**AcidoCEST MRI Analysis: Standard Operating Procedure**

Updated: 12/8/2022 by Renee

1. **Locate Files**
   1. If necessary, download acquisition files. Identify the RARE1, cestFISP\_Pre, and cestFISP\_Post scans based on the “E\_” number. The number of files in the DICOM folder ([numbered folder] -> pdata -> 1 -> dicom) will reflect the scan:

|  |  |
| --- | --- |
| Scan | Number of files in the DICOM folder |
| Localizer | 3 |
| RARE24 | 24 |
| RARE1 | 1 |
| cestFISP\_Pre | 176 |
| cestFISTP\_Post | 264 |

1. **Process Data**
   1. Open the MatLab by double-clicking “acidoCEST\_Pagel4\_ChemicalData\_20220104\_FinalVer”
   2. Ensure the “acidoCEST\_Pagel4\_TLi\_20220326.m” tab is selected, then click “Run” on the top bar
   3. Select the folder containing all of the scans (i.e. the folder containing folders labeled “1”, “2”, “3”, etc.)
   4. Input the folder number or scan number (“E\_”, these numbers are the same) correspondingly:
      1. Anatomical Scan: RARE 1 (I.e. input “3” if this scan is E3 or in folder labeled “3”)
      2. Anatomical Slice for CEST: “1”
      3. Pre-Injection Scan: cestFISP\_Pre (I.e. input “4” if this scan is E4 or in folder labeled “4”)
      4. Post-Injection Scan: cestFISP\_Post (I.e. input “5” if this scan is E5 or in folder labeled “5”)
   5. Circle the tumor, then click “Yes” when completed
   6. Circle an area around the corners of the scan for the noise without including the mouse. Ideally the area will be a little larger than the tumor. Click “Yes” when completed
   7. Select a folder to store results
   8. Allow the program to run. When the run is complete, “>>” will appear to the right of the “fx” input underneath the Command Window, and “Busy” will disappear from the bottom left corner of the screen
   9. When run is complete, type “figure;imagesc(pH\_results)” into the “fx” input to generate a pH map
   10. To adjust the pH scale, type “caxis([low value highvalue]) (i.e. “caxis([6 7.5])) into the “fx” input
   11. Save the pH map as a JPEG or TIFF image
   12. To determine the average pH, type “mean(nonzeros(pH\_results))” into the “fx” input
2. **Making Images Presentable (Note: this will use Photoshop)**
3. Open Adobe Photoshop
4. Open the RARE1 DICOM image and the MatLab-processed image
5. In the MatLab-processed image window, click the lock icon on the right underneath the “Layers” tab
6. Select the wand tool on the left bar, and click on any dark blue region in the MatLab-processed image
7. Delete the dark blue background as well as any other background beyond the tumor
8. Select the entire MatLab-processed image, copy it, and paste it over the RARE1 DICOM image
9. Right click the MatLab-processed image, and select “Free Transform”
10. Adjust the size of the MatLab-processed image as necessary to fit within the RARE1 DICOM image
11. Click the checkmark on the top bar when satisfied with the overlay
12. Export the image as a JPEG or TIFF file