# Deep Convolution Network for Brain Tumor Classification and Segmentation from MRI Data

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#### Abstract

This research aimed to perform the classification and segmentation of brain tumors from biomedical MRI data. Brain image data has been collected from multiple open sources for classification and segmentation purposes. The dataset consists of 7022 images of the human brain MRI which are classified into four classes: glioma, meningioma, pituitary, and healthy (no-tumor). A deep Convolutional Neural Network (CNN) is trained on brain tumor classification, and UNet based encoder-decoder approach is used for tumor segmentation for the selected MRI data. After trying several CNN models, a candidate CNN model is chosen for brain tumor classification based on the higher accuracy and simplicity of the CNN architecture. On the other hand, the UNet-based deep CNN model which consists of a contracting path to capture context and a symmetric expanding path that enables precise localization of brain tumors. It is found that the end-to-end UNet-based CNN outperforms the prior best sliding window-based convolutional neural network for tumor detection and segmentation which is also supported by the existing literature, also, the UNet-based network is faster. The application of deep learning models is shown to perform better in classifying and segmenting biomedical brain image data.

**Keywords:** Deep learning, CNN, classification, detection, segmentation, brain MRI, UNet-CNN

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# 1 Introduction

One of the fundamental problems of computer vision is image classification and segmentation, where the task is to know the location of the object(s) contained in the image besides classifying the images according to their labels. This helps to get a semantic understanding of the images and videos, and they are related to many real-world applications, such as tumor detection in medical images, face recognition, autonomous driving, etc. However, these tasks are not trivial, considering the computational cost and accuracy of prediction. In the deep learning context "object detection and segmentation" involves different sub-tasks such as localizing the objects in the image, finding informative regions, feature extraction, and classification [1].

For image classification purposes, the deep convolutional neural network is found to be one of the most effective approaches in the literature [2] [3]. On the other hand, for image segmentation purposes, an appropriate multiscale sliding window should be able to scan all the images and find the objects in the images that might appear in any position and have different aspect ratios and sizes [4]. After that, "feature extraction" will help to recognize different objects in the images for semantic and robust representation. Commonly used feature extraction methods are the scale-invariant feature transformation [5], histogram of oriented gradient (HOG) [6] etc. And then, a classifier will help to distinguish the object from one class to another.

A brain tumor is considered one of the most aggressive diseases among both children and adults [7]. Every year, around 11,700 people are diagnosed with a brain tumor [8]. Brain tumors are classified as benign, malignant, pituitary tumors, etc [9]. A proper and timely diagnosis can improve the odds of success in brain tumor treatment. The best way to detect brain tumors is using Magnetic Resonance Imaging (MRI). A huge amount of data is generated through the scans and examined, usually by radiologists. The manual examination can be error-prone due to the level of complexities involved in brain tumors and their properties. Hence, the application of automated classification techniques using machine learning and artificial intelligence has shown higher accuracy than manual classification. So, having a framework/model to classify and localize the brain tumor in MRI data will help doctors all around the world [10].

# 2 Data and Data Sources

### 2.1 Data Description

Initially, in the proposal of this study, it was mentioned that this study will use an open brain tumor data set called the BR35H::Brain Tumor Detection 2020 (BR35H) [11]. But the number of brain MRIs in this data set is fairly small to train the model, so two more related open data sets are also included. Hence, the dataset is a combination of three datasets: "figshare" [12], "SARTAJ" [13], and "Br35H". The combined dataset contains 7022 images of the human brain MRI which are classified into 4 classes: glioma, meningioma, no-tumor, and pituitary. No-tumor class is taken from the "Br35H" dataset. Here (figure: 1) are the sample images for all four classes.

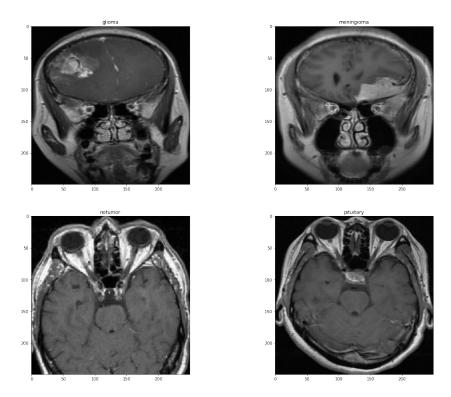


Figure 1: Cleaned (extra margin removed) sample brain MRI data for four classes

However, for the segmentation task, to avoid the computational burden, only a part of the dataset is used to train the model and to localize the tumors in the images.

# 2.2 Data processing

Data processing has been one of the key steps in this research. If we pay attention to the sample image in the figure: 3a before data processing, we will see that the actual size of the image in the dataset is different. For faster and more accurate results, we needed to resize the images by

removing the extra margins around the rectangular box in all the images. In the data processing stage, these extreme points on the image are identified and cropped in the rectangular box in the following way shown in figure: 2.

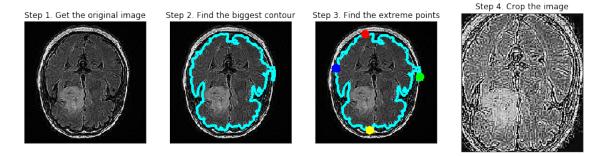
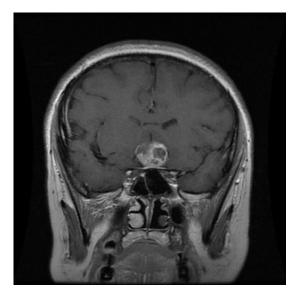
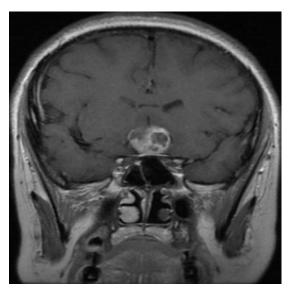


Figure 2: Steps followed in image processing to remove the extra margin

In the process, the images were thresholded, and then performed a series of erosions and dilations to remove any small regions of noise. The contours in the thresholded image were obtained, and the largest contour was grabbed to remove the noise. The new images were stored in separate files under training and test data for each of the classes. Here is a visual comparison of a sample image before and after the noise removal.



(a) An example pituitary MRI (Tr-pi\_0010) before data processing



(b) Same pituitary MRI (Tr-pi\_0010) after data processing

Figure 3: Cropping out the noise from the images

# 3 Method

#### 3.1 Deep CNN for brain tumor classification

In our dataset, we have four classes of brain tumor images: pituitary, meningioma, glioma, and no tumor. Our task is to train a deep convolution network to classify the tumors correctly. A CNN architecture which is used for classification with a different dataset is shown in the following figure: 4 [14]. Our CNN architecture is also similar and designed for classifying the classes of tumors. The following deep CNN architecture is trained on the brain tumor data having four classes.

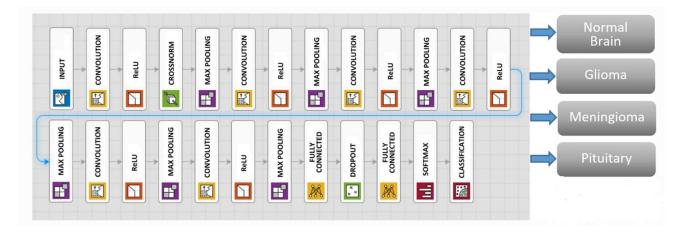


Figure 4: Architechture of the CNN model for brain tumor classification

# 3.2 U-net for segmentation

After performing the classification task, a special type of U-net-based deep CNN framework is used for image segmentation. In the UNet-based deep CNN, the convolution layers are arranged in such a way that results in image segmentation. The U-net CNN is designed for the semantic segmentation of images, especially for biomedical image data [15]. This architecture enables to have fast and precise segmentation of images. This is an end-to-end segmentation technique that takes a raw image as input and outputs a defined segmentation map of the image. The u-shaped architecture with a symmetric convolution network has a down-sampling contraction and up-sampling expansion path. In the contraction path of U-net, it is often called the encoder path and on the expansion path of it also called the decoder path. Combining both paths helps in image segmentation.

One of the advantages of the U-net convolution network is that it does data augmentation as a part of the model training which is useful when the number of raw inputs is smaller or difficult to obtain. Moreover, U-net architecture allows touching/identifying objects in the same class that requires to be correctly separated. Here, is an example of u-net architecture.

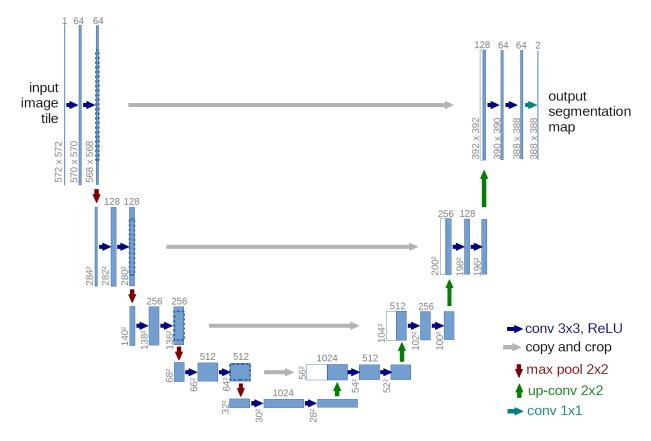


Figure 5: An example U-Net architecture [15]

In figure 5, an example of U-net architecture is shown, where each blue box indicates a multichannel feature map. The top box indicates the number of channels and the x-y size in the lower left edge of the box. And the white boxes represent copied feature maps. Finally, the arrows represent different operations [15].

According to [15], in the training model, the separation of the border is computed using the following weight map function:

$$\mathbf{w}(\mathbf{x}) = \mathbf{w_c}(\mathbf{X}) + \mathbf{w_0} \cdot exp(-\frac{(\mathbf{d_1}(\mathbf{X}) + \mathbf{d_2}(\mathbf{X}))^2}{2\sigma^2})$$

Where,  $\mathbf{w_c}$  is the weight map to balance the class frequencies,  $\mathbf{d_1}$  denotes the distance to the border of the nearest cell, and  $\mathbf{d_2}$  is the distance to the border of the second nearest cell. And the initial weights are taken from their [15] works as  $\mathbf{w_0} = \mathbf{10}$ , and  $\sigma = \mathbf{5}$  pixel.

# 4 Results

#### 4.1 Classification of tumors

In order to classify the brain tumors, the architecture of the implemented deep CNN is changed with different layers, optimizers, hyperparameters, etc. After running a couple of models, one model is chosen as the candidate model with comparatively higher accuracy (98.2%). This model also avoids the overfitting and underfitting problem more precisely. The architecture of the final model is in the appendix figure: 9. The following figure shows the mode performance.

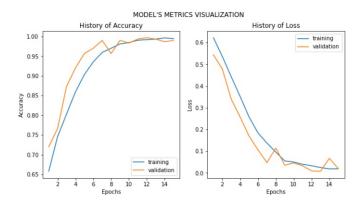


Figure 6: CNN model performance for brain tumor classification

Here is the sample (random) prediction of the tumors based on the final CNN model. In the prediction in the figure: 7, "0" indicates no tumor, "1" indicates pituitary tumor, "2" indicates meningioma tumor, and "3" indicates glioma tumor class.

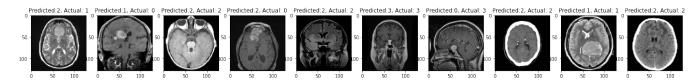


Figure 7: Deep CNN-based prediction for four classes of tumors from brain MRI data

# 4.2 Segmentation of tumors

One major challenge in brain tumor detection is to determine the tumor extent. The UNet-based image detection consists of two different elements: up sampling and down sampling. The downsampling component of the UNet CNN framework contains six convolution sub-modules, and each sub-module has three convolution layers. Each convolutional layer contains 32 filters with a  $3 \times 3$  window. The MRI of the brain of origin passes through each convolutional layer and generates posterior internal features. A pooling layer with average and maximum pooling is employed to decrease the size of the internal features in the convolutional layer. The average

pooling locates a  $3 \times 3$  mask on the inner feature set and obtains the mean of feature values as the estimated response from the pooling layer. On the other hand, maximum pooling locates a  $3 \times 3$  mask on the internal feature set and chooses the maximum of the feature values as the final response from the pooling layer. After concatenation, the convolution operation is applied on the two  $3 \times 3$  kernels, and ReLU is activated. Finally, by applying a  $1 \times 1$  convolution to the last layer, a vector of 56 components is assigned to the desired class. In the implemented framework, UNet CNN operates on zero padding for both up and downsampling. With the help of the gradient function, the tumor area is segmented out from the image. Here is the result of a sample segmentation of tumors in the images.

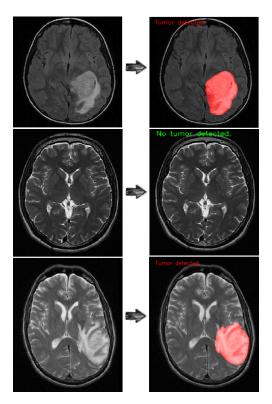


Figure 8: Image segmentation on the test image using the trained model

UNet-based CNN is considered the art-of-state model for image segmentation for biomedical image data. However, there is a scope for implementing this framework by incorporating different constraints and adjusting for computational easiness.

# 5 Conclusion

Brain tumors are complex in nature, and there are a lot of abnormalities in the size and location of the brain tumor(s). This is the main challenge for a complete understanding of the nature of the tumor. The classification of brain tumors is comparatively a trivial problem than the

detection or segmentation of brain tumors. In this study, the classification of brain tumors was done almost precisely (with more than 98% accuracy) with the deep CNN model. On the other hand, the UNet-based deep convolutional network is implemented for the detection and segmentation of the selected images for tumors. Image segmentation is considered a hard task, the implemented model could well detect and segment the tumor regions. However, there is scope for further improvement of the model by introducing constraints on the learning model for better computational complexity. Finally, With the application of deep learning-based methods, like any other field, medical imaging has also increased a solid status in modern-day healthcare systems. Different deep-learning methods can also be implemented in similar areas of biomedical image processing.

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# 6 Appendix

| Layer ( <u>type)</u>  | Output        | Shape          | Param # |
|---|---------------|----------------|---------|
| conv2d_29 (Conv2D)  | (None,        | 200, 200, 64)  | 3200    |
| batch_normalization_28  | (Batc (None,  | 200, 200, 64)  | 256     |
| max_pooling2d_28 (MaxP  | coling (None, | 100, 100, 64)  | 0       |
| conv2d_30 (Conv2D)  | (None,        | 100, 100, 128) | 401536  |
| batch_normalization_29  | (Batc (None,  | 100, 100, 128) | 512     |
| max_pooling2d_29 (MaxP  | coling (None, | 50, 50, 128)   | 0       |
| conv2d_31 (Conv2D)  | (None,        | 50, 50, 128)   | 802944  |
| batch_normalization_30  | (Batc (None,  | 50, 50, 128)   | 512     |
| max_pooling2d_30 (MaxP  | coling (None, | 25, 25, 128)   | 0       |
| conv2d_32 (Conv2D)  | (None,        | 25, 25, 256)   | 1605888 |
| batch_normalization_31  | (Batc (None,  | 25, 25, 256)   | 1024    |
| max_pooling2d_31 (MaxP  | soling (None, | 12, 12, 256)   | 0       |
| conv2d_33 (Conv2D)  | (None,        | 12, 12, 256)   | 3211520 |
| batch_normalization_32  | (Batc (None,  | 12, 12, 256)   | 1024    |
| max_pooling2d_32 (MaxP  | soling (None, | 6, 6, 256)     | 0       |
| conv2d_34 (Conv2D)  | (None,        | 6, 6, 512)     | 6423040 |
| batch_normalization_33  | (Batc (None,  | 6, 6, 512)     | 2048    |
| max_pooling2d_33 (MaxP  | soling (None, | 3, 3, 512)     | 0       |
| flatten_8 ( <u>Flatten)</u>   | (None,        | 4608)          | 0       |
| dense_24 ( <u>Dense)</u>  | (None,        | 1024)          | 4719616 |
| dropout_16 ( <u>Dropout)</u>  | (None,        | 1024)          | 0       |
| dense_25 ( <u>Dense)</u>  | (None,        | 512)           | 524800  |
| dropout_17 ( <u>Dropout)</u>  | (None,        | 512)           | 0       |
| dense_26 ( <u>Dense)</u>  | (None,        | 4)             | 2052    |
| Total params: 17,699,9<br>Trainable params: 17,6<br>Non-trainable params: | 97,284        |                |         |

Figure 9: Final CNN model architecture for brain tumor classification