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Effective High-grade gliomas segmentation based on H-Dense U-Net with CNN architecture.

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Abstract

In the medical field, brain tumor identification and segmentation is still a challenging task. Due to its complex structure, the region segmentation of the tumor from medical images is a strenuous process. Existing techniques are failed to predict the tumor cell from the brain in an accurate manner. To overcome this hindrance, we develop an H-Dense U-Net CNN architecture model fused with a pattern based learning strategy that ensures a better performance criterion. In every field of research, CNN plays a vital role and improvised system performance. The hybrid densely connected U-Net contains a 2D Dense U-Net which extracts the intra-slice features and 3D counterpart accumulating volumetric context. The intra-slice representation and inter-slice features are merged through a hybrid feature fusion layer (HFF). H-Dense U-Net also called an end to end system. We utilize the HGG Tumour imaging data from BRATS 2018 dataset where four different modalities are available (T1, T1c, T2, and FLAIR). Among the different modalities, we preferred FLAIR images. It is subject to preprocessing and then the segmentation process. After segmentation, the tumor region gets masked. Thus the tumor is detected and the system measures the area occupied by the tumor through region props. The key contribution of the paper is to segment the tumor accurately from the healthy tissue and provide better visualization for the physicians. The accuracy of our approach is about 98.74%. Hence our proposed system provides high accuracy and efficient value in segmenting the brain tumors. It also promotes the segmentation performance to the next level in the medical field.

Keywords: H-Dense U-Net, HFF, HGG Tumor, Mask, BRATS Dataset.

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Introduction

Convolution neural network (ConvNet/CNN) is a deep learning algorithm which has a major demand from last year due to its astonishing performance in different field of computer vision application [1]. It is also highly preferable in the medial analysis where CNN has to detect and segment the lesions from brain tissues. Based on the latest statistical report of the world cancer research Fund, it analysis that approximately 12.7 million people are affected by cancer where 7.6 million people are dying every year [2]. Different types and subtype of cancers are estimated in recent years. Brain cancer is one of the deadliest diseases among cancers. Based on different factors, the brain tumors are classified into 120 varieties [3]. So it is crucial to equip the physician to study the brain tumor in MR images. In the traditional method, the first step is to determine whether the MRI image contains any tumor. If the tumor is detected, then the physician has to outline the tumor countors. This outlining aid the physician for future proposes. However, tracking should be precise and accurate. Based on the size and shape of the tumor countor the cancer types also alter. A successful tumor diagnosis depends upon the accurate evaluation of the size and location of the brain tumor. The manual segmentation is a tedious process for the physician where they tried to improvise the accuracy by using some techniques such as image processing, machine learning, and computer vision. Still, they faced some challenges in separating the healthy tissues from tumor tissues due to tissue structure (gray matter, white matter, and cerebrospinal fluid). Analyzing the multi-spectral MRI images is a complicated process due to time-consuming and misalignment with the pairs of images. The aforementioned problem is solved by using a single MRI image which reduces the computational expenses and time consuming for segmentation. Medical imaging is an essential process for the diagnosis and prognosis of the disease. Several techniques are there to diagnosis the medical images such as Magnetic Resonance imaging

(MRI), Computed Tomography (CT), Positron Emission Tomography (PET). CT examines the body by passing the radioactive ray to the body. PET uses radioactive drugs to scanning the body. This radiation may affect or damage the cells in the human body. In order to prevent the damages, the MRI is suitable for diagnosing brain disease. MRI is a Magnetic Resonance Imaging is used to examine the inner part of the body through a strong magnetic field. It provides a 3D multi-modality scan of the brain. Radiologist and the doctor take a lot of time for identification and segmentation of the tumor cell from the brain tissues. The MRI is a non-invasive and it can predict the tissues at high resolution with good contrast. By applying different image acquisition protocols, we can take multiple images of the same tissues at different contrast levels. These different images enhance the accuracy level. The main aim of analyzing the brain tumor images is to extract the important features from it. This information's are embedded with the image data which can be used for further references. In manual detection, the doctor undergoes several stages to determine the lesions in MRI images. They inspect and investigate the MRI image multi-times before finalizing the result. It took a lot of involvement in the MRI image diagnosis process. There no assurance that the diagnosis is correct, there may be an occurrence of human error. To overcome these errors, an automatic segmentation system is needed in practice. But it is challenging to design an automatic segmenting system for brain tumor analysis. Due to the boundary detection and separation of healthy tissues from the lesions. After several decades, researchers found a solution for this segmentation problem through image processing. Brain tumors are categories into two types they are Primary and secondary brain tumor. Normally primary tumor wouldn't proliferate to another part of the body whereas the secondary tumor will be proliferating one. A malignant tumor is the most dangerous and life-threatening tumor and cancerous one which can easily penetrate and affect the parts of the body. Normally the human brain is affected by Glioma. Glioma is a tumor that occurs on the gluey supportive cells, which get energy from the surrounding nerve cells. It is a primary brain tumor that affects the function of the brain, the size and the location of the tumor decides the life-threatening of the human. It is classified as low grade (slow growing) and high grade (fast growing). The current treatments for glioma patients are surgery, chemotherapy, radiotherapy and sometimes they combine two different techniques for operation. So it is important to segment the glioma and its internal-tumor structure which gives more important information to the doctors. It will help in the analysis and evaluation of the tumors.

The most common image acquisition images are, T1-Weighted MRI which is image contrast where the tissues get relaxed (longitudinal) at a time of short T1 and brighter(hyper-intense). T2-Weighted MRI is an image contrast where the transverse relaxation of tissues takes place at the time of long T2. T1-c Weighted MRI where tumors show a signal enhancement after administration of the contrast agent. Segmentation is the process of partition the image into a region or parts, where each region is spatially contiguous and the pixels are homogenous respect to some criterion. The segmentation is a tedious process due to the anatomical structure of the brain. It is non-rigid and complex in shape and different for each patient. The shape and position of the tumors vary for each patient. The tumor cell may overlap on the healthy tissues, so there is a possibility of considering the healthy tissue as an unhealthy one. It is necessary to segment the brain tissues in a careful manner, the tissues have to be analyzed in a slice by slice manner. Sometimes, due to the presence of a large tumor, it may affect the structural property of neighboring tissues and demolish their and shape and structural. So it is most essential to find the tumor in an accurate manner. MATLAB or PYTHON tool is used to segment the image and detect the tumors in the image. In this analysis, pre-processing is the first step where the edges are marked properly which can separate the background and foreground of the image. After the pre-processing step, the image is segmented. There are several methods are available for the segmentation process such as K-means, Otsu's, CNN, H-Dense U-Net, etc.

The rest of the paper is organized as follow, section 2 explained the related work of the paper, section 3 describe the proposed work and its methodology, section 4 present the result and discussion of the method and conclusion in the final section.

Related Work

lhana et al. [2] expose a new threshold approach where the skull, brain images are obtained clearly. Warfield et al. [4,5] claimed a method in which elastic registration combined with statistical classification. Elastic registration assists to mask the brain from the surrounding region. Distance from binary boundary concept is used to separate the cluster in a multidimensional space. Olabarriage et al. [6], investigate a segmentation method where the semi-automatic process takes place in which both the computational and human expertise involve for this methodology. The segmentation process consists of a computational part, interactive part and user interface. Through this segmentation, the result is an effective one. In an unsupervised segmentation [7-9], based on the intensity level, the brain tumor area gets segmented. The K-means and fuzzy clustering are popular in this unsupervised segmentation. In this segmentation, the image is segmented into a tumor and edema. Initially, skull stripping will take place where the skull region removed and concentrate on the brain tissues. In a supervised algorithm, we can measure the series of the sample input with the expected response. Papageorgiou et al. [10], proposed a fully automatic segmentation method where there is no human intervention involved. Due to the lack of transparency and interpretability, it not gained any popularity among the clinical lab. Taheri et al. [11], proposed a level set approach for 3D segmentation of tumor which provides a good performance compared to region competition method. Muthukrishnan et al. [12], proposed a technique where the images get detached from the backgrounds to extract the features from the image. The key contribution of the techniques is to detect the edges properly. It provides an effective segmentation. Laxmi et al. [13], proposed a method to segment the tumor cells by the use of ROI (Region of Interest). Image scaling and geometric transformation are used to evaluate the feature points in the image. Gordillo et al. [14], proposed an approach that segments the images in a manual way. Manual segmentation requires a software tool that draws the region of interest of the brain tissues. But it is a tedious process, followed by an MRI scanner that provides multiple 2-D slices where the human expert has to mark the tumor properly. If the marking not in a proper manner then it produces jaggy images. Saritha et al. [15], proposed a method where wavelet entropy based spider web plot. There is integration between the wavelet entropy and probabilistic neural network. The wavelet entropy is used to extract the features from the image and spider web plot calculated the area and plot the values. Gopal et al. [16], investigate a method where the wavelet transformation is used to assemble the abnormal brain matter into a benign and malignant tumor. This system consists of four stages they are segmentation of ROI, discrete wavelet disintegration, feature abstraction, feature selection, organization, and evaluation. The SVM is used to segment the brain tumor. WST and WCT are used for feature extraction. The generic algorithm is used to select the optimal texture features in the brain image. PNN is used to detect the benign and malignant tumors in the brain tissues. Maru et al. [17], proposed a segmentation method through a watershed algorithm where the neighborhood pixels joint together which is considered as a disjoint region. It will analyze similar pixels from the image and connects it together. The principle of the algorithm is to locate the seeds and also called germs. It traces the grey level or intensity level and it continues its process until its criterion. Ali et al. [18], investigate the brain tumor area by enhancing the threshold algorithm. Vijayarangan et al. [19], proposed a method for brain segmentation through histogram thresholding. Hariharan et al. [20], proposed a method that extracts the multi-level information from the plain CNN model. In most of the computer vision task, this hyper column method is utilized but it is optimal in quality level. Cicek and Ronneberger et al. [21,22], proposed an H-Dense U-Net based architecture for image segmentation. Here the encoding done in downsampling whereas decoding is an upsampling one or deconvolution. The feature map is extracted in encoding and sends that information to the decoding part, concatenating all the information and finally predication take place. Nabizadeh et al. [23], proposed a method to segment the brain tumor from healthy tissues through a single contrast mechanism. Due to the density similarity, it is hard to remove the lesion from the healthy tissues. Sujan et al. [24] proposed a method to detect the brighter part of the tumor through the otusu method. Devakota et al. [25] proposed a method for early prediction of brain tumors where morphological reconstruction is used. Nabizadeh et al. [26] investigate the segmentation process using texture-based and contour-based algorithm.

In our proposed system, we adopt H-Dense U-Net architecture for image segmentation. The experiment is conducted on the recent brain tumor dataset i.e. BRATS 2018. From the experimental results, it demonstrates that the accuracy of the segmentation is better than the existing methods.

Proposed Work

Methodology

Our research focused on developing a segmentation technique that partitions the tumor region effectively and precisely. It should be time and cost effective. In Pre-Processing, images should be cropped into 240 × 240 in size, to prevent the complex computing which is illustrated in Figure 1. After the resize of an image, it proceeds for segmentation where features extracted from patches of the image. The process is repeated to extract numerous features from it in the form of iteration (Epoche). The Epoche is higher, then the output value also high. The iteration process extracts valuable information from the brain image. After the feature extraction, the data get stored in the .haf5 file. HGG tumor images are utilized for the segmentation process. The HGG (High-Grade Gliomas) tumor contains 4 types of cancer images. We select the FLAIR images for analyzing the tumors. At the end of the segmentation process, a mask is created around the tumor which segregates the healthy tissue from the unhealthy one. Thus it became quick identification for the physicians to detect the tumor cell in the brain. The segmented image can be a crop for isolating the tumor cell if required.

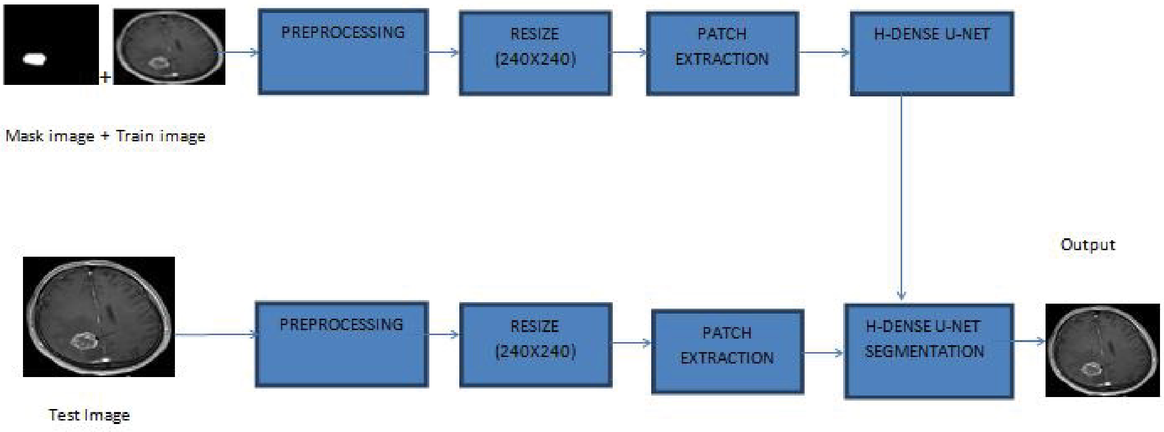


Figure 1. *Block Diagram of image segmentation using H-Dense U-Net architecture.*

The optimized result is gained through segmentation. The affected region is measured by calculating the area of the tumor cell occupied in the brain. To evaluate the affected area, the region prop is used. The python is used for implementing the segmentation process through H-Dense U-Net architecture.

Patch extraction

The 240X240 size image is subjected to patch extraction. The patch is determined as a container where numerous pixels get stored. Assume we have an image of size 100X100px, it has to be patched as a 10X10 ratio then the output contains 100 patches for a single image. The patches are then aligned in a random manner. Wang et al. [27] state that the patch extraction strategy improvises the accuracy of the segmentation.

Deep learning methods

Convolution Neural network is a feed-forward artificial neural network. It comprises of different receptive fields. The Conv-net has numerous advantages in the segmentation process. It can share the parameters among the network. Suppose the system needs filter then the layer and filter count get increased spontaneously. At the same time, the parameter count can be reduced by sharing it among the network. The layers are interconnected together which create the sparsity of connections that form the network to function together. Each layer input depends upon the previous neuron layer output. Images normally possess the pixel value and it is represented as a matrix. While checking the similarity between any two pixels of different images, it determines the feature matching. In this way, the system compares any two images for analyzing the similarity index. Using ConvNet, we can examine the matching features in the whole image. The matching feature is evaluated by split the images into patches where the patch value get a sum up and divided by a total number of pixels in the image. In spite of this partition and arithmetic estimation, it became easy for the system to map a similar feature between any two images. If any two-pixel values are similar then it assigns as one else it will be zero. Thus the image resemblance is identified.

Convolution operations are representing in arithmetic form in equation (1).

$$n_{out} = [\frac{n_{in} + 2p + k}{s}] + 1 \rightarrow (1)$$

n_{in}: Number of output features

n_{out}: Number of output features

k: Convolution kernel size

p: Convolution padding size

s: Convolution stride size

Convolution neural network is similar to the ordinary neural network where neurons are positioned which gets connected with all other neurons in the system. The information gets shared among these neurons. In a group of connection, all neuron share the information from the previous layer and there is no concentration between its own layers. At last, the information gets transfer to the output layer or fully connected layer. The convolution architecture consists of three-layer such as the Convolution layer, the pooling layer, and the fully connected layer which depicted in Figure 2. In the Convolution layer, patches are segmented among the matrix and the pooling layer will shrink the matrix where it stores only the useful information in it. Consider we have a matrix of 4*4.

Here we take 2*2 pooling and strides is 2 which is depicted in Figure 3. The maximum pooling is determined by selecting the maximum value from the matrix. There is a hyperparameter for the pooling layers, such as filter size, strides, and max or average pooling. After pooling, the matrix gets shrink to quarter size of the original image. From each window, it selected the maximum value in it. This maximum value indicates the best features in the window. At the end of the pooling, the total number of images will be the same but each image has less the number of pixels in it. This reduces the workload for the computer and reduces complexity in the calculation. Consider N is an input image Nh, Nw, Nc, in equation (2).

N_h: Height of the image

N_w: Width of the image

N_c: Channel of the image

F: Filter size

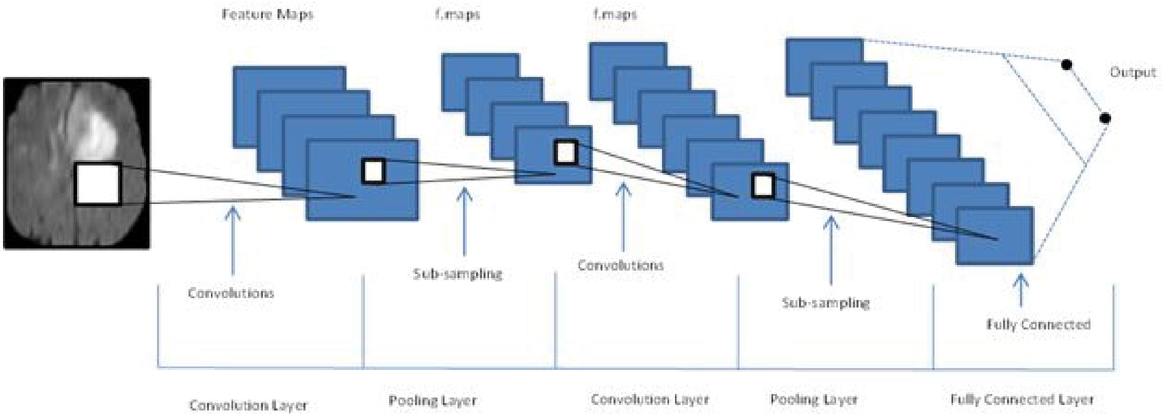


Figure 2. *Convolution Neural network.*

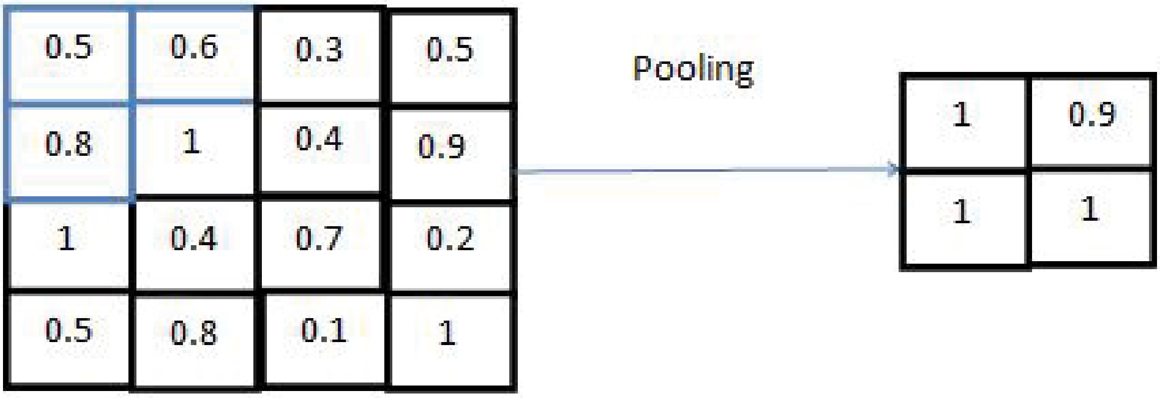


Figure 3. *Pooling process.*

p: Padding

s: Strides

$n_{[c]}$=No. of filter

$$Output = [\{\frac{Nh-f}{s+1}*\{\frac{Nw-f}{s+1}\}*\mathrm{Nc}] \rightarrow (2)$$

The Rectified Linear units (ReLU) are an important process in CNN where the negative numbers are converted into zeros which is illustrated in Figure 4.

In CNN, a raw image gets filtered, rectified, pooled and stacked as a filtered convoluted image and the process is done again and again.

General representation of the convolution layer whose matrix is N*N, Pre-nonlinearity input represent in equation (3).

x_{ij}^{l} =Pre-nonlinearity input

W: Filter.

$$x_{ij}^{l} = \sum_{a=0}^{m-1}\sum_{b=0}^{m-1} w_{ab} y_{(\mathrm{i+a})(\mathrm{j+b})}^{l-1} \rightarrow (3)$$

The total data get stored in a fully connected Layer. The feature mapping data get converted to a vector which is used for further classification. This conversion has some problems in retrieving the original data. To solve this problem H-Dense U-Net based CNN is proposed. It used the feature mapping concept for both the conversion and recovery process. This process takes place through contraction and expanding path. It prevents enormous loss and preserves the structural integrity of the image.

H-Dense U-Net

Inconsistent with FCN, SegNET, H-Dense U-Net act as a network of convolution layer for performing the semantic segmentation. H-Dense U-Net is considered as a standard CNN method. The image is segmented into different classes. It is a deep and efficient network compared to other existing systems. Based on the 2D convolution concept, it extracts the intra slice features. The main benefits of using a 2D layer we can fuse the densely connected path with U-Net which is illustrated in Figures 5 and 6. The densely connected path gained from a densely connected network (Dense net) which alleviates the arduous for training the deep network. In H-dense U-Net, we connect the U-Net between the encoder and decoder. It equipped the system to extract the low level of spatial features from the network. In order to explore the volumetric feature, our proposed approach extract inter-slice, and intra-slice features. These features are joined together by the Hybrid feature fusion layer. The 2D dense layer gets integrated with the 3D dense layer by auto context mechanism. The 2D dense U-Net optimization burden is alleviated from 3D dense U-Net. Moreover, the hybrid feature extraction provides better tumor recognition. Li [28-35] states that the hybrid dense U-Net occupied the 1st position in lesion segmentation. The dense network consists of a building block where each block connected with the subsequent layer which is depicted in Figure 6. One of the benefits of utilizing a dense network is the network provides an optimized output. This causes the creation of a k feature map and it is also called growth rate. Normally deep learning networks utilize several max-pooling which may lead to information loss of high-resolution features. The micro blocks in the 2D DenseUNet preserve the maximum information whereas U-Net is a long-range connection link that preserves the low-level information through the encoding and decoding part. The 2D dense layer consists of 167 convolution layer, pooling layer, dense block, transition layer, and upsampling layer.

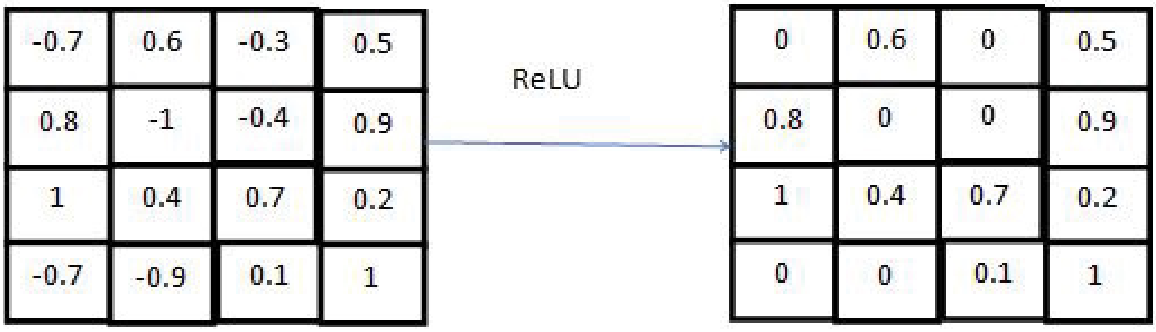
To compress the feature maps in the transition layer, the compression factor is used. It prevents the expansion of feature maps. The upsampling layer is executed by bilinear interpolation which summation with the low-level data obtain from the U-Net architecture and 3X3 Convolution layer. Before each layer, there will be a batch normalization and Rectified Linear unit (ReLU) [36-39].

Training

The segmented feature map from the input images is used to train the network with unpredictable gradient. The output image is smaller than the input image due to the unpadding convolution [40-44]. The final map value is combined with cross-entropy loss function which determines by an Energy function in equation (4).

$$E = \sum_{x=\sigma}[w(\mathrm{x})\log(\mathrm{p}_{l(\mathrm{x})}(\mathrm{x}) \rightarrow (4)$$

The weight map is computed through the equation w(x), in equation (5)



-0.7	0.6	-0.3	0.5
0.8	-1	-0.4	0.9
1	0.4	0.7	0.2
-0.7	-0.9	0.1	1

0	0.6	0	0.5
0.8	0	0	0.9
1	0.4	0.7	0.2
0	0	0.1	1

Figure 4. *ReLU process.*

Figure 5. *Representation of H-Dense U-NET Model.*

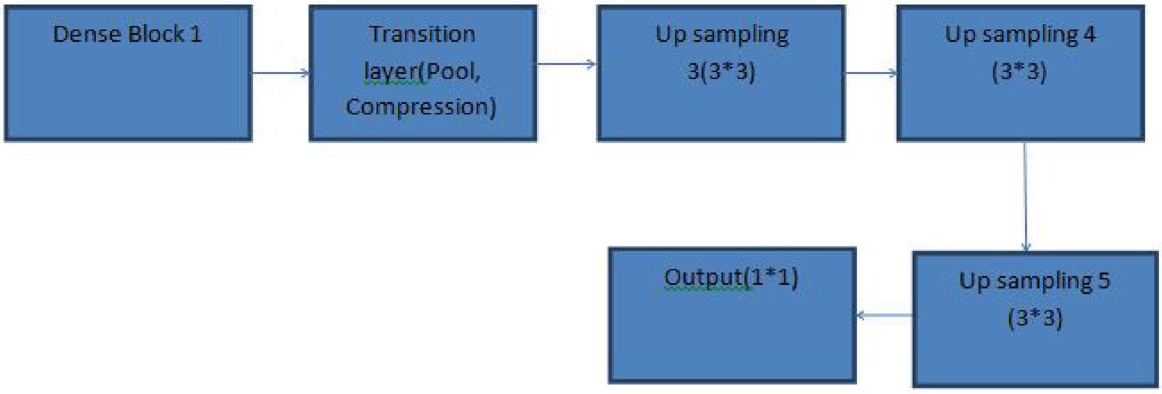


Figure 6. *Illustration of 2D dense U-Net.*

$$w(x)=w_c(x)+w_b.\exp\frac{(-d_1(x)+d_2(x))^2}{2\sigma^2}\rightarrow(5)$$

Wc: Weight map

d1: The distance between the border and nearest cell

d2: The distance between the border and second nearest cell.

Results and Discussion

We proposed a H-Dense U-Net based Convolution neural network for solving the segmentation problem. The test image is an MRI image where the skull part is removed from the brain, in order to avoid unnecessary information. Google Colab is the developing environment for brain segmentation. To segment the brain tumors from the healthy tissues, we need some configuration for the hardware device. For Hardware, it needs CPU in the range of 1*single core hyper thread Xeon Processors @2.3Ghz i.e.(1 core, 2 threads), GPU range is 1*Tesla K80, computer 3.7 which having CUDA cores, 12GB GDDR5 VRAM, RAM in the range of 12.6 GB, Disk range should be approximately 358 GB.

Dataset

The BRATS 2018 is collected from different medical institutions, notably UPenn's Center for Biomedical Image Computing Analysis (CBICA). The dataset comprises of 285 individual's brain tumor details. Each detail contains the age and survival information about the patients. These datasets are analyzed through expert neurologist, they labeled the tumor voxels which is gathered together and formed the BRATS 2018 dataset. We exploit BRATS 2018 dataset for the segmentation process, where validation (66 cases) and test set (191 cases). In those MRI scans, individual report each has four 3D MRI modalities (T1, T1c, T2, and FLAIR (Fluid Attenuated Inversion Recovery)). This dataset is divided into two categories (210 HGG and 75 LGG). The images are constructed to an isotropic resolution where it aligned and resampled into 1 × 1 × 1 mm. These datasets are collected from 19 institutes where physicians using different MRI scanner for scanning the brain. The input images are represented as a volume with X*Y* Z dimension of 240 × 240 × 155. The voxel images are categories into a tumor and non-tumor region. The Non-tumor region is labeled as 0 and tumor image is labeled as 1, 2 and 4 based on the severity of the tumors in that specific region.

Here the test images consist of tumor cells which have to segment from the healthy tissues which are depicted in Figure 7(a), where extracted cancer cell in Figure 6.

In Figure 8, shows the result of all input images and their predicted images. From the figure, it is clearly understood that the precise of the result. Compare to the existing system, the H-Dense U-Net based segmentation achieve good results and provided better performance.

In Figure 9, shows that from left to right is input image and predicted tumor cells. The tumor cell is highlighted by color.

After the Segmentation and detection of the tumor cell, the area of the tumor cell is calculated through region props. Based on the area value, the stage of cancer is determined may be flair, T1, T2 or T1c which is analyzed in Figure 10. From Figure 10, the area occupied by the tumor is about 3511pixels in the brain image. At last, the output is determined using H-Dense U-Net architecture.

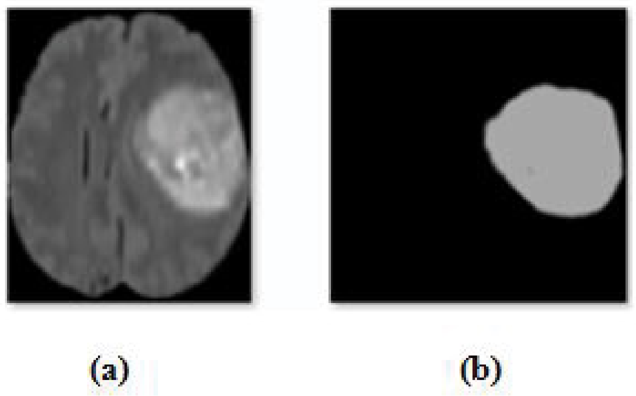


Figure 7. *a)Test Image b) Predicted Tumor cells.*

From Figure 11, calculated the accuracy of the system where the graph is plotted between accuracy and epoch.

Performance criteria

To compute the performance, the system accuracy, model loss, mean square error, and mean square absolute has to be evaluated through equations, the evaluated values are depicted in Table 1.

To evaluate the tumor in the brain tissues, the system sensitivity and specification has to be calculated through the equations (6) (7).

TP: True positive which detects the existing tumor correctly.

TN: True Negative which not detect the non-existing tumor.

FP: False Positive which detects the healthy part of the brain.

FN: False Negative which doesn't detect the tumor.

Sensitivity is defined as the determination of tumor in brain tissue. it is given by,

$$Sensitivity\ (\%) = \frac{TP}{TP+FN} * 100 \rightarrow (6)$$

Specificity is defined as the determination of non-tumor region in the brain, it given by,

$$Sensitivity\ (\%) = \frac{TN}{TP+FN} * 100 \rightarrow (7)$$

Accuracy is a term which defines the precision and trueness of any predicted value. Here the accuracy value is compared

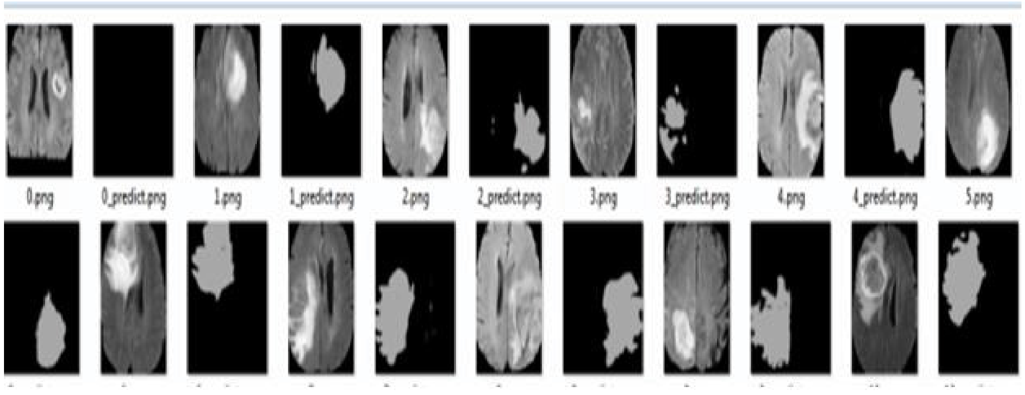


Figure 8. *Test images and its predicted results.*

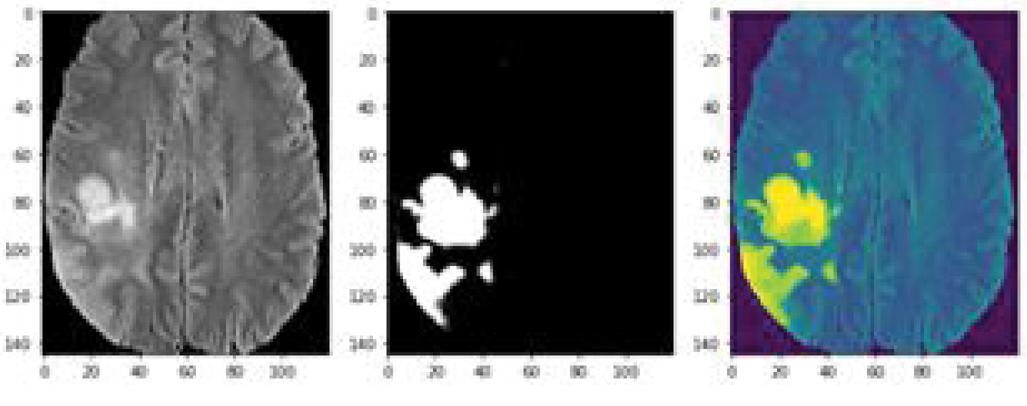


Figure 9. *Tumor cell detection and highlight.*

with the cent percentage. If the accuracy is high then the precision and trueness are high for the value in equation (8)

$$Accuracy = \frac{Number\ of\ correction\ prediction}{Total\ number\ of\ \ prediction} \rightarrow (8)$$

The accuracy calculated based on the binary value represent in equation (9)

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \rightarrow (9)$$

TP: True positive,

TN: True negative, FP-false positive,

FN: False negative

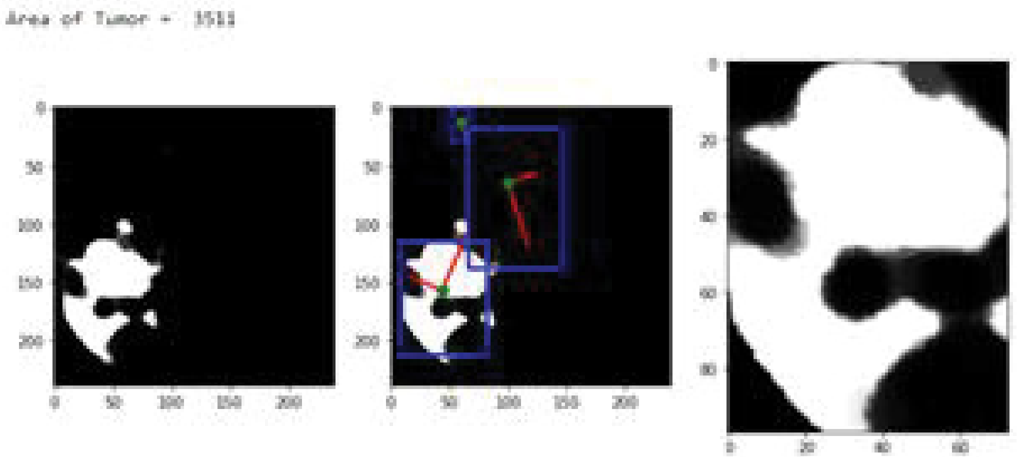


Figure 10. *Determining the tumor occupied area.*

Table 1. *Evaluated value.*

Evaluation measure	**Values**
Accuracy	0.987480539
Model Loss	0.068254539
Mean square Error	0.020643662
Mean square Absolute	0.049906712

Table 2. *Performance comparison of dataset.*

Article	**Dataset**	**Modality**	**Evaluation measure**	**Result**
Maleki et al. [29]	Clinical trial	FLAIR	Sensitivity Specificity Accuracy	0.961 0.975 0.929
Zikic et al. [30]	BRATS 2013	-	DSC	Complete 83.7%, Core 73.6%, Enhanced
Urban et al. [31]	BRATS 2013	T1, T1c, T2 and FLAIR	DSC	Complete 87.0%, Core 77.0%, Active 73.0%
Lyksborg et al. [32]	BRATS 2014	T1, T2, PD, and FLAIR	DSC	Complete 79.9%, Core 63.1%, Enhancing
Kleesiek et al. [33]	OASIS	T1	Specificity	99.36 ± 0.003
Brosch et al. [34]	MICCAI 2008	T1, T2, PD and FLAIR	VD TPR FPR	UNC 63.5%, CHB 52.0% UNC 47.1%, CHB 56.0% UNC 52.7%, CHB 49.8%
Havaei et al. [35]	BRATS 2013	T1, T1c,T2 and FLAIR	DSC Sensitivity Specificity	Complete 84.0%, Core 71.0%, Enhancing 0.57 Complete 0.88, Core 0.79, Enhancing 0.54 Complete 0.84, Core 0.72, Enhancing 0.68
Nuechterlein et al. [36]	LONI-LPBA40	T1	Mean DSC	0.844
Kamnitsas et al. [37]	BRATS 2015	T1, T1c, T2 and FLAIR	DSC Precision Sensitivity	Complete 84.9%, Core 66.7%, Enhanced 0.634 Complete 85.3%, Core 86.1%, Enhanced 0.634 Complete 87.7%, Core 60.0%, Enhanced 0.674
Proposed Method	BRATS 2018	T1, T1c,T2 and FLAIR	Accuracy	0.987

The accuracy value of the brain tumor segmentation is 0.9874

Model loss is defined a calculating the losses occurred in the system. The model loss for brain tumor segmentation is 0.0682.

Mean squared error (MSE) is a square difference between the estimated value and what is estimated in the process. The value will be strictly positive (No zero) due to the randomness. MSE is computed by an equation (10) where n sample is taken,

$$MSE = \frac{1}{n}\sum_{i=1}^{n}(y_i - y'_i)^2 \to (10)$$

N: Number of n data point in all variables

Y: Vector of the observed value

The MSE value for brain tumor segmentation is 0.2046.

Mean Square Absolute error is the measure of the difference between the continuous variables. It is a measure of the distance between each point and identity line in equation (11),

$$MSAE = \sum_{i=1}^{n}\frac{|y_i - x_i|}{n} = \sum_{i=1}^{n}\frac{|e_i|}{n} \to (11)$$

The MSAE value for brain tumor segmentation is 0.0499.

The mean absolute percentage error is defined as the measure of the accurate forecast system. It is the difference between the true value and forecast value in equation (12),

$$M = \frac{100}{n}\sum_{i=1}^{n}1|\frac{A_t - F_t}{A_t}| \to (12)$$

A_t: Absolute value, F_t-Forecast cast.

The performance of the different dataset is compared with our BRATS 2018 which is representing in Table 2.

From Table 3, we can understand the accuracy level of the proposed system. It provides the highest accuracy range compare to other existing methods. It is illustrated in the form of a graph in Figure 12.

Table 3. *Results of different approaches.*

Method	**Accuracy (%)**
New Threshold Approach [2]	96
Dense U-Net [27]	95.3
Seeded Region Growing (Compared Segmentation methods) [29]	92.5
Region Growing and level set evolution(BRATS -2012) [38]	95
Statistical features over Gabor wavelet features [39]	91.7
CAT(BRATS -2013) [40]	95.74
Bat algorithm (BA) and Tsallis based thresholding (BRATS-2015) [41]	97.53
Texture-based and contour-based algorithm[42]	92.3
Image Segmentation for Early Stage Brain Tumor Detection using Mathematical Morphological Reconstruction [43]	92
Bounding 3D-box-based Genetic Algorithm [44]	89
Proposed	98.7

Figure 11. *Model accuracy.*

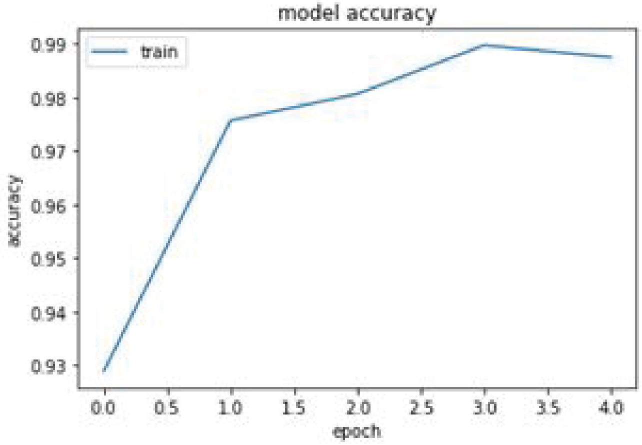
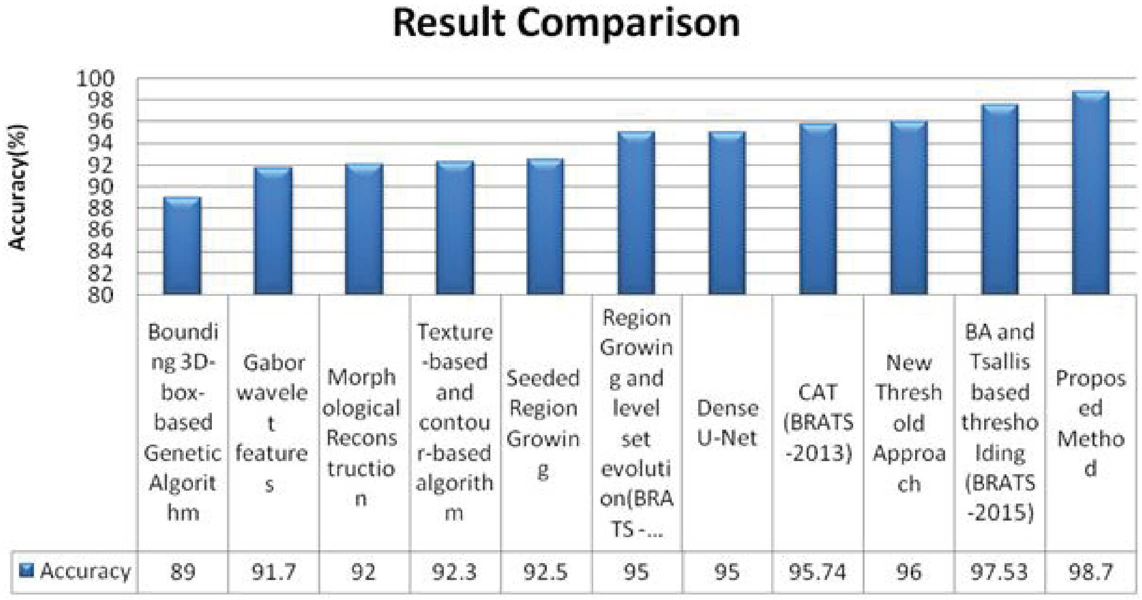


Figure 12. *Results comparison with existing methods.*



Conclusion

In summary, we proposed a novel approach for brain tumor segmentation in MRI images. The demonstration shows that our approach attains higher segmentation accuracy at a low computational cost. Glioma is one of the aggressive and life-threatening tumors. BRATS 2018 dataset (HGG) images are utilized for the segmentation process. The HGG tumor set consists of 210 folders where 4 types of cancer images are stored such as FLAIR, T1, T2, and T1C. The FLAIR images are trained through H-Dense U-Net organized in different classes. By the masking technique, the images get segmented under the labels. Based on the pixel value the test image gets compared with the training image. The accuracy level of our proposed system reaches 98.7% which is far better than the existing system. In the Future, we can enhance this segmentation and detection of a tumor cell to the next level. Thus our system became a promising solution for the segmentation and classification of the brain tumor.

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