**DCE MRI Lab**

Jan 31, 1-3pm

**Overview**

Please download the starter .m files and data files from the CLE.

Follow the steps below. It is fine to do steps in a different order or with different methods, as long as the final objective is the same and any major changes are explained.

Include images of figures and results and discussion as requested in the step-by-step guide by publishing your code + results in matlab and submitting on the CLE.

**Inputs:**

Image files are in:

data/E317/1009

they are a series of .DCM files of the prostate DCE MRI acquisition.

To load the data, the starter code will cd to the listed directory.

Before you rerun the code, you’ll need to cd back up to where you started. If you didn’t change the directory structure, this will be: cd ../../.. (also listed as the last section in the starter code – run this section to return to the starting directory).

**Step-by-step guide to the Lab**

**DCE MRI**

Use the DCE\_starter.m file

Make use of code from prior labs, if relevant.

This data is 4D. You may need to convert to 2D or 3D at times.

See the help on squeeze and/or consider making variables for part of the data.

* Helpful commands (you don’t need to use all of these – it depends on how you code)
  + squeeze
  + plot
  + hold on
  + double
  + diff
  + polyfit
* Be careful of your image math – make sure if you divide 2 integers you don’t lose fractional information (i.e. don’t let 1 / 2 \* 100 = 0).
* You can convert integers to floating points w/
  + Newvar = (double) integervar
  + It may be easier to make a temporary variable to hold your data, then assign it to your array.
* Be careful of units.
* When displaying images, you may well need to set the min and max to view easily.

You can just do all the steps on Slice 10. If you do this, you can convert your 4D raw data to 3D:

ImDCE (4D data: t,s,:,:) 🡺

Raw10 = squeeze(ImDCE(:,10,:,:); (3D data, now (t,x,y)

The steps involved are:

If using slice 10 data only:

**Step 4 (below) - Diagram**

Raw10 (t,x,y) (3D) 🡪 Enhance(t,x,y) (3D) 🡪 MaxPeak(x,y) (2D image)

(Raw10 scaled by baseline mean for each pixel) (Max vs. time)

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Slope(t,x,y) (calculate slope, initially as 2 point difference in Enhancement (then convert to %baseline / sec) set the first time point =0, the rest are the difference vs. the prior timepoint.

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* Maxslope(x,y) (2D image) (Max vs. time)

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| **Steps** |
| 1. Set up constants, file names. |
| 1. Read image acquisition parameters. |
| 1. Load 4D data. |
| 1. Calculate baseline intensity & Parameter Maps.    1. Make Enhancement maps for each timepoint.    2. Calculate max slope map ( a 2 point slope).    3. Calculate max peak map. |
| 1. Display baseline average image, image at timepoint 30, and parameter maps at a selected slice |
| 1. Create Right Peripheral Zone ROI and Left Peripheral Zone ROI (on a selected slice) – display on maxslope map. |
| 1. Calculate & print stats for the 2 ROIs for the parameter maps (Maxpeak and Maxslope) (mean, stdev, median) |
| 1. Plot uptake curves, i.e: Enhancement [%baseline] vs. time [sec] for cancer ROI and healthy ROI. (one plot with 2 curves on it, label) |
| 1. Calculate Washout slope [%baseline/minute] for the 2 ROIs as a linear fit to the last half of the timepoints. 🡪 just provide the slope measures.    1. Perform a linear fit of the mean enhancement in the ROI vs. time.    2. Do for both the left and right ROIs |
| **Questions** |
| Question 1 – Was the cancer likely on the patient’s right or the patient’s left?  Why do you say this? |
| Question 2 – Is this likely a moderate grade cancer, or could it be high grade? Why? |
| Question 3 – How easily can you tell cancer from normal on:   1. The baseline average image 2. The enhancement at time 30 3. The max peak map 4. The max slope map 5. Uptake curves |
| Question 4 – With these images, what are some challenges to viewing the cancer? |
| Question 5 – Suggest an image processing technique that will make it easier to view the cancer and/or make the measurements more accurate. Explain why. |