same were the best for ResNet50 with values 0.91 and 90% respectively. Its loss value came out to be 0.16 which is quite minimal. To conclude, segmentation is possible with good accuracy on large data sets by using ResNet50 and other neural network models. For future, I plan to implement the classification of tumors for the surgeons or the doctors to know whether the tumor is dangerous or mild. This can make it easy for them to know what surgery is needed to maintain patient's safety.

Keywords: Tumor Segmentation, Neural Networks, ResNet50, Unet, FPN

1. Introduction

1.1 An Overview of Brain Tumor

Brain being most complicated structure, functions with numerous different cells. Tumor develops as they shape an irregular community of cells across or throughout the skull. This group of cells may influence ordinary brain functioning and kill immune ones [1]. Persistent brain lumps with tumor and glioblastoma are the most prominent major brain cancers in individuals, present in nearly 80 per cent of positive tumors [2]. The word glioma comprises of multiple subsets, where tumor varies from slowly developing 'inferior' cancers to diverse, extremely malignant one. Even after major advancements in magnetic resonance imaging (MRI), chemo, radiation, and medical treatments, several forms of solid tumors, e.g. dominant are often deemed incurable with a median overall mortality expectancy of 8 to 2 percent in a decade [2].

1.2 Background and Motivation

Past findings displayed that the features of recently diagnosed tumors with MRI may be utilized to signify the possible plan of care [3]. The segmentation will have important findings which could be utilized as described in studies:(1) Approach carried out earlier on MR images leads the researchers by denoting what process can be followed; (2) Statistical MRI categorization tests can accurately track the occurrences, development or deformation of brain tumors by its measurements.

MRI feature extraction tests can accurately track the occurrences and development of brain tumors by its measurements, but here manual process is time consuming. Additionally, it is challenging to obtain repeatable outcomes even from the identical user. A completely automated, unbiased, and provable segmentation approach is strongly in need for a multidimensional, low, and randomized objective study [4]. Even after advances in labour saving and completely automated segmentation methods, many emerging issues remains, primarily owing to the extensive variability of tumors in scale, form, consistency, position, and diverse nature.

The popular form of machine learning, that is used for data processing brain tumor identification, involves primarily the Neural Network and the Support Vector Machine (SVM) [3]. Neural Network's performance also depends on the accurate choice of functionality and the appropriate range of various brain surfaces. Therefore, by storing a huge number of function vectors, the SVM approach is inefficient. Deep learning has been gaining interest in machine learning and object recognition over the period. Numerous deep learning studies, indeed, aims at identifying Alzheimer's and moderate cognitive disabilities. Outcomes of prior studies proves deep learning method produces physicians with an unbiased automated evaluation as a guideline and can even allow researchers or doctors prevent such mistakes in diagnosis and care.

Comparison of Neural network approaches are mentioned in [5] and as showed in Table 1., where small data sets were used, and the overall accuracy ranges out between 75 to 80%. One key factor being that these approaches were both manual and automatic. This motivates to find accuracy of a CNN model by bringing in such a novel approach which is fully automatic and trained on large data sets.

Method	Level of User Interaction	Performance (Dice)	
		Cure	Active
		Tumor	Tumor
Medical training and experience	Manual	0.93	0.74
CNN with 3x3 filters for deeper architecture	Fully Automatic	0.83	0.77
Generative model that performs joint			
segmentation	Semi-Automatic	0.78	0.72
Cascaded Two-pathway CNN	Fully Automatic	0.74	0.7
3D CNN architecture	Fully Automatic	0.71	0.65
Uses SVM; segmentation implemented			
within brain	Semi-Automatic	0.73	0.71
Local structured prediction with CNN and K-			
means	Fully Automatic	0.7	0.68

Table 1: Details of CNN models implemented trained on large data sets and Dice scores

1.3 Research Question

"To what extent can machine learning approaches help in segmenting brain tumors from MR images when they are trained on large data sets using Convolutionary Neural Network?"

The goal of this study is to address the above problem statement by understanding how significant improvements are generated by deep neural networks when trained on massive MR data sources and evaluated using Dice and IoU metrics. This would be done by

detecting the object i.e. the tumor. Since CNN has been considered producing good results for image processing and object detection; UNet, Feature Pyramid Network (FPN) and ResNet50 models are used.

1.4 Research Objectives

Objective defined to meet above research questions are as follows:

- Gathering massive MR Images and its pre-processing.
- Selection of best neural network models that would segment the tumor from MRI.
- Implementation of CNN models Unet, FPN, ResNet50.
- Evaluating based on Dice score and IoU metrics and optimizing it if needed.

The article is structured as Section 2 explaining the study conducted in the field preceded in Section 3 by the analytical methodology. Section 4 explains the models and performance metrics is discussed in section 5. The results are presented in Section 6 and concluding statement of the research done is mentioned in section 7.

2. Literature Review

Segmentation of the brain tumors is a tough task since the tumor has randomly oriented thicknesses and uncertain borders [6]. Frequencies, environment, and shape are typical features used in different research. Several researchers came up with various kind of approaches to segment the brain tumor, area development, gradient setting, the fuzzy clustering, and machine learning. In certain techniques while segmenting the tumor, human assistance was needed this had to be actioned upon [4]. This segment discusses in depth some earlier ideas or execution of the tumor segmentation outcomes obtained.

2.1 Related Work

Throughout the context of tumor segmentation, an image analysis program method for segmenting and tracking a customer's brain tumor using patient's MRI tests during the entire clinical procedure was described in [3]. Manual segmentation allows the physician using the MRI images' details including the biochemical and functional expertise gained throughout education and expertise [7]. Method requires the radiologist run through several samples of scans slice by slice, identify the tumor and cautiously identify the tumor areas physically [5]. The operation is preferred by manually labelling the region, or by defining tumor outlines. The primary challenge in manual delineation is the need for robust user interfaces. Additionally, the choice of tumor regions seems to have been a challenging and tedious task. In addition to long lasting task, manual segmentation is often reliant on radiologists, and the findings are subject to considerable variation in intra and inter rate [7]. In comparison, manual-based differentiation is commonly used in clinical research. Since many human skills and abilities are necessary in clinical studies to differentiate tissues, it has been frequently utilized [8]. Throughout the current studies, there are more over half a million tests handy for training of each class. Corresponding methods are, therefore, inefficient as generally performed [9].

A large amount of strategies has been introduced in [3] to categorize tumor cells at pixel level , depending upon unsupervised or supervised classifier. For segmentation of tumor, the absence of prior knowledge of form or size on the tumor makes it challenging to proceed in

an unsupervised way. A collection of training samples composed of labelled image data is considered to create prediction models for supervised technique in segmentation. Although RF models are confirmed to be effective during the classification of tumor [10]. Model-based approaches consider foreknowledge, like details about size and shape, which requires a series of pixels. A Bayesian geometry combining image recording and structural prior information is also suggested for specific tumors and tissue [3]. The suggested program in [11] takes feedback from fMRI images. Functional Magnetic Resonance Imaging (fMRI) contains comprehensive data on genetics and cellular system of tumors, allowing it to become a key diagnostic tool. The extracted decimal values from fMRI are Nacetylaspartate, Choline, Methylene protons of creatine and Creatine which makes human calculation difficult to confirm the tumor as there can be calculative errors. A further group of technique learns explicitly from the records in a distribution. While a training phase may be a drawback, these approaches may identify trends of tumors which does not fit a specific model [12]. Within active contour model (ACM), Sachdeva et al. utilized image content with strength to solve the problem found in earlier approaches such as FVF, boundary vector flow (BVF), and gradient vector flow (GVF) [6].Collection of false edges or false seeds contributes to the issue of merging and selecting of poor outlines contributes to division owing to the tumors edema. We reported a total accuracy (Dice score) of 62.3 percent for edema and 62.6 percent for tumor in the specific instances when tested with the Dice score using 4x7=28 voxels, 7 from each range [13]. While the suggested technique in [14] generally falls inside semi - auto techniques, it owns the classification technique with automated system, kept running on voxel useful for modelling and enhanced by a spatial dependence concept. Standard extracted features produce positive performance for stable to semi-balanced sets of data, but those with huge sample imbalances need systematic approach and advanced loss functions can be useful for obtaining targeted result [15].

Automatic detection of tumors and features allows for precise and testable measurements. It has tremendous ability for improved discovery, surgical preparation, and recovery evaluation [16]. As proposed in [17], approach integrates image data obtained in a standard clinical procedure, comprising traditional multiparametric MRI and circulatory. Limiting the method stems requiring to trace ROIs, which builds the original methodology semiautomatic and prone to variation intra- and inter observer. The thresholding-based technique and region-widening provides the option of a straightforward and fast segmentation but overlooked the spatial characteristics [18]. Throughout region-widening dependent segmentation, better user action is needed for seed selection. Seed is tumor cells hub; it may cause the question of homogeneity to worsen [5]. Following the rapid creation of semiautomatic and fully automated models, numerous emerging issues persist to this mission, primarily owing to the increasing variability in brain tumors in scale, form, frequency, position, sand variance [2]. Such approaches as mentioned in [19] drawbacks comprise the difficulty in choosing the optimal construction phase, and the susceptibility to slope and noises. In addition, convergence accelerations are sometimes low. The approach recommended in [20] involves human input to measure full tumor width. Researchers proposed a technique for the segmentation of subject particular to MR scans with a statistical guided level collection. The algorithm relies on a malignant approach, in which familiar data is collected utilizing spatial possibility from different Imaging methods. The model developed in [21] would be extended to the complex process of identifying and delineating child tumors using 3D MRI. This segmentation function is distinguished by high variations of both the pathology and the non-pathological brain tissue that surrounds it. A statistical assessment shows how reliable the suggested model is. The full operation with

one multi-spectral sample group involves no user intervention and consumes less effort than the strategies initially suggested [22].

In the analysis of [23], they concentrated about glioma, the most severe form of brain tumors. Researchers tackle the symptom as a classification model relying on a multi-layered feature vector that outlines each voxel towards its corresponding label. For certain instances, machine learning methods have proved to produce successful outcomes. Many voxel marks are heavily reliant on neighbours. Gliomas show up in any thickness at any place. Gliomas are also malignant cancers, which are hard to differentiate against healthy tissues. Unstructured data given by multiple processes should therefore be merged to resolve any such complexities [24]. S. Ravi implemented a technique using K means and Fuzzy c means (FCM) algorithm. Here the noise was eliminated and even produced good result, though, problem being the data set used had only 40 MR images which is quite small to know if the accuracy received could be better for large data sets and hence large data set would be needed [18]. Essential things to keep in mind for better performance involve pre-processing, data improvement, feature selection and image classification for error optimization technique. The impact of the same has been demonstrated in [15].

2.2 Data Mining in Brain Tumor Segmentation

The function of segmentation is to partition an image into sections that are relevant for the implementations in question. Data mining method is aimed at extracting insights and turning it into a comprehensible framework for further development. K-means was used by S. Ravi to remove the mass from the MRI, where, noise was removed during the pre-processing. The tumor dimensions are determined by the white pixels throughout the binary picture [18]. Problem with k-means could be in difficulty of predicting k-value as the tumor is of different size and shape and with global cluster k-means will not work well for a large data set [8]. Fuzzy c-means is another data mining method used for segmenting the tumor. The traditional FCM method worked efficiently on most noise-free images, which has a significant drawback, and it does not integrate spatial background knowledge, since it is noise-sensitive [25]. It does not take spatial data into consideration, making it quite noise sensitive. Due to their unusual feature vectors as mentioned in, a noisy node is falsely classified in a conventional FCM approach [2].

U-net based CNN method was implemented by H. Dong and team where five-fold cross validation technique was used to segment 54 cases were considered. Nevertheless, a simple specification for autonomous research data and more implementations for university - based and clinical datasets can be foreseen as mentioned in [2]. New advancements in deep learning with diagnostic implementations, like recognition of lung nodule disease and identification of lymph nodes, were successful in identifying risk factors for imaging. The existence of labelled medical information, indeed, provided a problem for the creation of successful prototypes [26]. New advancements in deep learning with diagnostic implementations, like recognition of lung nodule disease and identification of lymph nodes, were successful in identifying risk factors for imaging. The existence of labelled medical information, indeed, provided a problem for the creation of successful prototypes. Three systems are proposed-Interpolated Network, Skip Net, SE-Net, comprised of decoder and encoder design for which four main-blocks are used at each stage. We are used to note that after several training process, the Convolutionary patterns can easily erupt or disappear [15]. For 3D algorithms, consideration should be given to the relationship between receptive field, simulation time, and disk usage. The relatively high 3D areas for development, fortunately, burn a lot of ram, and thus constrain the finding and number of attributes in the

grid, resulting in restricted predictive accuracy and low recognition capability [16]. A CNN approach using ~270 MRI was proposed by A. Pinto to segment tumor. But as the augmentation and implementation takes a lot of space this was not implemented but proved to be beneficial on their research [12]. Hence, implementing tumor segmentation using deep learning and other data mining methods could prove to be more beneficial than other approaches described in the literature review above.

3. Methodology

A simplified step in building a Machine Learning Model is quite relevant for everyone operating on it. To assure that everyone should obey and do not skip any of the measures needed to build the application. CRISP-DM i.e. cross-industry process for data mining is one such methodology available and widely used framework. A systematic framework for preparing a data mining program is provided by the CRISP-DM framework. It is a reliable approach that has proved itself well and the same is displayed in Figure 1.

Proposed Approach: CRISP-DM for production



Figure 1: Tumor Segmentation - Design Methodology

3.1 Business Understanding

The thought of implementing Brain Tumor segmentation using data mining methods came up while analysing and knowing the limitations of the previous methods implemented and proposed. The goal now is to implement CNN models to segment the tumor through large data sets of MRI and knowing how good results do they produce. Additionally, planned how the structure of the approach would be and the same is displayed below in Figure 2.



3.2 Data Understanding

Data Source:

Data is obtained from Kaggle, but its primary source is an open source community / company 'Cancer Imaging Archive'. There are a total of 3886 MRI and its masks.

Primary source: https://www.cancerimagingarchive.net/collections/

Secondary Source: <u>https://www.kaggle.com/mateuszbuda/lgg-mri-segmentation?</u>

The data set did not contain any human participant or any sensitive data that could break any legal or ethical rules.

Data sets were gathered from 'Cancer Imaging Archive' for this implementation. All the files were in the form of .tif format. Out of the total 7863 files, 2 files represented the values of the tumor which were in the form of .csv file.86 MRI were duplicates.This data set was a combination of MRI and its masks which were used for the implementation purpose. The further distribution is as follows:

Table 2: Data set Description

	Count
Having Tumor	2500
Not Having Tumor	1386
Duplicates	86

The MRI images had to be considered as the Inpur image and the output would be the masked image.

3.3 Data Preparation

On the basis of Data understanding, issues related to the data were examined. One being duplicacy of images in the data. Hence, the list of images were stored in an excel sheet form where the duplicacy was found and were removed. The two extra files that were present were also seperated from the MRI and mask images. Also, the MRI and masked images were considered as two different data frames.



Figure 3: Distribution of Data

For splitting the data of 3886 MRI into Train, Test and Validation, first the data set was splitted into Train (90%) and Validation (10%). Then again the Train set was divided into

Distribution of data grouped by diagnosis

Train (85%) and Test (15%). The total numbers resulted for Train, Validation and Test sets were 2972, 389 and 525 respectively.



Figure 4: Splitting Data into Train, Test and Validation

3.4 Modelling

Modeling is carried out after Augmentation of data was done and this is the step in which the data is presented to produce the required implementation. Neural network models -Unet, FPN and ResNet50 are implemented. Detailed information on the working of these models are explained in Section 4

3.5 Evaluation

After the models are trained on train, validation and test sets of data, Dice co-efficient and IoU are used as the evaluation metrics to know how each model performed. Both the evaluation metrics have been explained in Section 5 along with the values obtained.

3.6 Deployment

Once the coding is tested and evaluated successfully, it would then be presented for real time assessment.

4. Implementation

This portion discusses in depth the application of Brain tumor segmentation through Data Mining. It involves the hardware / software specifics that will be needed for successful execution followed by the models.

4.1 Enviornment Setup and Requirements

This section provides information on the hardware and software requirements needed for the implementation of this proposal along with good network connection. The storage can also be done on cloud to avoid using large local space.

RAM	Mir	nimum 8gb ram
Processor	I5	and above
Speed 1.99 GHz		
Table 4 Software Pequirements		

Table 3. Hardware Requirements

Table 4. Software Requirements

Backup Storage	OneDrive, Google Drive
Language and Tools	Google Collab, Python, Web browser
Libraries	PyTorch, NumPy, pandas

4.2 Models Implemeted:

After studying the previous works implemented and proposed, data mining neural network models came out to be most successful in image processing and object detection. Hence, Unet, FPN and ResNet50 were chosen to be trained on large data sets of MRI and later segment the tumor from MR Images. The visualization of values is displayed along with the segmented tumor.

4.2.1 Unet:

Brain tumor representations typically include complex subject features, shapes, and vector object outline. Skip architectures incorporates high-level expression from dense sequencing layers to achieve accurate segmentation. Unet, which uses the skip architecture, achieves strong results in cell pattern recognition. Design comprises of three components: Contraction, Bottleneck, and Expansion. Portion of the expansion is made up of several sections of contraction. Every block receives an input that adds levels of convolution preceded by a max pooling limit. The lowest level moderates among the contraction layer and the expansion layer through which each block transfers the data to two layers of CNN accompanied by a sampling level.

Dice score recorded as per each Epoch can be seen in the graph displayed below in Figure 5. The Mean IoU recorded for Test set was 86%.



Figure 5: Dice coefficient of Unet model for each Epoch

4.2.2 Feature Pyramid Network (FPN):

Feature Pyramid Network (FPN) is a function remover built with precision and frequency for a pyramid model. It removes the scanner function such as Faster R-CNN and produces several surface maps levels with better attribute details than the standard image retrieval system to segment the tumor from MRI. The framework includes of a bottom-up and top-down system in which the bottom-up direction is the normal convolutionary network for retrieval of tumor information, and the image quality decreases as we move up.

The key finding while implementing the model is that the bottom layers have high resolution but are not used for object detection since it decreases the speed. Hence, the results are poor when the upper layers are used for tumor detection and segmentation specially when the tumor is small. The Dice to Epoch mapping for FPN train set is displayed in Figure 6. Below and Mean IoU recorded for Test set being 79%.



Figure 6: Dice coefficient of FPN model for each Epoch

Residual Networks (ResNet50):

The definition of skip connection was first implemented in ResNet model. It has usually 3 levels - convolution, block normalization and ReLu. The integration of the initial input x with the non-linear function F(x) provides us with benefits that helps initial surfaces to get permission from other layers to the differential signal. In other words, missing the F(x) functions makes earlier layers to reach a better differential signal. Consequently, this sort of interconnection is preferred as it eases deeper training process to segment the tumor.



Figure 7: Dice coefficient of ResNet50 model for each Epoch

The problem of acquiring low accuracy or dice scores during segmentation that occurred with FPN and Unet was solved by using ResNet. The dice and epoch mapping are displayed above in Figure 7 and Mean IoU recorded being 90%.

5. Evaluation Metrics

Evaluation metrics are necessary to evaluate and know how the model performed. After the models are trained on large data sets and used for segmentation, the prediction of tumor in MRI is done at first. The tumor is then segmented from MRI. For this process, the evaluation metrics used are Dice coefficients and Intersection of Union (IoU). Dice coefficients give the precision value whereas IoU gives the accuracy of a model and these two Evaluation metrics are best suitable for object detection processes.

Dice Co-efficient

It is a metric utilized to evaluate the closeness between two datasets or samples. The Coefficient of Dice is alike to the IoU. They are significantly linked, meaning that if the first approach says model A is superior to model B when segmenting a tumor, the latter says the same thing.

The values for loss, Dice coefficient and IoU should be 0,1 and greater than 0.5 respectively to be considered a good fit model. In implementation of Brain tumor segmentation with the help of Convolutional neural network models – Unet, FPN and ResNet all the models were a good fit. But the value of loss for FPN was close to 0.4 which was the maximum and that of ResNet50 was 0.16 which is close to 0 and the best.

Intersection over Union (IoU)

Intersection over Union is a statistical calculation used to calculate an object recognition's accuracy on a specified dataset. It is calculated by the below formula:

```
IOU = true_positive ÷ (true_positive + false_positive + false_negative)Or
```

The ratio of Area of Intersection to Area of Union

Similarly, the value for dice co-efficient and IoU were the best for ResNet50 model being 0.91 and 90% respectively which shows that out of the three, ResNet50 was the best fit to be implemented for Brain Tumor Segmentation when models were trained on large data sets.

The overall Dice scores and loss for all three models for 10 epochs are given below in the table 5.

Table 5: Performance comparison of models

	Models					
	Unet		FPN		ResNet50	
Mean value on Train - Epoch	Dice	Loss	Dice	Loss	Dice	Loss
Epoch 0	0.01	0.85	0.01	1.01	0.4	0.63
Epoch 2	0.54	0.53	0.44	0.63	0.79	0.23
Epoch 4	0.6	0.45	0.59	0.46	0.83	0.19
Epoch 6	0.62	0.43	0.61	0.43	0.84	0.18
Epoch 8	0.67	0.36	0.65	0.39	0.83	0.19
Epoch 10	0.74	0.35	0.68	0.37	0.91	0.16

The Mean IoU recorded for Test sets of each models are as below in Table 6:

Table 6: Mean IoU of Test Set

	Mean IoU for Test Set
UNet	86%
FPN	79%
ResNet50	90%

6. Result

As discussed above in Section 5., ResNet50 was the best model used for Brain tumor segmentation when models were trained on large data sets as the IoU was the highest of them all being 90% when at least 10 Epoch were executed and average time of execution being between 18-20 minutes.

As the ResNet50 was the best fit model among the three, displayed below in Figure 8 is the output captured after running the model. The tumor can be seen segmented from the Original MRI in the last picture.



Figure 8:Output after Segmentation

7. Conclusion and Discussion

Multiple manual and automated approaches were implemented and proposed for Brain tumor segmentation wherein some also gave good accuracy. But the manual approaches had a drawback of the calculations going wrong and could not be accurate while for that of automated approaches were trained on small data set. Hence, when models were trained on large data sets it did not produce good results.

This study aimed to provide a unique strategy by using neural network models to segment the brain tumour. These models are trained on large data sets with around 3890 MRI images. The implemented approach has the ability. The developed models can achieve better segmentation precision and obtaining a reasonable matching performance between the product of segmentation and the ground reality. In fact, some inaccurate segmentation may arise due to variance between eyesight and movement as surgeons physically segment the tumor. So, the automated segmentation output is often much higher. This approach will usually produce a more reliable outcome.

As per the outcomes from all three models implemented, ResNet50 produced an accuracy of 90% which was more compared to other models – FPN and Unet that came out to be 68% and 76% respectively. The loss was 0.16which was lowest compared to that of 0.35 and 0.37 of Unet and FPN, respectively. Hence, compared to other approaches which were studies the Neural network models can be used for segmentation of large MRI data sets to produce good results and get accurate segmented tumors.

To further strengthen the suggested procedure, tumor classification may be performed in various forms, irrespective of whether it is least / highly offensive or harmless, malignant. The gliomas may also be categorized into astrocytes, ependymal cells, and oligodendroglia cells. The limitation with the implementation is that it occurs large local space due to large MRI data set. But this can be solved by storing the data on cloud and performing operations on cloud. Hence to conclude unlike other approaches, our suggested solution to segmentation generates the tumor, safe place, and all sub-regions thereof. It adds strong spatial regularisation to its categorization and operates quickly on diagnostically available details.

8. Acknowledgement

I would like to convey my sincere appreciation to Prof. Hicham Rifai for his important and consistent advice, direction, motivation, and continuous help during the research without which this research would not be feasible. He took interest in looking over the paper and helping me improve it.

Information Sharing Statement:

Brain tumor MRI data used in this Research project was obtained by 'Cancer Imaging Achieve'¹², an open-source community resource [25]. I thank them for providing such huge data set for implementing Tumor segmentation using Neural network models.

¹<u>https://wiki.cancerimagingarchive.net/display/Public/TCGA-GBM#715bed1a14224923b50f1f2e7dae54a1</u> ²<u>https://wiki.cancerimagingarchive.net/display/Public/TCGA-GBM</u>

Bibliography

- [1] H. Mohsen, E.-S. A. El-Dahshan, E.-S. M. El-Horbaty, and A.-B. M. Salem, "Classification using deep learning neural networks for brain tumors," *Futur. Comput. Informatics J.*, vol. 3, no. 1, pp. 68–71, 2018, doi: 10.1016/j.fcij.2017.12.001.
- [2] S. E. A. Raza, L. Cheung, D. Epstein, S. Pelengaris, M. Khan, and N. M. R. B, "MIMONet: Gland Segmentation Using Neural Network," *Comput. Methods Programs Biomed.*, vol. 1, no. d, pp. 698–706, 2017, doi: 10.1007/978-3-319-60964-5.
- [3] N. Zhang, S. Ruan, S. Lebonvallet, Q. Liao, and Y. Zhu, "Kernel feature selection to fuse multi-spectral MRI images for brain tumor segmentation," *Comput. Vis. Image Underst.*, vol. 115, no. 2, pp. 256–269, 2011, doi: 10.1016/j.cviu.2010.09.007.
- [4] Z. Xiao *et al.*, "A deep learning-based segmentation method for brain tumor in MR images," 2016 IEEE 6th Int. Conf. Comput. Adv. Bio Med. Sci. ICCABS 2016, vol. 2016, no. 2015, pp. 5–7, 2016, doi: 10.1109/ICCABS.2016.7802771.
- [5] A. Işin, C. Direkoğlu, and M. Şah, "Review of MRI-based Brain Tumor Image Segmentation Using Deep Learning Methods," *Procedia Comput. Sci.*, vol. 102, no. August, pp. 317–324, 2016, doi: 10.1016/j.procs.2016.09.407.
- [6] K. Usman and K. Rajpoot, "Brain tumor classification from multi-modality MRI using wavelets and machine learning," *Pattern Anal. Appl.*, vol. 20, no. 3, pp. 871–881, 2017, doi: 10.1007/s10044-017-0597-8.
- [7] J. Kleesiek, A. Biller, G. Urban, U. Köthe, M. Bendszus, and F. A. Hamprecht, "ilastik for Multi-modal Brain Tumor Segmentation," *BraTS Chall. Manuscripts, MICCAI 2014*, vol. May, no. 2014, pp. 12–17, 2014, [Online]. Available: https://hci.iwr.uniheidelberg.de/sites/default/files/publications/files/1979342158/kleesiek_14_ilastik.pdf.
- [8] R. Gurusamy and V. Subramaniam, "A machine learning approach for MRI brain tumor classification," *Comput. Mater. Contin.*, vol. 53, no. 2, pp. 91–109, 2017.
- [9] M. Huang, W. Yang, Y. Wu, J. Jiang, W. Chen, and Q. Feng, "Brain tumor segmentation based on local independent projection-based classification," *IEEE Trans. Biomed. Eng.*, vol. 61, no. 10, pp. 2633–2645, 2014, doi: 10.1109/TBME.2014.2325410.
- [10] N. J. Tustison *et al.*, "Optimal Symmetric Multimodal Templates and Concatenated Random Forests for Supervised Brain Tumor Segmentation (Simplified) with ANTsR," *Neuroinformatics*, vol. 13, no. 2, pp. 209–225, 2015, doi: 10.1007/s12021-014-9245-2.
- [11] C. Engineering *et al.*, "Detection of Brain Tumor by Mining fMRI Images," *Int. J. Adv. Res. Comput. Commun. Eng.*, vol. 2, no. 4, pp. 1718–1722, 2013, [Online]. Available: https://www.semanticscholar.org/paper/Detection-of-Brain-Tumor-by-Mining-fMRI-Images-Nagori-Mutkule/508638838bb45d2a78b4c90e73a63d6d0c6ab510.
- [12] M. M. Thaha, K. P. M. Kumar, B. S. Murugan, S. Dhanasekeran, P. Vijayakarthick, and A. S. Selvi, "Brain Tumor Segmentation Using Convolutional Neural Networks in MRI Images," *J. Med. Syst.*, vol. 43, no. 9, pp. 1240–1251, 2019, doi: 10.1007/s10916-019-1416-0.

- [13] B. Menze, M. Reyes, A. Jakab, E. Gerstner, J. Kirby, and K. Farahani, "Proceedings of the MICCAI Challenge on Multimodal Brain Tumor Image Segmentation (BRATS) 2013," *MICCAI Chall. Multimodal Brain Tumor Image Segmentation*, vol. 57, no. October 2015, pp. 3–5, 2013, [Online]. Available: https://hal.inria.fr/hal-00912934/document#page=36.
- [14] M. Havaei, P. M. Jodoin, and H. Larochelle, "Efficient interactive brain tumor segmentation as within-brain kNN classification," *Proc. - Int. Conf. Pattern Recognit.*, no. June, pp. 556–561, 2014, doi: 10.1109/ICPR.2014.106.
- [15] S. Iqbal, M. U. Ghani, T. Saba, and A. Rehman, "Brain tumor segmentation in multispectral MRI using convolutional neural networks (CNN)," *Microsc. Res. Tech.*, vol. 81, no. 4, pp. 419–427, 2018, doi: 10.1002/jemt.22994.
- [16] A. Crimi *et al.*, "Brainlesion: Glioma , Multiple Sclerosis ," *Autom. Brain Tumor Segmentation using Convolutional Neural Networks with Test-Time Augment.*, vol. 10670, no. December 2017, pp. 138–149, 2017, doi: 10.1007/978-3-319-75238-9.
- [17] E. I. Zacharaki *et al.*, "Classification of brain tumor type and grade using MRI texture and shape in a machine learning scheme," *Magn. Reson. Med.*, vol. 62, no. 6, pp. 1609–1618, 2009, doi: 10.1002/mrm.22147.
- [18] D. D. Pingale and S. R. Todmal, "Brain Tumor Segmentation Using K-Means and Fuzzy C-Means Clustering and Its Area Calculation and Stage Using SVM Algorithm," *J. Adv. Sch. Res. Allied Educ.*, vol. 15, no. 3, pp. 27–32, 2018, doi: 10.29070/15/56750.
- [19] J. Zhou, K. L. Chan, V. F. H. Chong, and S. M. Krishnan, "Extraction of brain tumor from MR images using one-class support vector machine," *Annu. Int. Conf. IEEE Eng. Med. Biol. - Proc.*, vol. 7 VOLS, no. 2005, pp. 6411–6414, 2005, doi: 10.1109/iembs.2005.1615965.
- [20] A. Islam, S. M. S. Reza, and K. M. Iftekharuddin, "Multifractal texture estimation for detection and segmentation of brain tumors," *IEEE Trans. Biomed. Eng.*, vol. 60, no. 11, pp. 3204–3215, 2013, doi: 10.1109/TBME.2013.2271383.
- [21] M. Wels, G. Carneiro, A. Aplas, M. Huber, J. Hornegger, and D. Comaniciu, "A discriminative model-constrained graph cuts approach to fully automated pediatric brain tumor segmentation in 3-D MRI," *Lect. Notes Comput. Sci. (including Subser. Lect. Notes Artif. Intell. Lect. Notes Bioinformatics)*, vol. 5241 LNCS, no. PART 1, pp. 67–75, 2008, doi: 10.1007/978-3-540-85988-8_9.
- [22] X. Xuan and Q. Liao, "Statistical structure analysis in MRI brain tumor segmentation," *Proc. 4th Int. Conf. Image Graph. ICIG 2007*, vol. 2007, no. 2017, pp. 421–426, 2007, doi: 10.1109/ICIG.2007.181.
- [23] S. Bauer, L. P. Nolte, and M. Reyes, "Fully Automatic Segmentation of Brain Tumor Images Using Support Vector Machine Classification in Combination with Hierarchical Conditional Random Field Regularization," *Lect. Notes Comput. Sci. (including Subser. Lect. Notes Artif. Intell. Lect. Notes Bioinformatics)*, vol. 6893 LNCS, no. PART 3, pp. 354–361, 2011, doi: 10.1007/978-3-642-23626-6_44.
- [24] L. Zhao and K. Jia, "Multiscale CNNs for Brain Tumor Segmentation and Diagnosis,"

Comput. Math. Methods Med., vol. 2016, no. 2017, pp. 4–6, 2016, doi: 10.1155/2016/8356294.

- [25] K. Clark *et al.*, "The cancer imaging archive (TCIA): Maintaining and operating a public information repository," *J. Digit. Imaging*, vol. 26, no. 6, pp. 1045–1057, 2013, doi: 10.1007/s10278-013-9622-7.
- [26] X. M. Zhou *et al.*, "Radiomics in Brain Tumor: Image Assessment, Quantitative Feature Descriptors, and Machine-Learning Approaches ABBREVIATIONS: LBP local binary patterns; HOG histogram of oriented gradients; QIN Quantitative Imaging Network; SIFT scale-invariant feature," *Int. J. Comput. Appl.*, vol. 2018, no. 2018, pp. 4–6, 2018, doi: 10.3174/ajnr.A5391.