# MATLAB Homework 05

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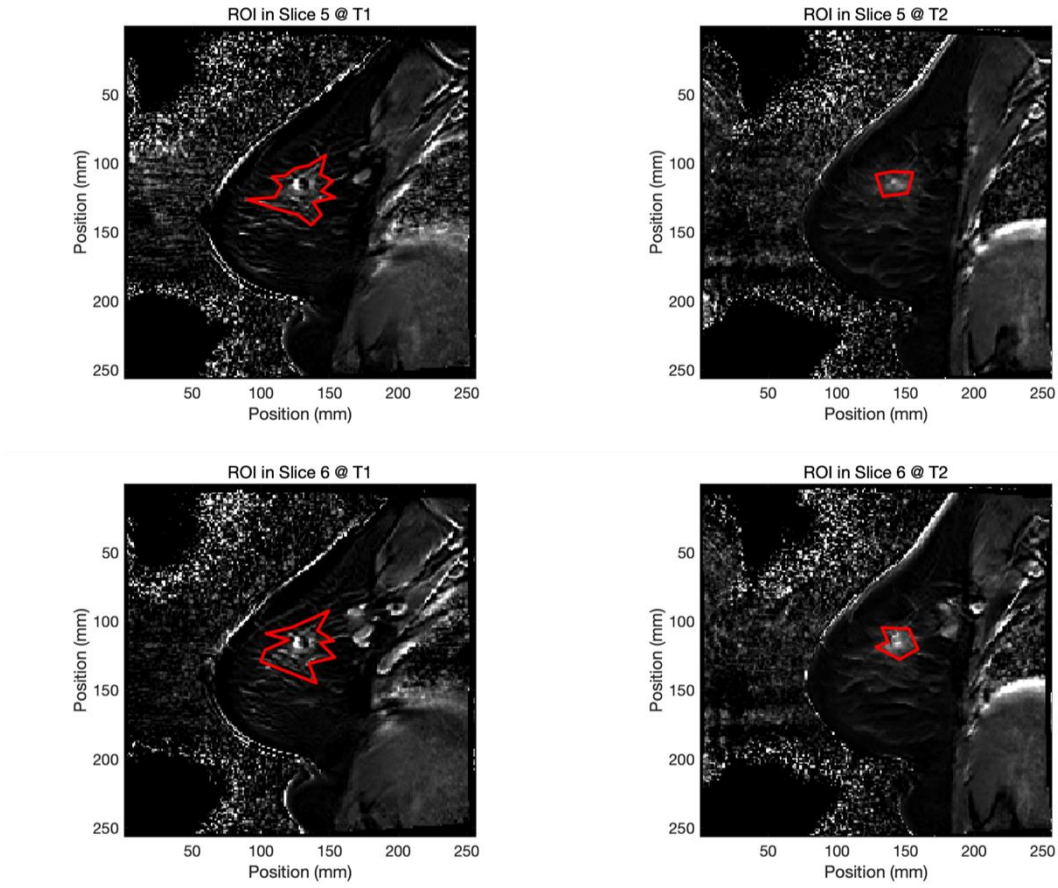
**Codes location:**

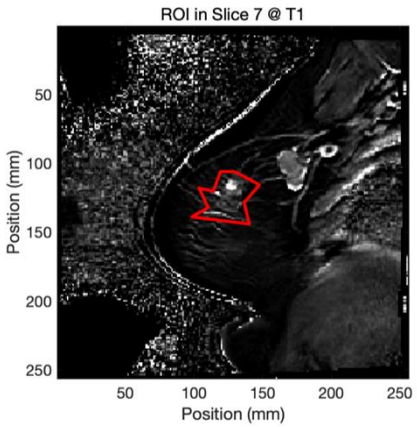
**https://github.com/yifuhhh/EE385J_Biomed_Image/tree/master/HW05/Submission**

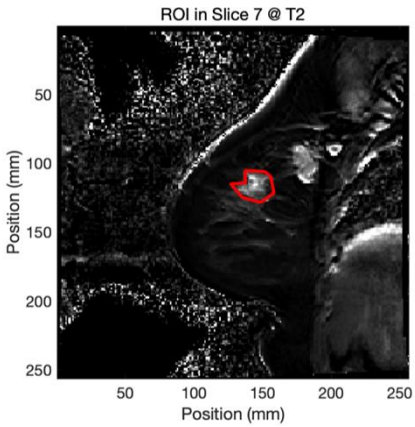
1. **For each patient, display the image slices with tumors, with your ROI displayed on top of it.**
   (a) Discuss how you determined what was cancerous from healthy tissue. (What were your assumptions).
   The slices with tumors are shown below. Slice 5 ~ 7 of Patient 1 and Slice 1 ~ 8 of Patient 2 are chosen here for ROI analysis.

   The criteria I determined what was cancerous from healthy tissue is based on the color and contrast in the image. The boundary of the tumor is blurry, and the shape is irregular.

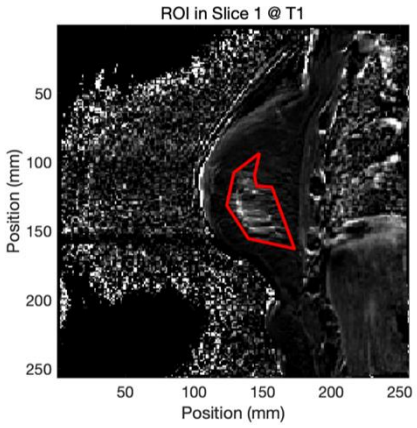
   **Patient 1:**

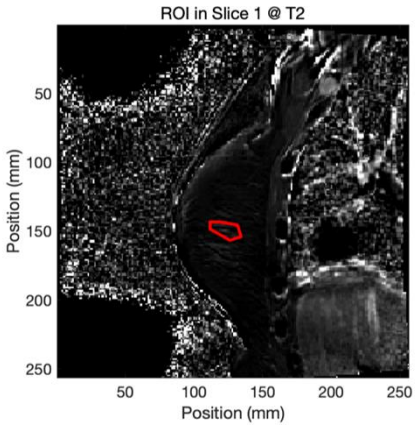


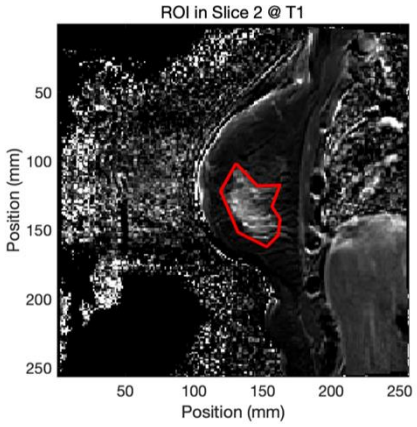

ROI in Slice 7 @ T1
Position (mm)
Position (mm)
50
100
150
200
250

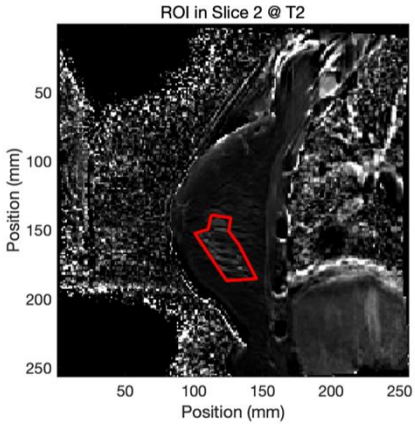

ROI in Slice 7 @ T2
Position (mm)
Position (mm)
50
100
150
200
250

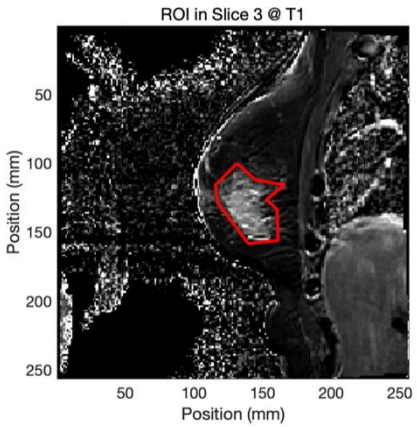
**Patient 2**

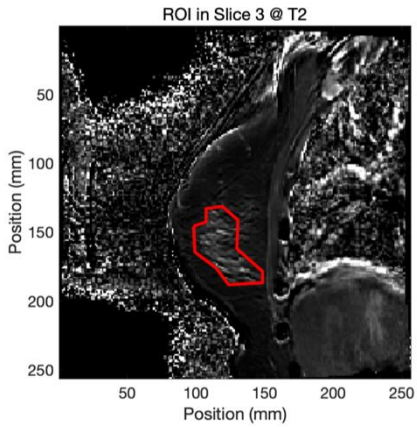

ROI in Slice 1 @ T1
Position (mm)
Position (mm)
50
100
150
200
250

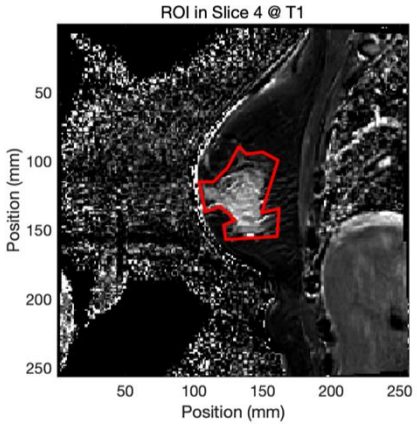

ROI in Slice 1 @ T2
Position (mm)
Position (mm)
50
100
150
200
250

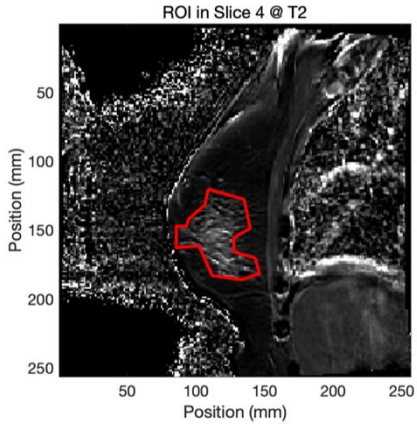

ROI in Slice 2 @ T1
Position (mm)
Position (mm)
50
100
150
200
250

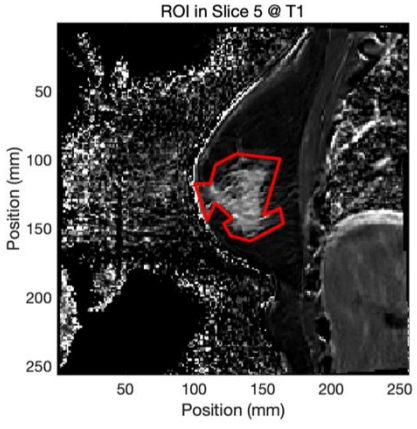

ROI in Slice 2 @ T2
Position (mm)
Position (mm)
50
100
150
200
250

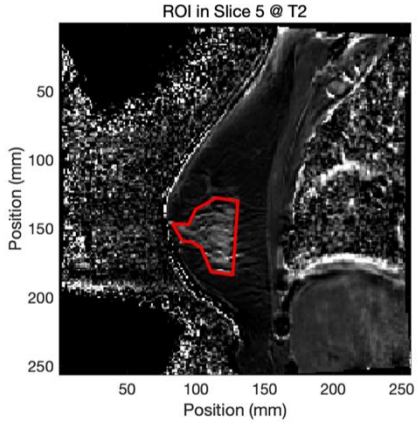

ROI in Slice 3 @ T1
Position (mm)
Position (mm)
50
100
150
200
250

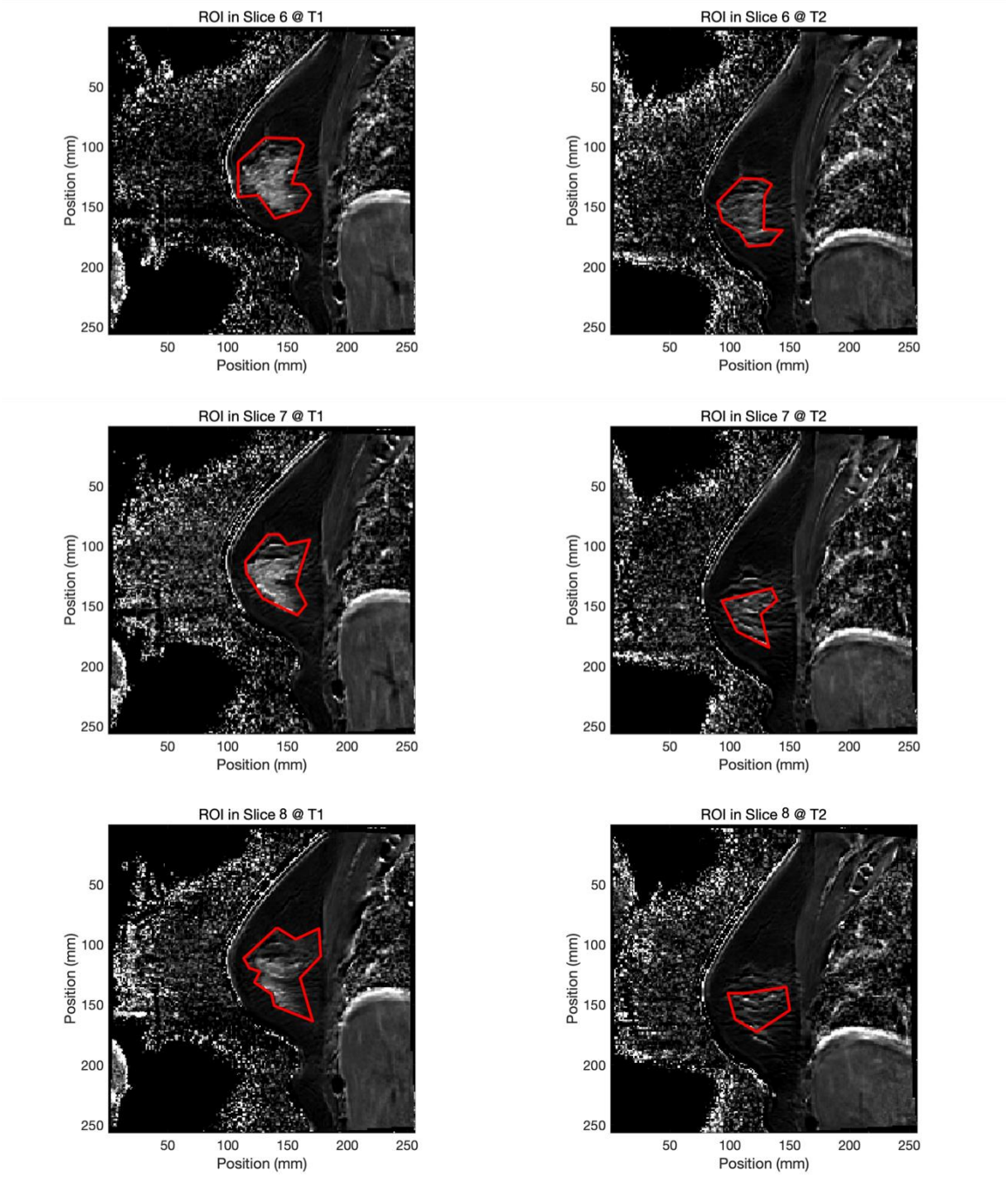

ROI in Slice 3 @ T2
Position (mm)
Position (mm)
50
100
150
200
250


ROI in Slice 4 @ T1
Position (mm)
Position (mm)
50
100
150
200
250


ROI in Slice 4 @ T2
Position (mm)
Position (mm)
50
100
150
200
250


ROI in Slice 5 @ T1
Position (mm)
Position (mm)
50
100
150
200
250


ROI in Slice 5 @ T2
Position (mm)
Position (mm)
50
100
150
200
250




**2. Create/code up a RECIST function that returns the longest dimensions at each time point, and the RECIST criteria (CR, PR, SD, PD).**

```
function maxdist = solvedist(mask)
    ind = find(mask == 1);
    [x, y, z] = ind2sub(size(mask), ind);
    tumor_arr = [x, y, z];
```

```
    npoints = size(tumor_arr);

    for i = 1 : npoints % select one voxel,
        for j = 1 : npoints % loop through all the other voxels, calculate distance
            dx = x(i) - x(j);
            dy = y(i) - y(j);
            dz = z(i) - z(j);
            dist(j) = sqrt(dx^2 + dy^2 + (dz * 5)^2);  % store distance for each voxel
        end
        mdist(i) = max(dist); % store maximum distance for voxel "i"
    end
    maxdist = max(mdist);
end
```

### 3. Calculate patient response

| | Volume change | RECIST criteria |
|---|---|---|
| **Patient 1** | -51.12% | PR |
| **Patient 2** | -14.91% | SD |

The advantage of RECIST is that it represents a common language of efficacy for clinical researchers across disease sites and clinical trial settings. The major disadvantage of RECIST is the reliance on human measurement.

It's hard to compare my results directly with others since different people have different measurement method to choose the ROI. However, we can analyze the results from all the students in the class by looking at the distribution of the RECIST criteria so that we can get a general idea of the situation of the patient response.