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A Comprehensive Review on Brain Tumour Segmentation Using Deep Learning Approach

Akshay, Varsha Bodade

Terna Engineering College, Neurl

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ABSTRACT

One of the most critical tasks in medical image processing is the analysis of brain tumour. Early detection of the disease however helps and assists in enhancing prior treatments and thereby increasing the survival rates of the patient. The process of conducting a manual segmentation through a series of MRI images of the brain helps to diagnose cancer. It is further accompanied through clinical routines and check-ups. The procedure of the same appears to be a tedious and time consuming job. Hence there is a need to automate the process by using advanced technologies such as machine learning and deep learning. The fundamental aim of this paper is to contribute in providing a detailed review of brain tumour segmentation methods along with the proposed method for final implementation. Automated form of brain segmentation has been widely adopted by various research scholars; wherein they use deep learning based algorithms to address the problems that remained restricted by using ML strategies. Many algorithms and techniques that fall under DL are capable to produce better results through objective evaluation on large amounts of MRI based patient data. With large and extensive research being done in the domain by using ML; this review paper differs by highlighting the trend and strategies used in DL. An introduction to brain tumours is presented in the paper followed by state-of-art algorithms which are to be proposed during the implementation phase. An assessment on current and existing work is also briefed and future directions to standardize the process of tumour segmentation are addressed.

Keywords: CNN, deep learning, EfficientNetB2, MRI, image processing

INTRODUCTION

A form of uncontrolled and unnatural grow of cells in the body is termed as cancer. Such occurrences leads to the division of cells and at times; an unnatural growth in the cells are also observed. When such changes occur in the brain tissues, the disease is called as brain tumour. While on one hand, where brain tumours are not that common; they can at times be lethal [1]. Depending on the source of origin of the growth cells, brain tumours can either be divided into primary and metastatic brain tumour. In primary brain tumour, the origin of the growth cells takes place in the brain; whereas in metastatic brain tumour; the origin of the tumour could be anywhere in the body which eventually spreads and resides into brain.

Gliomas tumour is a type of brain tumour that originates in the glial cells and appears to be as the point of research for many scholars and authors. The word glioma is a term which is used to refer various forms and types of tumour stages that occurs in the brain. Some of them include low intensity glioma such as astrocytomas and oligodendrogliomas [2]. On the other hand high intensity glioma comprises of glioblastoma multiform (GBM). Common and most observed forms of treating cancer are chemotherapy and radiotherapy [3]. Apart from this, medical imaging techniques such as Computed Tomography (CT), Positron Emission Tomography (PET), and Magnetic Resonance Imaging (MRI) are also used to derive valuable information about the tumour [4]. This information is further used to understand the location, size and metabolism of the tumour that resides within the brain.

While these clinical routines and medical imaging techniques being used; MRI is considered to be as the most accurate and reliable technique to understand the location of the tumour which resides in the brain. MRI is a non-invasive technique that makes use of radio frequency signals that triggers the targeted tissues and tends to

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produce an image of those tissues under the influence of powerful magnetic fields thus generated [5]. A sequence of brain images is generated and the modalities are later studied for tissue contrast image. Figure 1 depicts MRI modalities that represents the occurrence of gliomas in T1 weighted MRI, T2 weighted MRI and Fluid Attenuated Inversion Recovery (FLAIR).

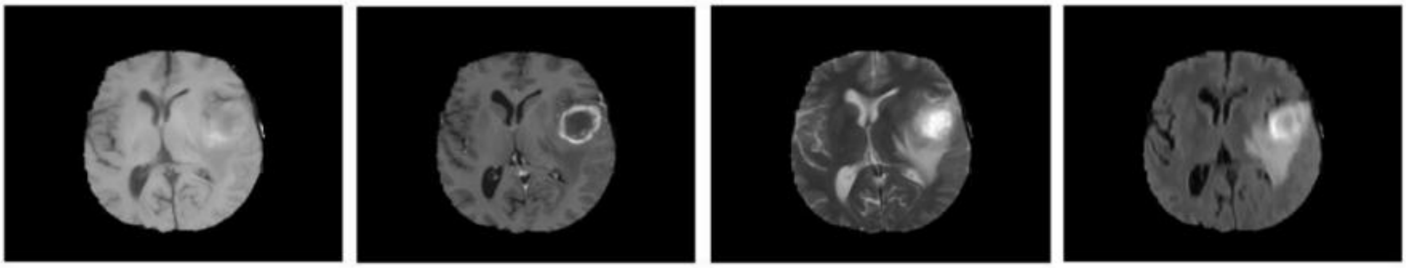

Figure 1: MRI Modalities showing types of glioma

The acquisition and image capturing through an MRI image can vary in different devices. An approximate number of 120 slices are expected to occur while capturing the 3D volume of the brain image. Later, when all the slices are eventually combined, the diagnosis of the modalities becomes complicated. In general terms, the T1 image of the glioma is used to differentiate between the healthy and unhealthy tissues; whereas the T2 images are used to perform segmentation on the bright signal region of the edema [5]. This edema region is responsible to detect active cell areas and further save it from tumour tissue. Finally, the FLAIR image of the glioma modality consists of water molecules within it and is later used to differentiate between the edema region and the region of Cerebrospinal Fluid (CSF).

Therefore it can be said that before applying any strategic therapy, it is mandatory for the doctor to check the stages of the unhealthy tissues that tends to disrupt the normal functioning of the human brain. The segmentation process usually involves diagnosis and separating the active tissues from unhealthy tissues; the necrotic regions from edema regions which also include the separation of grey matter (GM) with white matter (WM). The current process of clinical routine however comprises of segmentation, division, activation and manual annotation of the MRI images. With clinical routines and procedures being a time consuming job, the inclination of research scholars over robust and automated systems is highly observed.

Being in tangent with this methodology, the presented paper therefore focuses on image segmentation techniques which are used widely. It also focuses on the deep learning algorithms which are expected to be used during the implementation phase. A comparison of varying methods is also provided in the paper and the review finally ends by providing a research direction for future.

LITERATURE SURVEY

This section of the paper highlights the work done by other research scholars.

Authors in [6] made use of MRI images to diagnose brain tumour. They performed the same by implementing deep learning models such as CNN and transfer learning models. VGG16, MobileNet and InceptionV3 were used for the same. The dataset consisted on 10,000 images with an image resolution of 200 x 200 pixels. The dataset was further divided into two categories of healthy brain images and tumour brain images. A training accuracy of 92percent and a testing accuracy of 93.28percent were achieved. Similar work was obtained by authors in [7] wherein they used a DCNN model to detect brain tumours from MRI images. BRATS was used as the dataset which comprised of 950 Gliomas images, 600 tumour images and 940 meningioma images were present. The proposed model achieved a precision accuracy of 91.38percent by combing the model with DCNN and VGG19. SVM was also a part of the model implementation.

Authors in [8] tried to use a cutting edge automation technique that used CNN along with a correlation learning method (CLM). A total of 700 meningioma images and 1500 glioma images were present in the dataset. Additionally, 3000 brain tumour images were detected in the dataset and the CLM model achieved a precision accuracy of 91.32percent.

Authors Garg et al. in [9] proposed the implementation of ML based algorithms such as random forest, KNN, SVM and decision trees. For this purpose a hybrid model was encouraged and ensemble classifier was used. The classification of brain tumours was performed on 2500 brain tumour images. Thirteen feature extraction techniques were used and the ensemble classifier was able to generate an accuracy of 93.36percent. The accuracy however produced by the hybrid model was observed to be 94.28percent. Authors in [10] proposed the architecture of EfficientNetB2 along with CNN as a multi modal project. Brain tumor was diagnosed by scanning the MRI images. The authors also made use of transfer learning based models such as ResNet50, MobileNetV2 and InceptionV3. A total of 92percent accuracy was obtained through this model with an F1Score of 93.68percent. Authors in [11] developed a CNN based neural network that was implemented to diagnose brain tumours over a dataset of 2000 MRI images. BRATS was used for the same purpose and the findings and results were quite promising. The model accomplished an accuracy of 94.26percent under 100 epochs.

Authors Khalil et al. in [12] implemented the diagnosis of brain tumour by making use of two step dragonfly algorithm. The dataset used for the same comprised of 3D MRI images. One of the primary difficulties observed in this research was the understanding of the dataset due to the tumour size and structure in the MRI images. In order to overcome such challenges; a two-step method was adopted to extract a common point of origin. BRATS 2017 dataset was used for the same with 3D images of the brain. The results and findings of the study were further evaluated by using Fuzzy Means, SVM and decision trees as ML based algorithms. Parameters of evaluation such as accuracy, recall and precision score were calculated. The weakness of this study was further eliminated in a research work performed by authors in [13] wherein they used the BRATS dataset to diagnose regions of brain tumours. The analysis and validation of the same was done in a two-phase training method and regularization techniques such as dropout. The hybrid model thus developed attained an accuracy of 91percent and various segmentation methods of semiautomatic approach were used. The model was expected to perform better than CNN's.

Authors in [14] made use of ML based techniques such as SVM and KNN to analyze abnormalities in the fetal brain. A hybrid approach of combining RF, NB and decision trees was also proposed in the research. Once an evaluation of the model was done, BRATS dataset was later used for training and testing purpose. An accuracy of 91.36percetn was obtained. Authors Attallah et al. in [15] made use of various DL based algorithms to diagnose the presence of tumour in the brain. A series of detailed architecture was used and diagnosis of embryonic neurodevelopmental abnormalities (ENDs) was focused on.

Table 1: Comparative Analysis of various researches

Reference	Dataset	Model	Cons	GIST
[16]	11,000 MRI images were used	VGG-16, MobileNet	Due to smaller dataset, accuracy was not optimized	Image augmentation is required
[17]	3200 brain tumour images	DCNN, SVM	Varying types of images is required	Augmentation can be proposed
[18]	2500 MRI Images	CLM + CNN	Results were not optimized due to imbalance in the dataset	SMOTE could have been used to balance the dataset so that better results could have been obtained
[19]	2200 Images	Hybrid ensemble classifier	Number of evaluation parameters was less. Train and test ratios were not split in a decisive manner	A pre-trained model could have been used and planned ratios of train test and validation could have been proposed
[20]	3200 brain tumour images	ResNet50, MobileNet	A huge lack of performance metrics was observed due to smaller and imbalanced dataset	Proposal of SMOTE and other LDA techniques could have resolved the issue

[21]	BRATS 2015	Residual Network	Data processing was done in a slow manner with not much efficient algorithms which eventually resulted into over-fitting of the dataset	Over-fitting could have been avoided by using LDA and parameter tuning techniques
[22]	BRATS 2019	DCNN, VGG19, ENB2	Individual tumours per slice were trained and tested which increased the overall training and testing time of the model	Time complexity could have been reduced by ensuring planned ratio split of the dataset

Methods adopted for Image Segmentation

The methods used for segmenting brain tumour can be classified into three broad categories: manual, semi-automatic and fully automatic [23]. However the methods to be used in a specific project are determined by the level of interaction the project demands. Depending on that a specific category of brain tumour segmentation method can be selected.

3.1 Manual Method: this method is generally adopted by radiologists to extract tumour information from MRI images and further perform multi-modality segmentation on them through anatomical and physiological knowledge. However, the process to do the same involves the radiologist to clinically examine the tumour on MRI image, slice by slice and then diagnose the tumour and segregate the edema region. This method not only appears to be a time consuming task; but rather also involves dependency on the radiologist to examine the same.

3.2 Semi-Automatic Method: this method is generally adopted to initialize, intervene and generate feedback from the evaluation process thus done [24]. The process of initialization is done after segregating the tumour region from the healthy regions of the brain. It is in this stage, that various pre-processing methods are applied to the tumour dataset. Additionally, processing algorithms such as LDA and PDA are also used in this stage so that the project can be steered towards a desired result. The generated results are then evaluated and altered if not satisfactory. Once this process of initialization is done, a cellular automata (CA) is implemented on the segmented images so that a probabilistic vector mapping can be done. This approach of adapting to vector maps and later generating tumour images is called as MRI Modality through FLAIR. Results from initialization and CA are then combined to determine a final volume of the tumour [25]. In this stage, various DL and ML based classifiers are used so that data can be trained and tested on MRI images. The results however generated contain within them a series of noise and redundant data and must be removed so that tissue types from the brain image can be enhanced. For this purpose, special voxels from the dataset are selected and spatial coordinates are formed. The voxels thus created are in alignment to the corresponding type of the tissue. SVM’s and CNN’s are majorly used in this stage.

3.3 Fully Automatic Method: this type of brain segmentation method does not require any user interaction to be present in order to detect the tumour. However, there are certain challenges associated with the method. The primary challenge is to determine the gliomas in the MRI image. This segmentation of gliomas is a difficult task since the size and location of the gliomas tumour would vary from patient to patient. Also, with no boundaries and irregular regions in the MRI image, it becomes difficult to scan the edged in the MRI image. Additionally, introducing the manual efforts from radiologists would stretch the time and dramatically expose the health condition of the patient, if not treated on time. Hence, in such a scenario a fully automatic segmentation method is used which is performed by slicing different sections of the image and adjusting the intensities of every slice so that several modalities of the sliced image can be obtained and worked individually. The fully automatic segmentation method is further classified into descriptive and generative methods [26].

Descriptive: the descriptive method is a classification technique that tries to establish a relationship between the data input and its associated instances. A series of feature extraction and pre-processing stages are applied

Generative: the generative method on the other hand, works on probabilistic models who tends to differentiate between healthy tissues an unhealthy tissues by locating their spatial coordinates and determining the region of disease

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METHODOLOGY

This section of the paper briefs on the expected methodology which is to be implemented. It also summarizes on a workflow diagram and takes into account the usage of DL models.

Proposed Architecture

The primary aim of the expected research is to classify the occurrence of various types of brain tumours by using a GUI platform. The dataset consisting of MRI images is initially obtained from the Kaggle repository. In the next step, a series of data pre-processing is applied such as labeling the data, resizing the shape of the image etc. Once the dataset is pre-processed, a validation system is applied on the dataset wherein the data is divided and split into a planned ratio for training, testing and validation stages. The next step involves application of DL and transfer learning based algorithms such as CNN, EfficientNetB2 and VGG16. On application of algorithms, the programming model is able to classify the input given as one of the four types of brain tumour. In the end, results are calculated on the basis of accuracy and recall factors and finally, performance analysis of the same is determined. The entire classification application takes place on GUI platform using Flask; wherein the user can enter the image and the model shall classify it as either of one of the four types of brain tumour. Figure below explains the workflow of the research.

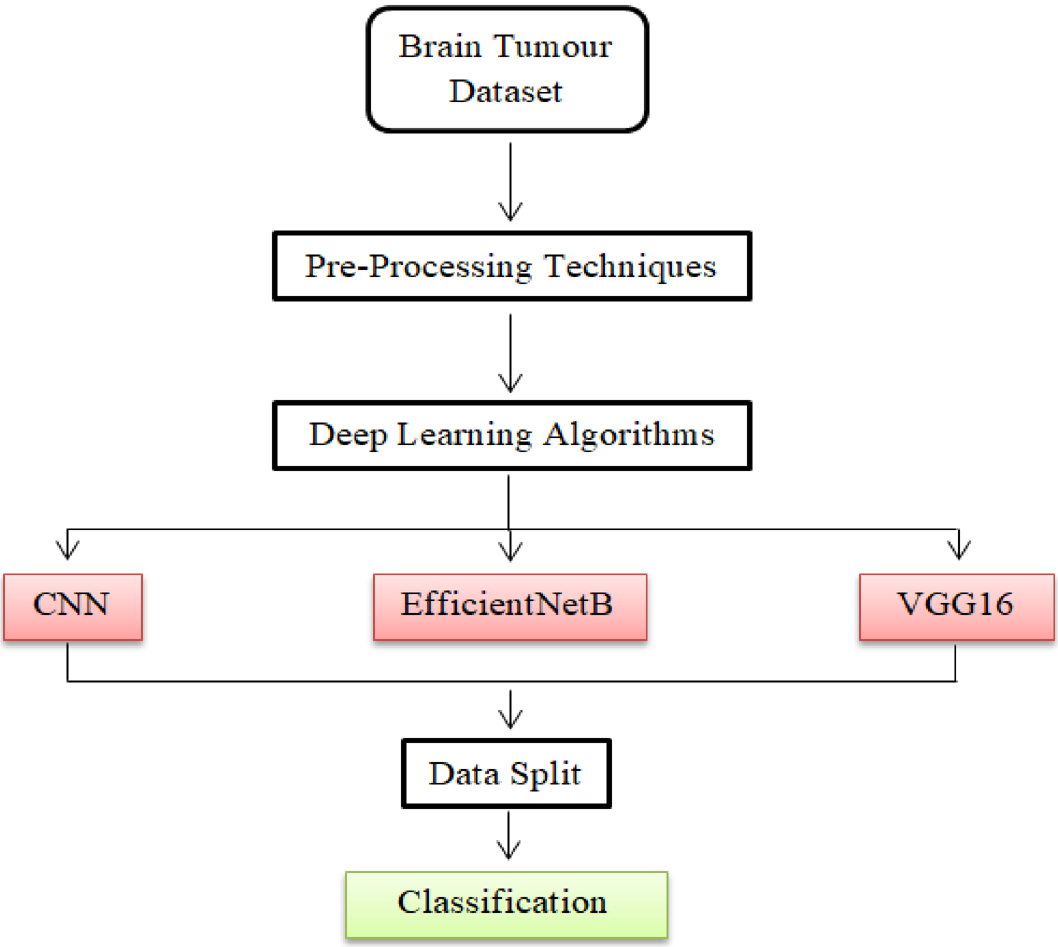

Figure 2: Proposed Workflow

Environmental Set up

The expected methodology is proposed to be performed on Flask wherein the user can upload an MRI image and the model can further classify it as either healthy image of the brain or presence of tumour in the brain. The platform makes use of 32GB RAM and the system is expected to train deep learning algorithms and generate optimized and efficient results.

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Dataset Used

The dataset required to implement the research is obtained from Kaggle repository [27]. MRI images are present in the dataset. A total of 920 Meningioma (a), 240 no tumour (b), 500 pituitary tumor (c) and 800 glioma (d) tumor MRI images are expected to be used in the training and testing phase of the model. Figure below displays the overview of the dataset.

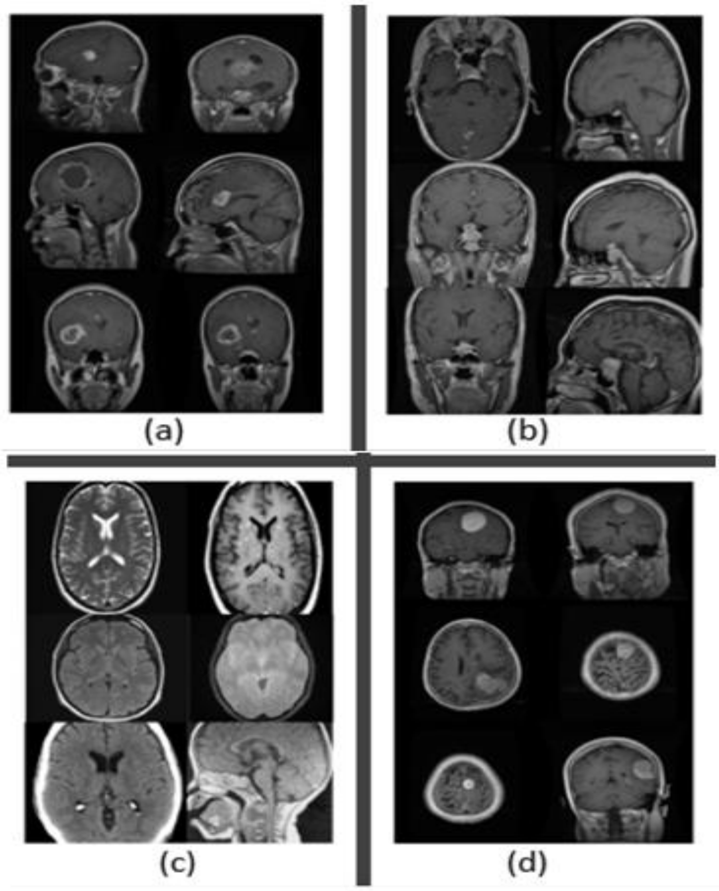

Figure 3: MRI Dataset

Data Pre-Processing

Pre-processing of data is one of the most essential and critical stages of any detection model. Once the dataset from the repository is obtained, it undergoes a few stages of pre-processing such as resizing the image, labeling the image, balancing the data etc. This is done so that high quality of database can be used and the MRI Images can be normalized so that efficient result generation can take place. Additionally, in order to smooth the MRI images obtained from the repository, the blurred mages from the background are removed so that a sense of image sharpness can be obtained in the original image. Various techniques such as Gaussian and Laplace filters are used to adopt the same.

Data Division

In scenarios where only small amounts of dataset is used; attaining better results and optimization becomes a challenging task. Since the working of neural networks requires large size of dataset to induce enhanced results, techniques such as augmentation and data division are used. Augmentation is a process of generating more images of data form a single source of dataset which is obtained through rotational practices. When images are horizontally, vertically and diagonally flipped, rotated, zoomed or shifted; a series of images are produced. This process is called as augmentation. However, the method can be fruitful if less number of MRI images is obtained from the repository. On the other hand, the process o f division leads to a planned and strategized categorization of dataset into ratios of training, testing and validation. Both the techniques can however be used to enhance the learning capacity of the model.

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Deep Learning Models

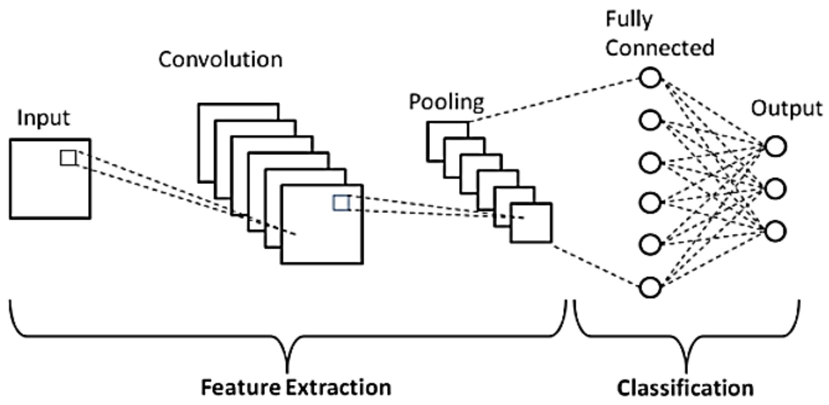

Figure 4: CNN Architecture

CNN: The research study begins by using an input image from the dataset with a pixel size of 32 x 32. This image is sent to a convolutional layer with 16 filters. The image is then expected to feature map the MRI images with a resolution of 32 x 32 x 16. A kernel size of 3 x 3 vector is used and the output is then forwarded to the next layer of the CNN which appears to be the max pooling layer. The pixels from the MRI Image are feature mapped and filter values of 32 is applied to the same. The repetition of these layers takes place in repetition wherein the convolutional layer and the pooling layer are feature mapped continuously so that a newly created 3 dimensional array vector could be created. The final layer is responsible to generate the output by making use of the activation function such as Softmax. Once the last layer generates the output, a dropout function of 0.5 is triggered and the CNN's architecture is configured. The figure below depicts the architecture of CNN:

VGG16: this algorithm appears to belong to transfer learning based model proposed by authors in [28]. A pre-trained model and heavy structure of the network is used to diagnose brain tumour, hence the usage of VGG 16 is justified by the author. It is capable to detect and classify heavily loaded datasets and can categorize the images with better and greater accuracy. One of the primary reasons of using VGG16, is that it performs better while dealing with larger datasets and attains optimization with complex data. A total of 5 layers are observed in the algorithm wherein the image of pixel resolution of 32 x 32 is used. ReLu is adapted to be as the activation function in this model and is further used to activate the hidden layers. Figure below depicts the architecture of VGG16.

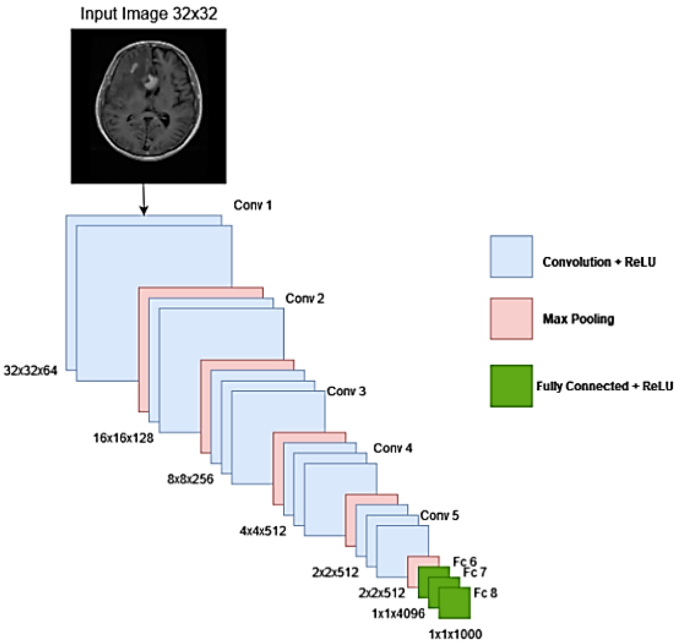

Figure 5: VGG16 Architecture

CONCLUSIONS

Detecting the presence of tumour in the brain at the right stage plays a vital role in preventing the rates of mortality. With varying sizes, location and structure of the tumour, the process of detection becomes a challenging task and is therefore influenced by multiple factors. In the early stages, the process of detection is done manually by doctors and technicians. However in complex scenarios, identification and segmentation of the tumour is a tedious task. Therefore analyzing, recognizing and categorizing become mandatory. To address issues of the same, algorithms and techniques of deep learning and transfer learning are used. A CNN based classification model for brain tumour detection is therefore proposed wherein the results are obtained by using MRI images obtained from Kaggle repository. The expected limitation of the research is the restriction of hidden layers and GPU capacity. Future work can be performed to better correctly identify brain cancers by using individual patient information gathered from any source.

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