# QSM analysis on Aortic Aneurysm

## Prerequisites

You will need MATLAB and FSL (<https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FslInstallation>) to run this analysis. You will also need to ensure the FSL Matlab toolbox is on your path (<https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FslInstallation/MacOsX#FslInstallation.2FFslMatlabConfiguration.Using_FSL_from_MATLAB>)

Alongside this you will need to download the MEDI toolbox and the iterative Tikhonov algorithm:

* MEDI toolbox (<http://pre.weill.cornell.edu/mri/pages/qsm.html>)
* Iterative Tikhonov algorithm (<https://xip.uclb.com/i/software/mri_qsm_tkd.html>)

Finally you will need the following files:

* qsm\_analysis.m (<https://github.com/stoneaj/qsm-toolbox>)
* Read\_Bruker\_raw\_singlecoil.m (<https://github.com/stoneaj/qsm_libraries/tree/master/MEDI_toolbox/functions>)

Note:

* Make sure all of these files and toolboxes are in your Matlab path.
* Let me know if there are any other dependencies I’ve missed out on (which is likely!) and I can help fill in the gaps
* Let me know if this set-up seems like a lot of work or is problematic. I’ll look into making it a bit more user friendly if there is interest but hopefully this will get you through

## Analysis

Now that you have all of the pre-requisites set-up we can begin the analysis.

## Step 1 - qsm\_AA\_init.m

This is the initial step that allows us to calculate the magnitude and R2\* images we will use to create masks from for the QSM calculation.

In this file you will need to edit the variables *fid\_dir* and *output\_dir*. You will need to manually edit these in the qsm\_AA\_init.m file. *fid\_dir* is the directory containing the Bruker fid file and *output\_dir* is the directory that you will output your analysis to. As we are only running preliminary processing the script automatically appends *\*\_mask* to the *output\_dir* to denote that this is where the masks are. This analysis will output the following nifty files:

Graphical user interface, application

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You can view the magnitude (mag\_\*.nii.gz) and R2\* (r2s.nii.gz) files using fsleyes

Graphical user interface, application, PowerPoint

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## Step 2 – qsm\_AA\_noise\_mask.sh

To create the mask we will use the results of the non-linear fit to the complex data (*ifreq\_raw.nii.gz* and *n\_std.nii.gz*). This is a bash script so make sure to change permission to make it executable (*chmod 755 qsm\_AA\_noise\_mask.sh*) and run through terminal. You’ll need to manually change the *output\_dir* to the one that you specified in Step 1. When running the analysis for real this mask might need further manual refinement i.e. remove some of the top and bottom slices and some of the mask voxels that appear outside the tube. For this example we’ll just stick with the thresholded mask.

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## Step 3 – qsm\_AA\_pmap.m

This MATLAB script calculates the final QSM map. As input variables it requires *fid\_dir* and *output\_dir* as set in the Step 1. It also requires *mask\_dir* which is specified as the output of Step 2. The scripts runs through a number of different preprocessing steps and outputs the intermediate preprocessed images as nifits in the output directory.

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After the script has finished the output will be in the *output\_dir*. The QSM map is *chi\_iterTik.nii.gz*

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*Note on susceptibility calculation*

Susceptibility calculation is performed using the Iterative Tikhonov method which is consistent with the previous *ex vivo* studies we’ve done. The regularisation parameter used is ɑ=0.02 which is the same as that in the *ex vivo* tissue models study. However, because the set-up has changed for the aorta sample (volume coil, different acquisition protocol**), L-curve optimisation might need to be performed to choose the optimal regularisation parameter.**