

Brain Tumor Detection and Segmentation Using RCNN

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Received: 25 August 2021; Accepted: 05 November 2021

Abstract: Brain tumors are considered as most fatal cancers. To reduce the risk of death, early identification of the disease is required. One of the best available methods to evaluate brain tumors is Magnetic resonance Images (MRI). Brain tumor detection and segmentation are tough as brain tumors may vary in size, shape, and location. That makes manual detection of brain tumors by exploring MRI a tedious job for radiologists and doctors'. So an automated brain tumor detection and segmentation is required. This work suggests a Region-based Convolution Neural Network (RCNN) approach for automated brain tumor identification and segmentation using MR images, which helps solve the difficulties of brain tumor identification efficiently and accurately. Our methodology is based on the accurate and efficient selection of tumorous areas. That reduces computational complexity and time. We have validated the designed experimental setup on a standard dataset, BraTS 2020. We used binary evaluation matrices based on Dice Similarity Coefficient (DSC) and Mean Average Precision (mAP). The segmentation results are compared with state-of-the-art methodologies to demonstrate the effectiveness of the proposed method. The suggested approach attained an average DSC of 0.92 and mAP 0.92 for 10 patients, while on the whole dataset, the scores are DSC 0.89 and mAP 0.90. The following results clearly show the performance efficiency of the proposed methodology.

Keywords: Brain tumor; MRI; preprocessing; image segmentation; brain tumor localization; medical; ML; RCNN; BraTS 2020; LGG; HGG

1 Introduction

A brain tumor is characterized by irregular brain cell growth that can affect the nervous system and be fatal in extreme cases. Brain tumors are known as malignant or benign brain tumors. Malignant is cancerous, while benign is a form of non-cancerous brain tumor. The growth rate of benign brain tumors is less severe than that of malignant tumors, considered the deadliest cancers. Brain tumors can be categorized as either depending on their initial origin, primary brain tumors, or metastatic



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cells that become malignant in another part of the body and spread to the brain [1,2]. Gliomas are more prevalent primary malignant brain tumors. Gliomas are tumors that originate in the glial cells of the brain. Low-Grade Gliomas (LGG) and High-Grade Gliomas (HGG) are two types of gliomas. Patients with low-grade gliomas might expect to live for several years.

On the other hand, high-Grade Gliomas are more severe and cystic, with most patients living less than two years after diagnosis [2–4]. MRI is mainly utilized to detect gliomas due to the excellent resolution of multi-planar MR images. For assessing tumor volume fluctuation, segmentation of the MR image is crucial [5].

MRI is one of the most effective procedures for evaluating brain malignancies. Because brain tumors vary in size, shape, and location, detecting and segmenting them can be difficult [6]. As a result, radiologists and physicians have a difficult time manually detecting brain cancers using MRI. Brain tumor identification and segmentation must be automated or semi-automatic techniques [3]. These automated techniques can help early find the exact size and location of the tumor that leads to further treatment planning. As a solution, different authors have already proposed multiple segmentation techniques, such as voting strategies, atlas, and machine learning [7].

In our contributions, we have:

Proposed a novel framework using deep learning technique to identify and segment brain tumor and through Active contour segmentation.

Compared the performance of the proposed framework through state-of-the-art methods to validate the findings.

Proposed framework will help medical practitioners and healthcare professionals for early diagnosis and better treatment of brain tumor.

Nowadays, researchers regularly work on machine learning-based techniques for tracing and analyzing medical images [8–12]. In this work, we proposed a method for *detecting and segmenting brain tumors using a regional convolutional neural network (RCNN)*. RCNN is a region-based technique of detection and segmentation. That can be proved helpful for smaller and larger datasets in different tasks [13]. RCNN can prove helpful even for datasets having an un-sufficient sample count. In such datasets, we can utilize unsupervised pre-training, supervised fine tuning, and localization of regions to achieve the best results. Our proposed RCNN based method is divided into three parts, Preprocessing to enhance the image quality and remove intensity inhomogeneity, brain tumor Localization using RCNN, and Segmentation for accurate extraction of the tumor area. State of the art BraTS 2020 is used to test the proposed methodology. For proving the efficacy of the suggested technique, the results are compared to state-of-the-art methodologies. For ten patients, the proposed method achieved an average DSC of 0.92 and mAP of 0.92, whereas the scores for the entire dataset were DSC 0.89 and mAP 0.90. The following data demonstrate the suggested methodology's performance efficiency.

This paper is structured as follows: A brief discussion on multiple previous studies is given in Section 2, Methodology used is presented in Section 3, Results and Discussions are given in Section 4, while Section 5 contains the Conclusions and Future work.

2 Literature Review

2.1 Machine Learning

Several machine learning and computer vision [14,15] based segmentation and classification algorithms exist to diagnose brain tumors, skin cancer, and lung cancer, common dangerous diseases in

humans [16]. Many machine learning segmentation techniques were used for brain tumor detection; most of them are classification-based. MRI intensities often reflect an a posteriori distribution in Generative techniques, whereas the appearance is represented by the probability function, while the prior reflects the prevalence of a condition, such as location [17–20].

2.2 Probability

Prastawa et al. [21] addressed the segmentation of brain tumors as outlier identification, as tumors are regions of abnormal intensity relative to healthy tissues. Other generative techniques use the probabilistic atlas to provide spatial information [18,20]. A probabilistic atlas is obtained after a registration stage, modelling the patient's brain structure. To overcome this issue, Kwon et al. [20] Anticipated a combined registration and segmentation technique, in which a healthy atlas template is transformed using a tumor development model to get the tumor and its sub-regions. Other approaches made advantage of the information from the surrounding tissues [17,18].

Zhao et al. [22] take tumor data into account at the regional level. A 3D joint histogram is used to evaluate a probability function using a clustering approach based on intensity similarity and context. Menze et al. [3] used MRFs to regularize segmentation in the neighborhood of a voxel, with a different cost for pairs of labels. Li et al. [23] used the MRF after using a dictionary learning technique to achieve an inadequate depiction of the data. A patch-based multi-atlas approach with a stratified voting scheme was introduced by Cordier et al. [24].

2.3 Support Vector Machine

The most frequent classifiers for the segmentation of brain tumors [3] and other applications [25–27] are Random Forests [28,29], association mining [30] and Support Vector Machines [31]. Bauer et al. [32] Proposed a hierarchical approach for SVMs that employed first-order intensities and statistics as features. The RF classifier [33] is employed, and the feature vector is extended to include gradient and symmetry information. The input from the generative and discriminative models was merged by Zikic et al. [34].

Tustison et al. [35] looked into utilizing the performance of a Gaussian Mixture Model as a feature in a two-step classification technique based on RF. Reza and Iftekhar Uddin [36] used point-based characteristics to give a broad summary of brain tissues. The second set of characteristics, primarily texture-based and includes fractal PTPSA, texton, and mBm, described the tumor. By converting the classifier Diverse Adaboost SVM to a Random forest, our technique extends Islam et al. [37]. A Random Forest classifier was also used by Festa et al. [38] with a set of characteristics that included context features. Convolutional Neural Networks (CNNs) have had much success in the computer vision field [39–41]. RCNN incorporate the idea of a local context by using kernel sets that are extended over pictures or image patches. The use of this characteristic in the segmentation of brain tumors has been studied [42–45].

2.4 Deep Learning

Das et al. [46] developed a deep learning-based framework for tumor diagnosis that uses a deep convolution neural network (Deep-CNN) that uses clinical presentations and traditional MRI studies. The Watershed segmentation approach was examined by Qaseem et al. [47] for brain tumor identification. The study used a large data set of pictures and found that the K-NN classification algorithm performed well in detecting brain tumors. Because brain tumors vary in form, structure, and volume, Havaei et al. [42] assessed cluster centroids (ABC populations) and used a level-set approach

to resolve contour differences. The results demonstrate that the model is more efficient than it was previously.

Our lead paper used RCNN, which enhances segmentation efficiency by computing deep features with a fair representation of Melanoma. The RCNN can identify numerous skin diseases in the same patient and diverse illnesses in separate individuals [48]. We propose a method of Brain tumor detection and segmentation for detecting and segmenting brain tumors using a deep regional convolutional neural network (RCNN) and the Active contour segmentation approach in this study. For object localization, by combining unsupervised pre-training and supervised fine-tuning areas, RCNN overcomes the problem of inadequate data [49,50].

3 Methodology

3.1 Dataset

The collection of data is called a dataset. The proposed algorithm is trained and tested on MRI brain slices containing tumors accessed from MICCAI BraTS 2020 [3,51,52]. The supplied MRI dataset has a multi-modal MR meta-images (MHA) file format. The dataset includes ground-truthed MR brain images of several individuals with brain tumors. Because patients are of varying ages and genders, tumor size, location, thickness, and color may differ. In each patient's brain scan, the number of MRI slices containing tumor varies. There are 369 training, 125 validations, and 169 test multi-modal brain MR studies. The MR picture comprises 155 slices of the brain taken along any of the three axes, with each slice measuring 240×240 pixels. After analyzing the medical pictures and obtaining the raw pixel data, we retrieved the 240240 2D slices from the 3D photos.

3.2 System Overview

In this paper, we presented a three-phase method, with the first being preprocessing, the second being localization, and the third being segmentation. In the first phase, to reduce the, only those slices are selected which contain tumor. Preprocessing is done where we applied median filter followed by bias field correction for intensity inhomogeneity. In the localization phase, RCNN (Region-based Convolutional Network) is applied for locating and extracting the brain tumor region. RCNN is applied to localize the brain tumor regions because it correctly detects the numerous tumors in the shape of a bounding box. We have used the completed BRAT 2020 experiment, but for the simplicity of the paper, we described various examples from 10 sample images.

The RCNN considers the brain tumor region a region of interest (ROI) after training, whereas the remainder of the picture is considered background. The RCNN then used a regression layer and selective search approach to locate brain tumor areas using a pre-trained AlexNet model. The suggested model's performance is measured using the DSC and is tested using a leave-one-out strategy (DSC). Fig. 1 depicts the technique described in this study for automated brain tumor identification and segmentation.

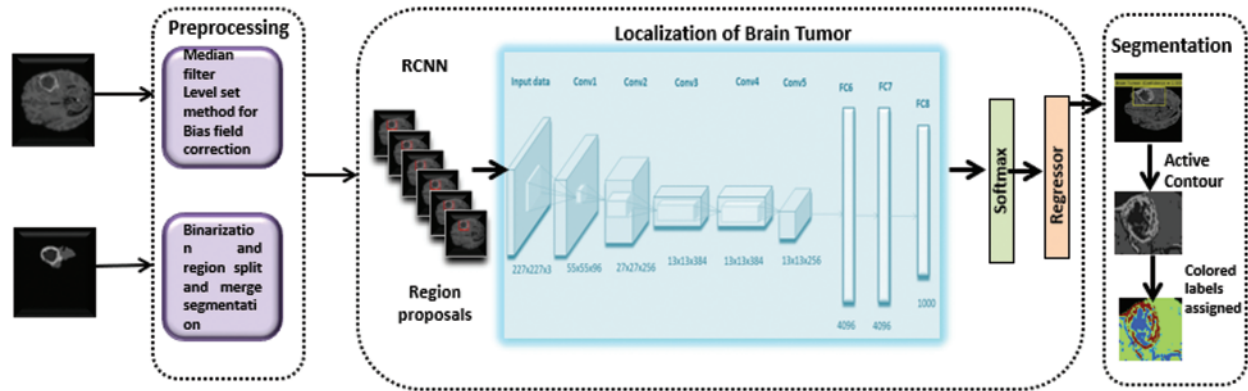


Figure 1: An architecture of proposed methodology for Brain tumor detection and segmentation, divided into three phases, Preprocessing, localization, and segmentation of Brain tumor

3.3 Image Acquisition and Selection

In this proposed framework, only the T1c sequence is used rather than considering all sequences for the tumor segmentation because T1c has the highest spatial resolution [50]. Then slices having tumors are identified and selected.

3.4 Preprocessing

There might be a bias field or intensity inhomogeneity in MR pictures obtained by various MRI machines. It's an artifact that has to be eliminated since it might skew segmentation findings. For bias field correction, we used the level set technique in the preprocessing stage [53]. The median filter is used to remove noise from the image to obtain the improved image. A nonlinear filter called median filtering is an efficient approach for removing noise while retaining edges. A window glides pixel by pixel over the image in this sort of filtering procedure. During this movement, algorithm replaces each pixel's value with the median value of surrounding pixels. All of the pixels' values are sorted first, and then the median value is used to replace the pixel value to determine the median value. When it comes to removing noise, the median filter outperforms linear filtering [54]. After that, the ground truth images are rehabilitated to binary image and region split, and merge segmentation [55] is applied to ensure precise brain tumor detection through RCNN. In region Split and merge Segmentation, similar regions are merged, and different regions are split until there are no more similar regions to merge, or different regions are left to split.

3.5 Brain Tumor Detection and Localization Using RCNN

The input image $I_p(x, y)$ proposes region against RCNN. The SoftMax layer procreated the predicted confidence score for classifying each region proposal as a tumor or non-tumorous region [42]. Afterwards, we apply the greedy suppression algorithm [56] to exhaustive search the brain tumor regions, and bounding boxes are created over the affected area as

$$BOI(x, y, w, h) \quad (1)$$

Box over the image (BOI) the bounded area is centered at (x, y) coordinates and height and width are depicted by w, h of the bounding box. In our proposed methodology, in the training phase of

RCNN, training pairs comprise the detected and ground-truth regions. The training pairs are presented as: $\{(BOI^i, GTI^i)\}_{i=1, \dots, N}$, where i shows training samples index N and GT^i is used to represent the ground-truth areas. The GT I (Ground truth in image prediction) can be represented as:

$$GTI(x, y, w, h) \quad (2)$$

3.5.1 Feature Extraction

CNN has shown a dramatic increase in performance efficiency for object detection as compared with object detection methods. But they are computationally costly because of the sliding window method they utilize for object detection. RCNN presented a selective search algorithm that uses fewer region proposals, saves computation time, and increases the CNN's efficiency to overcome this limitation.

Generally, the brain tumor varies in shape, size, and location; therefore, the image pyramid enables RCNN to downsample the input image, and deep feature representations are obtained to detect disease at various aspect ratios. The image pyramid $BOI_j(x, y, w, h)$ represents the image $I_p(x, y)$ by frequent smoothing and down-sampling, and various levels of the image pyramid are depicted as the subscript: $j = \{1, 2, \dots, 4\}$. The smoothing and down-sampling complete process can be denoted as

$$BOI_j(x, y) = I_p(x, y) - 4 \sum_{m=-2}^2 \sum_{n=-2}^2 \varpi(m, n) I_r \left(\frac{x-m}{2}, \frac{y-n}{2} \right) \quad (3)$$

The selective search step of RCNN collects texture, color, and intensity representation of tumor areas across many layers. We ran RCNN with different parameters values during experimentation found the best values and different selected parameters for precise modelling of brain tumor features as given in [13].

3.5.2 Regression

To accurately find the region affected by tumor disease, we used regression. The regression layer creates a bounding box around that detected tumor area. Optimal transformation functions are utilized to prevent any mislocalization. The four transformation functions for error reduction $b_x(BOI)$, $b_y(BOI)$, $b_w(BOI)$ and $b_h(BOI)$ were used from our previous work [13]. The projected tumor area is mapped over the ground truth using these transformation functions. The $b_x(BOI)$ and $b_y(BOI)$ scale-invariant mappings of the center are presented as a box over the image (BOI). The input region suggestions were converted into anticipated ground truth brain tumor regions after learning optimum transformation maps.

Regression targets are designated as Reg^* in the proposed algorithm for training pairs (BOI, GTI) and are numerically described as follows:

$$Reg_x = \frac{(GTI_x - BOI_x)}{BOI_w} \quad (4)$$

$$Reg_y = \frac{(GTI_y - BOI_y)}{BOI_h} \quad (5)$$

$$Reg_w = \text{Log} \left(\frac{GTI_w}{BOI_w} \right) \quad (6)$$

$$Reg_h = \text{Log} \left(\frac{GTI_h}{BOI_h} \right) \quad (7)$$

The predicted **BOI** is then assigned to the ground-truth **GTI**, yielding an intersection over the union (IoU) score. We've defined 0.7 as the intersection over the union threshold; if the IoT score is more than 0.7, it's deemed a tumor region, while a lower number indicates a non-tumor region.

3.5.3 Training Parameters for RCNN

To accurately classify and localize brain tumor regions, AlexNet is fine-tuned by transfer learning using auxiliary labeled dataset CIFAR10 [57]. After attaining good accuracy compared to the state-of-the-art, Alexnet was tuned, and brain tumor classification was performed [58].

Ground truth labels and region suggestions obtained by the selective search were utilized for training the network. Optimized weights were obtained using a stochastic gradient descent algorithm to decrease the error rate for brain tumor classification. Throughout the training phase, the learning rate was automatically modified using a piecewise learning scheme. Five hundred epochs were used for the optimized cost function to reduce brain tumor mislocalization. RCNN is performed 500 times during training to improve brain tumor localization.

3.6 Brain Tumor Detection at the Test Time

In image testing, selective searches were used to extract region suggestions, then wrapped to make the regions suitable for presentation to Alex Net's input layer. For the identification of the brain tumor regions, SoftMax cross-entropy probabilities are utilized. Confidence scores are computed when deep convolutional features are fed into the SoftMax layer [42].

3.7 Brain Tumor Segmentation Using Active Contour

After the brain tumor has been located, the cropped portion of the MR image is used as the ROI (Region of Interest). The Active Contour Segmentation Algorithm, commonly known as snakes, takes this ROI and segments the tumor area.

An inactive contour algorithm takes boundary as an initial step. Which are usually in spline curves shape and, depending upon the application underway, it spread out in a specific manner. The curve is created, resulting in an image consisting of several regions. In this process, expansion/contraction operations are implemented based on energy function.

3.8 Limitation of the Approach

The efficacy of our approach has been validated by a series of tests using the BraTS 2020 open-source dataset. We utilized unsupervised pre-training, supervised fine tuning, and localization of regions to achieve the best results, which was a time-costly procedure. To overcome this problem, we will apply our methodology to other variants of RCNN, i.e., Fast RCNN. We will extend our work by applying the proposed methodology to all the BraTS dataset variants to observe if the proposed method is efficient for the current BraTS or all.

4 Results and Discussion

The findings achieved using the suggested method at each phase of brain tumor identification and segmentation is detailed in this part.

4.1 Evaluation Metrics

The evaluation metrics for each phase of the proposed system are presented in this section.

4.1.1 Results of Preprocessing

After the image is acquired, preprocessing is applied. For image enhancement, a median filter is applied, and level set method is used for bias field correction [53]; then connected component analysis of ground truth is done to find the largest connected object, which gives the location information of tumor, i.e., (x, y, w, h).

4.1.2 Brain Tumor Localization

In preprocessing step, bias field correction and median filter were applied for image enhancement; after that, the enhanced image was then passed to the pre-trained Alex Net model for brain tumor localization. The soft-max layer of this model; classify the tumorous region and non-tumorous region by generating the feature map. We can see the localization results of test images and perceive that RCNN has accurately detected the tumor region in the test MRI scans. For localization of tumor region, convolutional layers assign different probabilities to tumorous and non-tumorous regions.

Selective search generates region proposals from which RCNN extracts convolutional features, and then the AlexNet model uses them to classify the region proposal. For the localization of brain tumors, training of binary classifier is performed, and the tumorous region is assumed as a positive instance while the non-tumorous region is considered a negative instance. For labelling the region as tumor region, the IoU measure is used, and after several experimental runs, the threshold value was set to 0.7. We performed k-fold validation for each patient, and the value of k is set at 5. Afterwards, we calculated precision for every patient and, based on these precision scores, we accumulated mAP. For example, P_4 gives the highest precision of 0.99 among all patients after 5 runs, while P_8 shows the least precision. The IoU overlapping value higher than 0.7 is considered as tumor region detected, and lower than this threshold is declared non-tumorous. [Tab. 1](#) P_i indicates the patient number and precision of algorithm performance found for each patient after localization of brain tumor regions at the regression layer and achieving mAP of 0.92 for 10 patients.

Table 1: mAP Score to localize brain tumor using RCNN

Patient ID	P_1	P_2	P_3	P_4	P_5	P_6	P_7	P_8	P_9	P_{10}	mAP
Precision	0.97	0.98	0.93	0.99	0.89	0.87	0.95	0.84	0.85	0.93	0.92

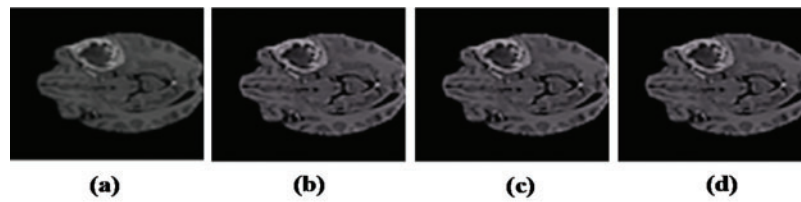


Figure 2: Resulted images after Preprocessing: (a) Input image with artifacts. (b) Image after bias field correction. (c) Median filter applied. (d) Resultant preprocessed image

4.1.3 Brain Tumor Segmentation Using Active Contours

The tumor region has to be correctly segmented to compute the segmentation performance of the brain tumor region. Active contour was used to segment the tumor area. In Fig. 3, segmentation results are shown after implementing Active Contour and the segmented pictures produced are highly comparable to the ground truth images.

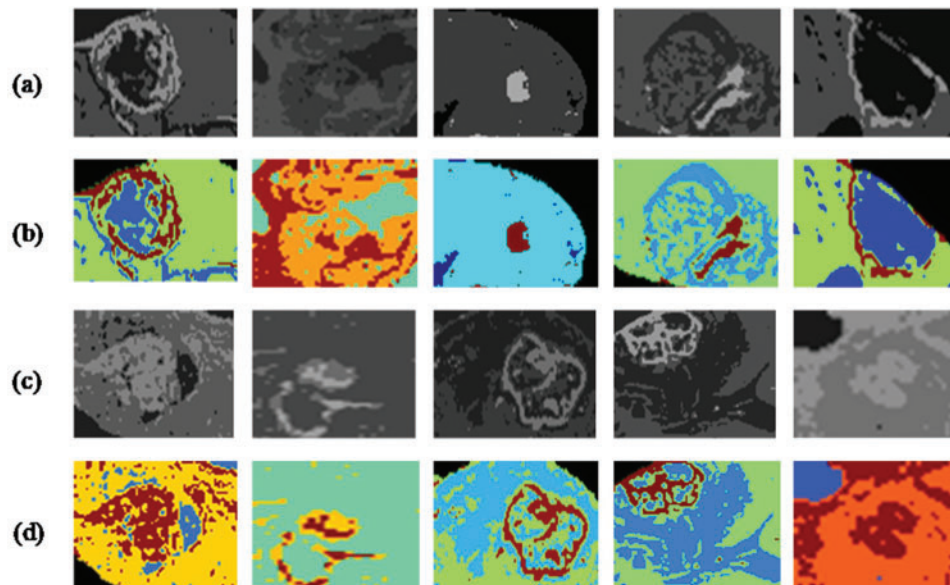


Figure 3: Segmentation results and localized brain tumor images (a), (c). Localization results using RCNN (b), (d). Segmentation results using active contour segmentation

The DSC score is used to measure the segmentation phase's performance. Our method achieved an average DSC score of 0.92, representing good segmentation performance compared with other techniques. Results achieved based on Fig. 3 are then compared with state-of-the-art techniques. The proposed method performed well because of the accurate localization results by using RCNN.

The above box plot shows the DSC score of each patient. It also gives the highest and lowest DSC score range. For P_1 , which represents Patient 1, the minimum DSC score is 0.3, and the maximum DSC score is more than 0.8. Similarly, it gives the maximum and minimum range of the DSC. However, in a few images, the brain tumor was not localized accurately by RCNN because of the complex brain structure and visual similarity between tumor and non-tumor regions. The False positive MRI slices that were not detected correctly because of the complex brain structure are shown in Fig. 2, which

illustrates the difficulty in brain tumor detection. In [Tab. 2](#), we depict DSC scores for each of the selected ten patients along with true positive and true negatives; at the end of the table, we also represent average results for DSC. The highest DSC score was of P_4 and P_7 of 1, while P_{10} shows the least DSC score. [Fig. 4](#) represents the boxplot of DSC of all ten patients. [Fig. 5](#) shows the heat map of all ten patients with HGG.

Table 2: DSC Score, true positive, true negative

Patient ID	True positive	True negative	DSC index
P_1	61	12	0.876
P_2	45	16	0.891
P_3	64	18	0.916
P_4	55	18	1
P_5	61	15	0.920
P_6	48	36	0.922
P_7	41	17	1
P_8	56	17	0.908
P_9	57	17	0.915
P_{10}	22	19	0.858
Avg result	510	185	0.920

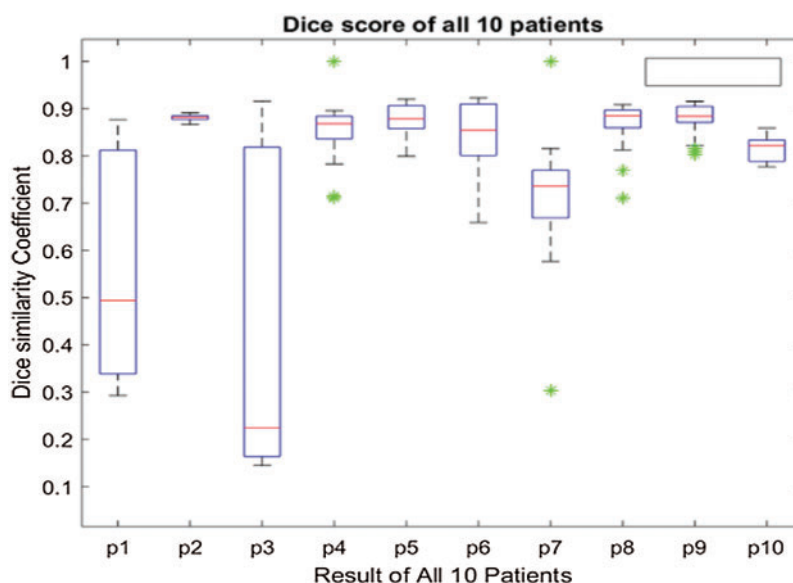


Figure 4: Boxplot of 10 patients of HGG (High-Grade Glioma) showing DSC score of each patient

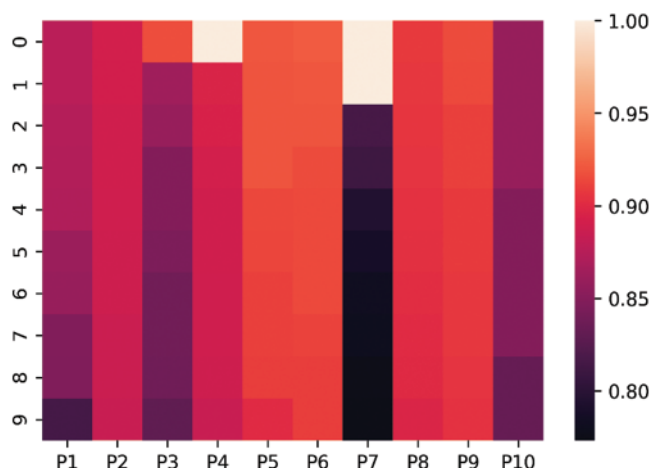


Figure 5: Heat-map of 10 patients with High-Grade Gliomas (HGG)

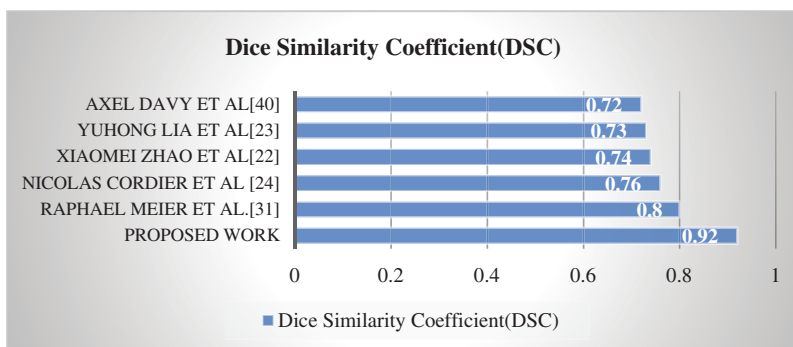


Figure 6: Comparison of proposed method with state-of-the-art techniques

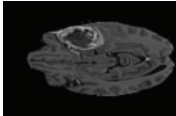
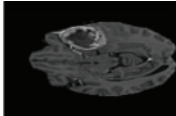
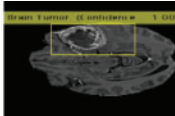
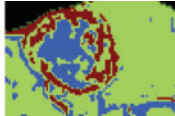
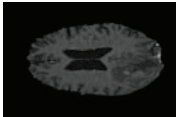
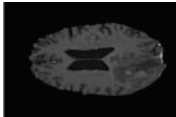
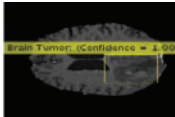
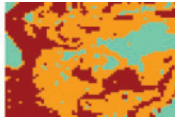
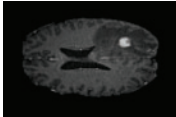
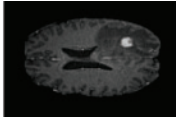
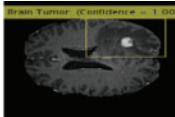
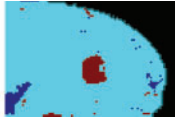
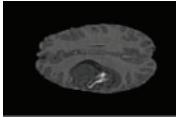
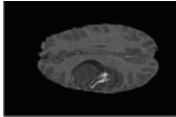
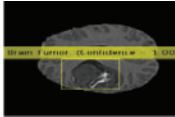
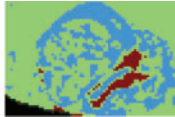
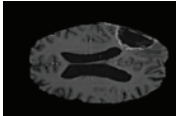
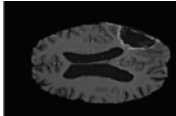
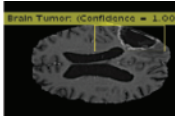
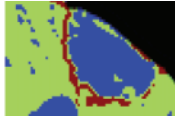
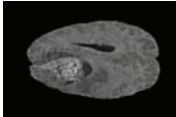
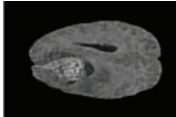
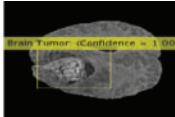
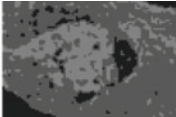
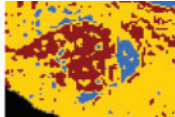
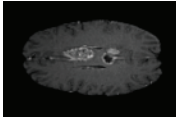
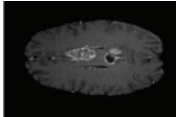
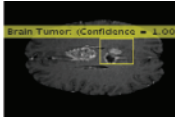
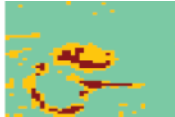
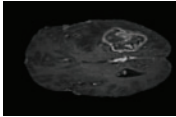
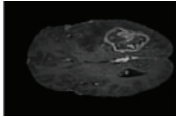
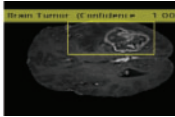
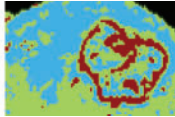
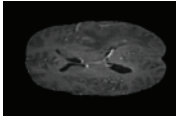
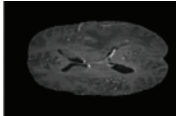
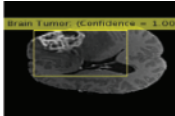
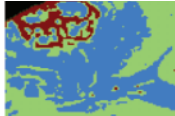
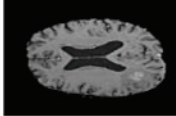
4.2 Comparison with State-of-the-Art Techniques:

Compared to our suggested technique, the DSC score value obtained for the BraTS 2020 dataset was 0.92. The suggested approach is compared to state-of-the-art methods in [Fig 6](#).

Compared to previous techniques [22–24,33,42], [Fig. 6](#) demonstrates that the suggested model has greater computational efficiency. However, the task's complexity is shown by the task's overall low DSC scores. This research aims to develop a system that can accurately and efficiently preprocess, locate, and segment a brain tumor. Preprocessing, identifying the brain tumor, and subsequently, tumor segmentation is phases in the proposed technique. The effectiveness of a completely automated CAD system for the identification of brain tumors was investigated. BraTS 2020 was the dataset used in this study.

In [Tab. 3](#), we have represented images of 5 phases for each sample patients are given. In the first column, the original image is shown before preprocessing stage. Then preprocessing is done, and the results are given in preprocessing column. In the localized tumor column, results of the localized tumor are shown, and the other two columns show results after applying segmentation and then assigning a color label to a segmented image.

Table 3: Results of preprocessing, localization, and segmentation

Patient Id	Original Image	Preprocessed Image	Localized tumor	Segmented Image	Color labeled Image
P1					
P2					
P3					
P4					
P5					
P6					
P7					
P8					
P9					
P10					

5 Conclusion and Future Work

This work proposed a novel technique for practical, precise, and automated brain tumor area segmentation using MR images based on RCNN and Active contour segmentation. Preprocessing, brain tumor region identification and brain tumor segmentation are the three phases in our approach. Compared to state-of-the-art systems, the RCNN can assess deep features with good brain tumor representation, improving segmentation efficiency. In addition, our method may be utilized to address complex medical picture segmentation issues. Several experiments were performed using the BraTS 2020 open-source dataset. In addition, our method may be utilized to address complex medical picture segmentation issues. The efficacy of our approach has been validated by a series of tests using the BraTS 2020 open-source dataset. We utilized unsupervised pre-training, supervised fine tuning, and localization of regions to achieve the best results. We will apply our methodology to other variants of RCNN, i.e., Fast RCNN, and will extend our work by applying the proposed methodology to all the BraTS dataset variants to observe if the proposed method is efficient for the current BraTS or all. We will extend our work with following [59–62]. Later on, this work can be reached out to assess the findings of other BraTS challenge datasets to identify sub-tumor areas, such as complete, focus, and improve tumor.

Acknowledgement: This work was supported in part by the Basic Science Research Program through the National Research Foundation of Korea (NRF).

Funding Statement: This work was funded by the Ministry of Education under Grant NRF-2019R1A2C1006159 and Grant NRF-2021R1A6A1A03039493.

Conflicts of Interest: The authors declare that they have no conflicts of interest to report regarding the present study.

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