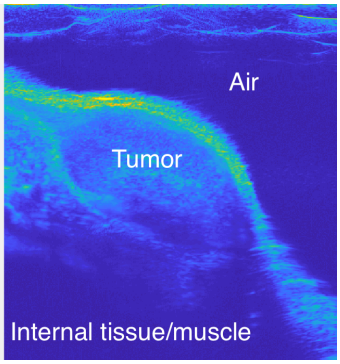
Assignment: Ultrasound Analysis
Due Friday, 10/25/2019 by 11:59 pm
Complete the deliverables listed below and upload to Canvas.
Please upload each file separately (i.e., don't compress them or make a .zip file)

- Matlab m-file with code to answer the following questions
- A report (saved as a pdf) of answers and figures (if necessary) to support your answer
- Make sure each plot/figure has a title, labeled axes, and is displayed in the correct aspect ratio.

We have collected some contrast enhanced ultrasound data. In this study, we used microbubbles filled with perflurocarbon as a contrast agent. Microbubbles create a stark contrast between tissue and the bubble itself. Due to their size, these microbubbles cannot enter the tissue from the vasculature, so they remain primarily within the vasculature. We will perform different types of analysis on this dynamic data to understand how it could be used to study tumor vasculature. In this study, a tumor was implanted in the hind limb of a mouse. The image to the right shows some of the general landmarks when looking at these images. There are three images within this .mat file. First, bmdata this is a 3D array (2D in space, 1 in time) showing pre-, and post-contrast images. The time at which each image was collected is stored in "t". Second, we have a pre-contrast image ("pre") and a post-contrast image ("post"). We will not use the pre and post images.



(1) (5 pts) Compared to the other images we have looked at so far (MRI, PET, CT), what are some differences between this US image and those other images?

(2) (5 pts) Create a "for" loop to loop through each image in time (Matlab Monday 00), as you watch the the playback, what do you notice happening? What could be the potential cause of this? Can you think of anyways we could address this? Are you able to see the contrast enhancement?

(3) (20 pts) Using the *imresize* function, resize the image to 15% of its original value. (Since this is a 3D image, you will have to loop through time to resize each time point)

a. For each voxel, we want to calculate the baseline signal intensity. To calculate the baseline signal intensity, we will simply average the first 5 time points at each voxel. Display the baseline signal intensity (on one plot) and the standard deviation (on a second plot). What could the standard deviation tell us about the image?
b. Segment the tumor tissue. Display your segmentation on top of one of the images.
c. Within the segmented tumor: Find the maximum value at each voxel within the tumor. Then divide 2D array of maximum values by the baseline signal intensity. Use the colormap 'hot' to display your results. Set the display range in imagesc to be from 1 to 1.3. Add a colorbar. What does this image tell us?
d. Within the segmented tumor: Create 4 plots showing which voxels are greater than baseline + 1*SD, + 2*SD, + 4*SD, and +8*SD (Where SD = baseline standard deviation). What do these images tell us?
e. Within the segmented tumor: Find at what time point the maximum value occurs in each voxel within the tumor. Display with a colorbar. Comment on what this map might tell us

(4) (10 pts) Using *lsqcurvefit* and a scripted function to fit each voxel's timecourse using the logistic growth model consisting of parameters P_1 and P_2. Before fitting, normalize the signal to the baseline signal intensity. Assume the parameters have a lower bound of 0, and no upper bound.

$$S(t,P) = P_1\left(1-\exp\left(-P_2 \cdot t\right)\right)$$

(a) What does P_1 and P_2 represent in terms of the tumor biology?
(b) Create a plot of P_1 and P_2 within the tumor

(5) (10 points). Using the results of (4) and (5) what are the best and worst perfused regions? What could the impact of this be on tumor growth? What could the impact of this be on a tumor's response to treatment?