QIBA/NIST
Dynamic Susceptibility Contrast Phantom
User Manual

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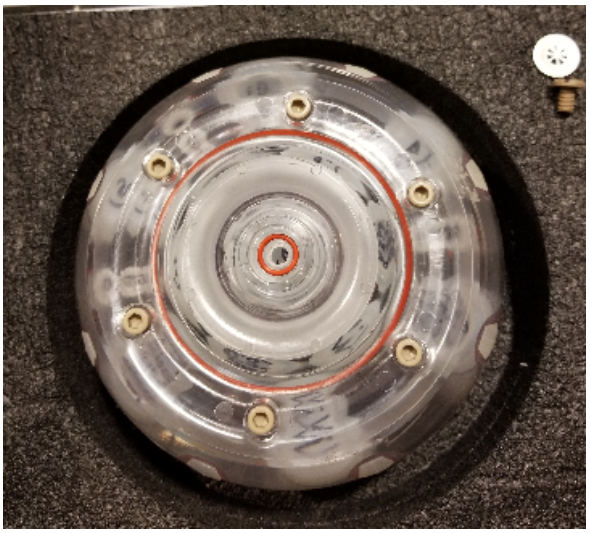
1.0 Introduction

This guide features sections on how to acquire data on the NIST/QIBA Dynamic Susceptibility Contrast (DSC) Phantom, analyze the DSC echo planar image (EPI) “perfusion” data to estimate ΔR2*, and calculate R_2* values for comparison. The analysis software requires at a minimum: Matlab R2015b, and "Image_Toolbox" v37. The Phantom shell is from HPD, the components were developed by the Magnetic Imaging Group at NIST, and software developed at MGH with support from HHSN268201500021C(H-1).

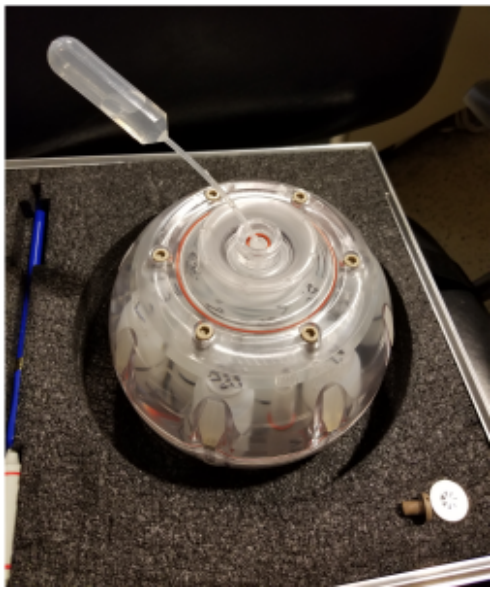
2.0 Instructions for Phantom Acquisition

1. Fill phantom with distilled water at least 24 hours before expected scan data to allow air bubbles to settle. Carry phantom to scanner bay carefully to avoid creation of air bubbles.

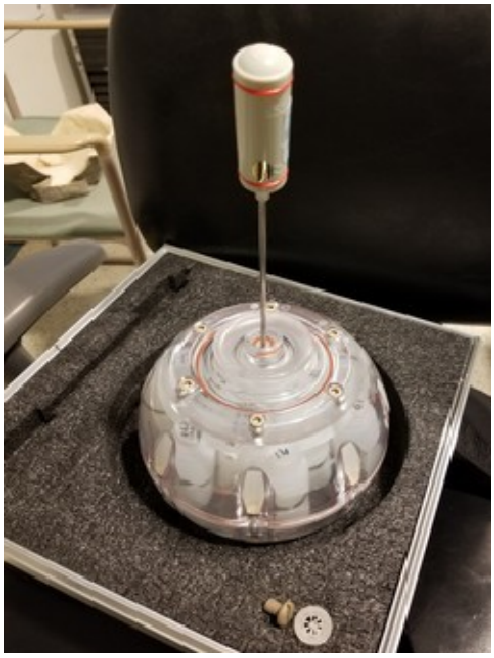
2. In scanner console room, before study, open portal as shown using provided disk.



3) Fill dropper with water and put water into the portal

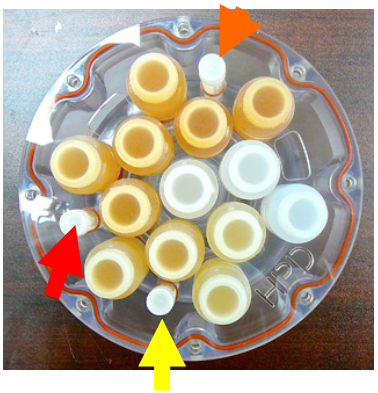


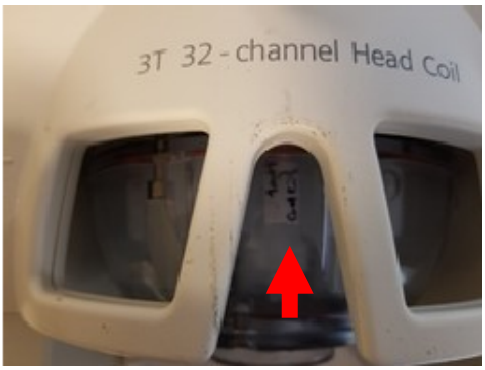
4) Measure and record temperature of phantom with provided temperature probe (outside of the scanner since temperature probe is not MRI compliant)



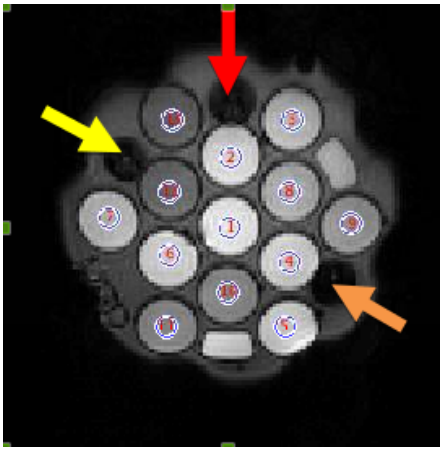
5) Close portal and place in the head coil in preparation for axial scans through the center plate.

6) For first scan, make sure middle gadolinium vial (red arrow) is aligned along the nasion. Make sure Plate with HPD logo (e.g. bottle tops) is facing the bottom of the coil.

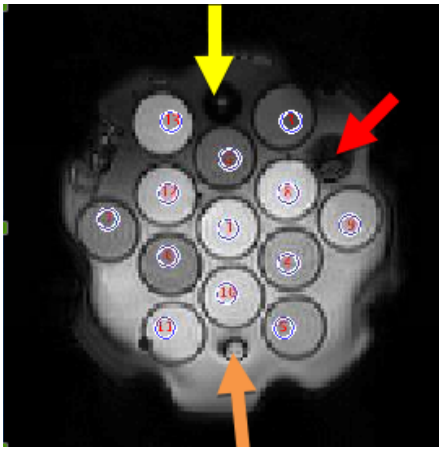




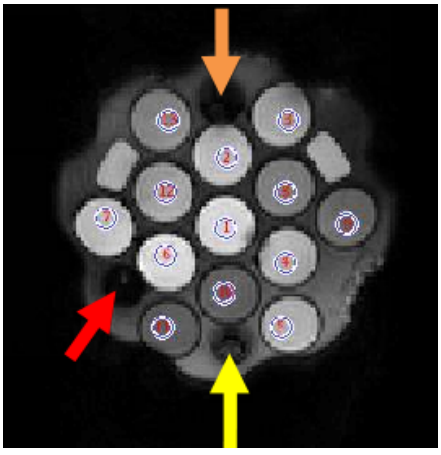
7) Run scanner protocol (localizer, EPI, T2* mapping). The resulting image center slice should look like this, with HPD logo in the lower left corner.



8) Take phantom out, and rotate, making sure vial to left (yellow arrow) is now aligned along the nasion. Repeat 7, with resulting center slice image looking as follows, with HPD logo in upper left.



9) Take phantom out and rotate, making sure vial 180 degrees (orange arrow) is now centered along the nasion. Repeat 7, with resulting center slice image appearing as follows, with HPD logo in lower right corner.

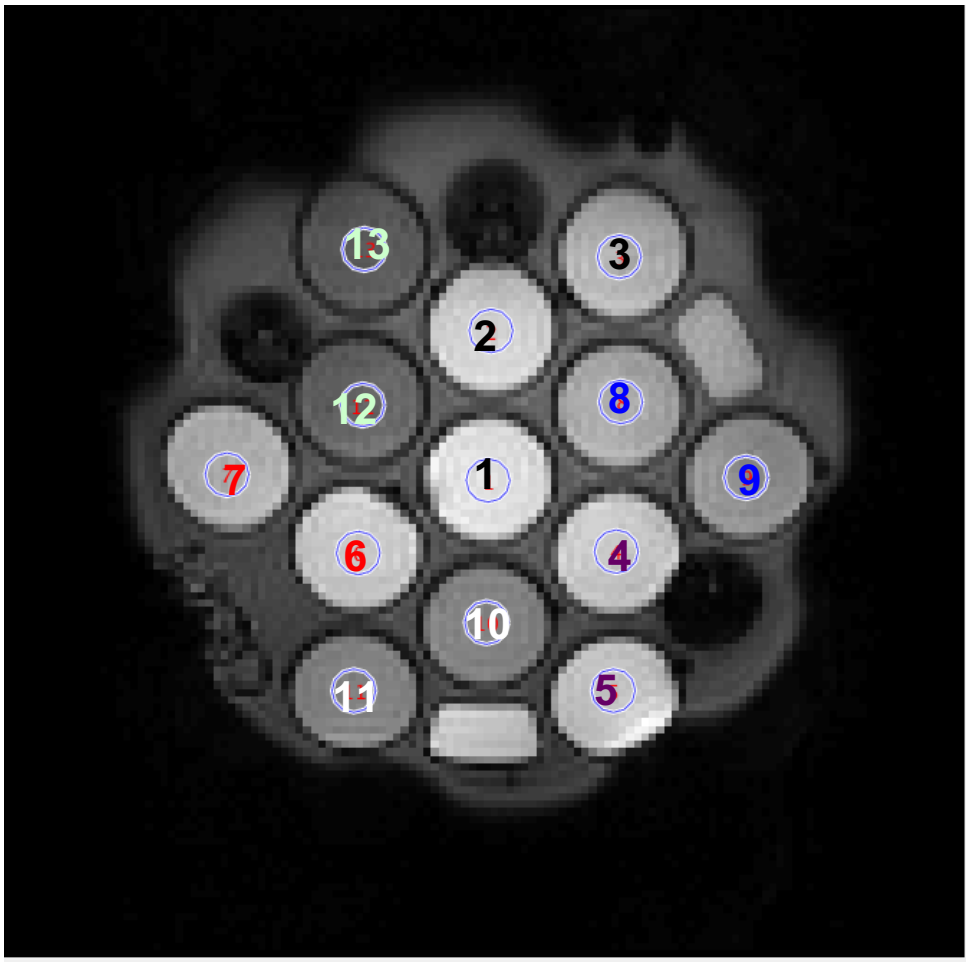


10) Take phantom out, move phantom to console room, open portal (step 2), measure temperature of phantom (step 4), record, close portal and return phantom to carrying case.

3.0 Instructions for EPI Data Analysis

The assumed layout of the phantom vials for software analysis is as follows:

ROIs	Sample
1, 2, 3	0.01 mM $GdCl_3$
4, 5	0.01 mM $GdCl_3$ + 0.2% agarose
6, 7	0.01 mM $GdCl_3$ + 0.5% agarose
8, 9	0.01 mM $GdCl_3$ + 1.0% agarose
10, 11	0.01 mM $GdCl_3$ + 2.0% agarose
12, 13	0.01 mM $GdCl_3$ + 3.0% agarose



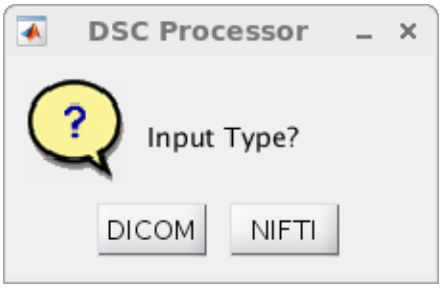
1) Run qiba_dsc_process_EPI in matlab. You have the option of running with or without arguments or outputs. More information can be obtained by typing:

>> help qiba_dsc_process_EPI

2) For this example we will save outputs and run in interactive mode:

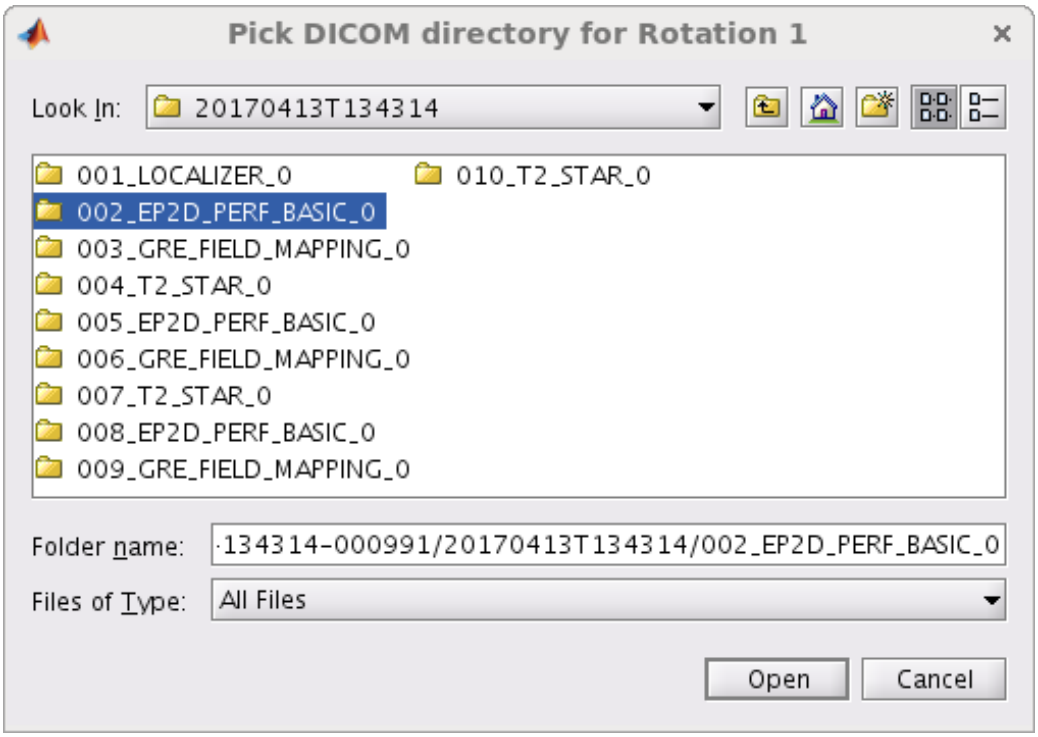
[av,sd,inner,outer,conc,imstack,roistack,raw]=qiba_dsc_process_EPI();

You will be prompted to choose an input type.



Choose an input type, DICOM or NIFTI.

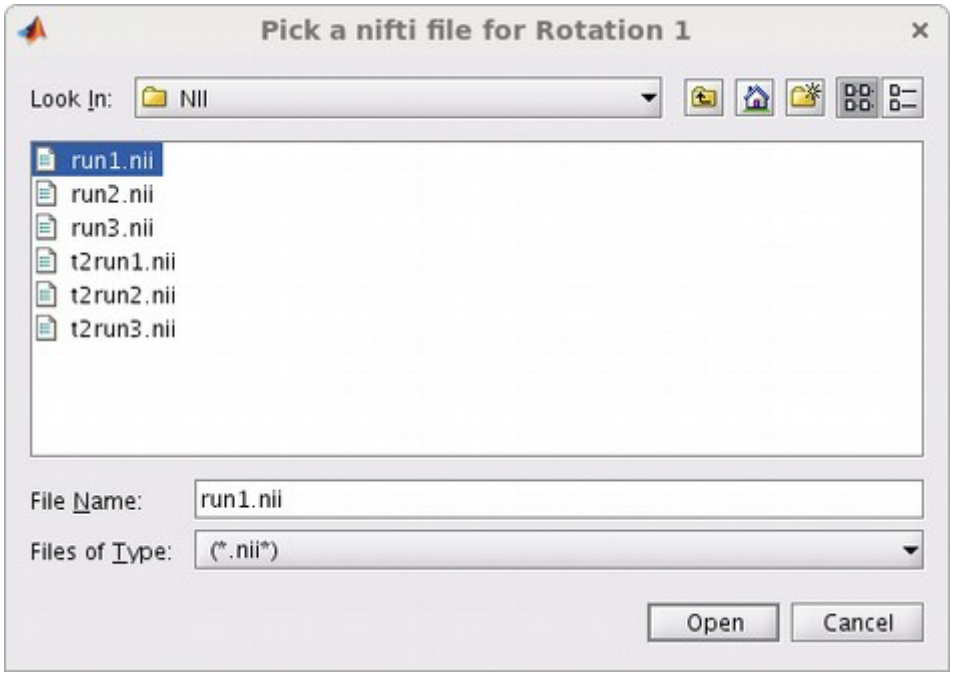
3A) If you choose DICOM, choose separate directories for each of rotations 1-3. It is assumed each folder contains only DICOM files for each individual run of DSC EPI acquisitions.



When you find the folder matching the correct rotation number, click open; proceed for

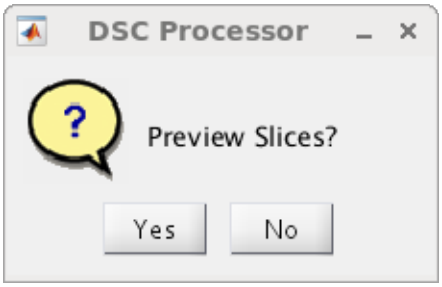
rotations 1-3. (See Section 2 on Acquisition).

3B) If you choose NIFTI, choose separate NIFTI files for each of rotations 1-3. It is assumed each NIFTI file is a 4D file containing all data from a single DSC EPI acquisition.

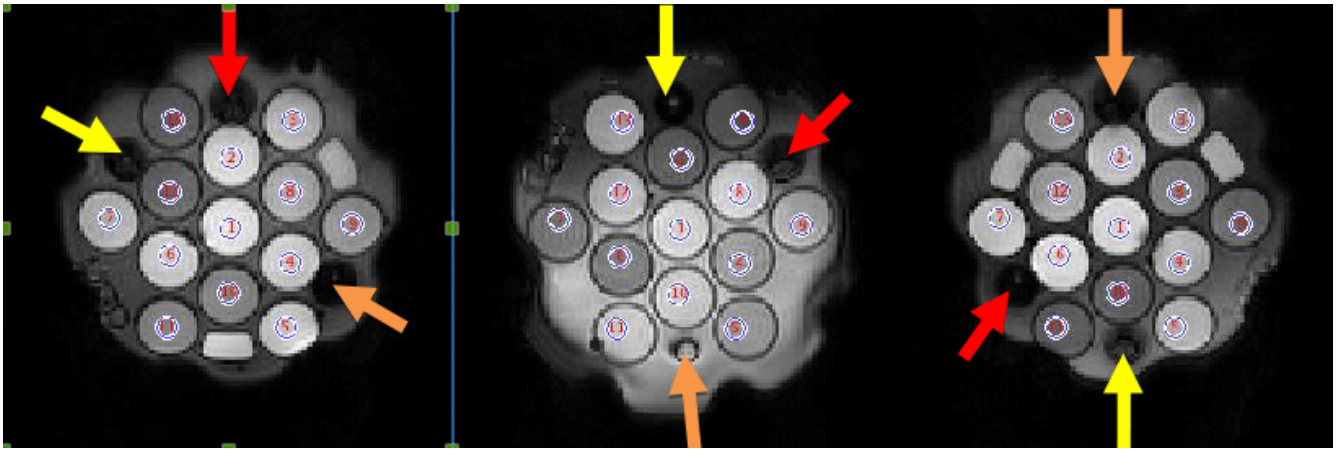


When you find the file matching the correct rotation number, click open; proceed for rotations 1-3. (See Section 2 on Acquisition).

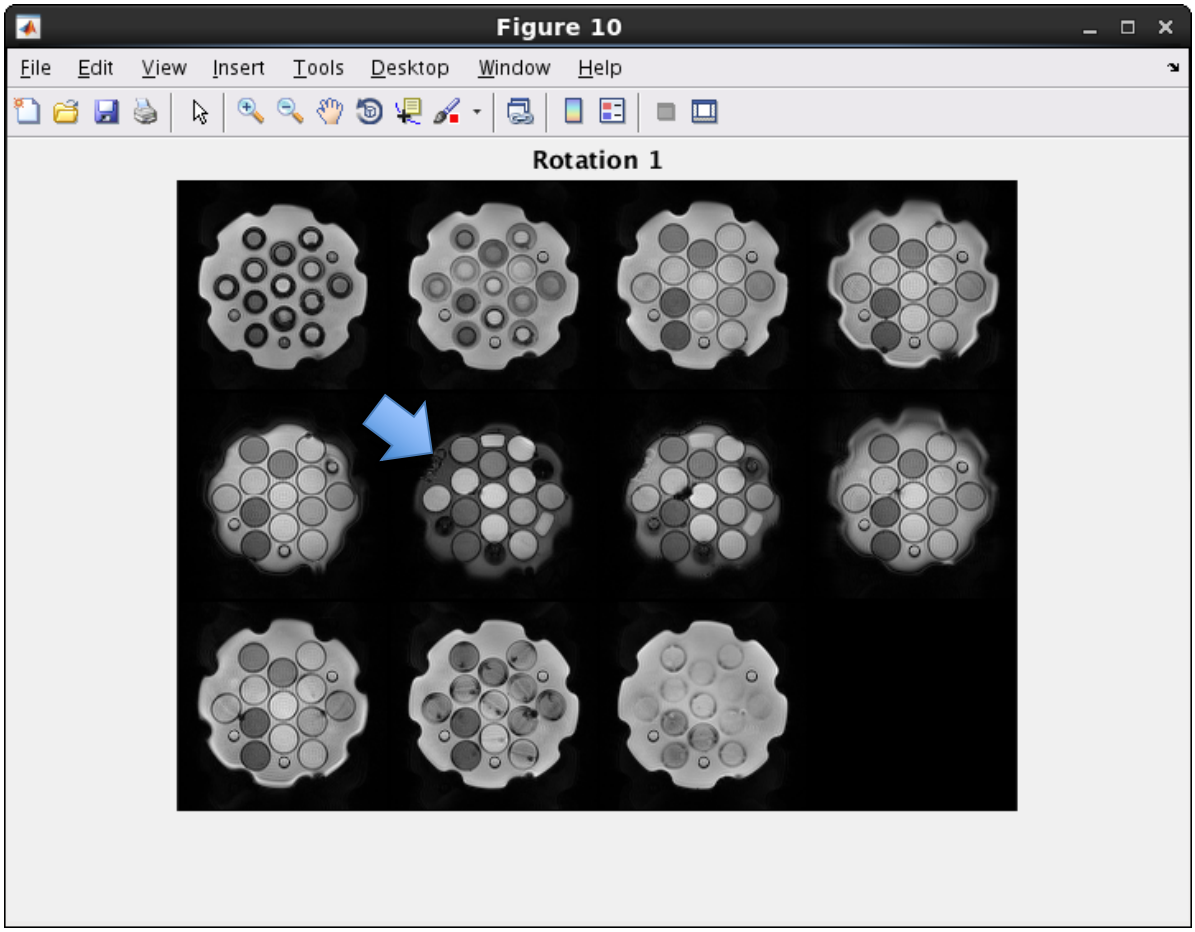
4) Preview files to ensure they are the correct files and they are oriented properly, flip vertically if necessary. **TIP:** It is suggested that if it is the first time analyzing the dataset to Preview the slices.



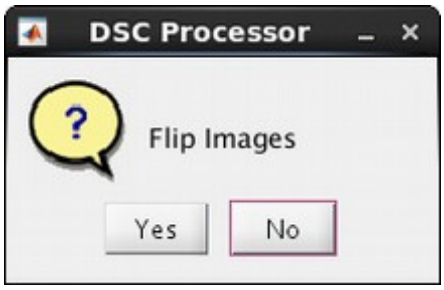
Make sure each rotation's slices are oriented as they are depicted below. Use the position of the fiducials (arrows) for guidance using the slice containing the central slice. (Left) Rotation 1. (Middle) Rotation 2. (Right) Rotation 3.



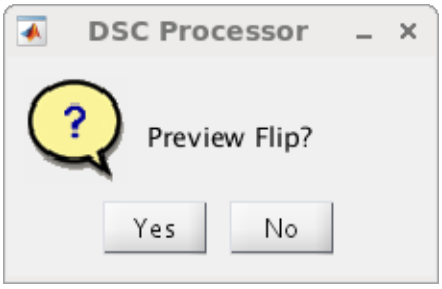
An example of a preview that needs to be flipped is shown below. If the HPD logo appears flipped vertically in the central slice (arrow), Flip the Images. This often occurs for NII images depending on the software that was used to convert the DICOM files:



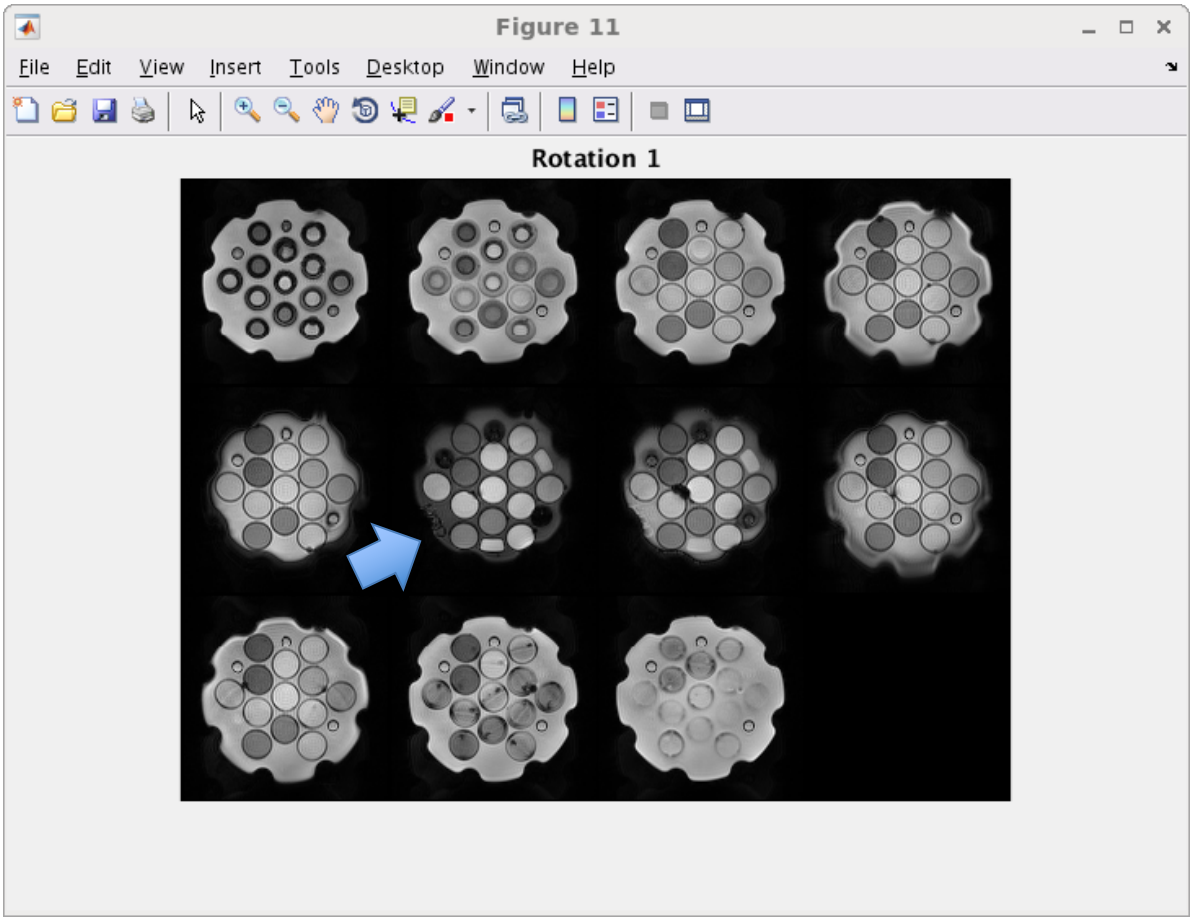
To flip the image above select yes when asked to Flip Images.



You will have the option to view the flipped images to check the results.



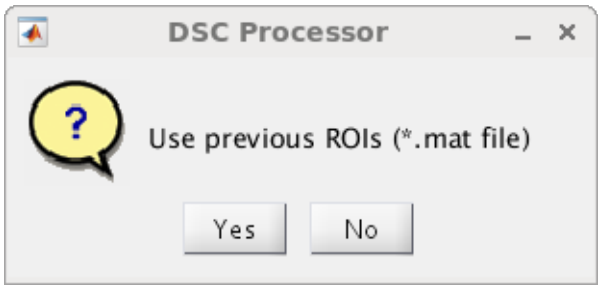
Below is the preview of the flipped, corrected slices.



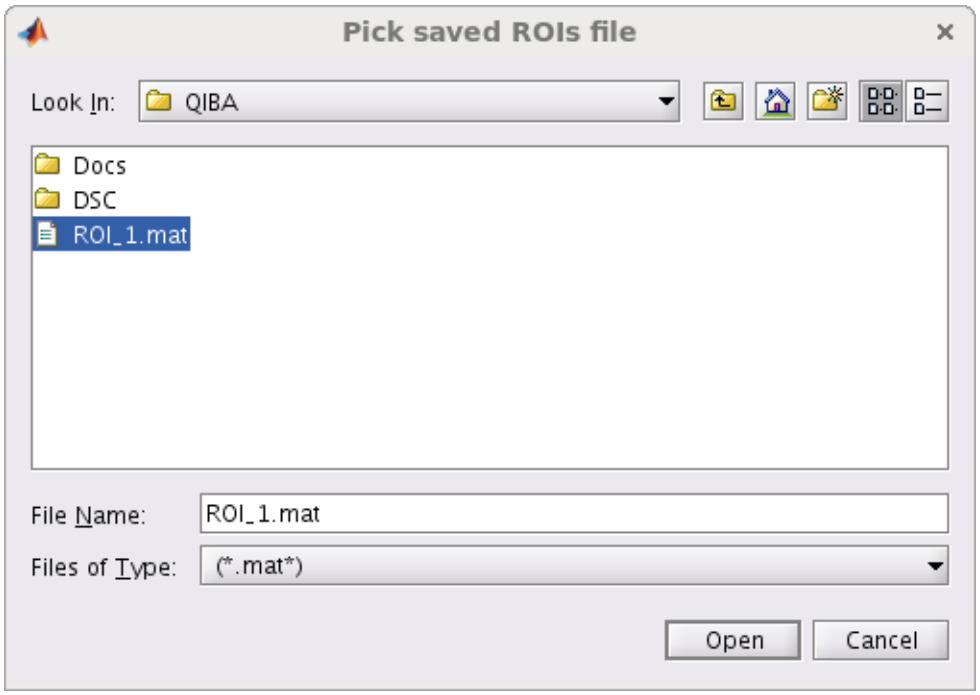
Notice the HPD logo on slice 6 (arrow), indicating the central slice for this rotation.

If the images still do not appear to be oriented correctly, you may need to reformat the NII files from the original DICOM files. Another option would be to change the numbering and ordering of the vials in the following steps to match the ordering of vials to match your positioning.

5) Next you will be asked if you would like to use a previous region of interest (ROI). If you have ROIs to use, you can click yes and select a previous ROI (assumed matlab format). We have included a previous rois.mat that consists of central 3 slices, 5 mm radius ROIs.

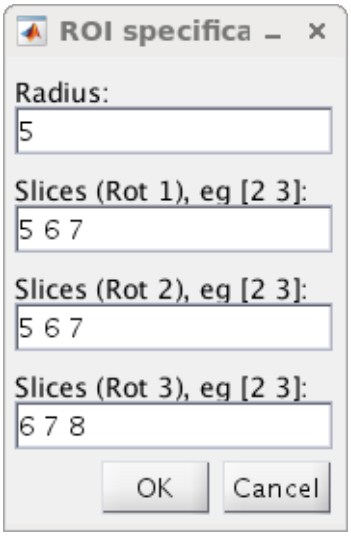


6A) If you have a previously saved ROI file, a prompt appears asking for the filename of a previous ROI.



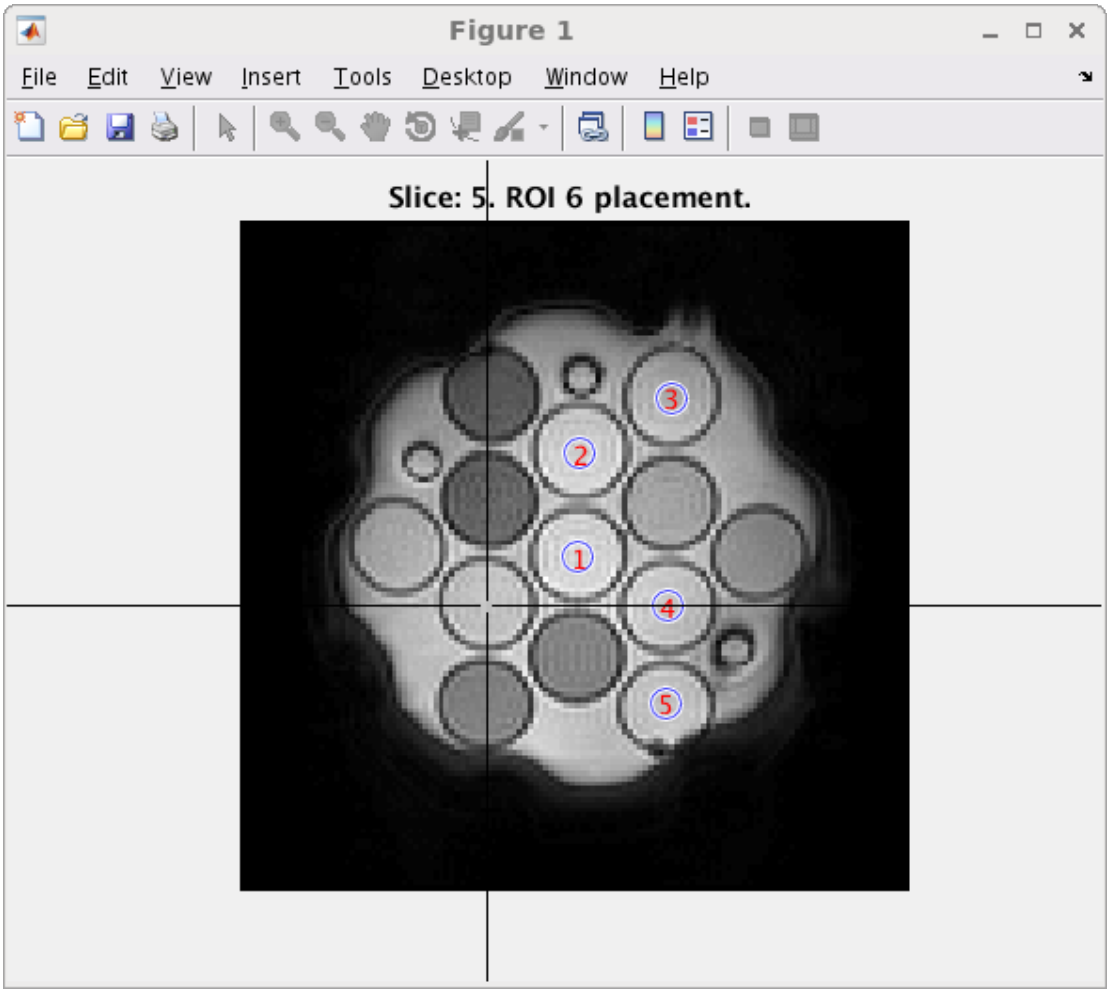
You will see ROIs autopopulate on slices for each rotation. Continue with step 9.

6B) If not, select your ROI's radius in the ROI specification window. By default, all slices in the acquisition are shown.

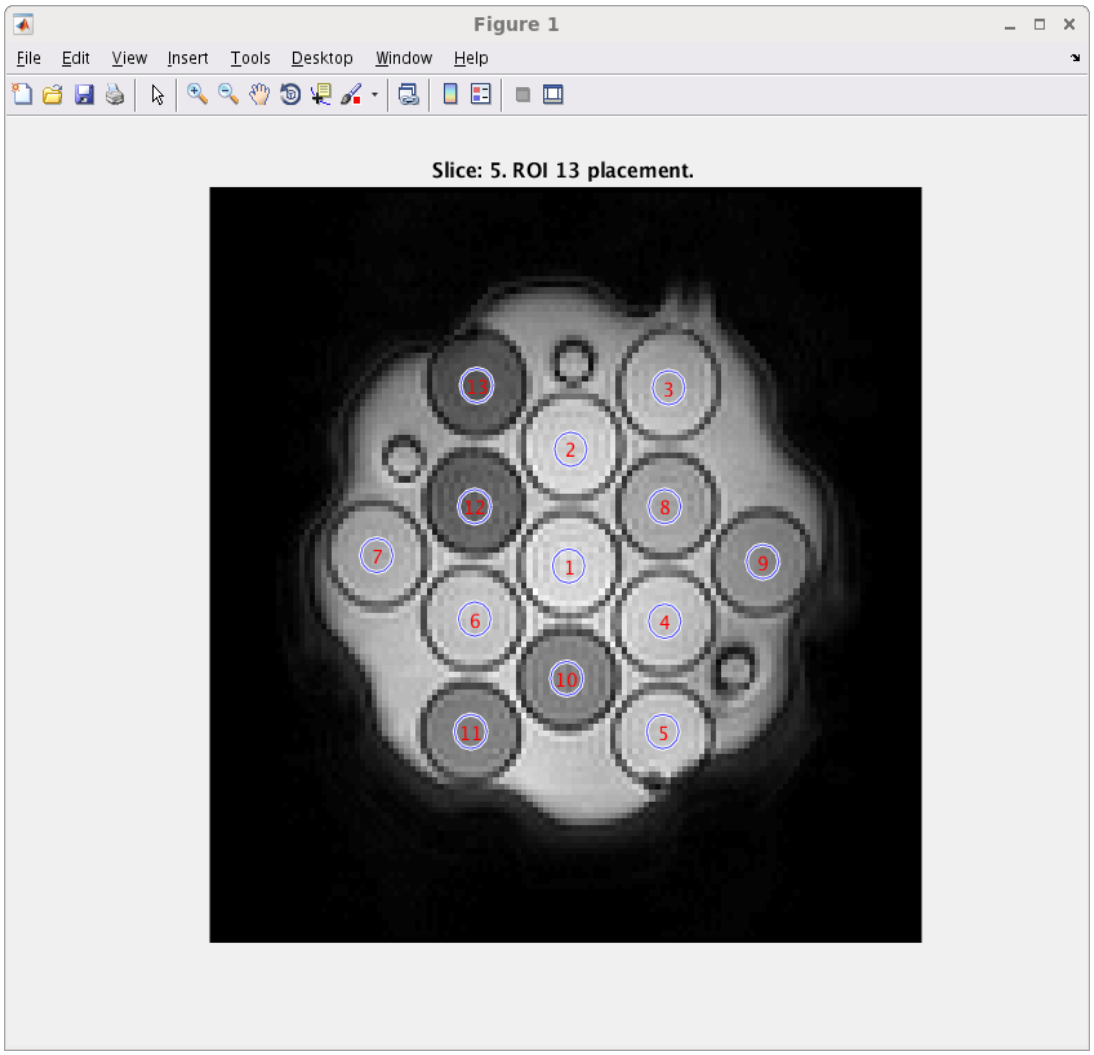


TIP: It is recommended that you restrict the analysis to the central reference slice (with HPD logo) and the slices before and after it. You can restrict the analysis to the slices you want by entering the slice numbers separated by spaces. For example, if your central slice is 6 in rotation 1, you would enter 5 6 7 in that box. The same number of slices should be used for the other rotations. In this example, the 3rd rotation was slightly off, and hence the central slice was in slice 7.

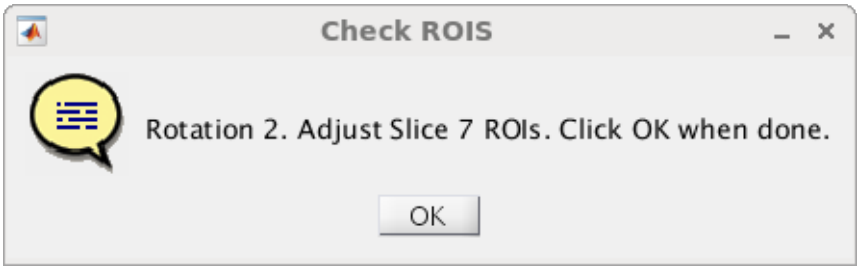
7) ROI Placement: Using your mouse, mark the center of the 13 ROI's per slice, 1 for each vial. Below shows how to mark the ROI for vial 6 after having marked the ROI for vials 1-5. **TIP**: Making the window larger can make ROI placement easier.



Once you have placed ROIs for all vials, you will have an image as follows:

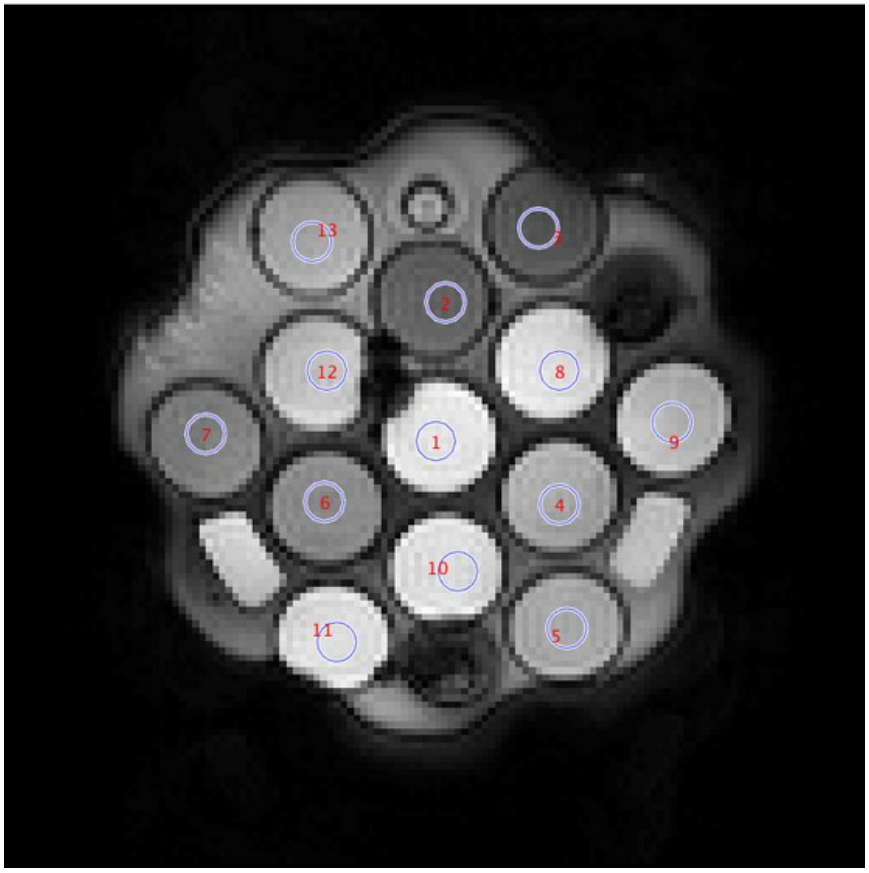


8) Once you are done placing all ROIs, you are given the option to adjust the placement of your ROIs. These ROIs are then propagated to all the slices. **TIP**: ROI placement for the first slice of each rotation is the most important. Good placement of the first slice will limit the need to adjust ROIs on the subsequent slices.



When the check ROIs box pops up, you will be able to drag your ROIs to a new location. Click okay when you are satisfied with the ROIs positions. Note that the red numbering of the ROIs will not move, only the outer ring indicating the ROI will move

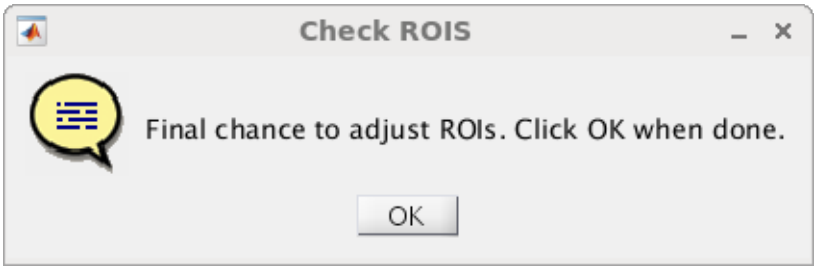
when you adjust your ROIs. Confirm the placement of your ROIs for all slices. **TIP:** If you have problems moving the ROIs, making the figure larger can help. The cursor will change to a hand when positioned correctly on the ROI.



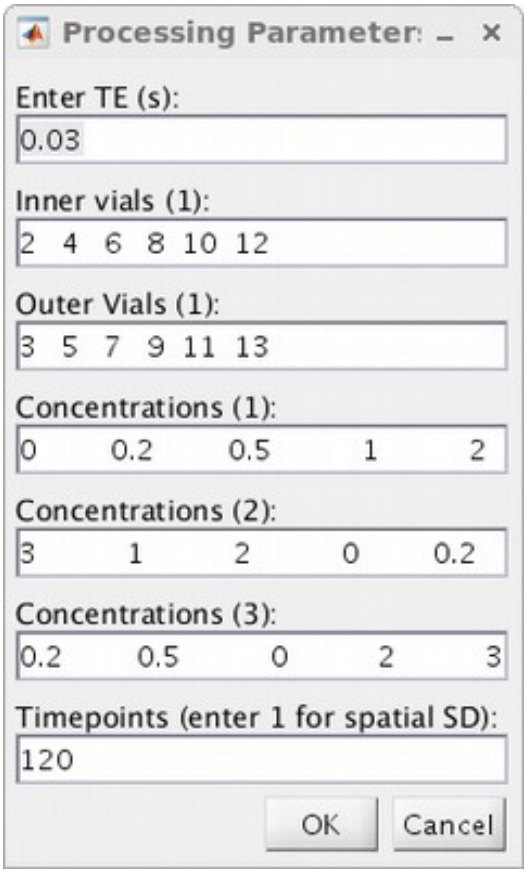
Repeat until you are done adjusting the ROIs for the last slice of the 3rd rotation.

9) You will be given one last time to adjust the ROIs for all slices for all rotations.

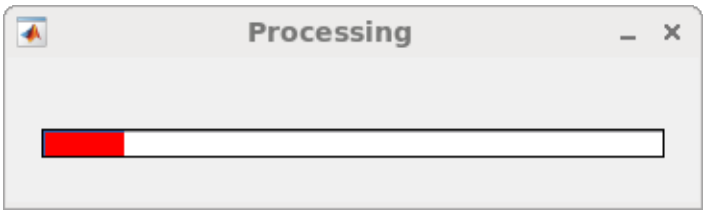
Once you have confirmed ROI placements, the red text will be centered in the ROIs in their final positions. If unsatisfied with ROI positions, the matlab program can be restarted.



10) Next you can confirm your Processing Parameters. The default parameters assume that the vials are placed as shown in Step 4. It is assumed that all EPI datasets were acquired with the same TE. Timepoints specify the number of timepoints to estimate variance. To estimate noise in a single timepoint, set to 1. Hit ok when done.

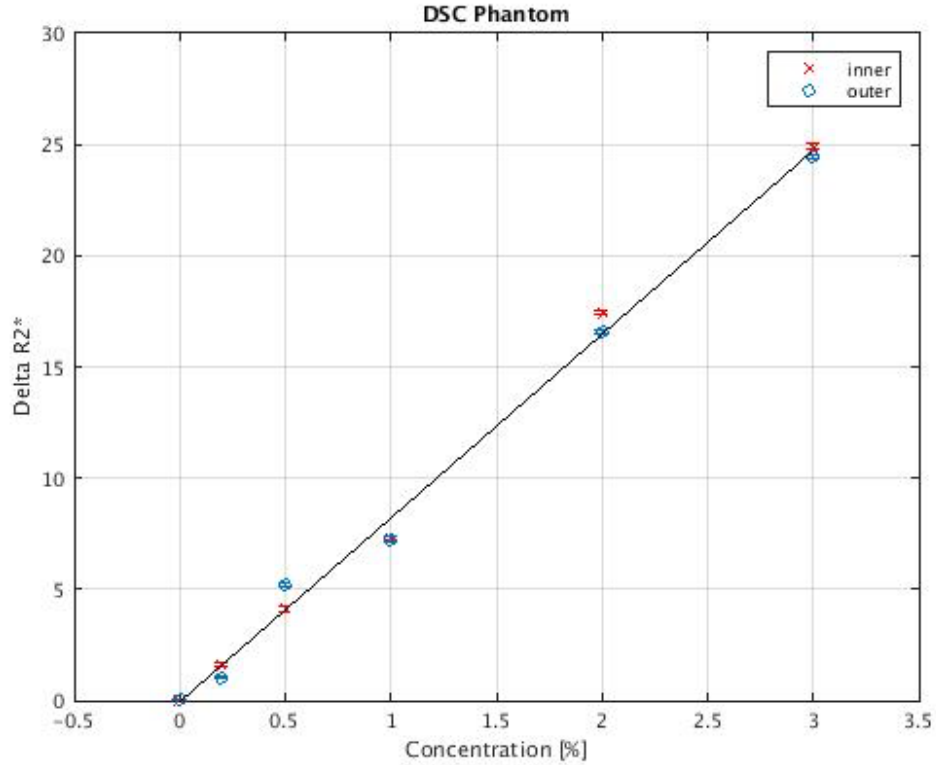


11) Previous figures with ROIs will close. You will be shown a processing progress bar.

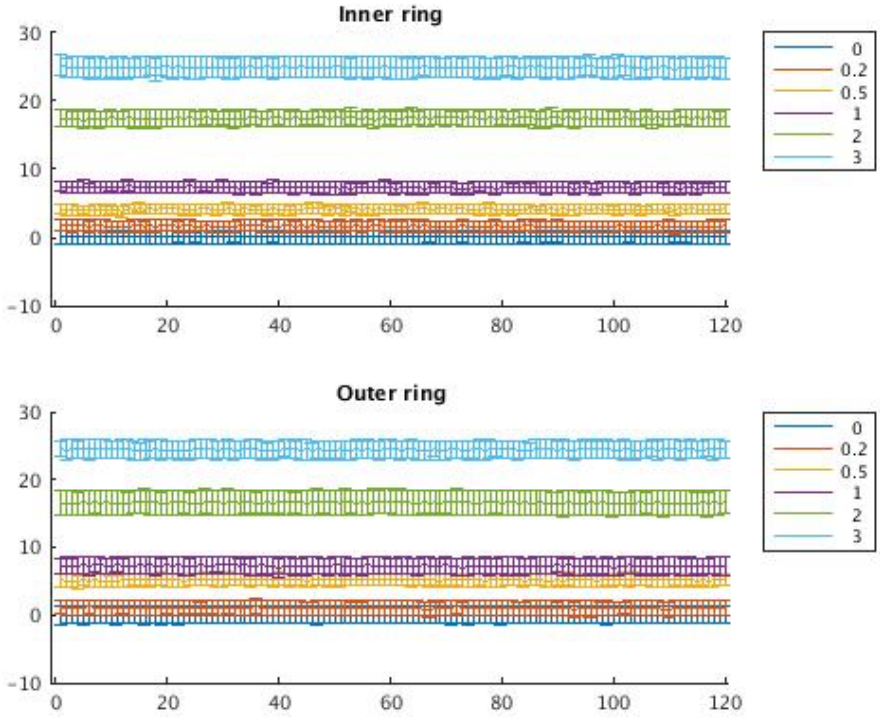


When Processing is complete, results will appear as two figures.

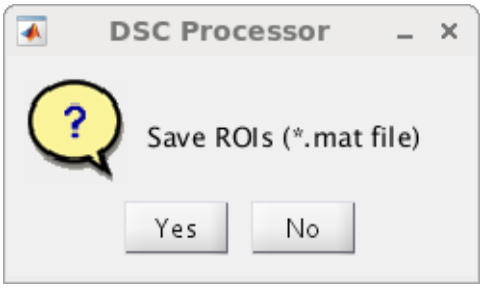
The first figure shows the change in calculated R2* with respect to the 0% concentration vial in the other rotations along with error bars (standard deviation within ROIs across the specified number of time points. Results are organized by inner and outer vial rings:

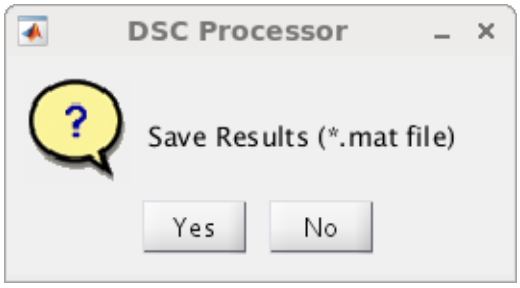


The second figure shows the estimated ΔR2* at each timepoint to understand fluctuation of estimates as a function of scanner time. Results are also shown as a function of inner and outer vials.



12) If the results appear satisfactory, you can choose to Save your ROI's and results for future use if you wish.





13) If one does not choose to save the results, if the program was run as described in Step 2, one can interact with the returned results directly:

av average values in ROI across times
- inner vial numbers of 1st rotation
- outer vial numbers of 1st rotation
- conc concentration in each vial
- imstack dR2* values over time for each rotation
- roistack ROIs used per vial (eg timept 13 = vial 13 roi)
- raw 1x3 cell of raw 4D images

14) The script can also be run in non-interactive mode by passing arguments:

These values must be specified

'InteractiveMode'	0 or 1 (default)
'ROI'	saved ROI filename
'type'	'NIFTI' or 'DICOM'
'rot1'	DICOM directory or NIFTI filename of rotation 1
'rot2'	DICOM directory or NIFTI filename of rotation 2
'rot3'	DICOM directory or NIFTI filename of rotation 3

Optional:

'Flip'	0 (default) or 1 - flip image in A/P direction
'radius'	5 (default) - radius for ROI
'TE'	0.030 (s default) - TE
'Nrois'	13 (default)
'Nrots'	3 (default)

4.0 Instructions for R_2* Mapping

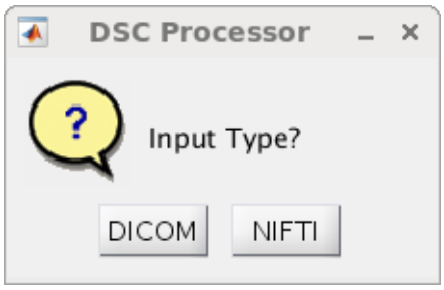
1) Run qiba_dsc_process_T2 in matlab. You have the option of running with or without arguments or outputs. More information can be obtained by typing:

```
>> help qiba_dsc_process_T2
```

2) For this example we will save outputs and run in interactive mode:

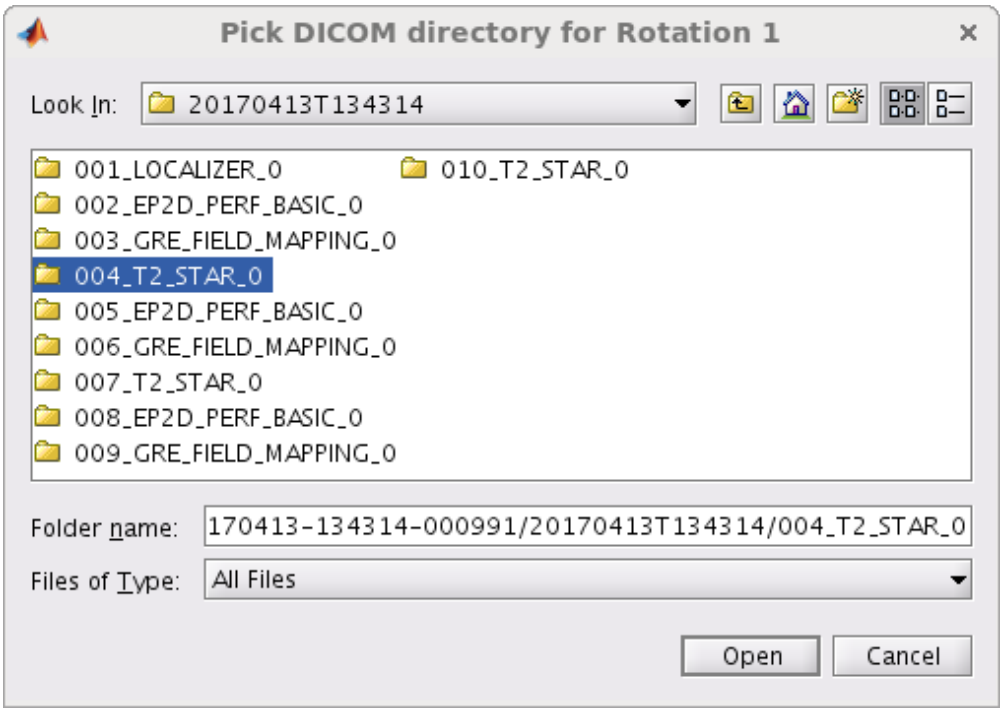
```
[av,sd,inner,outer,conc,imstack,roistack,raw]=qiba_dsc_process_T2();
```

You will be prompted to choose an input type.



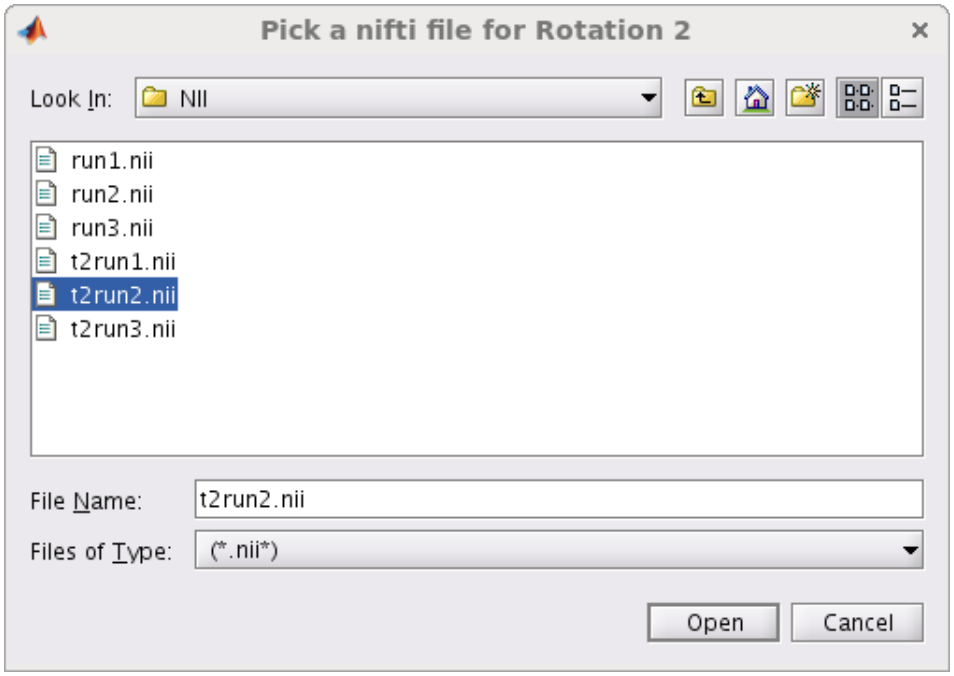
Choose an input type, DICOM or NIFTI.

3A) If you choose DICOM, choose separate directories for each of rotations 1-3. It is assumed each folder contains only DICOM files for each individual run of multi-echo gradient echo acquisitions.



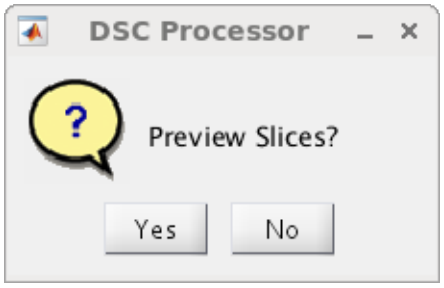
When you find the folder matching the correct rotation number, click open; proceed for rotations 1-3.

3B) If you choose NIFTI, choose separate NIFIT files for each of rotations 1-3. It is assumed each NIFTI file is a 4D file containing all data from a single multi-echo gradient echo acquisition.

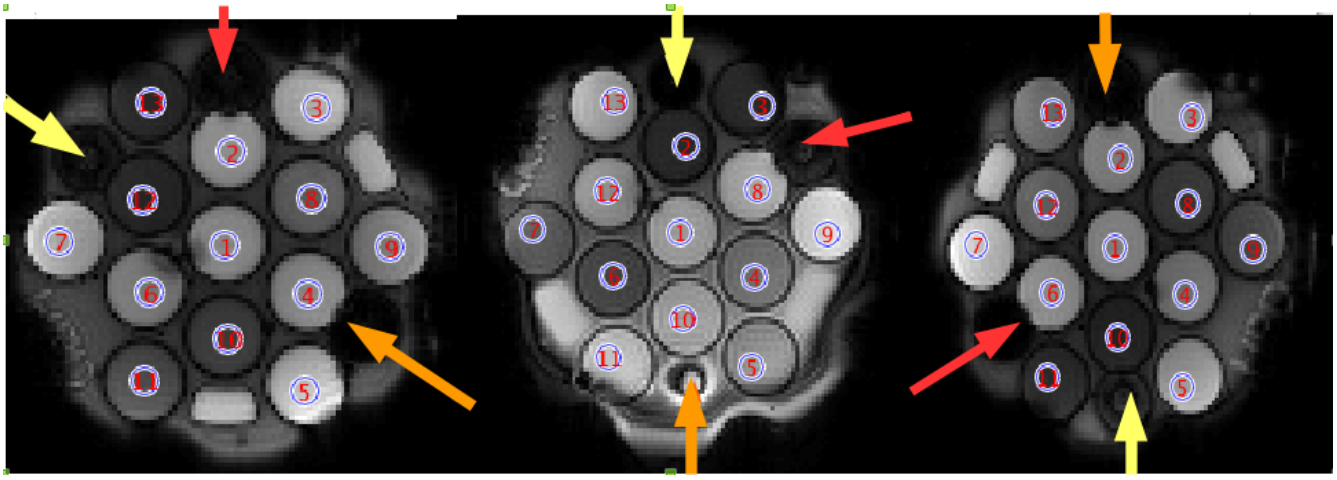


When you find the file matching the correct rotation number, click open; proceed for rotations 1-3.

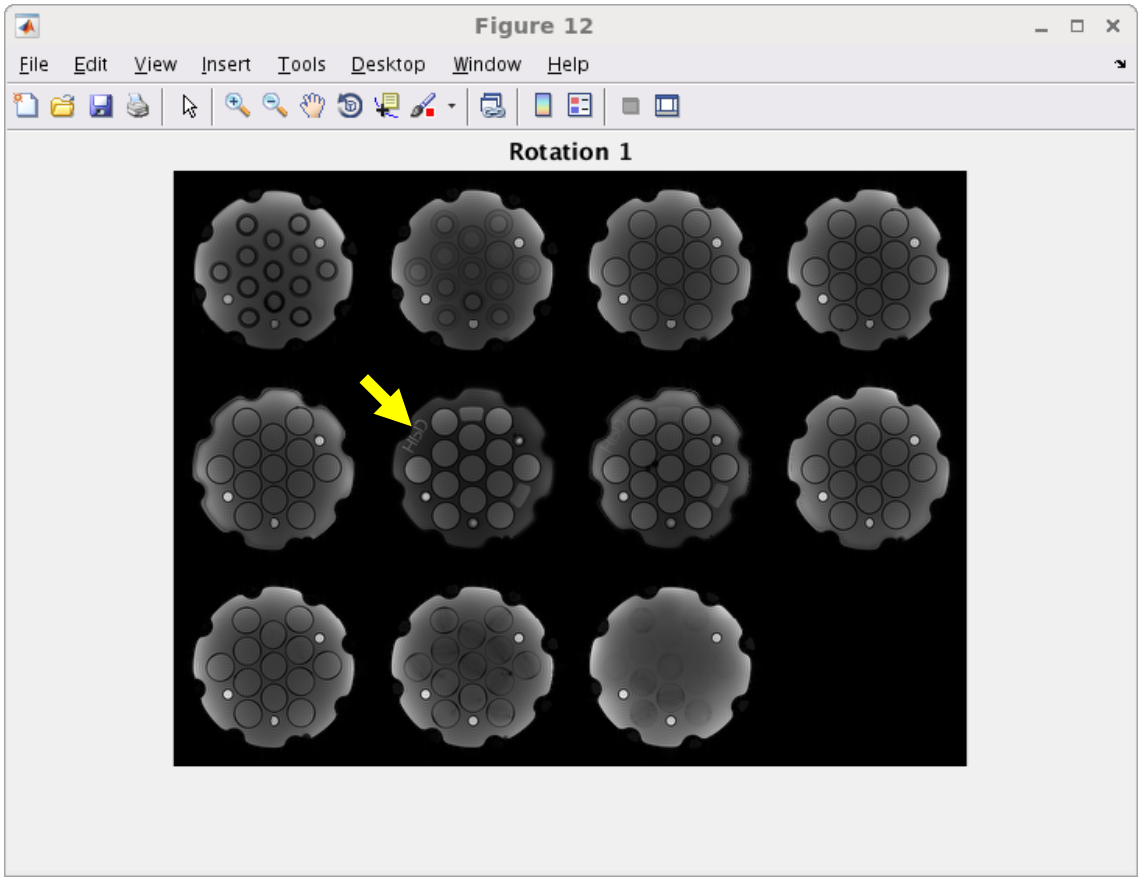
4) Preview files to ensure they are the correct files and they are oriented properly, flip vertically if necessary. **TIP:** It is suggested that if it is the first time analyzing the dataset to Preview the slices.



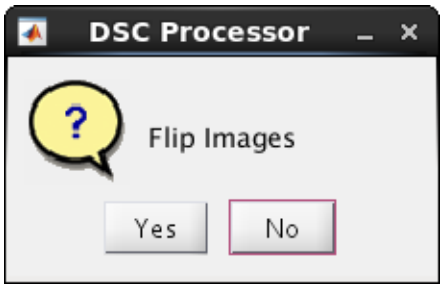
Make sure each rotation's slices are orientated as they are depicted below. Use the position of the fiducials (arrows) for guidance using the slice containing the central slice. (Left) Rotation 1. (Middle) Rotation 2. (Right) Rotation 3.



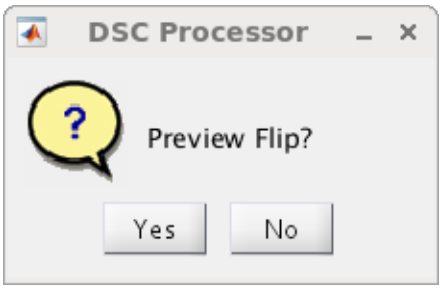
Below is an example of a first rotation that needs to be flipped. If the HPD logo appears flipped vertically in the central slice (arrow), flip the Images. This often occurs for NII images depending on the software that was used to convert the DICOM files:



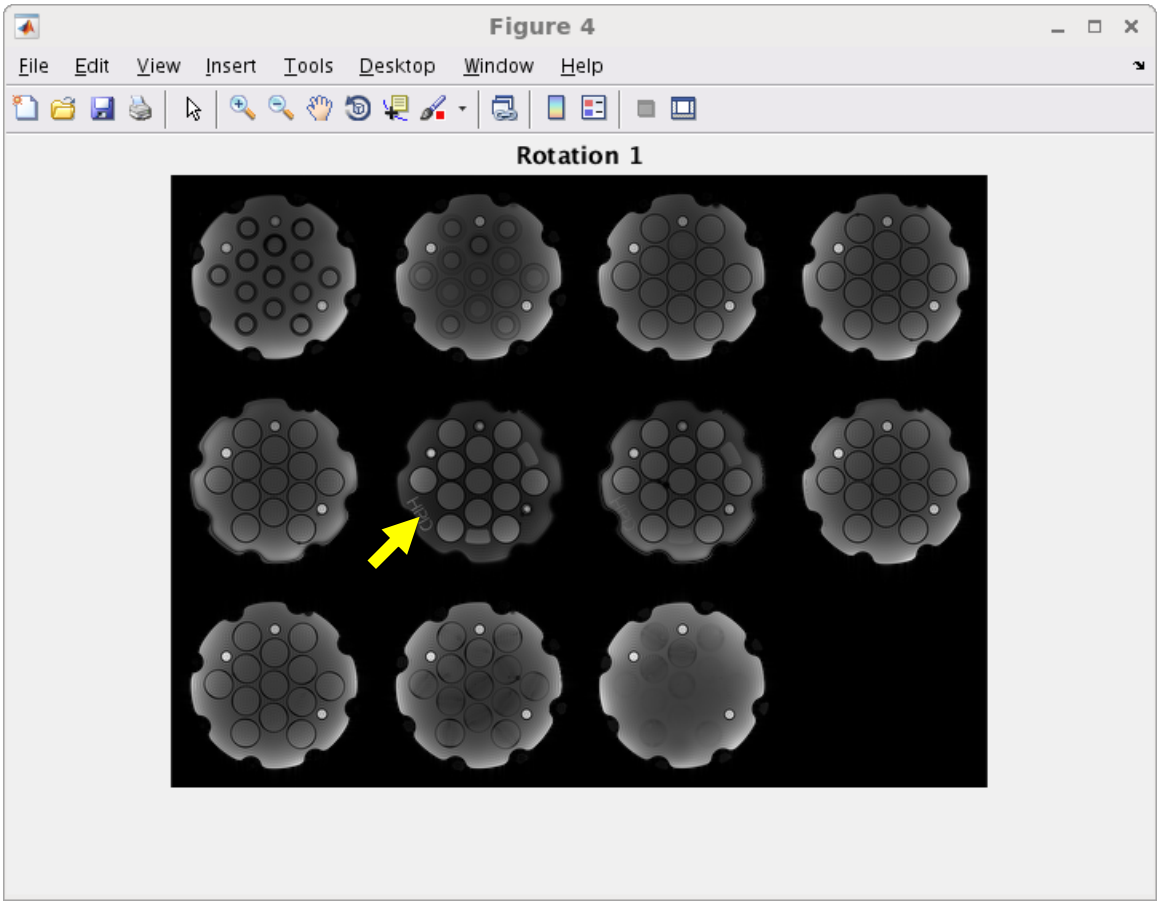
To flip the image above select yes when asked to Flip Images.



You will have the option to view the flipped images to check the results.



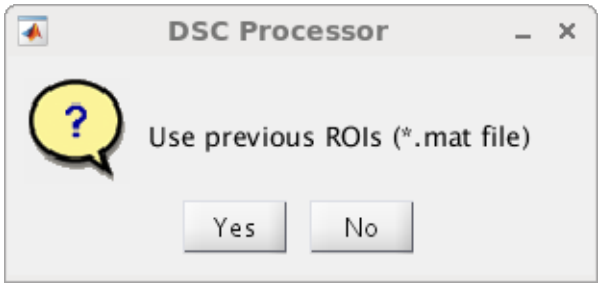
Below is an example of rotation one after it has been corrected by flipping.



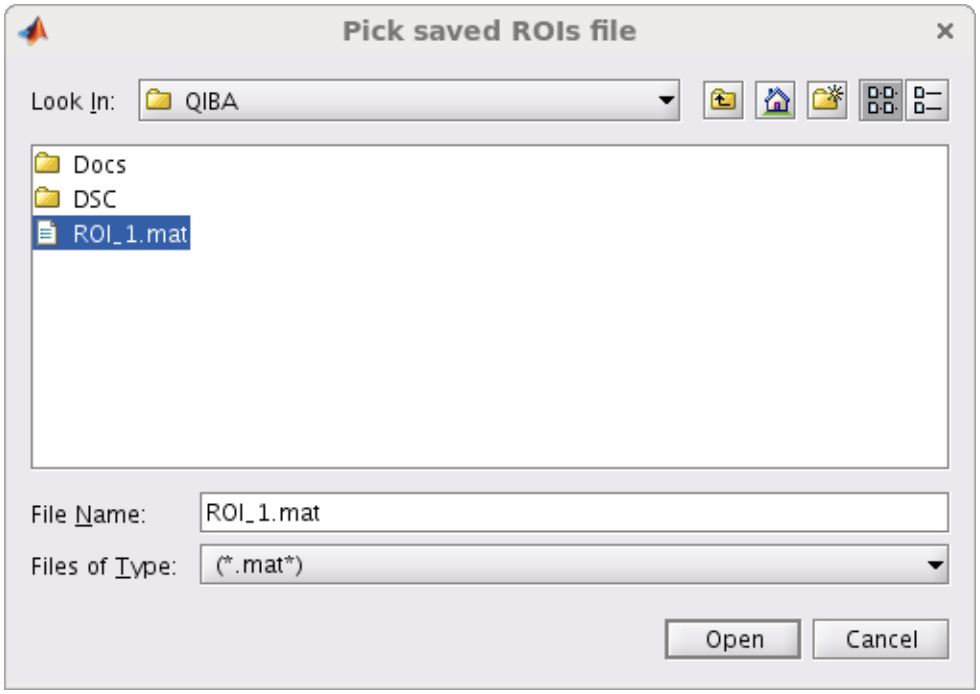
Notice the HPD logo on slice 6 (arrow), indicating the central slice for this rotation.

If the images still do not appear to be oriented correctly, you may need to reformat the NII files from the original DICOM files. Another option would be to change the numbering and ordering of the vials in the following steps to match the ordering of vials to match your positioning.

5) Next you will be asked if you would like to use a previous region of interest (ROI). If you have ROIs to use, you can click yes and select a previous ROI (assumed matlab format). We have included a previous rois.mat that consists of central 3 slices, 5 mm radius ROIs. **TIP**: If you use the same ROIs as used for EPI analysis, you can compare results.

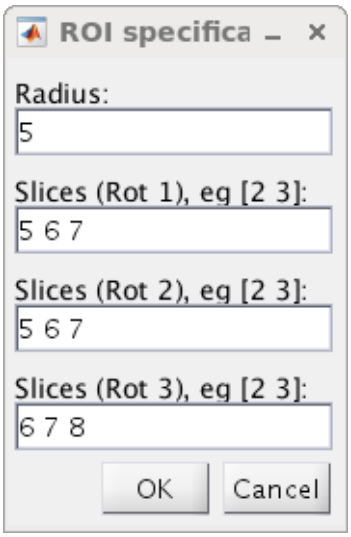


6A) If you have a previously saved ROI file, a prompt appears asking for the filename of a previous ROI.



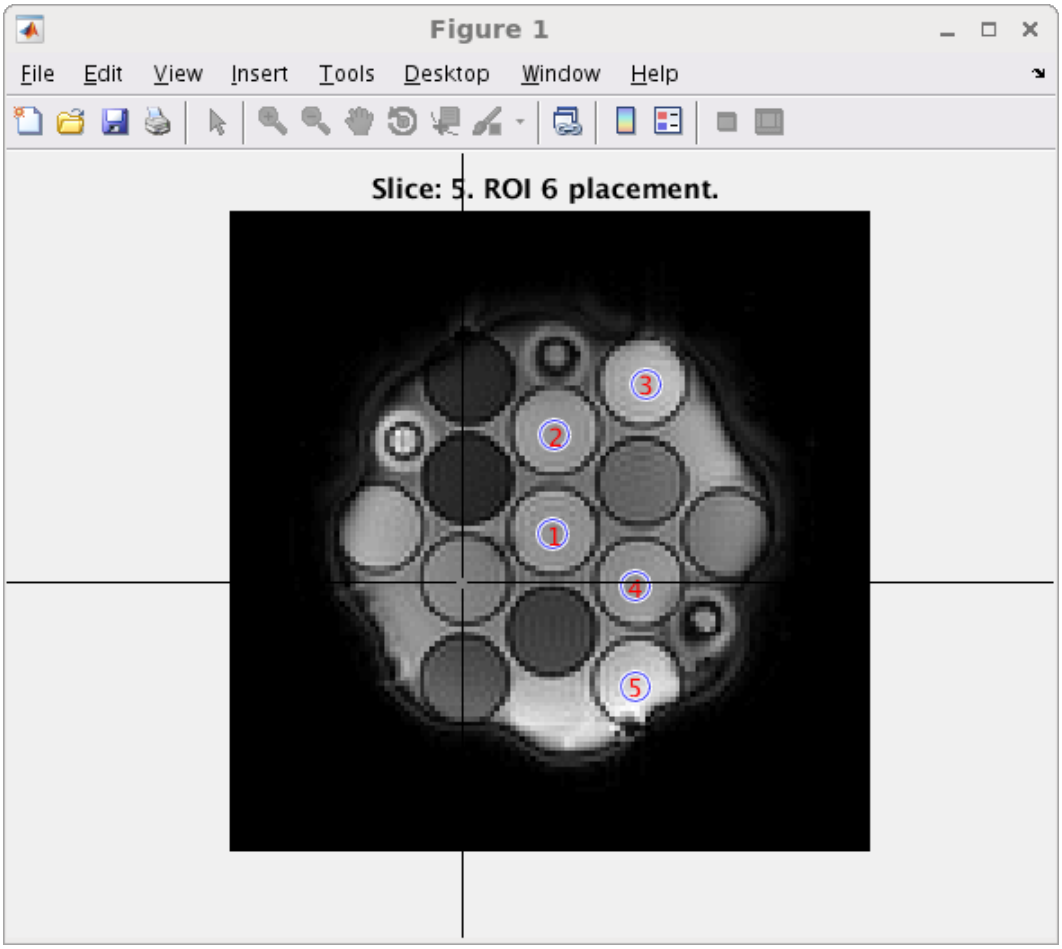
You will see ROIs autopopulate on slices for each rotation. Continue with step 9.

6B) If not, select your ROI radius in the ROI specification window. By default, all slices in the acquisition are shown.

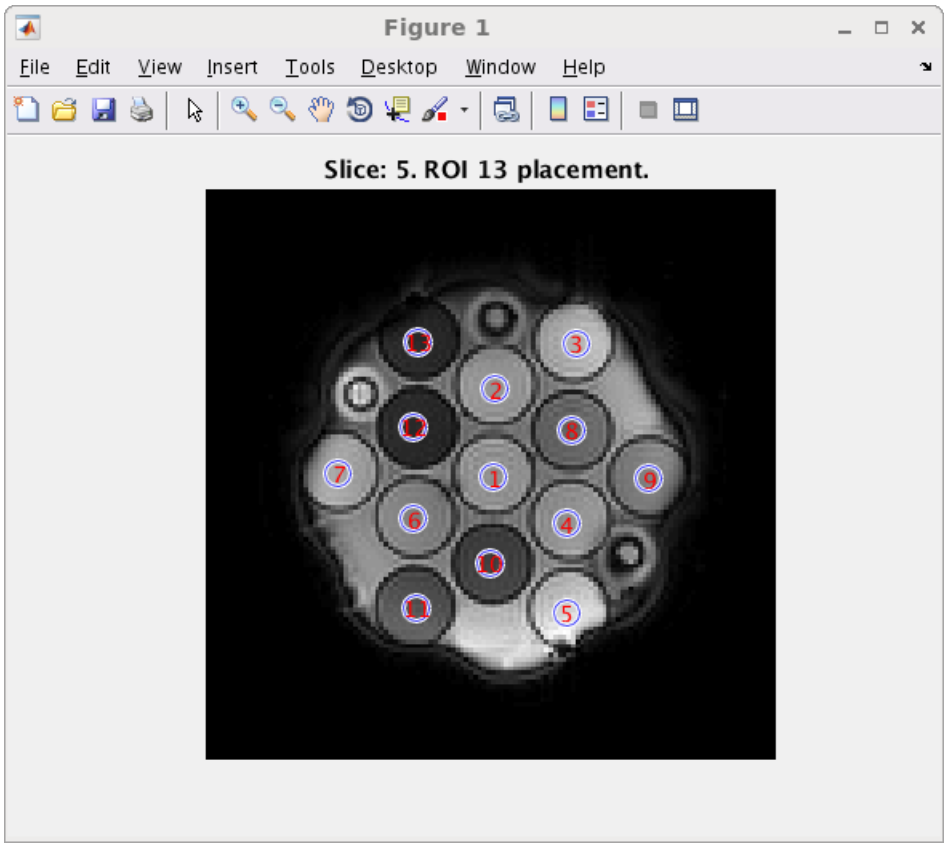


TIP: It is recommended that you restrict the analysis to the central reference slice (with HPD logo) and the slices before and after it. You can restrict the analysis to the slices you want by entering the slice numbers separated by spaces. For example, if your central slice is 6 in rotation 1, you would enter 5 6 7 in that box. The same number of slices should be used for the other rotations. In this example, the 3rd rotation was slightly off, and hence the central slice was in slice 7.

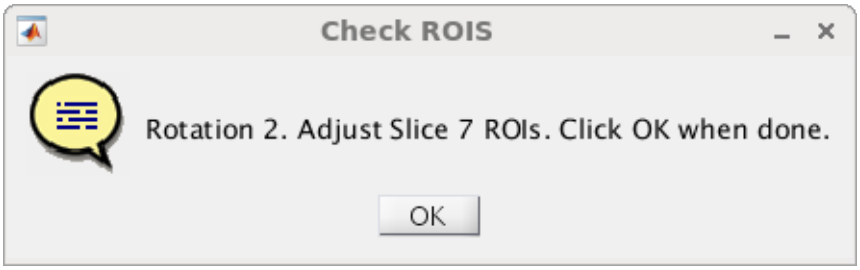
7) ROI Placement: Using your mouse, mark the center of the 13 ROIs per slice, 1 for each vial. Below shows how to mark the ROI for vial 6 after having marked the ROI for vials 1-5. **TIP**: Making the window larger can make ROI placement easier.



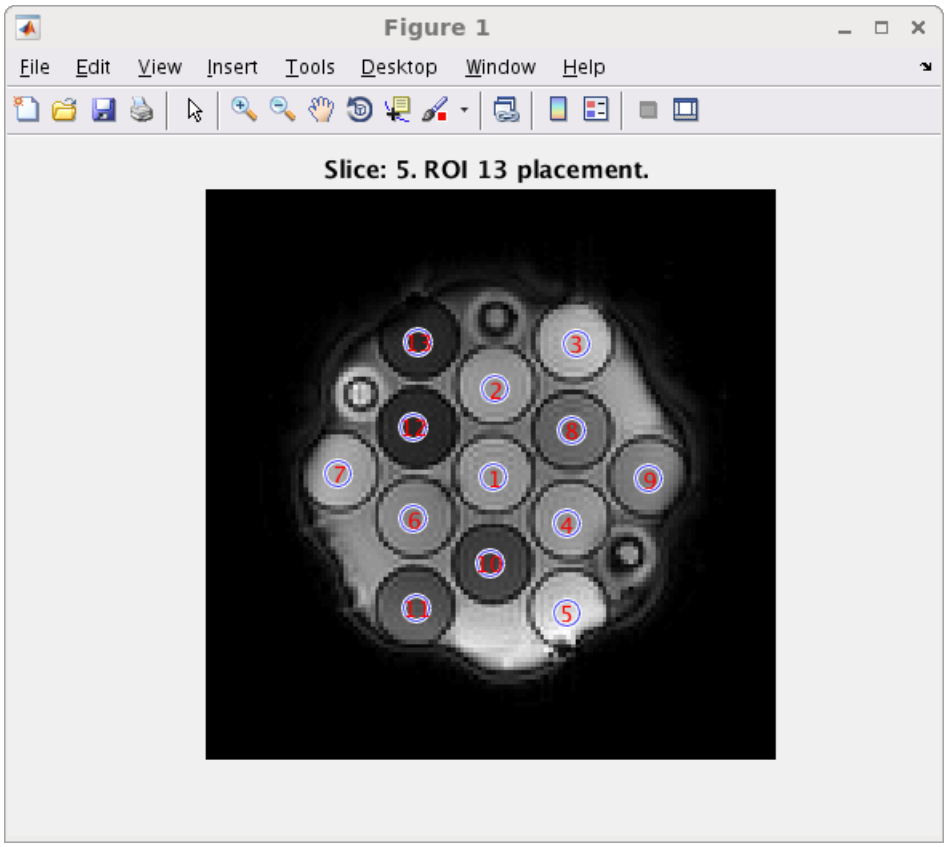
Once you have placed ROIs for all vials, you will have an image as follows:



8) Once you are done placing all ROIs, you are given the option to adjust the placement of your ROIs. These ROIs are then propagated to all the slices. **TIP**: ROI placement for the first slice of each rotation is the most important. Good placement of the first slice will limit the need to adjust ROIs on the subsequent slices.

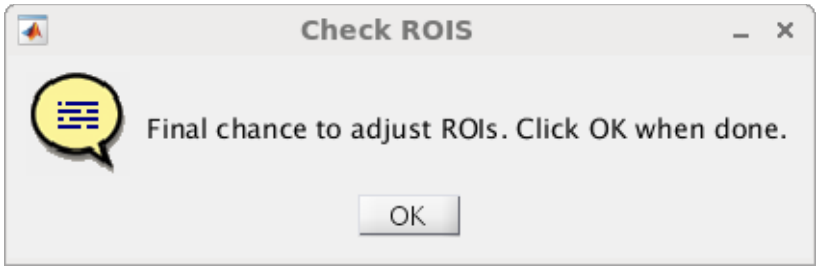


When the check ROIs box pops up, you will be able to drag your ROIs to a new location. Click okay when you are satisfied with the ROIs positions. Note that the red numbering of the ROIs will not move, only the outer ring indicating the ROI will move when you adjust your ROIs. Confirm the placement of your ROIs for all slices. **TIP:** If you have problems moving the ROIs, making the figure larger can help. The cursor will change to a hand when positioned correctly on the ROI.



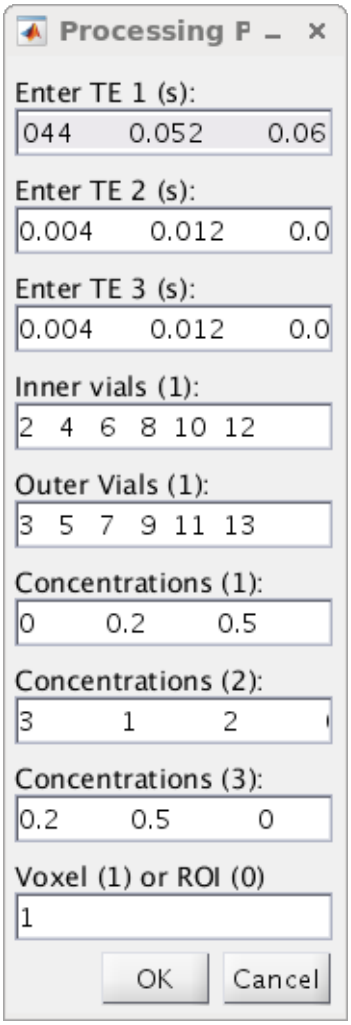
Repeat until you are done adjusting the ROIs for the last slice of the 3rd rotation.

9) You will be given one last time to adjust the ROIs for all slices for all rotations.

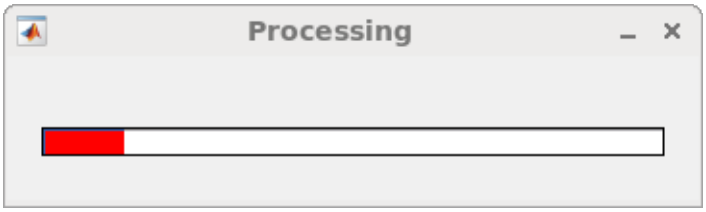


Once you have confirmed ROI placements, the red text will be centered in the ROIs in their final positions. If unsatisfied with ROI positions, the matlab program can be restarted.

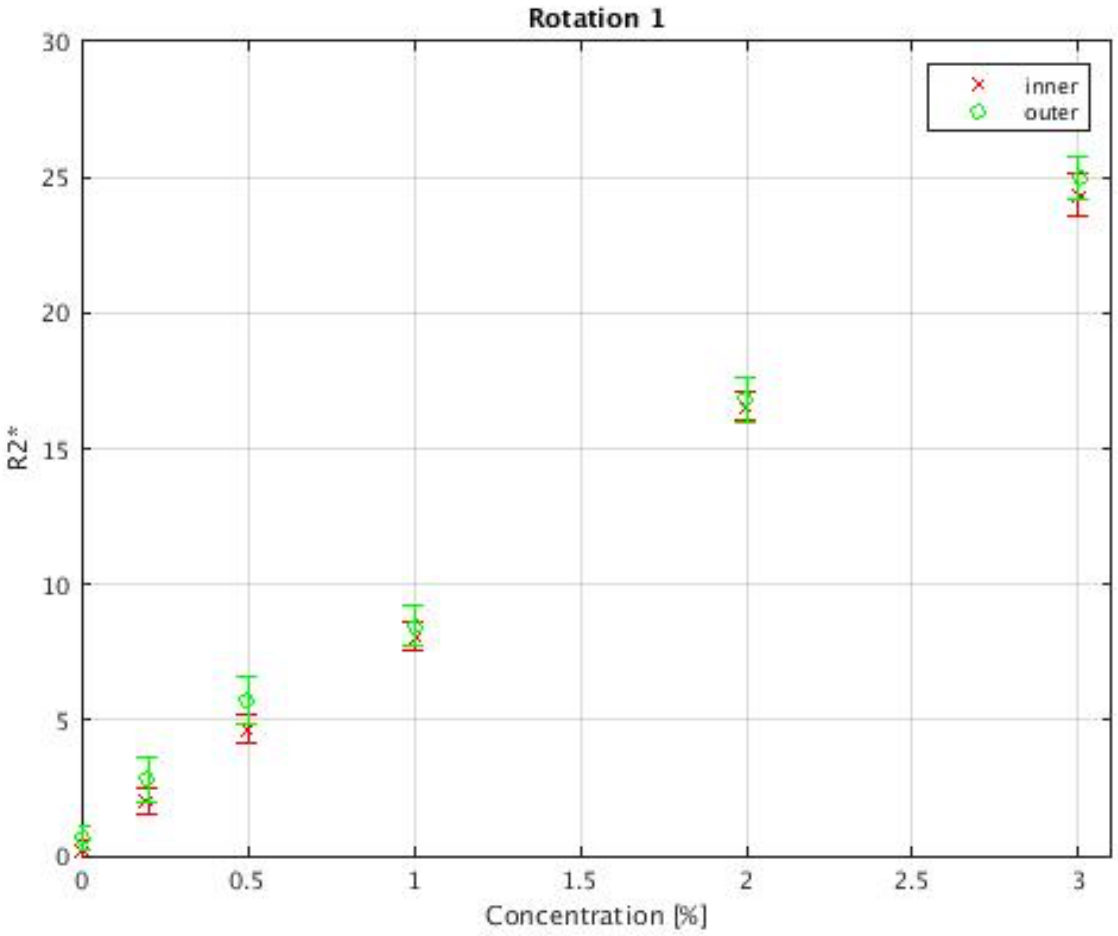
10) Next you can confirm your Processing Parameters. The default parameters assume that the vials are places as shown in Step 1, Section 3 EPI Processing. It is assumed that all datasets were acquired with the same TE steps. Voxel or ROI field specify whether T2* calculations will be performed on an individual voxel basis or on the mean ROI signal intensity. Hit ok when done.



Previous figures with ROIs will close. You will be shown a processing progress bar. This will take several minutes to complete depending on whether voxel-wise analysis or ROI analysis was chosen.

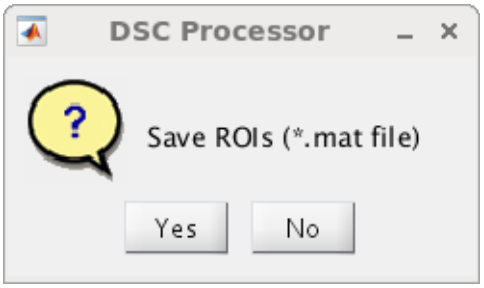


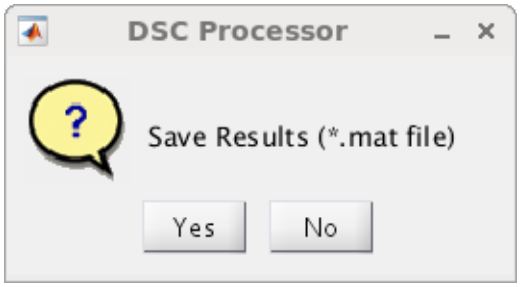
11) Your results will be given as 3 curves for each of the three rotations. A scatter plot for Rotation 1 results is shown below. Results are also shown as a function of inner and outer vials.



To compare results with those from EPI Processing, one can subtract R2* values measured in the baseline vials (2, 3) from the other (Inner, Outer) vials.

12) If the results appear satisfactory, you can choose to Save your ROIs and results for future use if you wish.





13) If one does not choose to save the results, if the program was run as described in Step 2, one can interact with the returned results directly:

av	average values in ROI across times
inner	vial numbers of 1st rotation
outer	vial numbers of 1st rotation
conc	concentration in each vial
imstack	dR2* values over time for each rotation
roistack	ROIs used per vial (eg timept 13 = vial 13 roi)
raw	1x3 cell of raw 4D images

14) The script can also be run in non-interactive mode by passing arguments:

These values must be specified

'InteractiveMode'	0 or 1 (default)
'ROI'	saved ROI filename
'type'	'NIFTI' or 'DICOM'
'rot1'	DICOM directory or NIFTI filename of rotation 1
'rot2'	DICOM directory or NIFTI filename of rotation 2
'rot3'	DICOM directory or NIFTI filename of rotation 3

Optional:

'Flip'	0 (default) or 1 - flip image in A/P direction
'radius'	5 (default) - default radius for ROI
'voxmethod'	1 (default) or 0 - calculate R2* on a voxel basis
'TE'	[0.004 0.0120 0.0200 0.0280 0.0360 0.0440 0.0520 0.0600] (default)
'Nrois'	13 (default)
'Nrots'	3 (default)