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Automated medical image classification using deep learning

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***Abstract*---**Medical imaging is extremely important in the domain of medicine. Image classification is now utilized to distinguish aberrant tissues from healthy tissue in brain imaging. The brain tumor is identified from MRI images by using some classification techniques, where the area of the tumor as well as the tumor size is detected. Automatic tumor detection using brain MRI is efficient and time- saving, assisting the neurologists in diagnosis. Tumors can increase the risk of cancer, which is the most common cause of

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death or major cause of mortality worldwide. To detect brain tumors at the moment, effective automation of tumor detection is essential. Marker based Watershed algorithm is a typical segmentation technique which is used for identifying brain tumors. For brain tumor detection, we performed marker based watershed classification on MRI images with the use of gray scale images, then by noise removal and morphological operations. The steps in the methodology are as follows: Gray-level and sharpening was used in the pre-processing, and the image was segmented using thresholding as well as the marker based watershed algorithm, and the CNN was used for classifying the images. Finally, the tumor's location and size were determined. A marker is used to identify the damaged portion of the brain, as well as the overall shape of the tumor, from an MRI scan.

***Keywords*---**Brain Tumor, MRI (Magnetic Resonance Imaging), Marker based Watershed Algorithm, CNN Algorithm, Morphological Operations, Thresholding.

Introduction

A tumor is a collection of aberrant cells that forms a mass of tissues. Normal cell growth, aging, death, and replacement by new cells occurs in our bodies, but cancer as well as other tumors disrupt this cycle. Tumor cells proliferate even if the body doesn't want them to. Unlike the normal cells, these cells don't die quickly, which results in tumors or cancer. The tumor continues to expand as the process progresses, and many cells are added to the bulk of tumor cells. Throughout the area of medical research, deep learning produces difficult results. The suggested medical image classification system uses image segmentation as well as classification to attain 98 percent accuracy.

It is useful for medical specialists in this field. The syntactic level classification as well as segmentation techniques are used for classification of brain tumor images. This includes advance knowledge of testing and training datasets, using Convolutional Neural Networks (CNN) for image realization, removing noise from the input image and Thresholding. Segmentation of the input image is done by using Marker based Watershed Algorithm, and finally, the determination is done (i.e. whether the input MRI scan image is a brain tumor image or not). Using deep learning techniques, this automated process would assist the medical image analysts in identifying the Brain Tumor in the patient. Medical analysts just have to input a MRI scan human brain image into the system. Further, the algorithm will detect whether or not the image is altered by tumor.

Materials and Methods

(Valanarasu et al., 2020) developed the KiUNet, which is a cascade network, to achieve brain dissection classification. Vanilla U-performance Net's is substantially limited when detecting minute anatomical structures with fuzzy noise borders. To address this issue, the authors created the Ki-Net, a different structure in which the spatial dimension of the intermediate layer is greater than the spatial dimension of the inserted figures. As a result, the presented Ki-Net gives better result in terms of retrieving edges, resulting in increased overall classification accuracy. Ki-Net improves classification accuracy in addition to that. Furthermore, by combining Ki-Net with U-Net, it achieves rapid confluence for minute anatomical features and uncertain borders. (Ibtehaz et al., 2020) introduced MultiResUNet, which incorporates ResPath, a Residual Path that needs encoder qualities to execute more convolution operations before integrating with equivalent decoder qualities. They also stressed the importance of the MultiRes U-Net being adaptable to future investigations across multiple domains.

The variability of image features, namely the scales of a brain tumor, is one of the challenges in biomedical image categorization. After employing further convolutional filters of sizes 3x3, 5x5, and 7x7 at the same time, they incorporated the resulting image characteristics. A persistent connection was also introduced, which has been found to be successful in medicinal image classification. Ultimately, they added a 1x1 convolutional layer to handle more spatial data. This form of modification is known as a MultiRes block. A downside of skip connections is that the first link joins the encoder and decoder before its first pooling and in the final deconvolution phase. Because the decoder's qualities contained poor reports and the encoder's qualities had rising reports, a possible syntactic difference between the two data sets was discovered.

By expanding intensity separating complication to the building of 3D networks, (Meng et al., 2020) proposed a "V-Net" (LV-Net) that conducts a lesser amount of procedure than V-Net during liver analysis. A moderate VNet was used to investigate the relevant variables created at multiple network levels supervised on the Human Liver datasets. The alert access points provide an approximate sketch of the organs at the two highest network stages, but not at the low levels of granularity. The moderate VNet was used to investigate the second classification images created at low levels of the system supervised on the Human Liver datasets. (Brochard et al., 2020) used VGG-11 as an encoder of a categorization to segment Mri scans of the shoulders, which were received training quite well over ImageNet. Using a pre-trained system to boost accuracy rate was shown to be effective in experiments. A pre-trained system using ImageNet might identify certain basic qualities needed for both pharmaceutical and naturalistic images, eliminating the requirement for restarting while fine-tuning is advantageous to design training. The domain addictive qualities might have been a difficult task when converting pre-trained models of naturalistic sceneries to medicinal computer vision tasks. To detect brain tumors, (Deepa et al., 2021) adopted transfer learning methodology. Transfer learning is used to create the stated network structure. They used a batch normalization size of 200 for 20 iterations. To begin with, the network has been trained and qualified. Second, the system is tested and validated using MRI scans.

The models categorize the input data into two groups: tumors and non-tumors. As a result, the presence of a tumor might be detected in specific MRI images. The "Deep Network Designer" is a MATLAB toolkit for network implementation. They compared different ResNet versions such as ResNet-50, ResNet-101, and ResNet-152. The transfer learning process affects all the networks. SAU-Net was introduced by (Darbeha et al., 2020), and it is focused on model's readability and stability. The proposed architecture uses supplementary-shaped channels to emphasize the issues with poor edges classification results in medical images. Shaped channels and standard texture channels can both capture a lot of shape-dependent data at the same time. Furthermore, the decoder uses spatial as well as channel attentiveness structures to provide information about the model's learning performance at each U-Net levels. Finally, by retrieving learned shapes, one may classify the severely activated area of each decoder's blocks. The learned shape patterns are also utilized to figure out the standard form of the model's intriguing sections. Using a controlled shape stream, the SAU-Net could learn challenging attributes of items. It's a more understandable model than previous work.

Results and Discussions

Architecture of the Project:

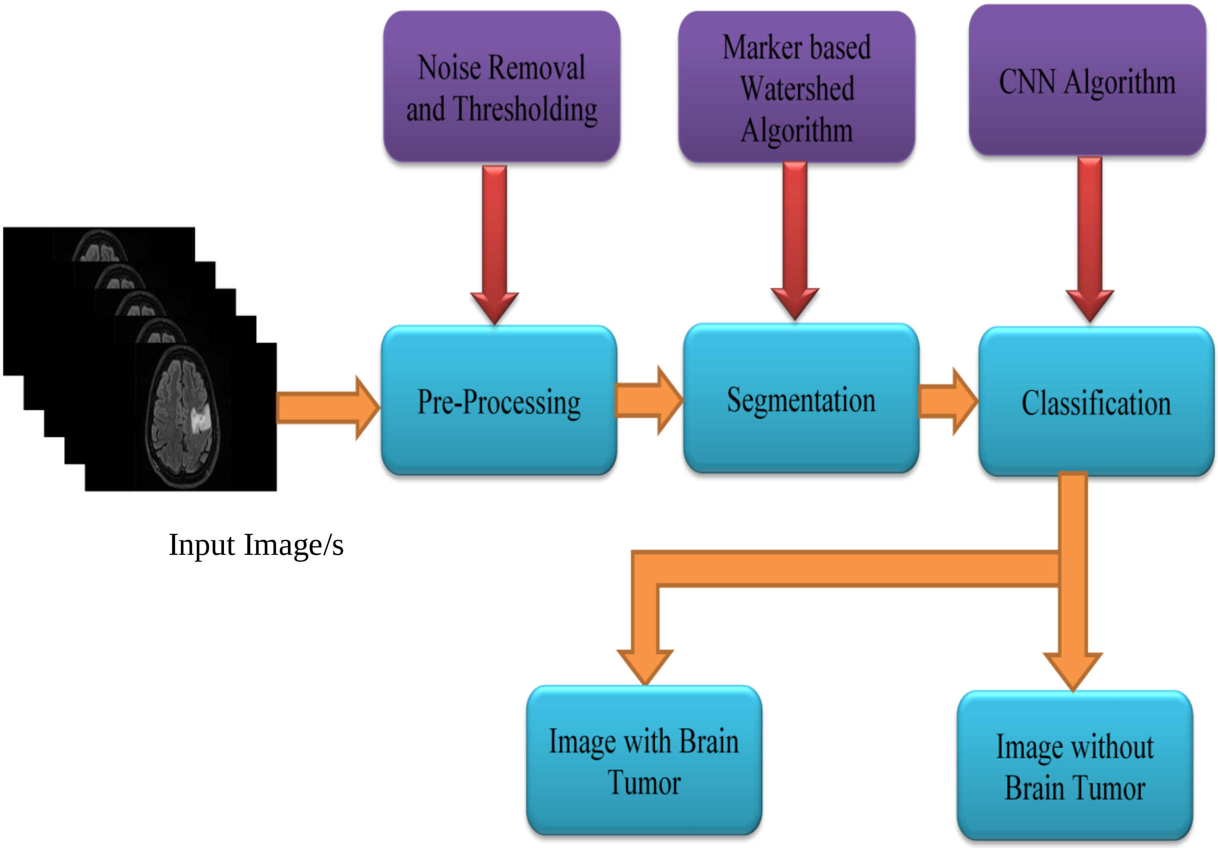


Figure 1: Architecture of the Project

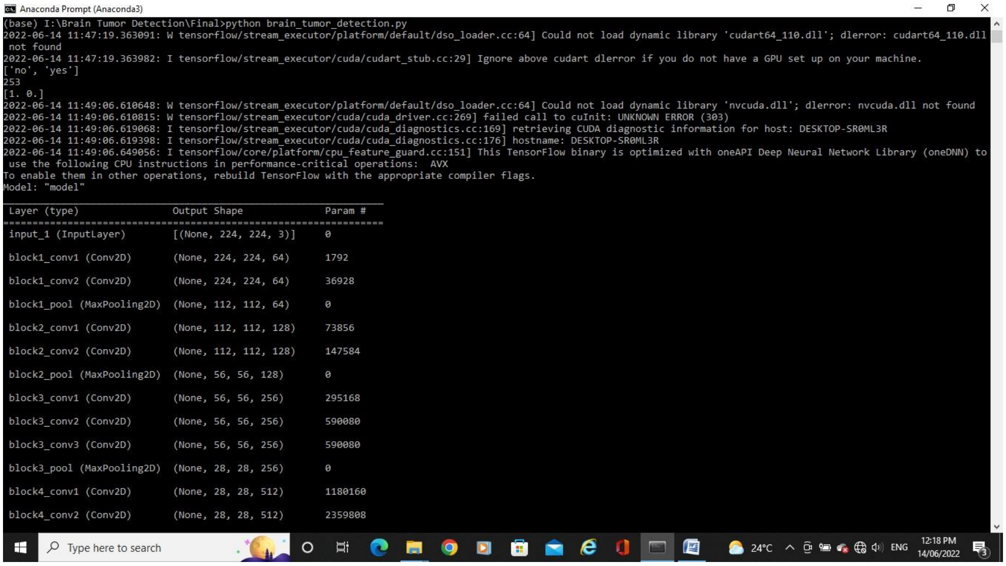
The project's architecture is depicted in the diagram above. The Brain MRI image is loaded into the application first, as can be seen. The image is then pre- processed, which includes thresholding and noise removal from the raw image. The input brain MRI image is separated into two important regions during the segmentation process. There are two types of images: tumor and non-tumor. The data is segmented using the Marker-based Watershed Algorithm. Finally, we can detect Tumor and Non-Tumor images using the CNN Algorithm.

Pre-processing:

The goal of this phase is to turn raw data into aligned and usable model input. Each pixel in the raw image is retrieved and scaled to 227 x 227 pixels. The pixel values are resized between 0 to 1 as well as every pixel is calculated by subtracting from its global mean image. This process is done to verify that the input image should be on the same scale. The image's noise is eliminated, by performing thresholding.

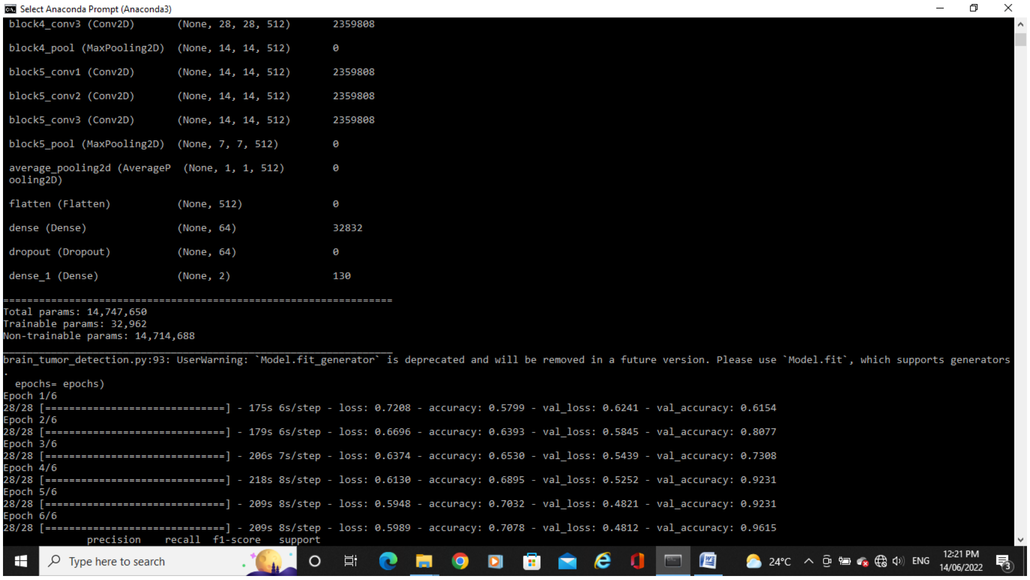
Feature Extraction

To realize the specific patterns throughout the training images, this research proposes a convolutional network. Models are repeatedly trained using training and testing datasets. This returns the most accurate stored model that was developed throughout the training job. The model is evaluated using metrics such as “Accuracy”, “Precision”, “Recall”, and “F1-Score”. This phase is presented in *Figures 2(a), 2(b), 2(c), and Figure 3.*



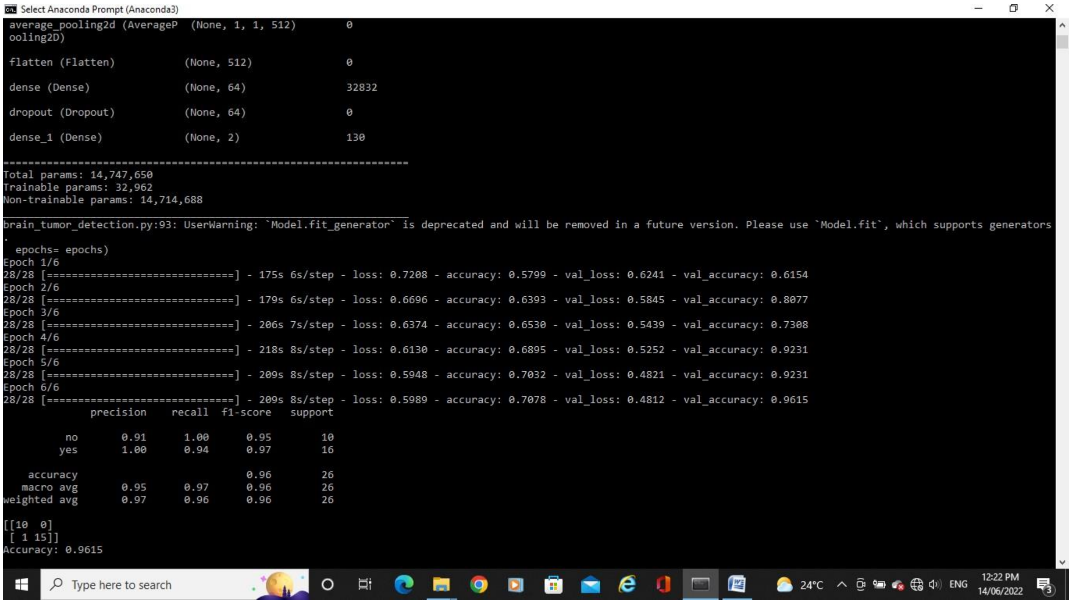
```
(base) I:\Brain Tumor Detection\Final>python brain_tumor_detection.py
2022-06-14 11:47:19.363091: W tensorflow/stream_executor/platform/default/dso_loader.cc:64] Could not load dynamic library 'cudart64_110.dll'; dlerror: cudart64_110.dll
 not found
2022-06-14 11:47:19.363982: I tensorflow/stream_executor/cuda/cudart_stub.cc:29] Ignore above cudart dlerror if you do not have a GPU set up on your machine.
['no', 'yes']
253
[1. 0.]
2022-06-14 11:49:06.610648: W tensorflow/stream_executor/platform/default/dso_loader.cc:64] Could not load dynamic library 'nvcuda.dll'; dlerror: nvcuda.dll not found
2022-06-14 11:49:06.610815: W tensorflow/stream_executor/cuda/cuda_driver.cc:269] failed call to cuInit: UNKNOWN ERROR (303)
2022-06-14 11:49:06.619068: I tensorflow/stream_executor/cuda/cuda_diagnostics.cc:169] retrieving CUDA diagnostic information for host: DESKTOP-SR0ML3R
2022-06-14 11:49:06.619398: I tensorflow/stream_executor/cuda/cuda_diagnostics.cc:176] hostname: DESKTOP-SR0ML3R
2022-06-14 11:49:06.649056: I tensorflow/core/platform/cpu_feature_guard.cc:151] This TensorFlow binary is optimized with oneAPI Deep Neural Network Library (oneDNN) to
 use the following CPU instructions in performance-critical operations:  AVX
To enable them in other operations, rebuild TensorFlow with the appropriate compiler flags.
Model: "model"
_________________________________________________________________
 Layer (type)                Output Shape              Param #
=================================================================
 input_1 (InputLayer)        [(None, 224, 224, 3)]     0

 block1_conv1 (Conv2D)       (None, 224, 224, 64)      1792

 block1_conv2 (Conv2D)       (None, 224, 224, 64)      36928

 block1_pool (MaxPooling2D)  (None, 112, 112, 64)      0

 block2_conv1 (Conv2D)       (None, 112, 112, 128)     73856

 block2_conv2 (Conv2D)       (None, 112, 112, 128)     147584

 block2_pool (MaxPooling2D)  (None, 56, 56, 128)       0

 block3_conv1 (Conv2D)       (None, 56, 56, 256)       295168

 block3_conv2 (Conv2D)       (None, 56, 56, 256)       590080

 block3_conv3 (Conv2D)       (None, 56, 56, 256)       590080

 block3_pool (MaxPooling2D)  (None, 28, 28, 256)       0

 block4_conv1 (Conv2D)       (None, 28, 28, 512)       1180160

 block4_conv2 (Conv2D)       (None, 28, 28, 512)       2359808
```

Figure 2(a): Training process



```
 block4_conv3 (Conv2D)       (None, 28, 28, 512)       2359808

 block4_pool (MaxPooling2D)  (None, 14, 14, 512)       0

 block5_conv1 (Conv2D)       (None, 14, 14, 512)       2359808

 block5_conv2 (Conv2D)       (None, 14, 14, 512)       2359808

 block5_conv3 (Conv2D)       (None, 14, 14, 512)       2359808

 block5_pool (MaxPooling2D)  (None, 7, 7, 512)         0

 average_pooling2d (AverageP  (None, 1, 1, 512)        0
 ooling2D)

 flatten (Flatten)           (None, 512)               0

 dense (Dense)               (None, 64)                32832

 dropout (Dropout)           (None, 64)                0

 dense_1 (Dense)             (None, 2)                 130

=================================================================
Total params: 14,747,650
Trainable params: 32,962
Non-trainable params: 14,714,688
_________________________________________________________________
brain_tumor_detection.py:93: UserWarning: `Model.fit_generator` is deprecated and will be removed in a future version. Please use `Model.fit`, which supports generators
.
  epochs= epochs)
Epoch 1/6
28/28 [==============================] - 175s 6s/step - loss: 0.7208 - accuracy: 0.5799 - val_loss: 0.6241 - val_accuracy: 0.6154
Epoch 2/6
28/28 [==============================] - 179s 6s/step - loss: 0.6696 - accuracy: 0.6393 - val_loss: 0.5845 - val_accuracy: 0.8077
Epoch 3/6
28/28 [==============================] - 206s 7s/step - loss: 0.6374 - accuracy: 0.6530 - val_loss: 0.5439 - val_accuracy: 0.7308
Epoch 4/6
28/28 [==============================] - 218s 8s/step - loss: 0.6130 - accuracy: 0.6895 - val_loss: 0.5252 - val_accuracy: 0.9231
Epoch 5/6
28/28 [==============================] - 209s 8s/step - loss: 0.5948 - accuracy: 0.7032 - val_loss: 0.4821 - val_accuracy: 0.9231
Epoch 6/6
28/28 [==============================] - 209s 8s/step - loss: 0.5989 - accuracy: 0.7078 - val_loss: 0.4812 - val_accuracy: 0.9615
              precision    recall  f1-score   support
```

Figure 2(b): Epoches



```
 average_pooling2d (AverageP  (None, 1, 1, 512)        0
 ooling2D)

 flatten (Flatten)           (None, 512)               0

 dense (Dense)               (None, 64)                32832

 dropout (Dropout)           (None, 64)                0

 dense_1 (Dense)             (None, 2)                 130

=================================================================
Total params: 14,747,650
Trainable params: 32,962
Non-trainable params: 14,714,688
_________________________________________________________________
brain_tumor_detection.py:93: UserWarning: `Model.fit_generator` is deprecated and will be removed in a future version. Please use `Model.fit`, which supports generators
.
  epochs= epochs)
Epoch 1/6
28/28 [==============================] - 175s 6s/step - loss: 0.7208 - accuracy: 0.5799 - val_loss: 0.6241 - val_accuracy: 0.6154
Epoch 2/6
28/28 [==============================] - 179s 6s/step - loss: 0.6696 - accuracy: 0.6393 - val_loss: 0.5845 - val_accuracy: 0.8077
Epoch 3/6
28/28 [==============================] - 206s 7s/step - loss: 0.6374 - accuracy: 0.6530 - val_loss: 0.5439 - val_accuracy: 0.7308
Epoch 4/6
28/28 [==============================] - 218s 8s/step - loss: 0.6130 - accuracy: 0.6895 - val_loss: 0.5252 - val_accuracy: 0.9231
Epoch 5/6
28/28 [==============================] - 209s 8s/step - loss: 0.5948 - accuracy: 0.7032 - val_loss: 0.4821 - val_accuracy: 0.9231
Epoch 6/6
28/28 [==============================] - 209s 8s/step - loss: 0.5989 - accuracy: 0.7078 - val_loss: 0.4812 - val_accuracy: 0.9615
              precision    recall  f1-score   support

          no       0.91      1.00      0.95        10
         yes       1.00      0.94      0.97        16

    accuracy                           0.96        26
   macro avg       0.95      0.97      0.96        26
weighted avg       0.97      0.96      0.96        26

[[10  0]
 [ 1 15]]
Accuracy: 0.9615
```

Figure 2(c): Accuracy

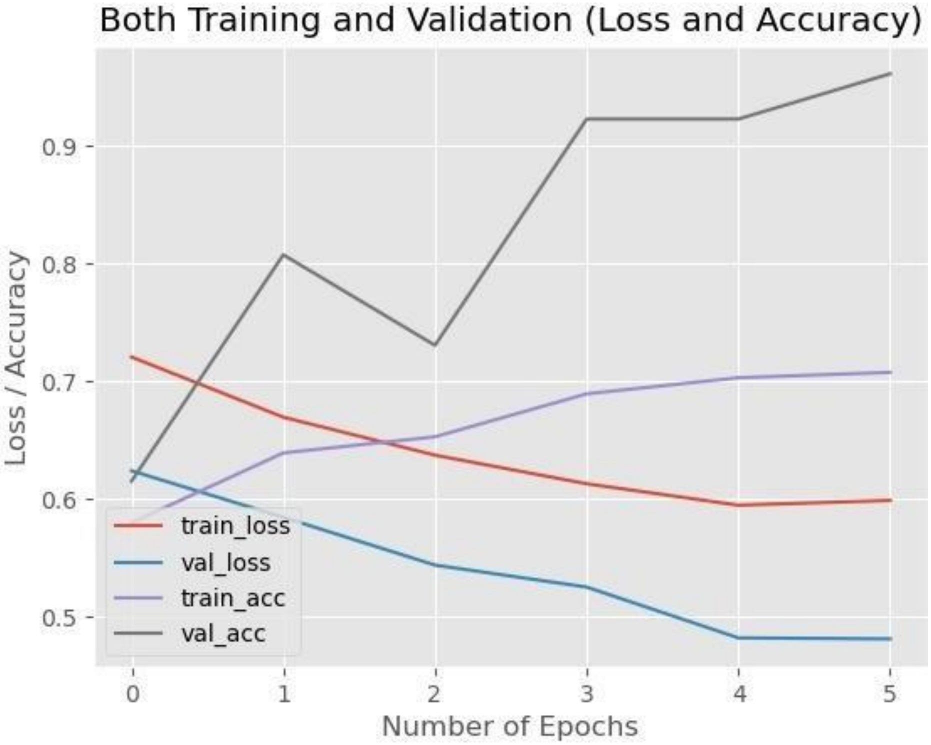


Figure 3: “Training and Validation” Accuracy and Loss Graph

Segmentation

We split the brain images containing tumors in order to deliver them to the classification algorithm. We found two significant sections in the image after segmentation: tumor and non-tumor. The Marker based Watershed Algorithm is used to segment the data.

Marker based Watershed Algorithm

A marker-based water-shed approach, which is an interactive picture segmentation method, was implemented by OpenCV. It assigns various labels to the item. Firstly, find the sure background objects using morphological operations like dilation and mark them with one color. Second, find the sure foreground objects sing dilation transform and mark them with another color (or intensity). *Figures 4(c) and 5(b)* depict the above-mentioned two steps. Thirdly, find the objects that neither lies in foreground nor background (Unknown area). This region is labeled with 0. That's where we'll put our marker. After that, use the watershed algorithm. The boundaries of entities will have value '-1'. The marker will be modified with the labels that are provided. The third phase of the Marker-based Watershed Algorithm is depicted *in Figures 4(d) and 5(c).*

Detection

The final outcome is produced in this phase. The program determines whether or not the input brain MRI image is a brain tumor image.

Output 1: Loading and Detecting a Tumor Image

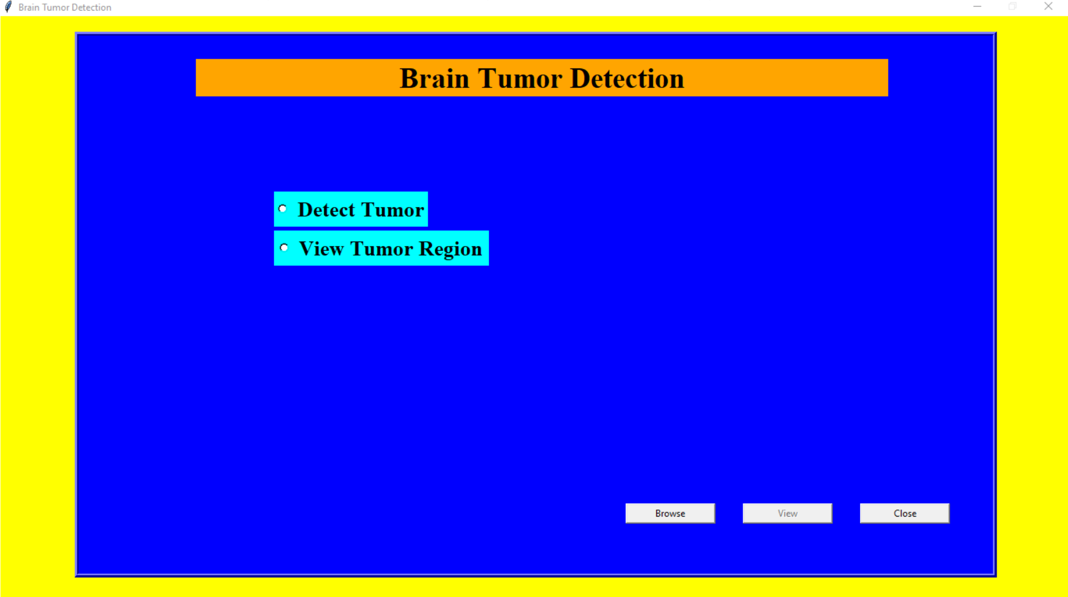
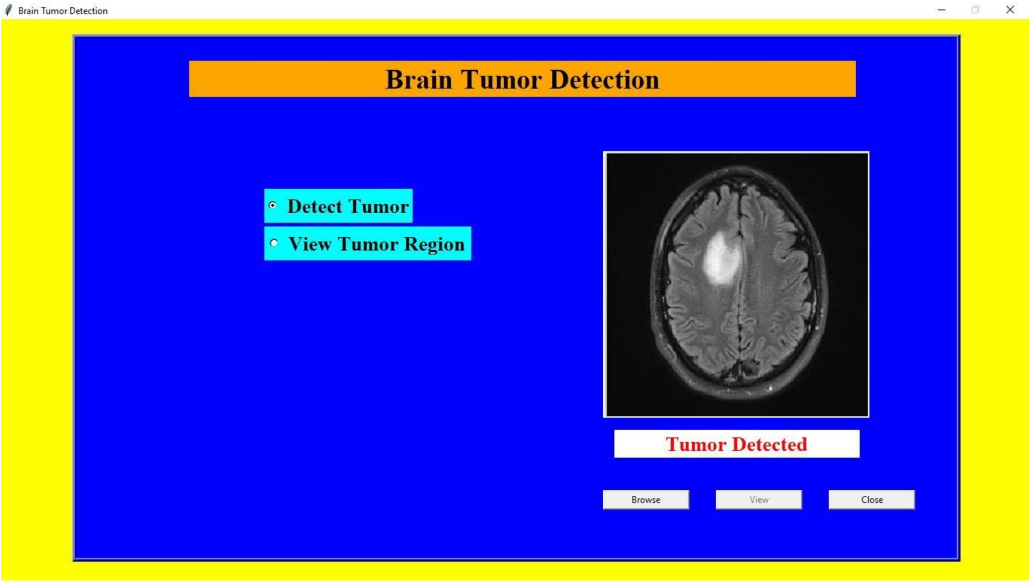


Figure 4(a): Home Page

The project's primary screen is depicted in *Figure 4(a)*. To upload an image, the user must first select the browse option, after which he or she can upload either a tumor or a non-tumor image of the brain.



Tumor Detected

Figure 4(b): Brain MRI image having Tumor

A brain MRI image with a tumor is loaded in *Figure 4(b)*. When the user selects Detect Tumor, the program/algorithm recognizes that the image is of a tumor. As a result, the output will be labeled “Tumor Detected” in red.

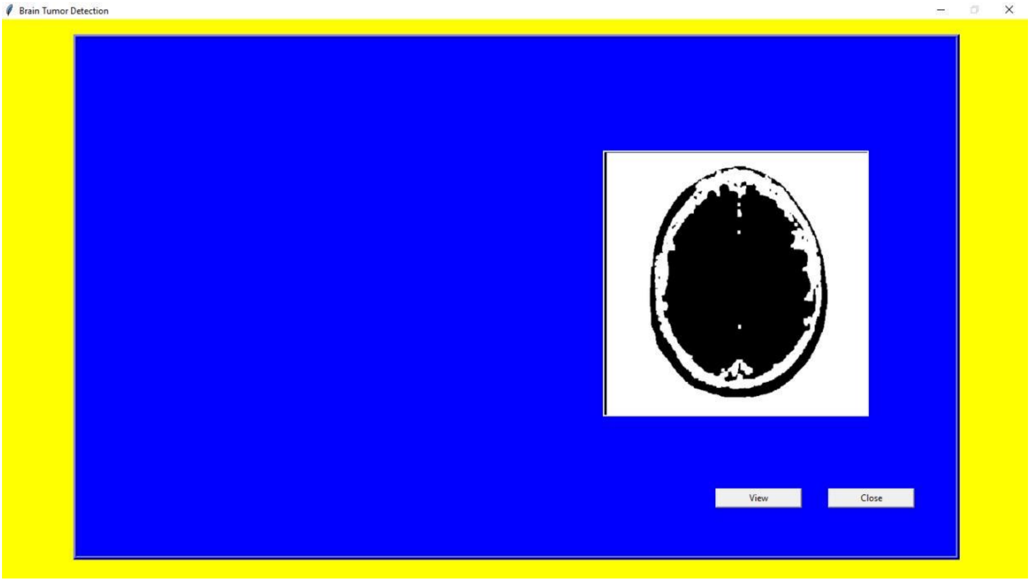


Figure 4(c): Segmentation (1)

The result of the segmentation operation is shown in *Figure 4(c)*. Certain foreground and background objects are recognized and segmented in this step.

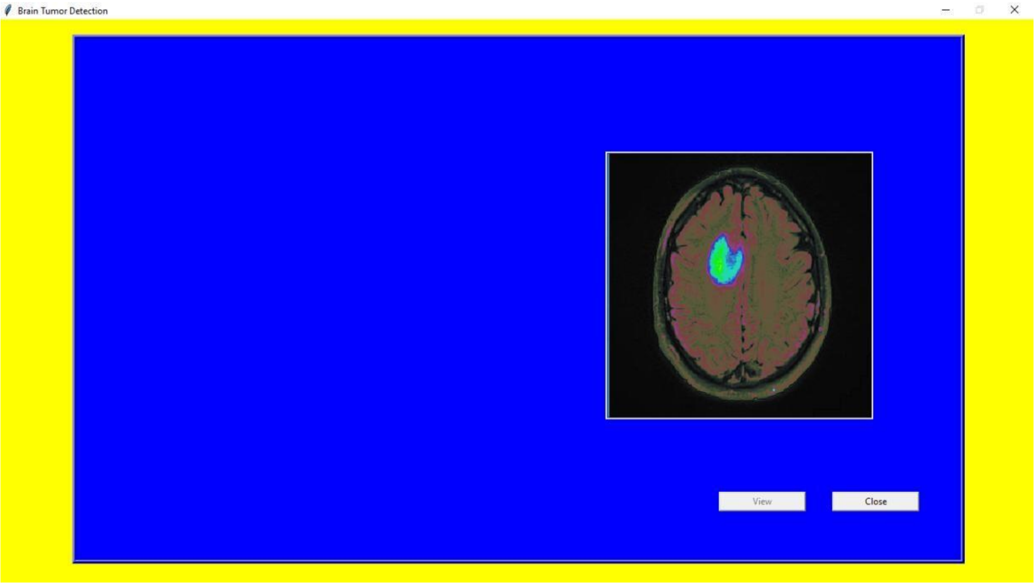
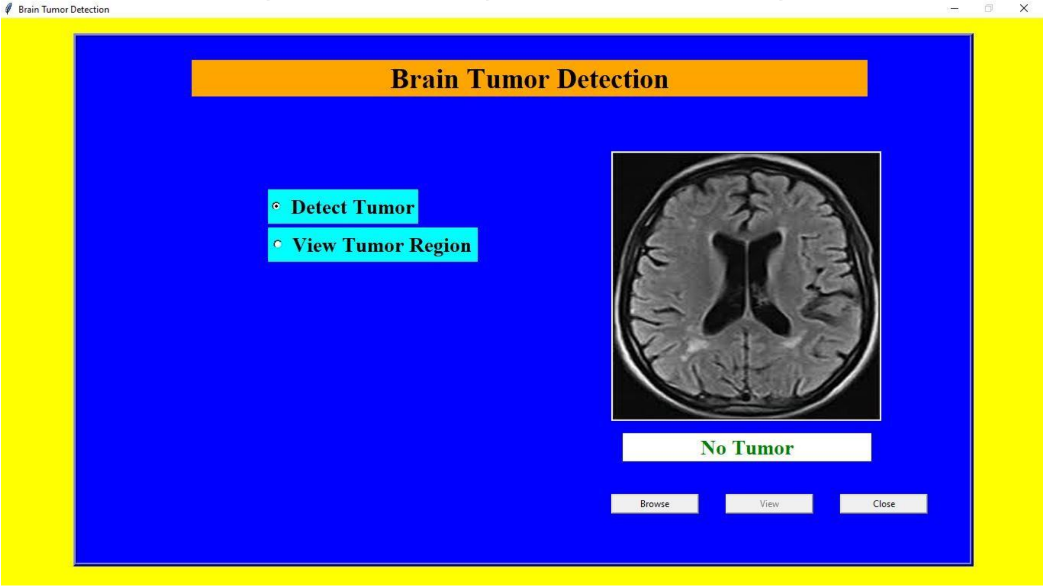


Figure 4(d): Tumor area marked by the Marker

The marker detects and marks the objects lying in the unknown area (i.e. neither foreground nor background) in *Figure 4(d)*. This is the part of the brain that has a tumor or is malignant.

Output 2: Loading and Detecting a Non-Tumor Image



● Detect Tumor
○ View Tumor Region

No Tumor

Figure 5(a): Brain MRI image not having Tumor

A brain MRI scan without a tumor is loaded in *Figure 5(a)*. When the user selects Detect Tumor, the program/algorithm recognizes that the image is not of a tumor. As a result, the output will be labeled "No Tumor" in green.

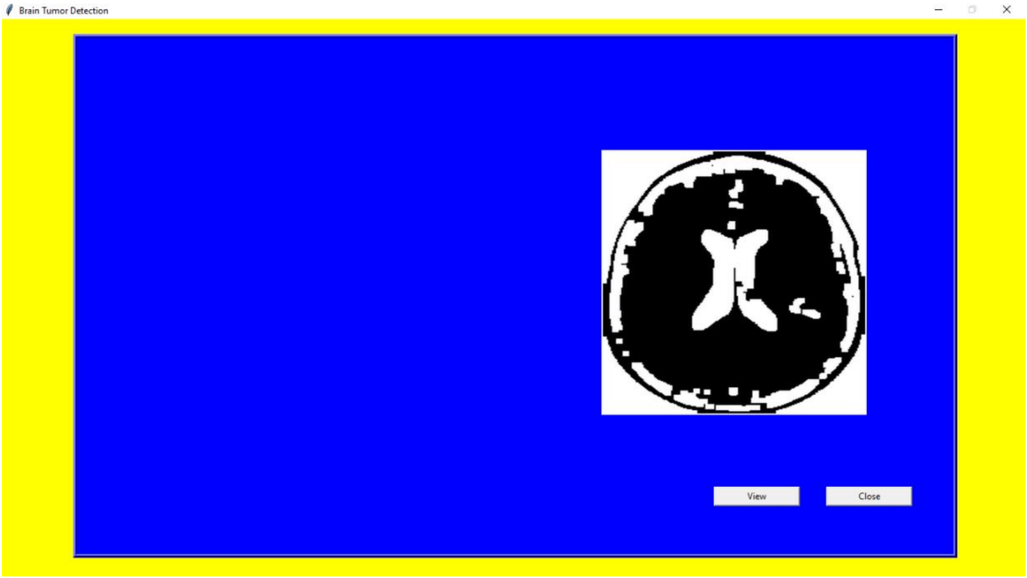


Figure 5(b): Segmentation (2)

The result of the segmentation operation is shown in *Figure 5(b)*. Certain foreground and background objects are recognized and segmented in this step.

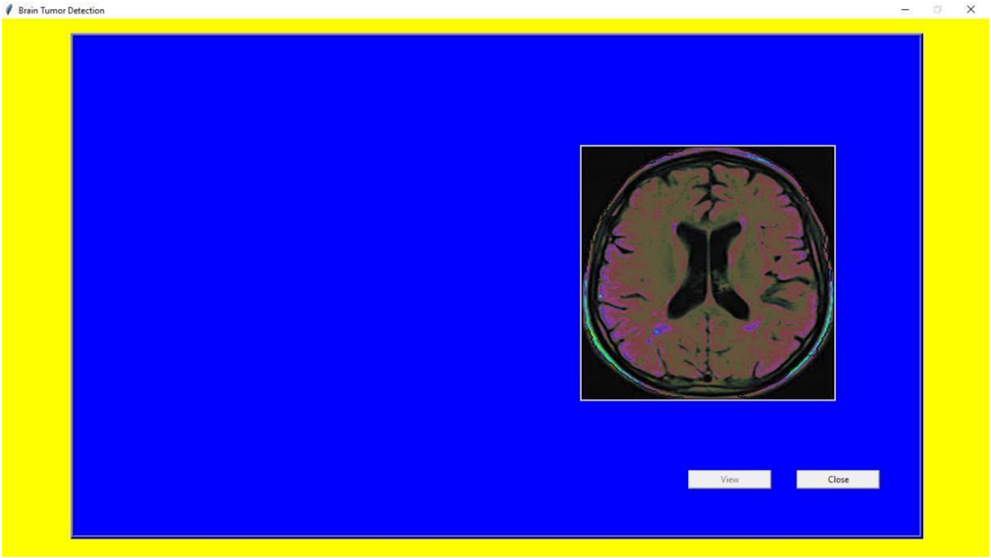


Figure 5(c): No Tumor

The marker detects and marks the objects lying in the unknown area (i.e. neither foreground nor background) in *Figure 5(c)*. No part of the brain image has been marked by the marker. As a result, the brain MRI image supplied by the user does not include any tumor.

Because we are automatically segmenting and classifying the tumor, the amount of time taken by a doctor to identify and categorize the tumor is greatly reduced. Furthermore it helps in minimizing the number of errors committed when segmenting and classifying tumors to some extent.

Conclusion

Utilizing marker based watershed algorithm and CNN approaches; a brain tumor detection project work has been done using MRI data received from locally accessible sources. Pre-processing was used to improve the input brain MRI image and eliminate noise from the brain MRI image in order to detect brain tumors. Multiple morphological operators were utilized to modify the image as per the requirements, which proved to be quite helpful in extracting the tumors from the image. Filtering, gray-leveling, and image adjustment were used in the pre- processing. Because the tumor isn't really always in the same region/position, different values must be supplied to specific operators for multiple input images.

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