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```
% Anuhya Reddy & Vishal Kandagatla
% Image Processing with MATLAB:applications in Medicine Project
% Final Take Home Project
```

clear workspace

```
clc;
clear all;
close all;
```

question 2:Load MRI dicom files

```
mri=zeros(256,256,56);
for i=0:55
    if i>9
        imgrd=['0000' num2str(i) '.dcm'];%num2str used to convert to string format
    else
        imgrd=['00000' num2str(i) '.dcm'];
    end

    %saving all the read dicom files into mri matrix
    mri(:,:,i+1)=uint8(dicomread(imgrd));

    %extracting the information of MRI slices using dicominfo
    info = dicominfo(imgrd);

    %slice location of each MRI slice
    slice_loc(i+1) = info.SliceLocation;
    %slice thickness of each MRI slice
    slice_thk(i+1) = info.SliceThickness;

    %saving the filenames of each and every MRI slice in the variable...
    %image_Slice_name
```

```

image_slice_name(i+1,:) = imgrd;

vox_size=[info.PixelSpacing; info.SliceThickness]';
end

```

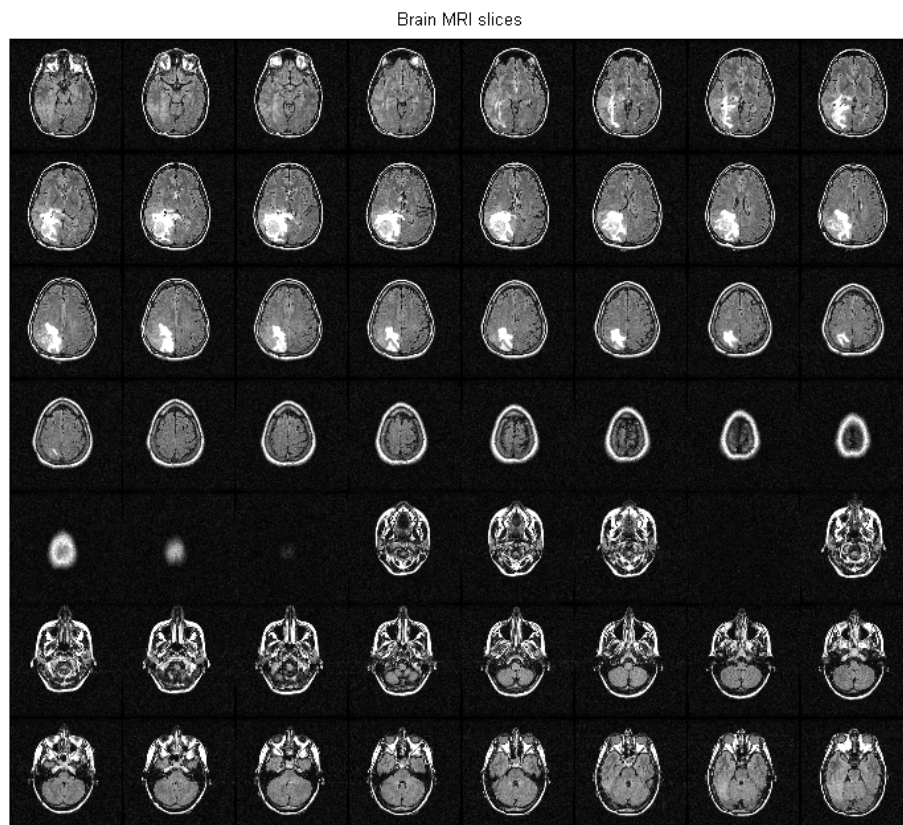
Question 2: Generate Montage

```

figure(1)
montage(reshape(uint8(mri),[size(mri,1),size(mri,2),1,size(mri,3)]));
title('Brain MRI slices');

```

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



Question 3: Anatomically organized order from top to bottom

```

%sorting the slice thicknesses of the MRI slices
sort_slice_loc = sort(slice_loc,'descend');

for i = 1: length(sort_slice_loc)
    for j = 1: length(slice_loc)
        if sort_slice_loc(i) == slice_loc(j)

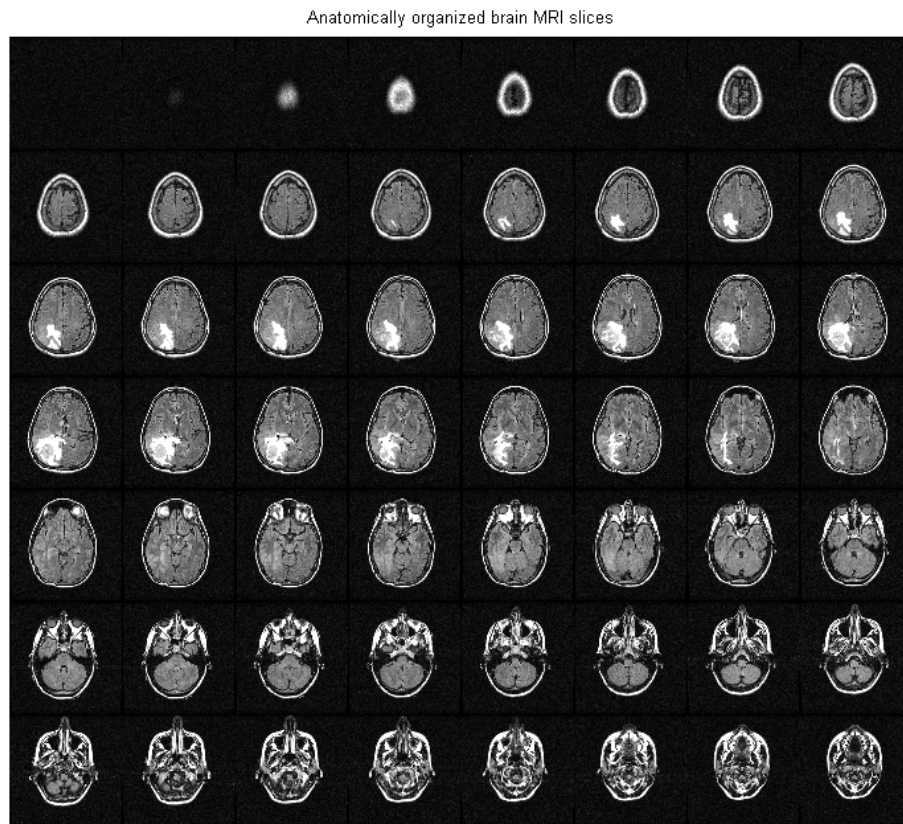
```

```

        sorted_mri(:,:,i) = uint16(dicomread(image_slice_name(j,:)));
    end
end
end

%plotting the top to bottom ordered MRI slices
figure(2)
montage(reshape(uint8(sorted_mri),[size(sorted_mri,1),size(sorted_mri,2),1,size(so
title('Anatomically organized brain MRI slices');
```

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

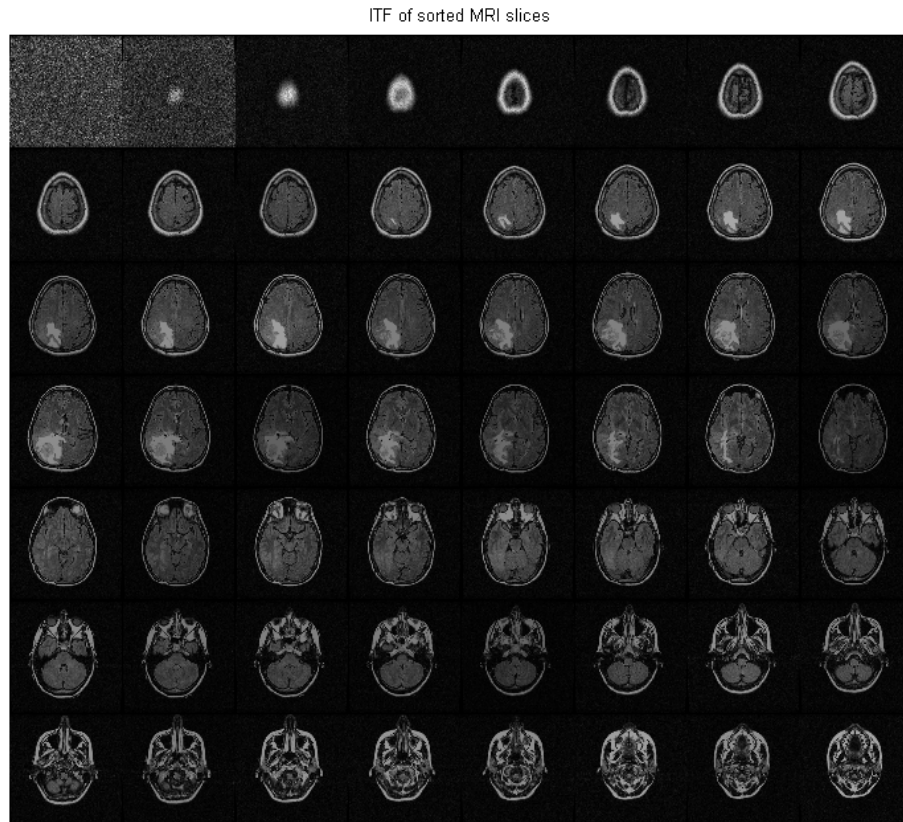


Question 4: ITF of sorted MRI slices

```

for i=1:56
    sorted_trans = itf_img(sorted_mri(:,:,i));
    trans_sort(:,:,i)=sorted_trans;
end
figure(3)
montage(reshape(uint8(trans_sort),[size(trans_sort,1),size(trans_sort,2),1,size(tr
title('ITF of sorted MRI slices');
```

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



Question 4 & 5: Segmenting the brain tissue

```
figure(4)
colormap jet(100)
%performing intensity transform function
%Using itf_img.m function program to execute intensity transform function
%for i=1:56
selected_img = itf_img(sorted_mri(:,:,25));
subplot(2,2,1)
image(selected_img)
title('intensity transformed MRI slice')

%Using Region_grow.m function program for segmentation
%Segmented brain with skull and scalp eliminated
subplot(2,2,2)
segmented=region_grow(152,173,selected_img);
image(segmented)
title('segmented brain with skull & scalp removed')

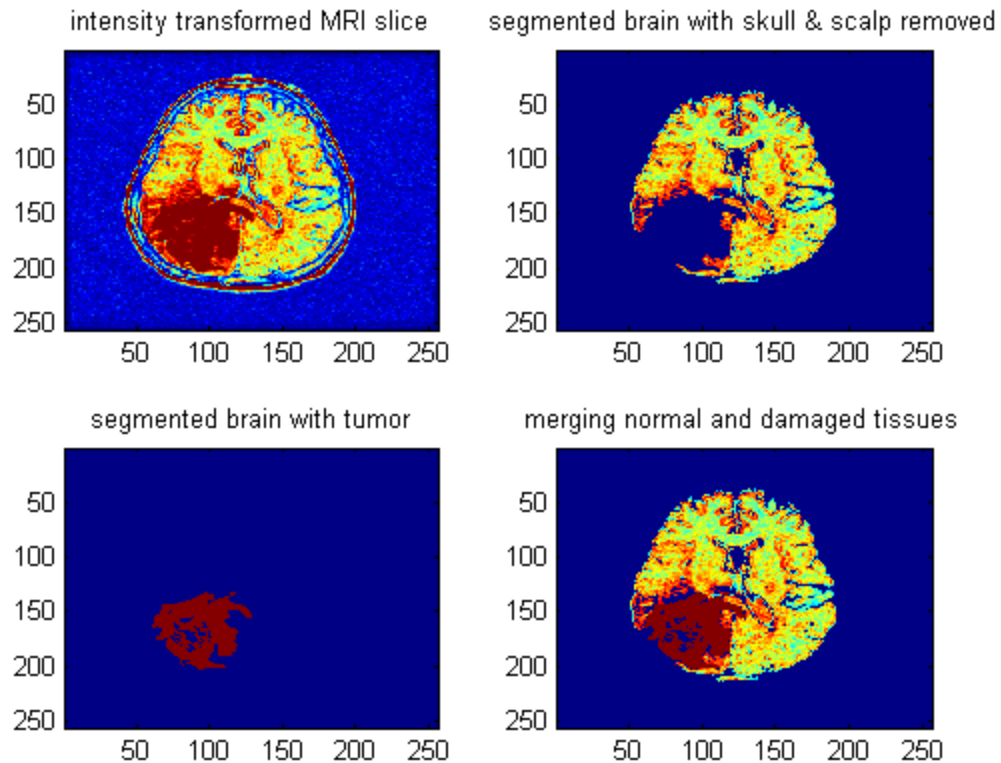
%Using Region_grow.m function program for segmentation
%Segmenting the brain(isolateing normal tissue)
subplot(2,2,3)
tum_segmented=region_grow(96,197,selected_img);
```

```

image(tum_segmented)
title('segmented brain with tumor')

%merging normal and damaged tissues together
subplot(2,2,4)
colormap jet(100)
tot_segmented=segmented + tum_segmented;
image(tot_segmented)
title('merging normal and damaged tissues')

```



Question 6: Contrast map the healthy and diseased brain region

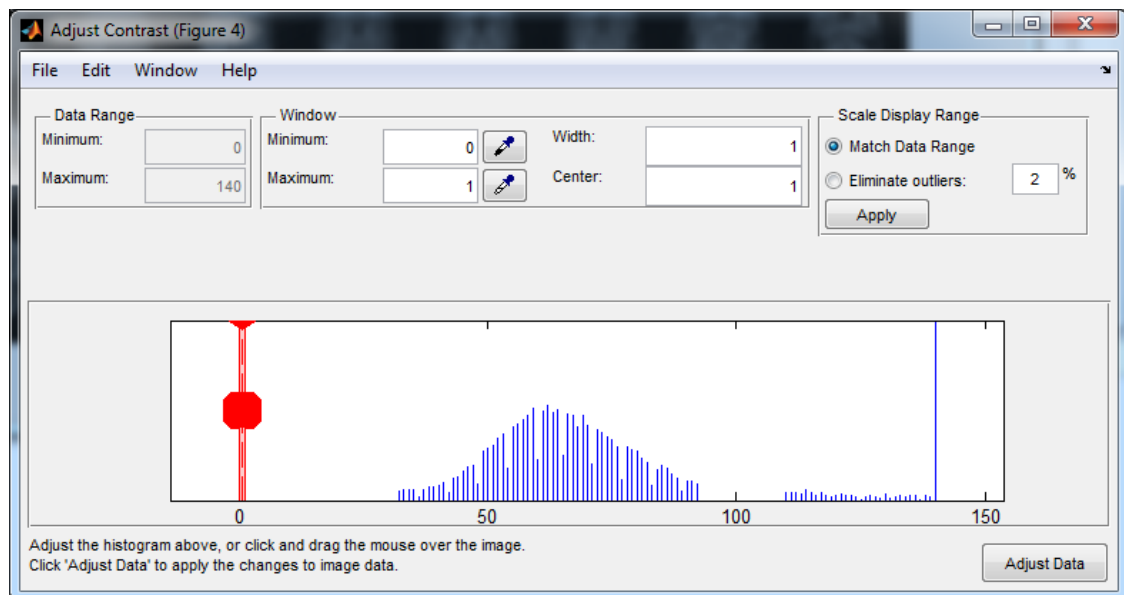
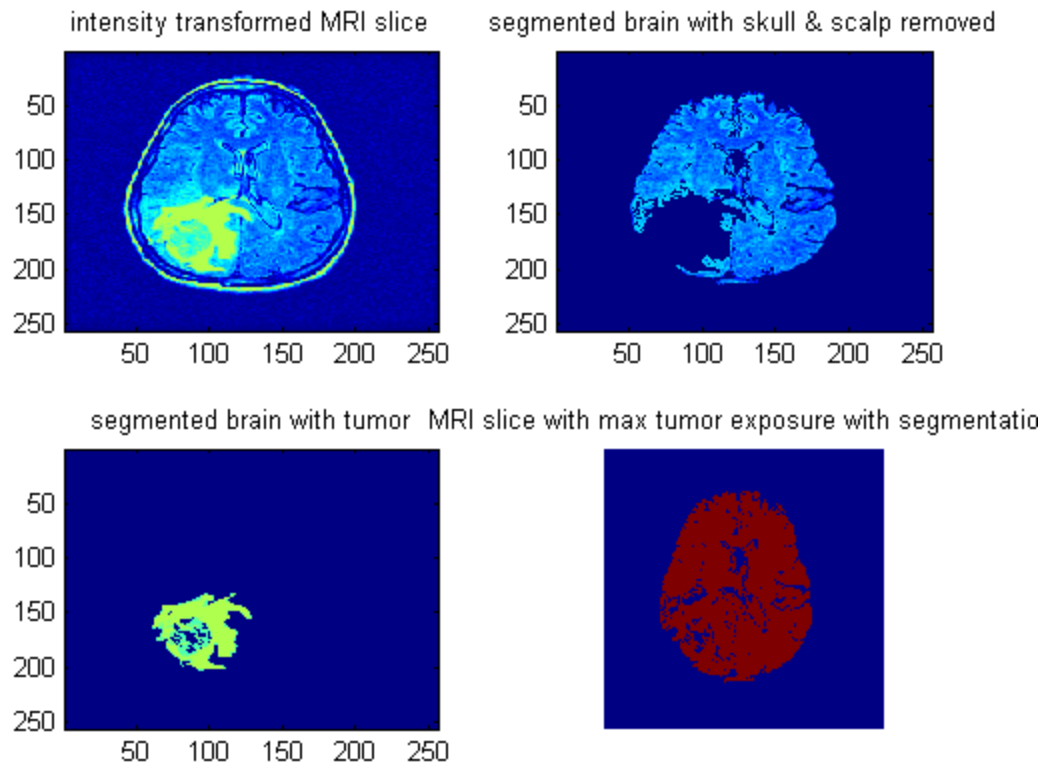
```

%Contrasting damaged and normal tissues of the brain using imcontrast
b=imshow(tot_segmented)
title('MRI slice with max tumor exposure with segmentation')
colormap jet
imcontrast(b)

```

$b =$

720.0032

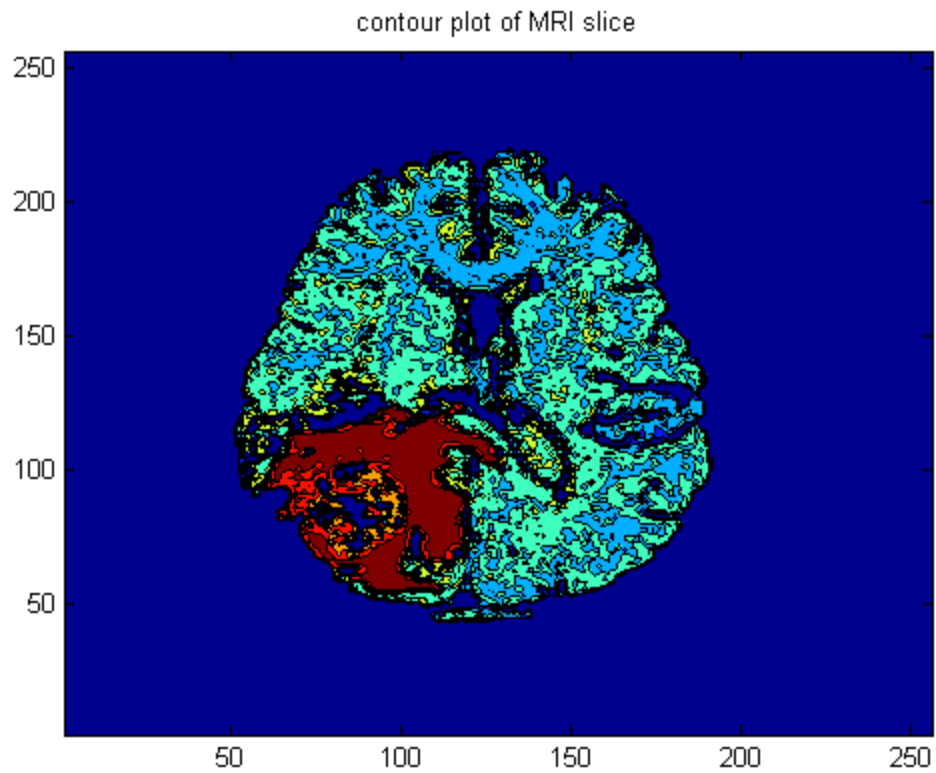


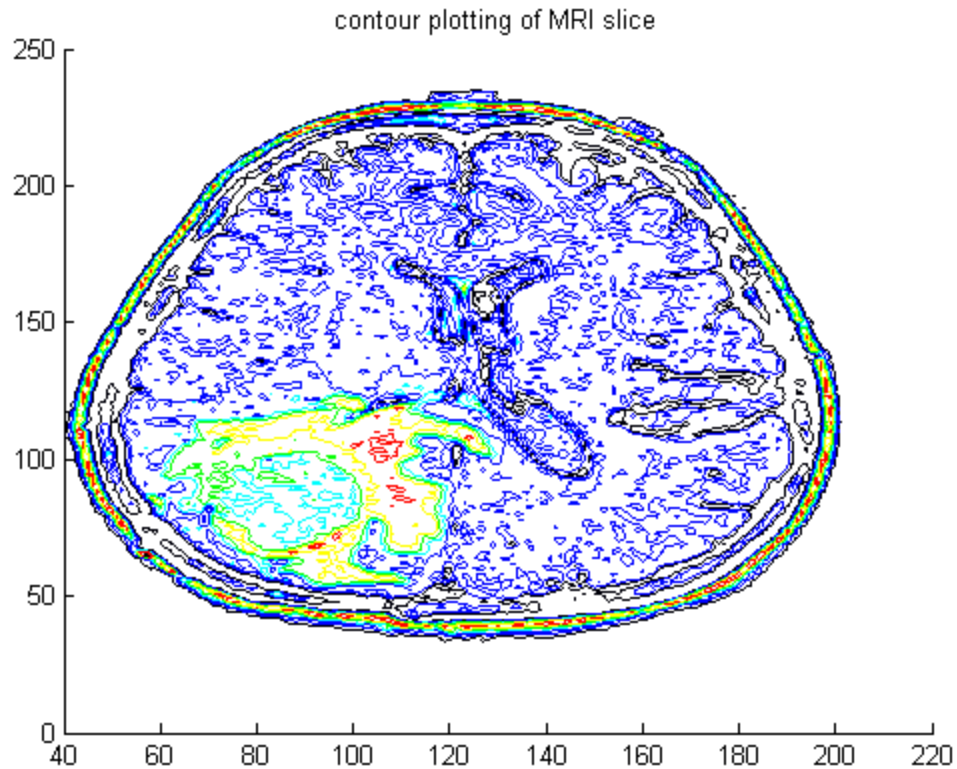
Question 7:Contour plotting

```
figure(5)
%creates contour plot of the image data
contourf(flipdim(tot_segmented,1))
title('contour plot of MRI slice')
```

```
% flipdim is used for altering dimensions

%contour plotting in volume slice planes
image_num=25;
cm=brighten(jet(100),-0.8);
figure('Colormap',cm)
contourslice(flipdim((sorted_mri),1),[],[],image_num)
title('contour plotting of MRI slice')
```





Question 9:3-D plot

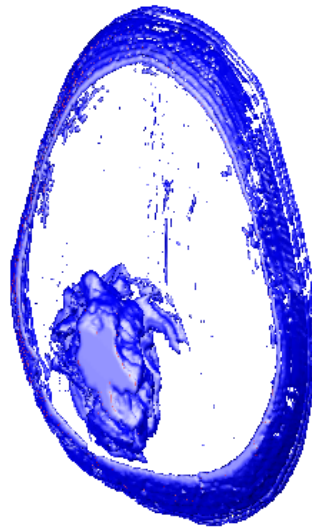
```
%selecting the MRI slices which have the tumor
%performing intensity transform function for those slices
for range=14:30
    selected_img = itf_img(sorted_mri(:, :, range));
    selected_set(:, :, range)=selected_img;
end

%down sampling
ds=selected_set;
ds=flipdim(ds,1);
%ds=flipdim(ds,2);
%rearranges the dimensions of 'ds' so that they are in the order specified by
%the vector order
ds=permute(ds,[3 2 1]);
vox_size2=vox_size([1 3 2]).*[4 1 4];
%isosurface obtains similar isosurface values from volume data ds
tissue=isosurface(ds,109);
tumor=isosurface(ds,150);
h=figure('visible','off','outerposition',[0 0 800 600]);
title('3D view of selected slices')

patch(tissue,'FaceColor','b','EdgeColor','none');
patch(tumor,'FaceColor','r','EdgeColor','none','FaceAlpha',0.5);
```

```
view(45,15);  
daspect(1./vox_size2);  
axis tight;  
axis off;  
camlight;  
camlight(-80,-10);  
lighting phong;  
movegui(h,'center');  
set(h,'visible','on');
```

3D view of selected slices



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