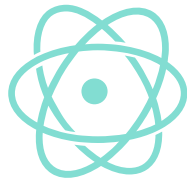


Computer Applications for BME



Identifying Gliomas through Computer Led MR Image Analysis

Biomedical Gals

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OUTLINE

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Project Overview

- Our project is centered around tumor identification in MR images of the human brain.
- The code that we've created can take an MR image with a tumor present, and provide a size estimate of the tumor, a location estimate, a treatment scope, and the original MR image with the tumor highlighted.
- By creating this program, the diagnosis of gliomas, or brain tumors, is a more streamlined process and allows for a higher survival rate of patients, due to a quicker diagnosis.



Problem at Hand

- The problem that we are solving is diagnosis time in gliomas. Neurology is highly dependent on efficient and accurate diagnosis. Gliomas are fast spreading, malignant tumors, and the quicker one can be identified and classified, the higher the patient chance of survival is. Gliomas are one of the most dangerous types of cancer, due to the intense effects they can have on the brain, and by creating a program to aid in their diagnosis, we are hoping to decrease their effects on patients as much as possible.

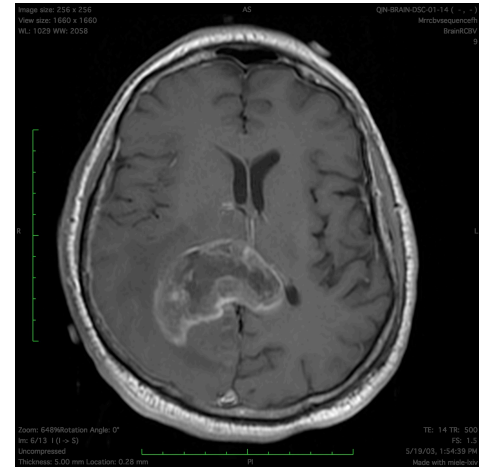
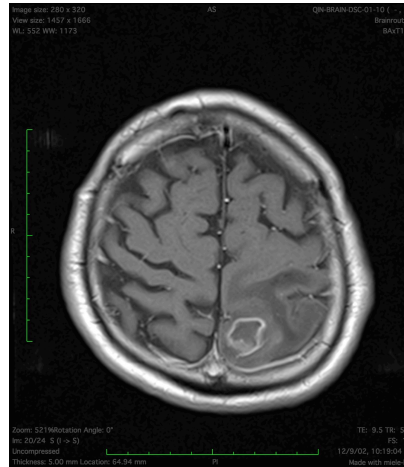
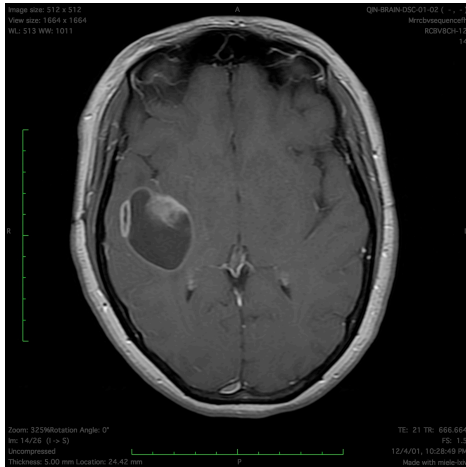


Significance

- By creating this program, we are allowing the diagnosis of gliomas to become more efficient and streamlined. Once a doctor sees a glioma in an MR image, it can be plugged into our program, which outputs a location, size, highlighted image, and treatment plan. This eliminates the need for anyone to go through each process individually, saving time and resources. By making this process more efficient and streamlined, we can increase patient survival rates, as the treatment of gliomas is very dependent on their progression, which happens very quickly.

Data Set

- Our data set for code development and testing comes from The Cancer Imaging Archive. This data set contains MR images of gliomas of all sizes, ranging from 0.5cm^2 to 20cm^2 , as well as various locations and centralization levels.

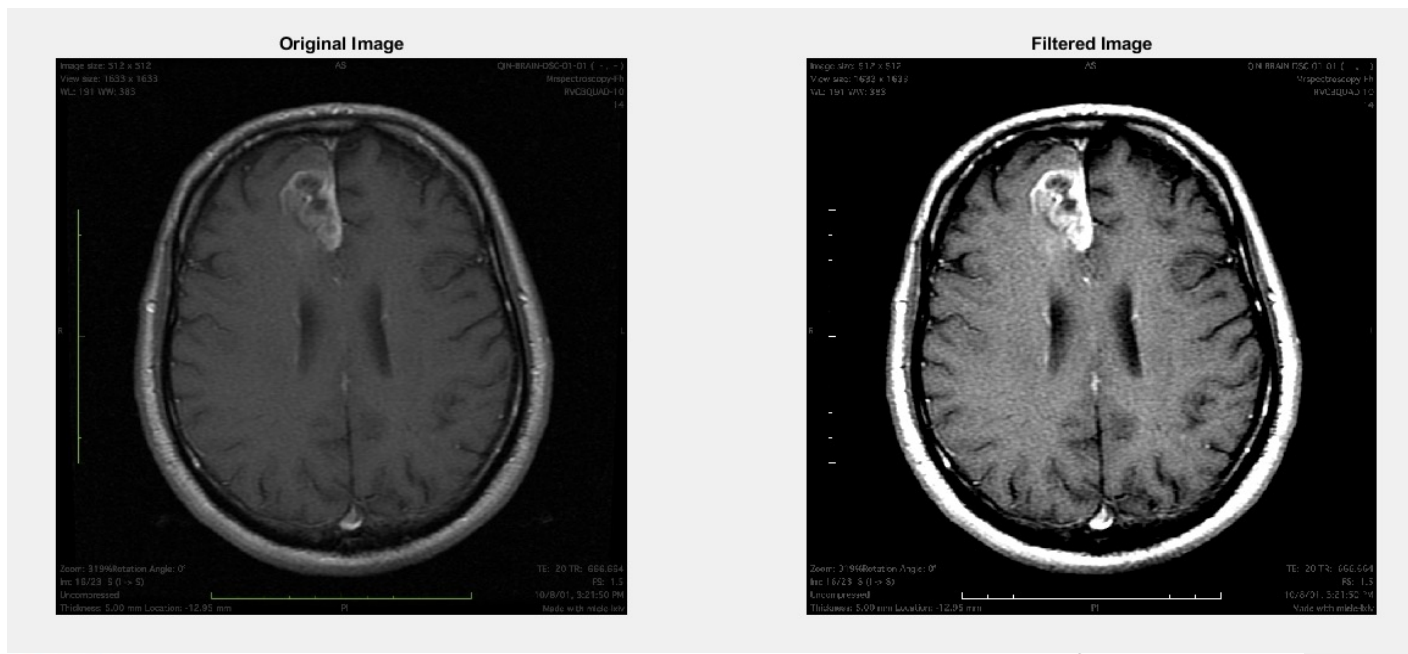




Methodology

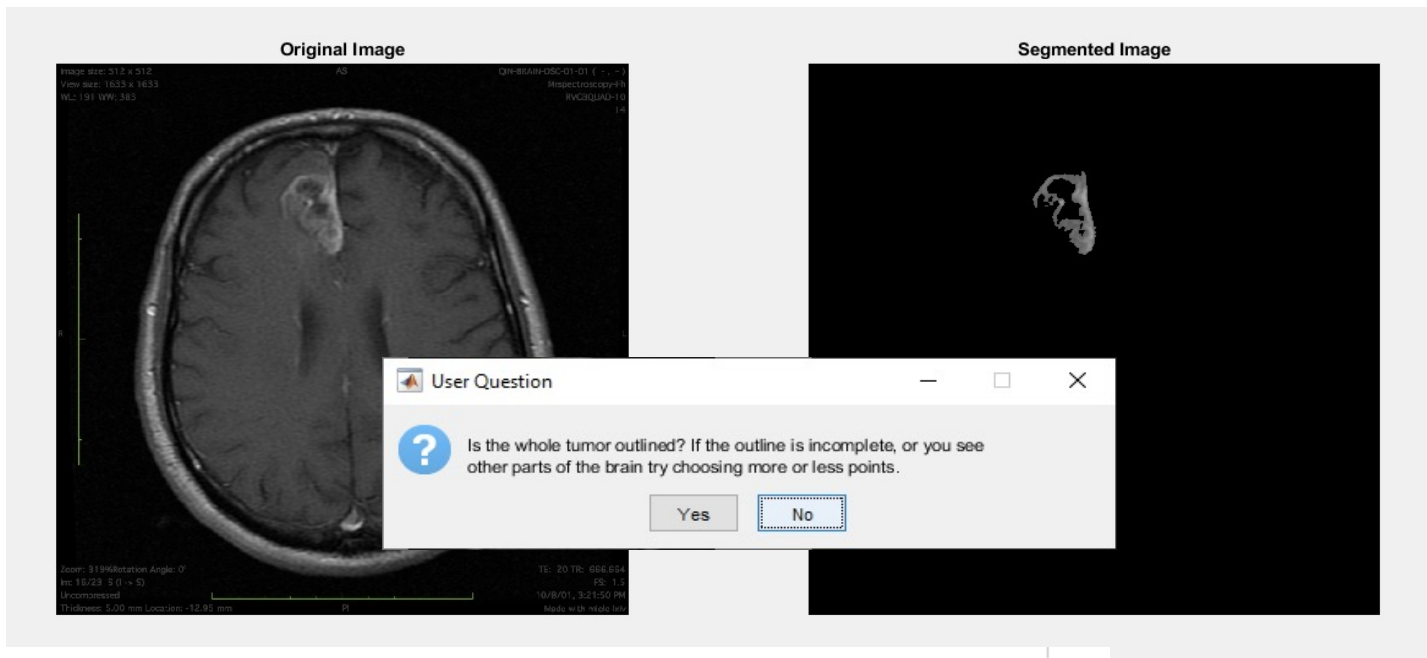
- Our code has a lot of parts, but the basic components are as follows:
 - Filter the image for a higher contrast, and have the user select several edge points on the tumor to establish an outline.
 - Fill in the tumor outline and calculate the area of the tumor.
 - Determine the location of the tumor based on centralization and where the majority of the tumor lies in the brain.
 - Determine a treatment recommendation based on the size and location of the tumor
 - Apply a blue highlight over the tumor for ease of viewing
 - Output a final highlighted image of the tumor with a caption listing the size, location, and treatment recommendation.

Image Filtering



```
Idouble = im2double(gray_I);  
avg = mean2(Idouble);  
sigma = std2(Idouble);  
filter_I = imadjust(gray_I, [abs(avg-n*sigma) abs(avg+n*sigma)], []);
```


Outline the Tumor

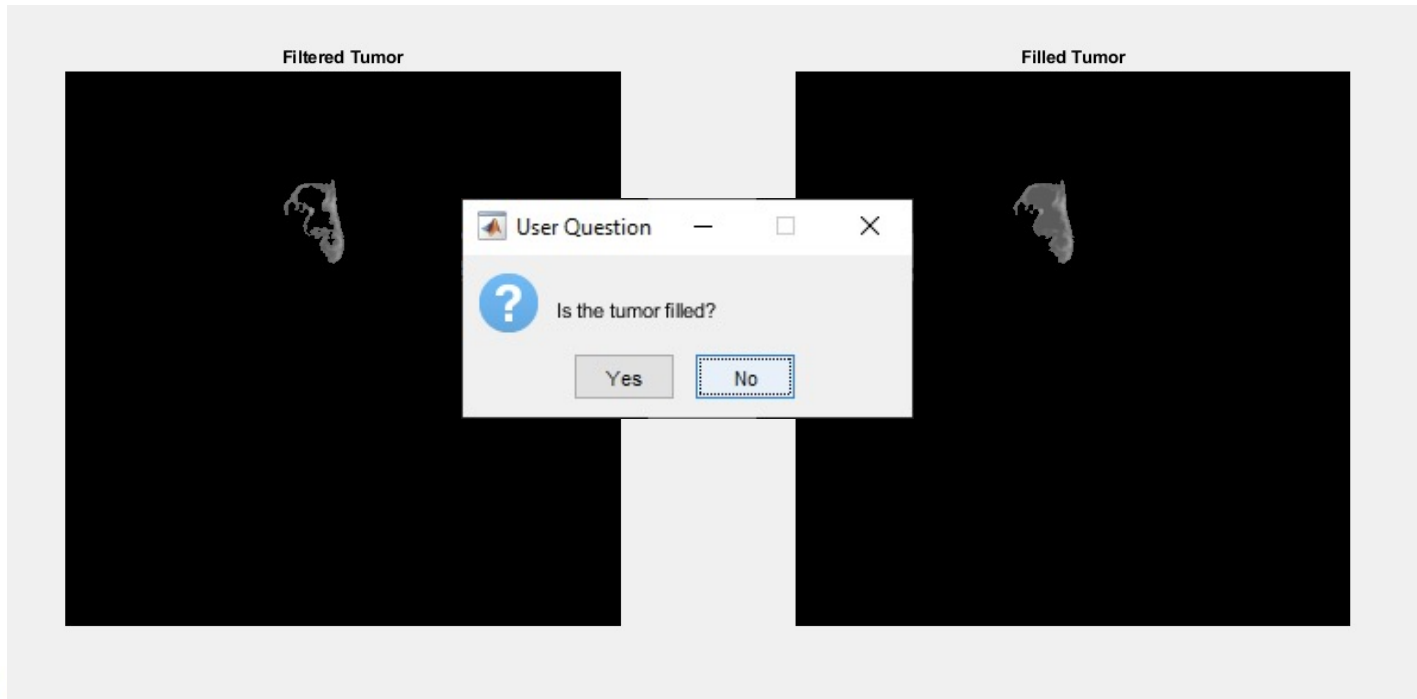


`%Thresholding`

`Ithresh = gray I; %Create new variable`

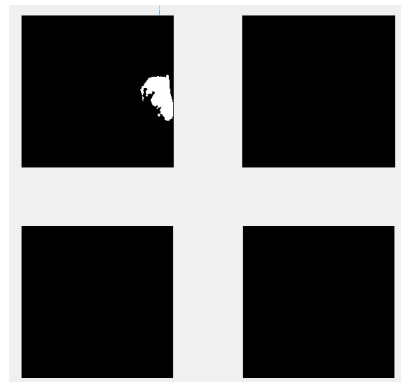
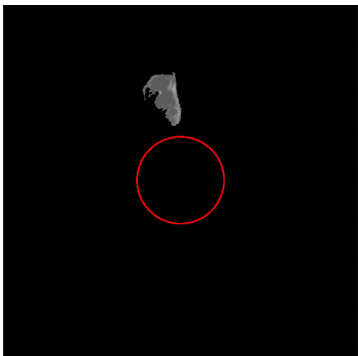
`Ithresh(Ithresh<pmin) = 0; %Binary threshold`

Size the Tumor



```
[row,col] = find(L==1);  
%Find the Length of the scale bar  
dis = row(end) - row(1);  
%Use the length of the scale bar to find the area of the tumor in cm  
areacm = (100/dis^2)*area;
```

Find the Location of the Tumor



%Calculating the circle to be used for masking

```
th = 0:pi/50:2*pi;  
xunit = r*cos(th) + x;  
yunit = r*sin(th) + y;
```

%Creating a mask of the same size as the circle created

```
mask = poly2mask(xunit, yunit, rows, columns);
```

%Masking the image with the circle mask created

```
if colorchannels == 1  
    maskedimage = Ifill;  
    maskedimage(~mask) = 0;  
else  
    maskedimage = bsxfun(@times, Ifill, cast(mask, class(Ifill)));  
end
```

%Splitting image into 4 equal quadrants

```
I1=I(1:(round(rows/2)),1:(round(columns/2)),:);  
I2=I((round(rows/2))+1:rows,1:(round(columns/2)),:);  
I3=I(1:(round(rows/2)),(round(columns/2))+1:columns,:);  
I4=I((round(rows/2))+1:rows,(round(columns/2))+1:columns,:);
```

%Finding the area of the tumor in each quadrant

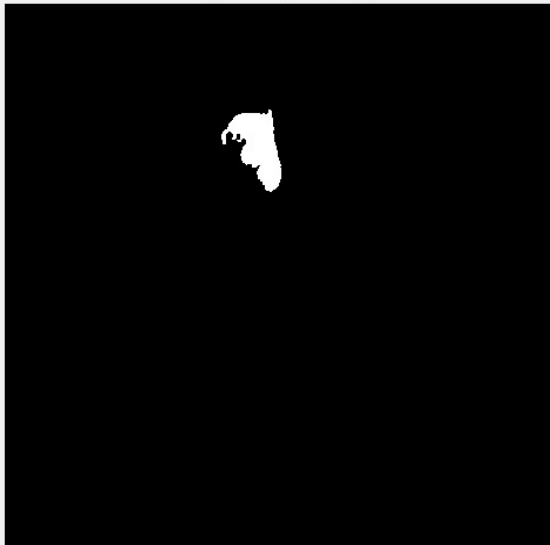
```
A1 = bwarea(I1);  
A2 = bwarea(I2);  
A3 = bwarea(I3);  
A4 = bwarea(I4);
```

%Setting a vector up with the areas, and finding the largest value

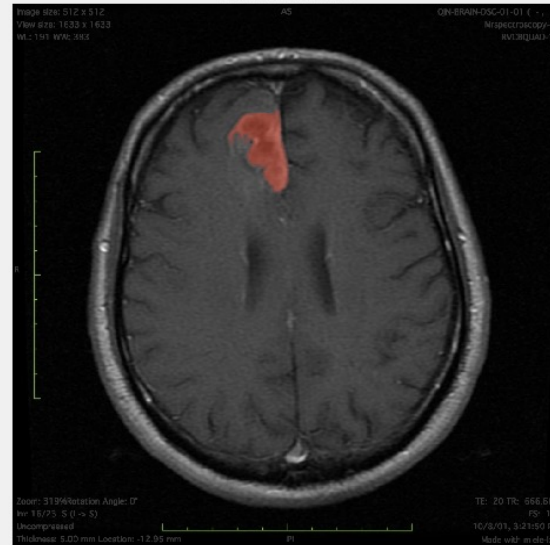
```
vec = [A1 A2 A3 A4];  
maximum = find(vec == max(vec));
```

Highlight the Tumor

Binarize the Filled Tumor

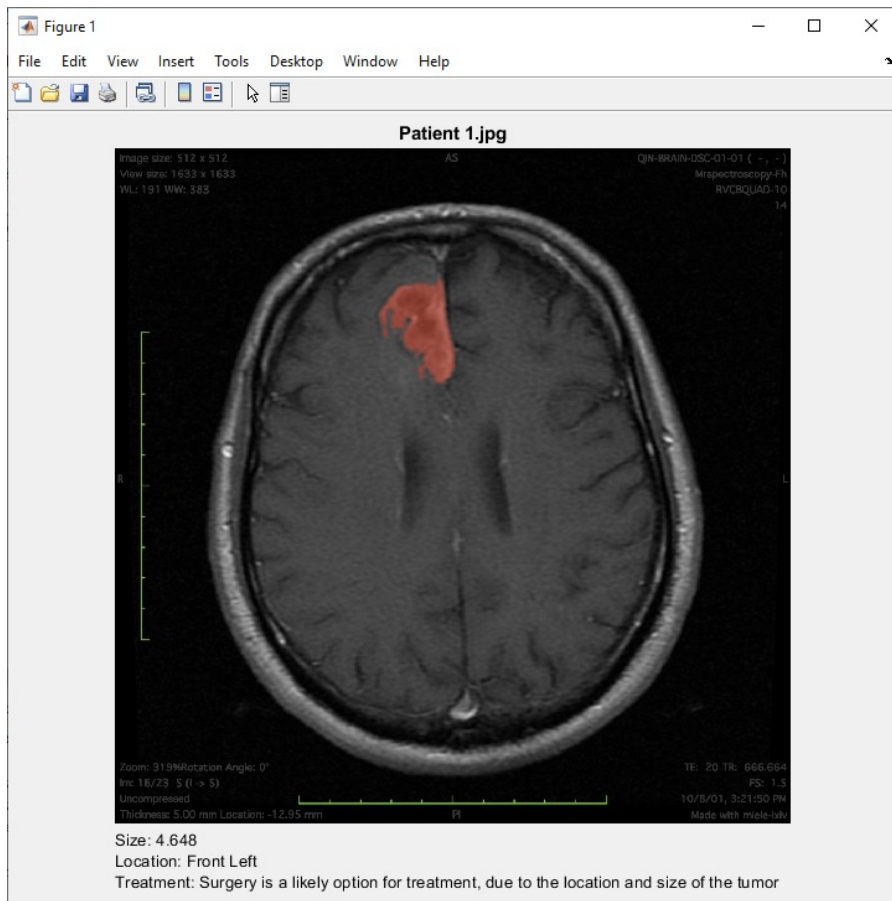


Overlaid Image



```
I = imbinarize(Ifill);  
bw = im2uint8(I); %Change to uint8 so the gray connected works  
W = bw;  
for f = 1:k %For all the chosen points  
    J = grayconnected(bw,round(y1(f)),round(x1(f)));%include all the chosen points  
    W = imfuse(W,J,'blend');  
end
```

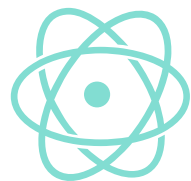
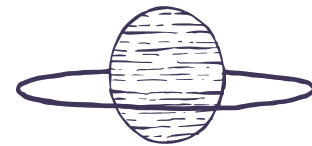
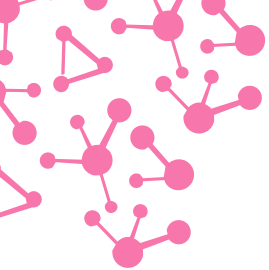
Final Product



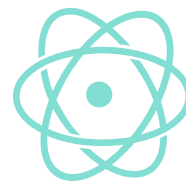


Results

- With our program, we have been successful in our entire methodology and created a program to help streamline tumor identification and treatment. The program runs smoothly, if operated correctly, and outputs an image of the highlighted tumor with useful information to help doctors quickly treat gliomas, increasing the chances of survival for the patients.



Demo Time!



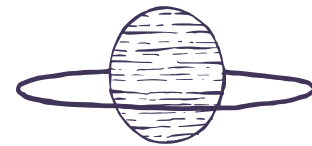
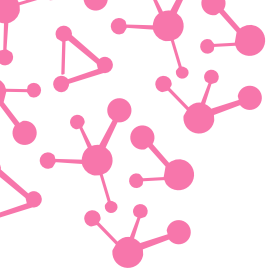
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Thanks for Watching!

♥ Sarah and Gianna ♥



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