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Detection of the Brain Tumor Existance Using a Traditional Deep Learning Technique and Determination of Exact Tumor Locations Using K-Means Segmentation from MR Images

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Abstract

Tumors occur in the brain as the cells in the brain tissue grow abnormally. Since a large amount of tumors in the brain are cancerous, it can have consequences until the death of the sick person. Magnetic Resonance (MR) imaging is widely used as a means of imaging brain tumors. MR images can distinguish diseased and healthy areas using the image's texture, contrast, brightness and boundary information. In this way, planning of the treatment process of the disease can be made by finding the shape, location, size and area of the brain tumor. In this study, the detection of the brain tumor in MR images by using deep learning and the segmentation with K-means are performed. As a result of the study, the accuracy obtained in detecting of the brain tumor is 84.45%, and the sensitivity is 95.04%. The study proposed detection and segmentation of the brain tumor and, extracting the tumor area automatically.

Keywords: Magnetic resonance imaging, Brain tumor detection, Brain tumor segmentation, Deep learning, K-means

Beyin Tümörü Varlığının Geleneksel Derin Öğrenme Tekniği Kullanılarak Tespiti ve MR Görüntülerinden K-Means Segmentasyonu Kullanılarak Kesin Tümör Konumlarının Belirlenmesi

Özet

Beyin dokusunda bulunan hücrelerin anormal bir şekilde büyümesi ile beyinde tümörler meydana gelmektedir. Beyinde bulunan tümörlerin büyük bir miktarı kanserli olduğu için, tümörlü beyin hasta kişinin ölümüne kadar sonuçlar doğurabilir. Beyin tümörlerinin görüntülenmesinde yaygın olarak Manyetik Rezonans (MR) görüntüleme araç olarak kullanılmaktadır. MR görüntüleri, görüntünün doku, karşıtlık, parlaklık ve sınır bilgilerini kullanarak hastalıklı ile sağlıklı bölgeleri ayırabilmektedir. Bu sayede, beyin tümörünün şekli, konumu, büyüklüğü, alanı bulunarak hastalığın tedavi sürecinin planlaması yapılabilmektedir. Bu çalışmada, derin öğrenme yardımı ile MR görüntülerinde beyin tümörünün tespit edilmesi ve K-means ile bölütlenmesi işlemi yapılmaktadır. Çalışma sonucunda beyin tümörünün tespit edilmesinde elde edilen doğruluk oranı %84,45, hassasiyet %95,04 olarak bulunmuştur. Çalışma ile, tam otomatik bir beyin tümörü tespit etme ve bölütleme önerilerek, tümörlü bölgenin doğru bir şekilde çıkarılması amaçlanmıştır.

Anahtar kelimeler: Manyetik rezonans görüntüleme, Beyin tümör tanıma, Beyin tümörü bölütleme, Derin öğrenme, K-means

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1. INTRODUCTION

A brain tumor is an abnormal growth of cells in the brain tissue. Although some of the tumors occurring in the brain are benign, some are cancerous and can have consequences until the death of the person. Brain tumors can be shown in detail by imaging methods such as Ultrasonography, Computed Tomography (CT), Magnetic Resonance Imaging (MRI), and can provide medical doctor who study the case to understand the tumors and know the location of tumors.

Magnetic Resonance Imaging (MRI) is one of the most used methods for imaging the build of the human body. In particular, it has an important place in detecting diseases that may occur in the brain, as it can offer much more contrast between the soft tissues of the body. It can give higher resolution and less harm than CT. By using brain MR images, brain diseases such as Alzheimer's, Epilepsy, Schizophrenia, Multiple Sclerosis (MS), and brain tumor can be recognized and used for treatment. Four standard MRI sequences (T1-weighted, T2-weighted, T1-Gd-gadolinium enhanced and FLAIR - Fluid Attenuated Inversion Recovery) can be used for brain tumor diagnoses that are given in Figure 1. The data produced by MR imaging is quite large, which makes it very difficult to process, store, and segment the data.

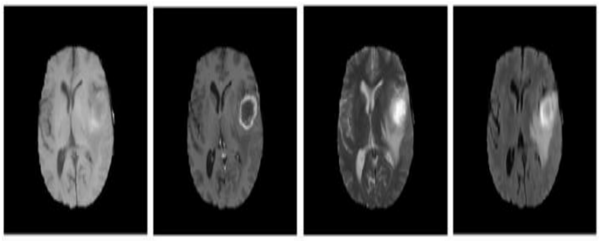

Figure 1. 4 different MR modalities. From left to right: T1-weighted, T2-weighted, T1-Gd and FLAIR. Images taken from BRATS 2013 dataset (Menze et al., 2015).

Detection and segmentation of brain tumor by using MR images is an important issue. Treatment can be planned for the disease by detecting and marking the tumor, and treatment can be tailored according to the structure of the tumor. In the segmentation process, normal brain tissues can be separated from diseased tissues, the location of the tumor region can be determined and the area of the region can be calculated by using different features of the image, such as tissue, contrast, brightness and borders. Segmentation of tumors in MR images can be quite difficult due to factors such as shape, size, and location of the tumor.

In this study, brain tumor detection has been made on MR images with deep learning, and after the brain tumor has been detected, marking of the tumor area has been performed by K-means segmentation. In the section 2, literature review is given, and the section 3, proposed method is explained in detail. The test results obtained in section 4 are given and performance of the study is measured with evaluation criteria. In the last chapter, the results are interpreted and future studies are mentioned.

2. LITERATURE REVIEW

The detection and location of the brain tumor is very important in the treatment process of the disease. Thanks to the deep learning algorithms developed in recent years, a lot of work has been done on the subject (Havaei et al. (2017), Soltaninejad et al. (2019), Damodharan and Raghavan (2015), Pereira et al. (2016), Gurusamy and Subramaniam (2017), Arunkumar et al. (2019), Iqbal et al. (2018), Khan et al. (2019)). Kaya et al., (2017) focused on T1-weighted MR images for brain tumor segmentation using different Principal Component Analysis (PCA) algorithms (CPCA, PPCA, EM-PCA, GHA, APEX). They made a comparison between the differences in PCA algorithms in MR images. Saouli et al., (2018) proposed a fully automated end-to-end method for segmentation of a brain tumor using three deep learning models (2CNet, 3CNet, EnsembleNet). Cabria and Gondra (2017), presented an algorithm based on the analogy of the concept of potential fields in physics. They proposed a new approach by combining the new algorithm called Potential Field Segmentation with other segmentation algorithms and tested the work on the BRATS dataset. Dong et al., (2017) performed the U-net based (Ronneberger et al. (2015)) which is very popular and fast in biomedical image segmentation, brain tumor segmentation in the BRATS 2015 dataset. Nazir et al., (2019) firstly, decomposed the image into wavelet subbands, and then divided it into high-energy subband blocks. Finally, the high variance properties of each block were selected by separate cosine transforms and sent to the neural network for classification. Bahadure et al., (2017) proposed a method for image segmentation based on the Berkeley wavelet transform. They also analyzed images with a Support Vector Machine (SVM) based classifier. Bobotov and Bene (2016), proposed automatic tumor segmentation. Firstly, they removed the cranium region. Later, they analyzed histogram parameters with the mixture of Gaussians and applied morphological reconstruction and threshold applications. Finally, they performed segmentation with the Grab Cut algorithm.

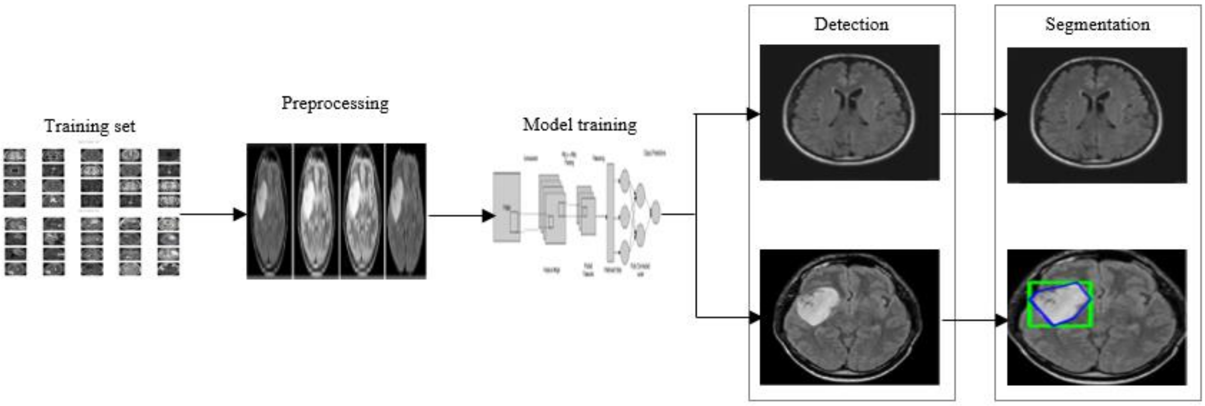

Figure 2. Proposed method flow diagram

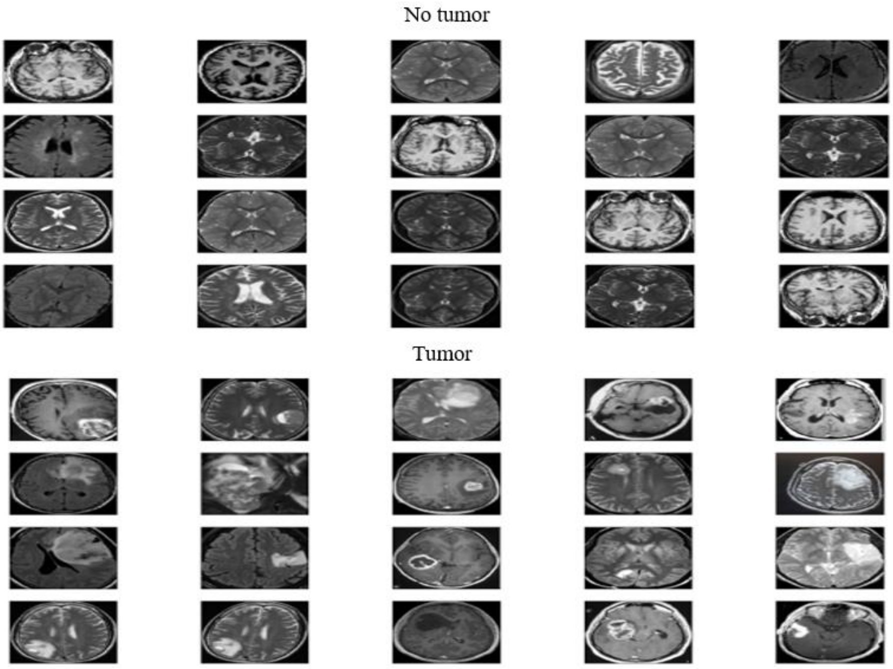

Figure 3. Samples randomly taken from the database. Top side displays negative samples, bottom side displays positive samples

3. PROPOSED METHOD

Detecting the brain tumor and its location in the brain, determining the shape, size and type of the tumor are very important in terms of planning the treatment process. In this study, the dataset consisting of MR images have been preprocessed, a deep learning model has been created and training has been performed. The trained model has been tested with images from the test sets and it has been determined whether there is a tumor in the MR image. At the last stage, the segmentation of the tumor region performed on the images determined to be tumors. The general flow diagram of the study is given in Figure 2; details are explained in the following sub-sections.

3.1. Dataset and Its Augmentation

In the study, the database in Kaggle (2019) was modified and additionally, The Whole Brain Atlas (2019) resource from Harvard University were used. 101 of the 277 MR images in total consist of negative images (without brain tumor) and 176 of positive images (with brain tumor). In order to increase the success of the trainings with a small number of images, data augmentation is frequently used, especially in the biomedical research. New data samples are generated by applying random operations (scale changing, density changing, rotating the image, etc.) in data augmentation. In this study, the data augmentation has been done by flipping the images horizontally and vertically, rotating the images and extending along the axes. With the data augmentation, there are 2486 images in the database, 1476 positive and 1010 negative. Random samples of both classes are given in Figure 3 in the augmented dataset.

3.2. Preprocessing MR Images

Some pre-processing steps have been implemented before starting the training of MR images. First, the image has been converted to a gray level. In the image converted to gray level, the Otsu's thresholding method was used to remove the cranium region from the image. In the new image obtained, the histogram equalization method used to contrast enhancement. Thus, the difference between contrasts in the brain MRI image increased, making it possible to see the possible tumor region and the brain region more clearly. After histogram equalization, a 5x5 Gauss filter used to eliminate small noises in the image and the image blurred. Erosion is applied to remove small noisy areas. Then, by performing the dilation process, the image was restored to its original shape after the noise removed. The MR images obtained were converted to 256x256x3 size and made ready for training. The original MR image and the performed preprocess steps on the image are given in Figure 4.

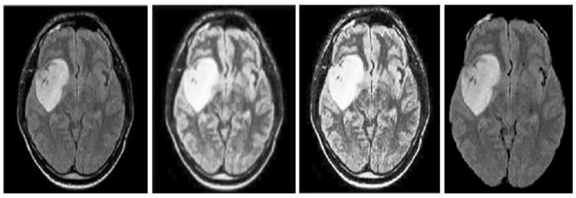

Figure 4. Pre-processing steps. From left to right: gray level image, histogram equalization and image blurring, applying morphological processes, removing cranium region from image.

3.3. Model Building and Training Phase

2486 MR images in the augmented dataset splitted randomly for the 70% for training phase, 15% for the validation phase and 15% for the test phase. Images for training phase are brought to size 256x256, they first go through 64 convolution filters with size 5x5, then normalize the filter outputs and activate with the Rectified Linear Unit (ReLU) activation function. After this stage, it passes through the maximum pooling layer to reduce computational complexity. These stages were done 2 more times and at the last stage, the data flattened and the model gives output. 211,585 parameters are available in the model, 211,201 parameters are trainable and 384 parameters are non-trainable.

3.4. Testing and Segmentation Processes

Using the trained model, the presence of tumor in the MR image for testing detected and the results are evaluated with performance criteria. Then, in the MR images where the tumor detected, the region of the tumor is segmented and marked on the original image. Before performing the segmentation process, the test images passed through the preprocessing stages used for training. The resulting image is segmented by using the K-means algorithm. The K-means is one of the well-known data clustering method for unsupervised learning. In this study, there are three classes to segmentate the MR images into background, tumor and the non-tumor areas. By using these different 3-class tumor location is easily extracted from the MR images. After the K-Means method, a black-and-white image obtained with the threshold method in the image, small noises in the obtained image eliminated with some morphological processes. Finally, the location of the tumor region was found and removed from the image. The tumor area in the segmented image is marked in the original image. The steps applied in the segmentation process are given in Figure 5.

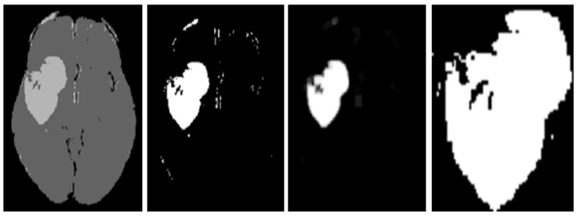

Figure 5. Segmentation steps. From left to right: Using the K-means algorithm, white regions obtained as a result of segmentation, application of morphological processes, application of the threshold method

4. EXPERIMENTAL WORKS

The study was performed on a PC with Ubuntu 16.04 and Nvidia GeForce GTX 1050 graphics card. The created model is trained to batch size 16 and epoch 25. The training took 9 minutes and 32 seconds on the GPU. The graph of the loss functions and accuracy functions for the training set and the validation set at the end of the training is given in Figure 6. As you seen in the Figure 6 that, the validation loss and accuracy is converged when they are reached to the sufficient epoch size.

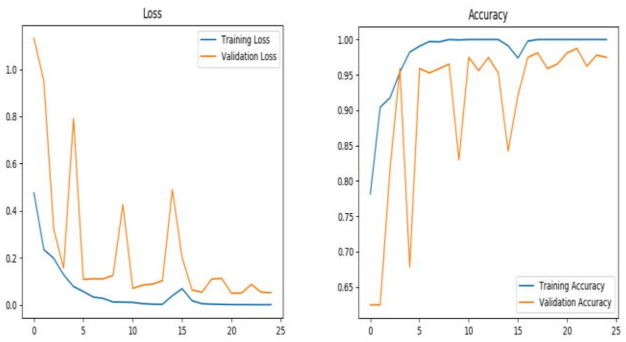

Figure 6. Loss function (left), accuracy function (right) for training and validation sets

According to the results obtained at the end of the training, the test MR images (221 tumors – positive, 152 healthy – negative) evaluated according to the following performance criteria.

Confusion matrix: The confusion matrix includes True Positive - TP (tumor with a tumor MRI image), False Positive - FP (tumor with a healthy MR image), False Negative - FN (healthy with a MR image with tumor), and True Negative - TN (healthy to a healthy MR image). At the end of the study, the confusion matrix formed as follows.

$$\text{Confusion } Matrix = \begin{bmatrix} 211 & 47 \\ 11 & 104 \end{bmatrix}$$

The accuracy of the study (whether there is a tumor in the MR image or not) calculated according to the following equation.

$$Accuracy = \frac{TP+TN}{(P+N)} = \frac{211+104}{211+47+11+104} = 0.8445 \qquad (1)$$

Precision in the study (how many of the images called tumors are actually tumors) calculated according to the following equation.

$$Precision = \frac{TP}{(TP+FP)} = \frac{211}{211+47} = 0.8178 \qquad (2)$$

Sensitivity in the study (the rate of accurately detecting tumor MR images) calculated according to the following equation.

$$Sensitivity = \frac{TP}{(TP+FN)} = \frac{211}{211+11} = 0.9504 \qquad (3)$$

The F1 score (harmonic mean of precision and sensitivity) in the study calculated according to the following equation.

$$F1 = 2 * \frac{precision*sensitivity}{precision+sensitivity} = \frac{0.8178 \times 0.9504}{0.8178 + 0.9504} = 0.8792 \qquad (4)$$

A comparison between the proposed method and some studies found in especially the recent literature is given in the Table 1 by considering the metrics of accuracy, sensitivity and F1 score.

Table 1. Comparison between our proposed method and studies found in the recent literature by considering three different performance metrics.

Research Paper (Year)	**Performance Metrics**		
	Accuracy	**Sensitivity**	**F1 Score**
Damadhoran and Raghavan (2015)	83.00%	100%	-
Akkus et al. (2016)	87.70%	93.30%	-
Hussain et al. (2017)	-	82.00%	80.00%
Soltaninejad et.al (2018)	-	96.00%	89.00%
Thaha et al. (2019)	92.00%	90.00%	-
Proposed Method (2020)	84.45%	95.04%	87.92%

When we examined the table given above, it was observed that the accuracy obtained in our study is less successful than the other studies specifically the recent literature (2015-2020); but higher values have been evaluated with respect to the metrics of sensitivity and F1 score. The accuracy is a kind of metric that measures whether there is a tumor in an MR image or not, and therefore it is not sufficient to express the success of any study alone. Along with the accuracy, the sensitivity, indicating that the proportion of positives that are correctly identified (e.g., the percentage of MR images with tumor which are correctly classified as having cancer), is a frequently used metric to measure the comprehensive success of a research study. Considering 95.04% as sensitivity metric obtained in the proposed study, MR images with tumor in the database was detected with a very high ratio. It has been also observed that the F1 score, which is the harmonic mean of the precision and sensitivity metrics, gives quite close results compared with the studies given in the Table 1. As it is understood from the evaluation criteria, it has been determined that the presence of a brain tumor in MR images is high with the built model.

After the information that the test image contains a tumor, the image segmented to find the location of the tumor area. In Figure 7, there are examples for accurate and false tumor region segmentation.

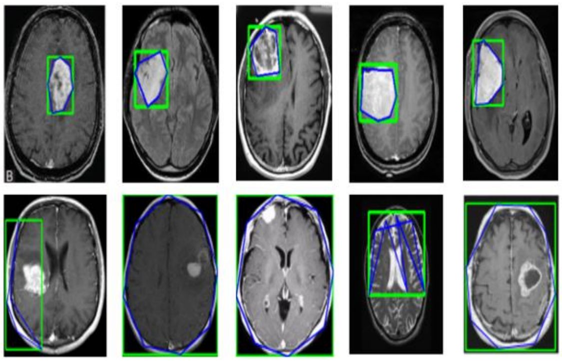

Figure 7. Accurate segmentation results (top), false segmentation results (bottom) in test MR image

It was observed that main causes of the false segmentation results in MR images are removal cranium area and different MR images modalities.

5. CONCLUSION

In this study, by using MR images, determined whether there is a brain tumor in the image, and then, in the test images with tumor, segmentation and display of the tumor region with the K-means algorithm is realized. A brain tumor is detected with 84.45% accuracy and 95.04% sensitivity in the study. In images containing the detected brain tumor, segmentation has been successfully performed. With the study, it has been aimed to plan disease treatment more easily by making a fully automatic tumor detection and segmentation. In future studies, it is aimed to increase the accuracy of the system by combining segmentation algorithms that include more than one method.

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