



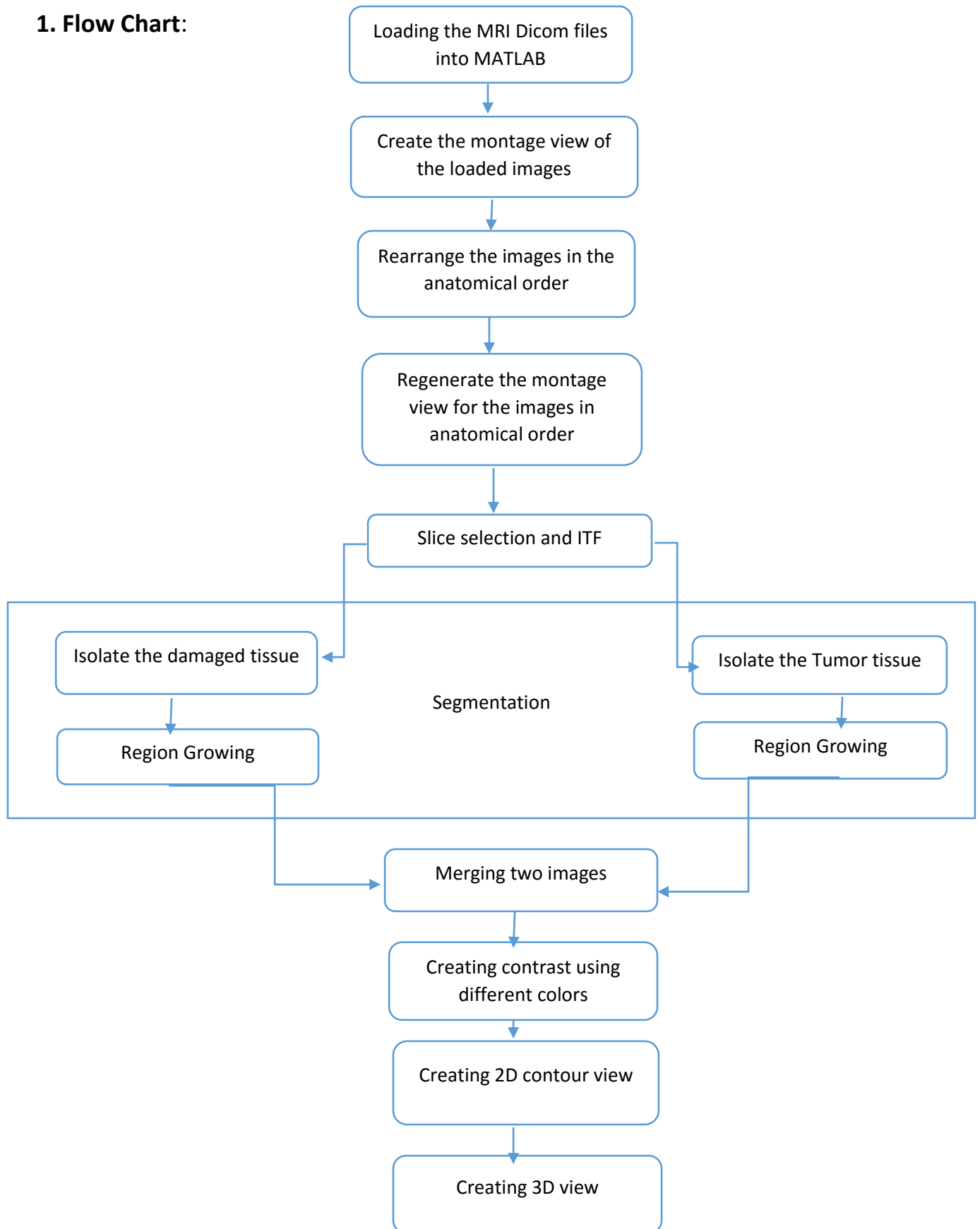
IMAGE PROCESSING WITH MATLAB: APPLICATIONS IN MEDICINE & BIOLOGY PROJECT

Anuhya Reddy(1001239464), Vishal Kandagatla(1001275803)



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DEPARTMENT OF BIOENGINEERING
UNIVERSITY OF TEXAS ARLINGTON

1. Flow Chart:



2. Loading MRI data

Loading data

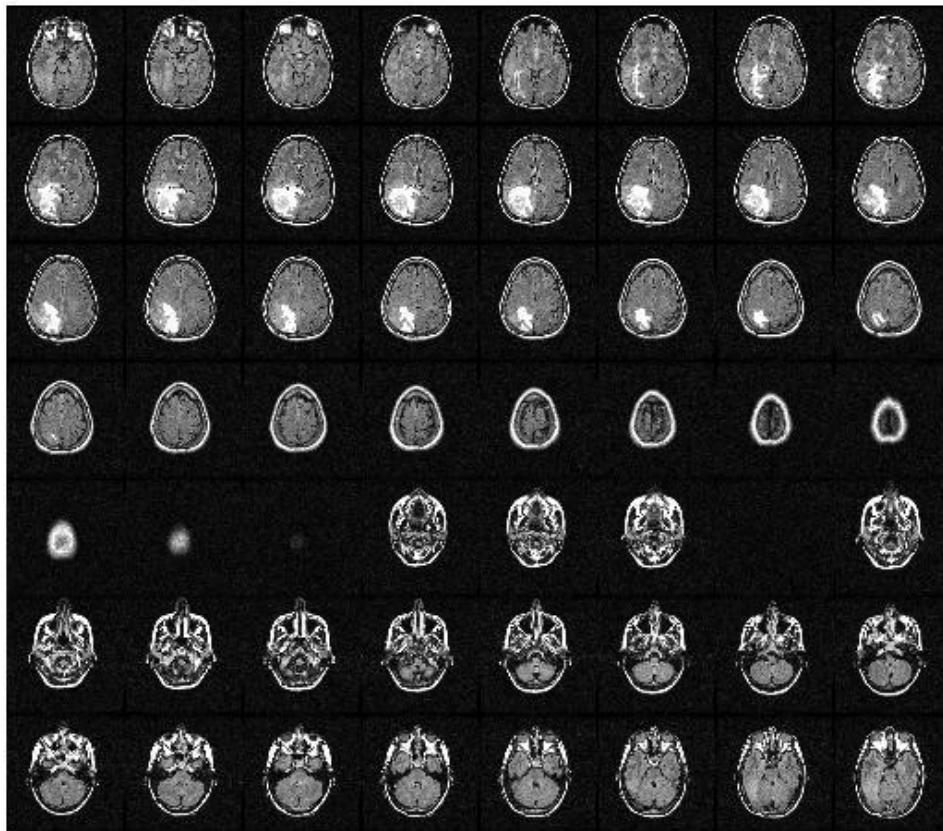
There were a total of 56 MRI brain images that had to be loaded into MATLAB in order to perform image processing procedures. We need the current folder as a string. Hence we made use of 'num2str' function to convert the numeric data into string. Thereafter, 'dicomread' command was used to read all the 56 images in the variable 'imgrd' using a 'for' loop onto a variable 'mri'.

Plotting images:

After loading all the images in to MATLAB the next step was to generate a montage view of the MRI data in order to create a more comfortable viewing experience. Hence, to display all the dicom images we have into one single rectangular frame we used the 'montage' function available in MATLAB. Again for loop was applied (where i=1 to 56) and images were plotted using 'montage' function. Reshape command is used to change the dimensions of

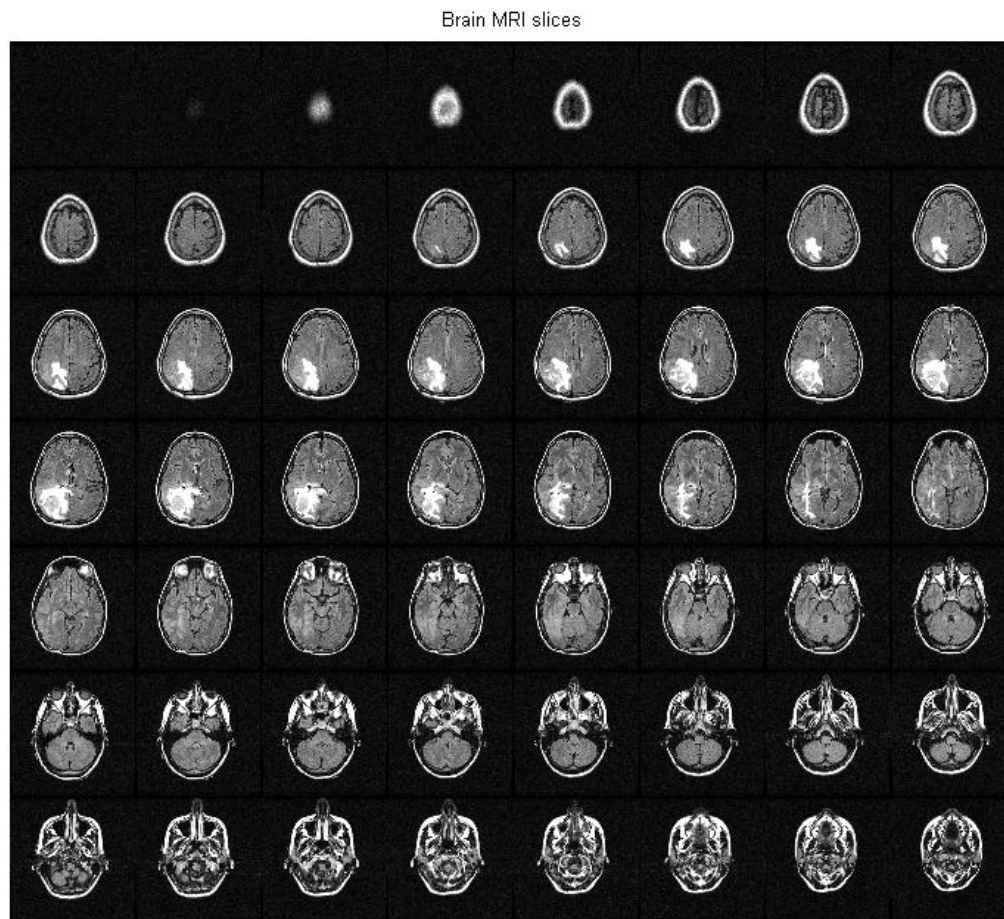
Loading the images:

Brain MRI slices



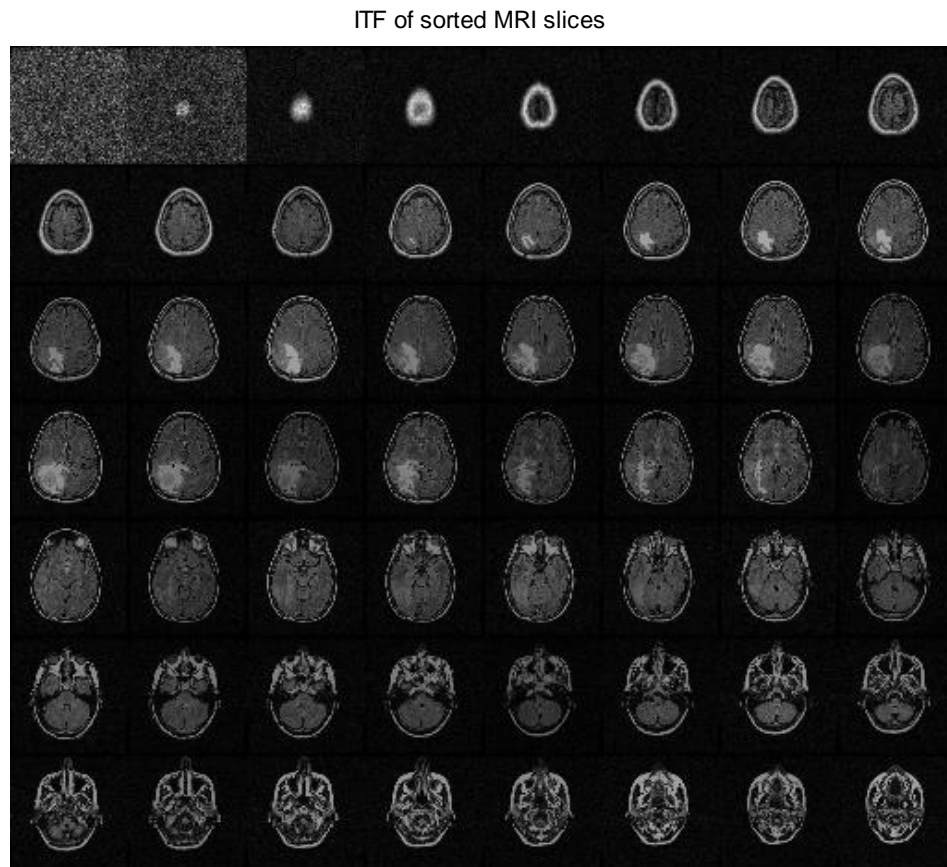
3. Replotting it in an anatomical order from top to bottom:

We have sorted the given MRI slices in top to bottom order and saved it in variable 'sorted_mri'. Syntax 'Descend' is used to get the loaded images in descending order i.e., from top to bottom of the head. We displayed all the dicom images we have read in 'sorted_mri' variable into one single rectangular frame we used the 'montage' function available in MATLAB.

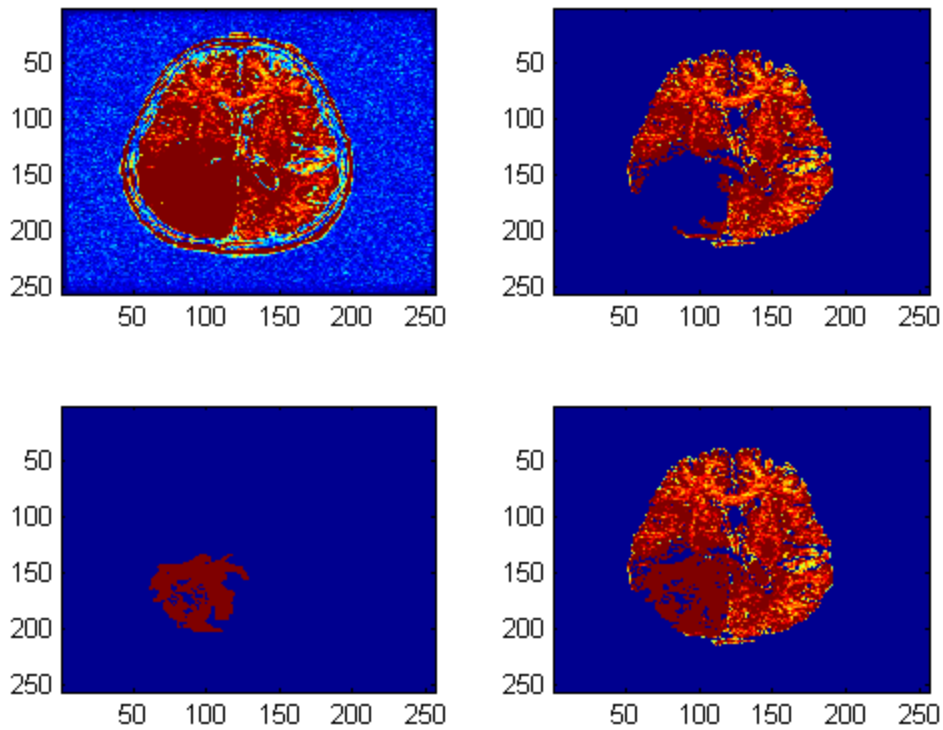


4. Image Segmentation:

We are performing intensity transform function on all the sorted MRI slices before segmentation because to brighten or darken the intensities of an image. The ITF performed MRI slices are displayed using montage view from the variable 'trans_sort'.

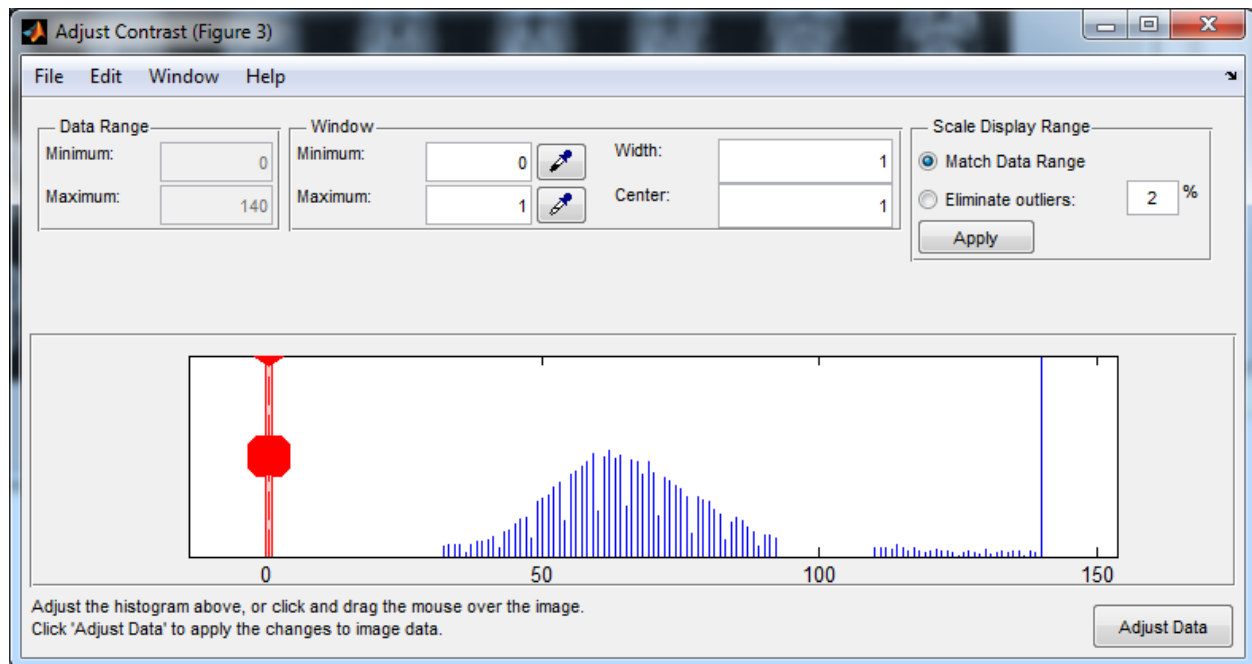


We have selected a MRI slice with maximum tumor area in it. Segmentation was performed for that slice using the region growing technique with a function call file 'region_grow.m'. Seedmask is used to isolate the tumor region from the healthy tissue and then plotted the healthy tissue. Another seedmask is selected to isolate the normal brain tissue from the slice and then it is plotted. We then merged both the isolated tissue and tumor images into one variable 'tot_segmented'.



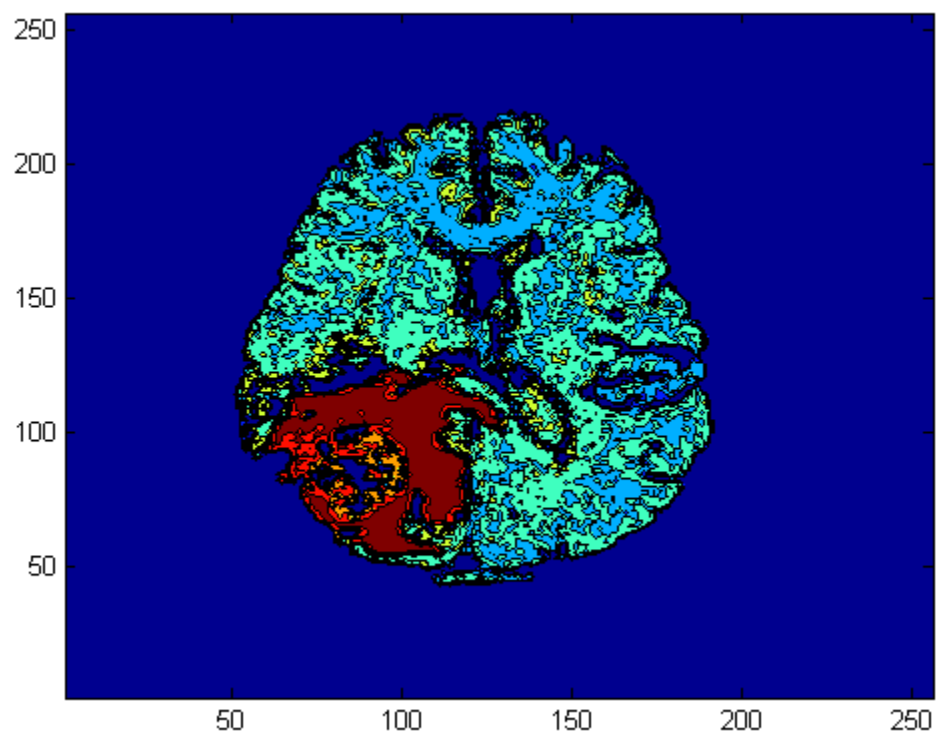
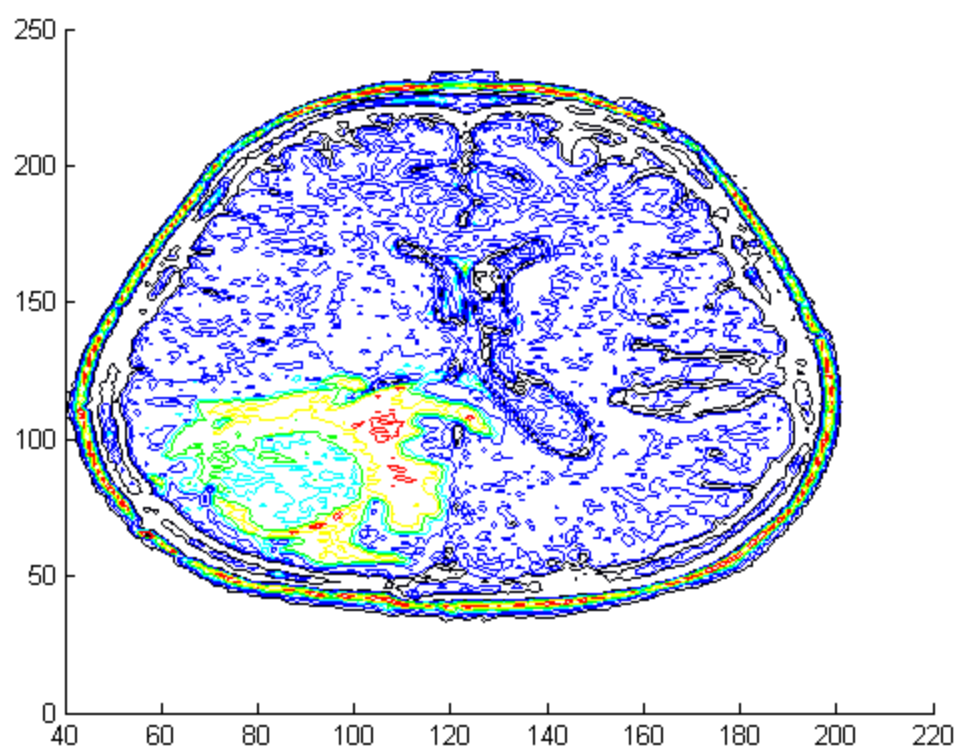
6. Contrast Mapping :

We have used `imcontrast` command to interactively adjust the contrast in a separate figure 'Adjust contrast (Fig \$)' that is associated with colormap `jet` image in a current figure, called the target image 'tot_segmented'. The adjust contrast tool is an interactive contrast and brightness adjustment tool which changes the actual pixel values of target image.



7. Performing the 2D Contour view

In order to perform the contour view we applied a function in MATLAB that lets us create a contour plot of the image data. The command used to display the contour plot was 'contourf' which sets up the axis of the image automatically such that it matches the aspect ratio of the given image. And 'flipdm' to flip the array along the specific dimension(row-wise down).To generate a contour in the volume slice plane 'contourslice' command is used.



8. Publishing the Report

We have published the script files using the publish function in the matlab.

9. Generating the 3D image of both normal and tumor tissue

We have selected the tumor region to plot it in 3D, i.e. 14-30 images in the image stack. To extract the isosurface data of the volume 'Isosurface' command is used for both the tumor and the normal tissue. To differentiate the normal tissue with the tumor tissue 'patch' command is used to color the different regions.

3D view of selected slices

