
Table of Contents

.....	1
Loading MRI slices	1
Creating Montage view	1
Thresholding and Segmentation using Region Growing	2
Tumour segmentation	2
Displaying Segmented Image and Tumor	3
Contour Slice	4
3D Isosurface rendering of Segmented brain tissue	5
3D Rendering of tumour tissue	6
Montage of the segmented brain image	7
Montage of the tumor	8
References	8

```
%Matlab Final Take Home Project
%Anand and Hemanth
```

```
clc
clear all
close all
```

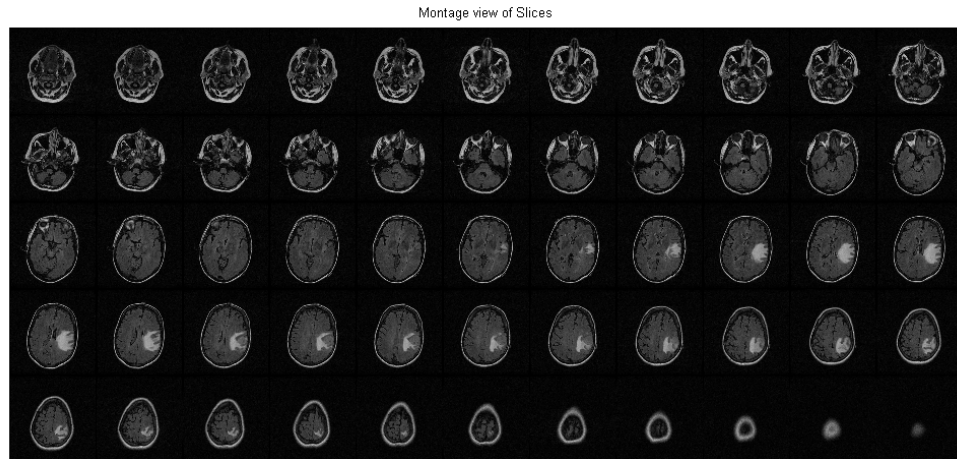
Loading MRI slices

```
FileFolder=fullfile(pwd,'Project');
files=dir(fullfile(FileFolder,'*.dcm'));
fileNames={files.name};
mri=zeros(256,256,length(files));
```

Creating Montage view

```
for i=1: length(files)
    mri(:,:,i)=dicomread(fileNames{i});
end
new=reshape(mri,[256 256 1 length(files)]);
montage(new,'DisplayRange',[],'Size',[5 11])
title('Montage view of Slices')
```

Warning: Image is too big to fit on screen; displaying at 33%



Thresholding and Segmentation using Region Growing

```
for i=1:length(files)

    img =mri(:,:,i);
    img=img.*(img>150);
    % Finding the starting seed
    %imagesc(img),colormap(gray)
    %[x,y]=ginput(1);
    %x=round(x);y=round(y);
    x=134;y=140;
    % seed(x,y,img,rmin,rmax) is a user defined function for region growing
    seedmask=seed(x,y,img,50,340);
    se=strel('square',2);
    seedmask=imdilate(seedmask,se);
    seg_img(:,:,i)=img.*(seedmask>1);

end
```

Tumour segmentation

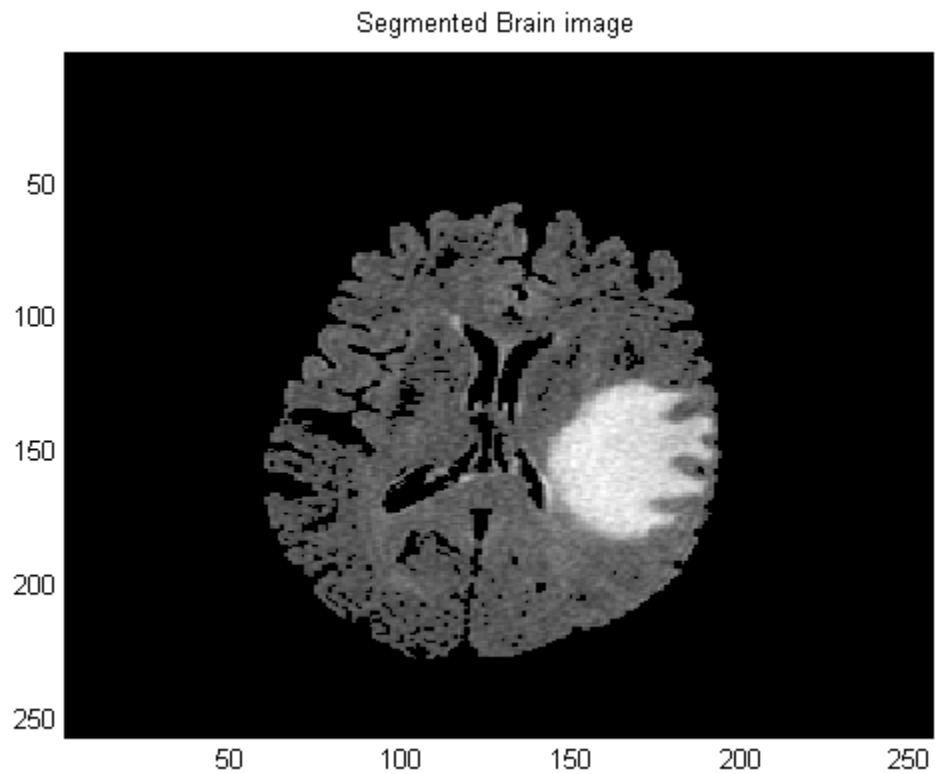
Finding the seed for tumour

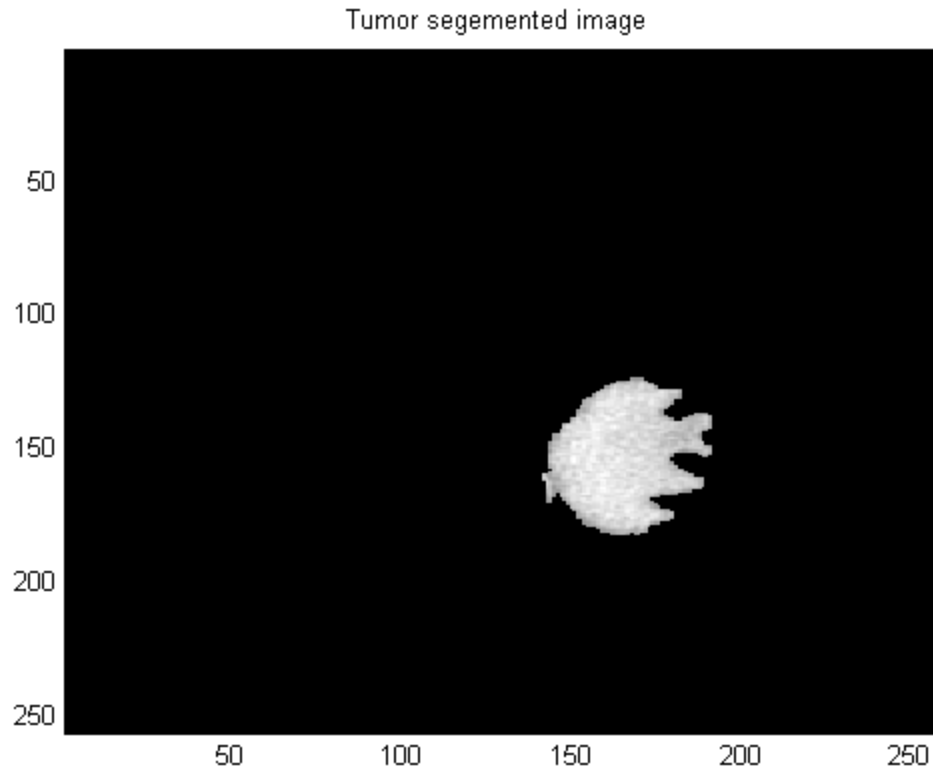
```
%imagesc(seg_img),colormap(gray)
[x,y]=ginput(1);
%x=round(x);y=round(y);
x=174;y=153;
tumourmask=seed(x,y,img,100,150);
se=strel('square',2);
tumourmask=imopen(tumourmask,se);
tumour_img(:,:,i)=img.*(tumourmask>1);

end
```

Displaying Segmented Image and Tumor

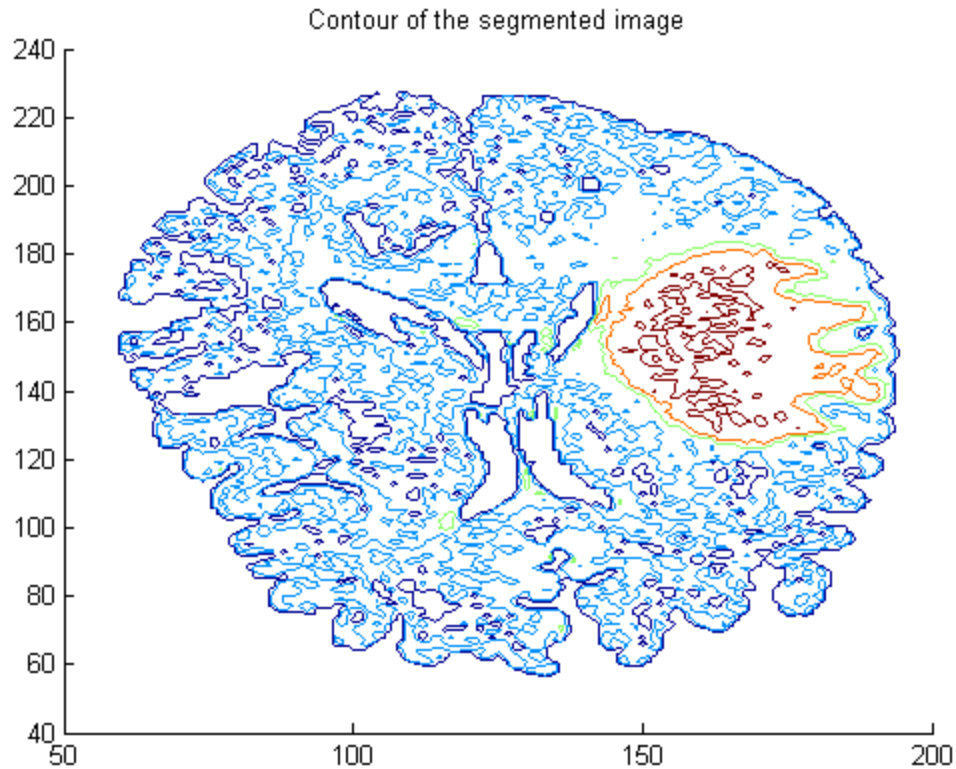
```
figure
imagesc(seg_img(:,:,32)),colormap(gray),title('Segmented Brain image')
figure
imagesc(tumour_img(:,:,32)),colormap(gray),title('Tumor segemented image')
```





Contour Slice

```
figure  
contourslice(seg_img,[],[],32),title('Contour of the segmented image')
```



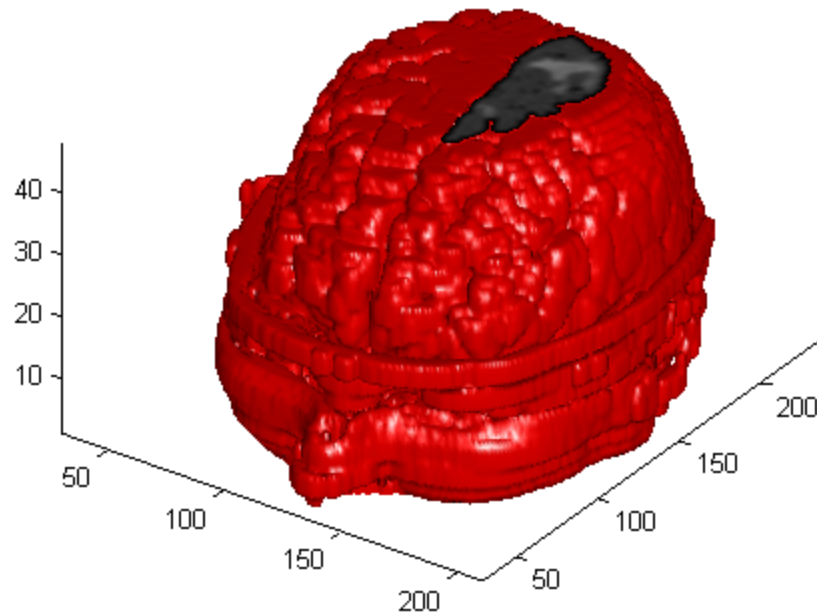
3D Isosurface rendering of Segmented brain tissue

```
figure
colormap(gray)
Ds = smooth3(seg_img(:,:,1:48));
hiso = patch(isosurface(Ds,5), 'FaceColor', 'r', 'EdgeColor', 'none');
title('Segmented brain in 3D')
isonormals(Ds,hiso)
hcap = patch(isocaps(Ds,10), 'FaceColor', 'interp', 'EdgeColor', 'none');
view(35,30)
axis tight
daspect([1,1,.4])
lightangle(45,30);
lighting gouraud
hcap.AmbientStrength = 0.6;
hiso.SpecularColorReflectance = 0;
hiso.SpecularExponent = 50;
```

Warning: Struct field assignment overwrites a value with class "double". See MATLAB R14SP2 Release Notes, Assigning Nonstructure Variables As Structure Displays Warning, for details.

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Segmented brain in 3D

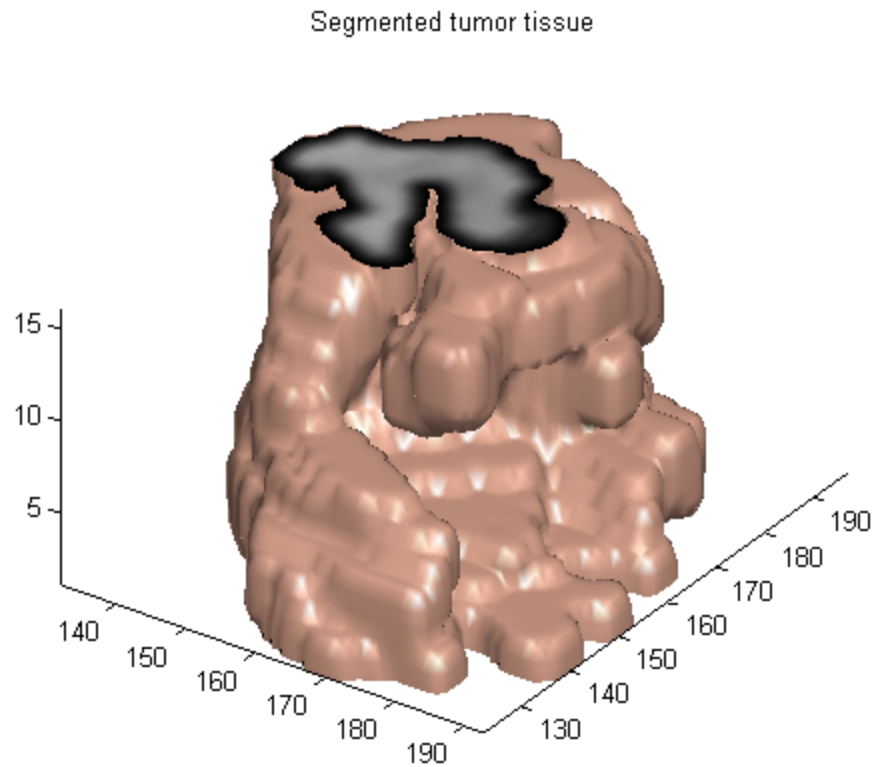


3D Rendering of tumour tissue

```
figure
colormap(gray)
Ts= smooth3(tumour_img(:,:,32:47));
% Ds = smooth3(seg_img(:,:,1:48));
bs=isosurface(Ts,5);
hiso = patch(bs,'FaceColor',[1,.75,.65],'EdgeColor','none');
isonormals(Ts,hiso),title('Segmented tumor tissue')
hcap = patch(isocaps(Ts,10),'FaceColor','interp','EdgeColor','none');
view(35,30)
axis tight
daspect([1,1,.4])
lightangle(45,45);
lighting gouraud
hcap.AmbientStrength = 0.6;
hiso.SpecularColorReflectance = 0;
hiso.SpecularExponent = 50;
```

Warning: Struct field assignment overwrites a value with class "double". See MATLAB R14SP2 Release Notes, Assigning Nonstructure Variables As Structure Displays Warning, for details.

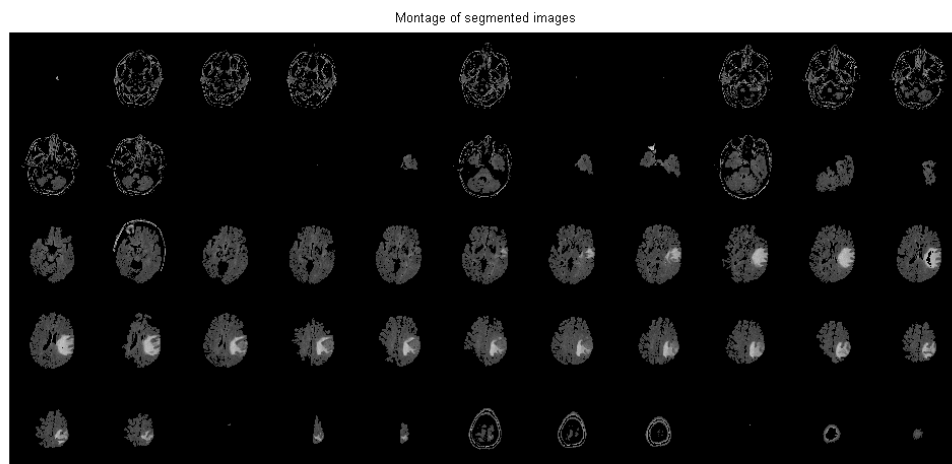
Warning: Struct field assignment overwrites a value with class "double". See MATLAB R14SP2 Release Notes, Assigning Nonstructure Variables As Structure Displays Warning, for details.



Montage of the segmented brain image

```
figure
new_seg=reshape(seg_img,[256 256 1 length(files)]);
montage(new_seg,'DisplayRange',[0,1], 'Size', [5 11])
title('Montage of segmented images')
```

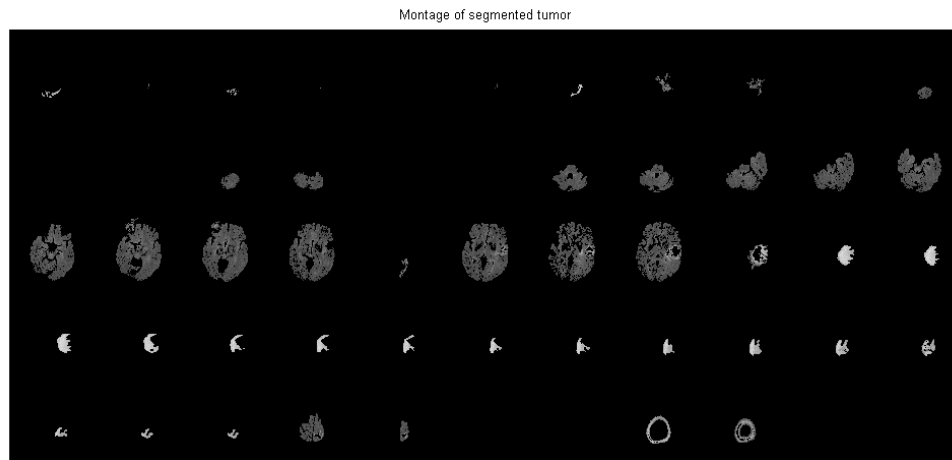
Warning: Image is too big to fit on screen; displaying at 33%



Montage of the tumor

```
figure
new_tum=reshape(tumour_img,[256 256 1 length(files)]);
montage(new_tum,'DisplayRange',[],'Size',[5 11])
title('Montage of segmented tumor')
```

Warning: Image is too big to fit on screen; displaying at 33%



References

- 1)<http://www.mathworks.com/help/matlab/visualize/techniques-for-visualizing-scalar-volume-data.html?refresh=true>
- 2)<http://www.mathworks.com/videos/medical-image-processing-with-matlab-81890.html>

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