ACQUIRING AND PROCESSING SUSCEPTIBILITY WEIGHTED IMAGING (SWI) DATA ON GE 3.0T

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Overview

Susceptibility Weighted Imaging (SWI) is a relatively new data acquisition and processing technique that provides the high resolution mapping of the brain's venous vasculature. It combines the phase and magnitude data to generate an image whose contrast is sensitive to venous blood and iron content.

This manual explains the data acquisition and post processing steps needed to generate SWI images and the minimum Intensity Projection (mIP). The mIP is a two-dimensional top down view of a stack of processed SWI images where each pixel corresponds to the minimum signal intensity.

It's important to note that the post processing program requires a P-file to generate the SWI images. Make sure to save the P-file at the end of your scan as described in this manual.

Data Acquisition

The SWI protocol is available both on the 3TE and 3TW scanners. The protocol name is SWI-CFMRI and is located under Site/Head. For SWI, the product 3D SPGR sequence with flow compensation is used. Other relevant scan parameters are: TR: 31ms, TE: 20ms, Flip Angle: 12°, BW: 27.78 kHz. These parameters are optimized for 3T and changes are not recommended.

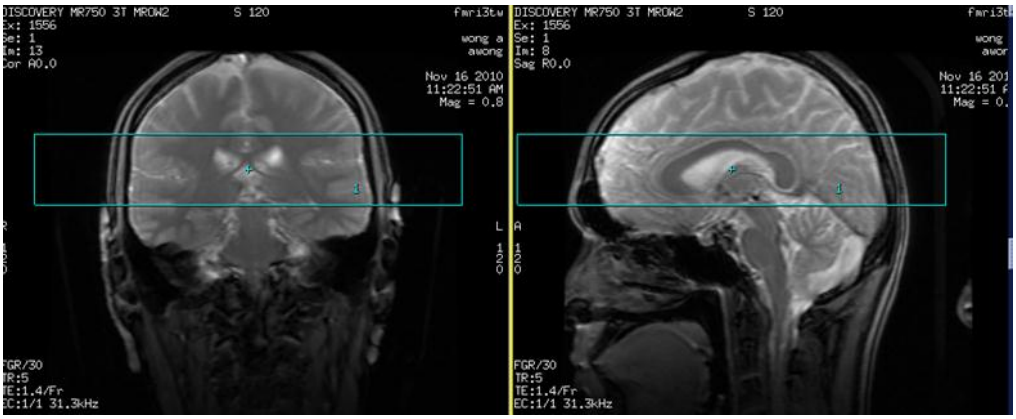
Below are the instructions on how to prescribe and complete the SWI scan.

1. Select the 3-Plane Localizer series and click scan.
2. Double click the SWI series.
3. Using the graphic RX tool, prescribe slices.

<u>Considerations for slice prescription:</u> The default prescription is set to axial, 1.5mm thickness, and 28 slices per slab, which results in the total scan time of 8:30 min. The figure below shows the extent of brain coverage that can be achieved using this default setting. The coverage can be extended by increasing the number of slice selective phase encodes (# of Scan Locs on the GE Rx window), but at the expense of increased scan time. If desirable, the image orientation can also be set to coronal or sagittal.

4. Save series.
5. Click on the arrow at the right edge of the Scan button. A small window appears.
6. Click on Research, and Display CVs.
7. Set the CV 'autolock' to 1.

   <u>Note:</u> This CV ensures that the P-file is saved at the end of the scan.
8. Click Scan.



Data Transfer

The SWI data is stored as a P-file in directory **/usr/g/mrraw**. Open a command tool and follow the instructions below:

1. cd /usr/g/mrraw
2. ls –ltr P* to locate the latest P-file.
3. Transfer the latest P-file to a local computer where the post processing will be done.

Important Notes:

The space available in directory /usr/g/mrraw is NOT reflected in the storage bar on the GE GUI. It is recommended that you check the space available before running SWI scans to avoid possible loss of the P-files. Do this by typing df –k in the command line after cd-ing to /usr/g/mrraw.

Post Processing using SWI Program

Program Installation

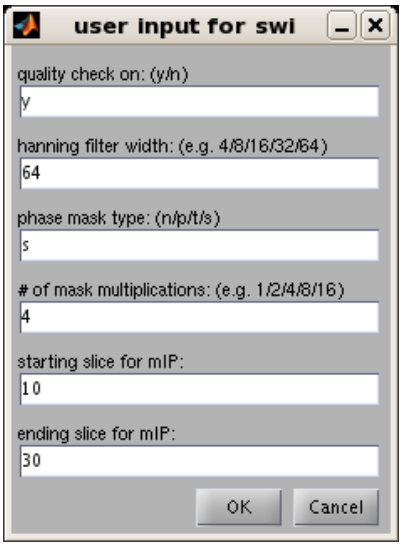
- Download swi_v1.tar from the CFMRI website: http://fmri.ucsd.edu/Howto/swi.shtml
- Untar the file (in Linux: tar –xvf swi_v1.tar).
- Add the swi_v1 folder to your MATLAB path.

Note: The program has been tested with MATLAB versions R2010, R2009, and R2008. Older versions may very well work but they haven't been tested.

SWI Data Processing Steps

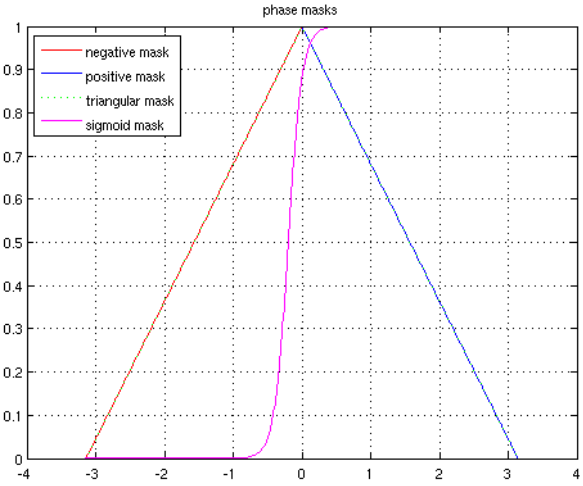
- Start MATLAB
- In MATLAB command window, type: swi.p

A MATLAB input dialog box will appear as shown in the figure below. This box is where all user options are set.



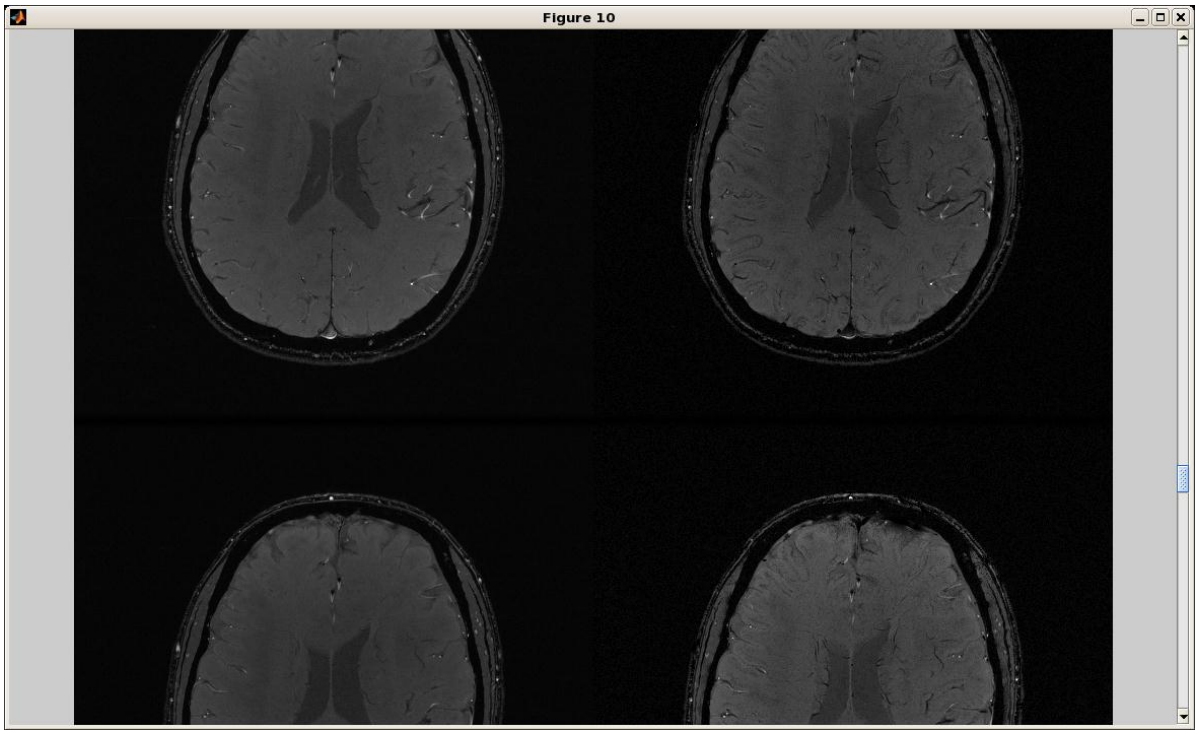
The Table below provides a description of each user option and its default setting. More detailed descriptions of these options can be found from the literature. A few recommended publications are included in the Reference Section.

User Option	Default	Description
Quality Check	On	Provides intermediate image reconstruction and post processing steps. If this option is turned off, the output is limited to processed SWI images and the mIP.
Hanning Filter Width	64	Sets the filter size to create a high-pass filtered phase mask. This step removes the low spatial frequency components caused by the global geometry of the brain and inhomogeneities in the main magnetic field. Higher filter width means more aggressive removal of these components.
Phase Mask Type	Negative	Phase mask is used to increase the visibility of the venous vasculature. Negative mask is the default. This specific mask sets all positive phase values (between 0 to π) to 1 while all negative phase values (between $-\pi$ to 0) are linearly scaled between 0 and 1. Figure below shows all phase masking schemes that are available. The venous blood phase depends on the vessel orientation relative to the main field. The negative mask provides the best vein contrast for vessels with orientation less than 55°. For vessels with orientation between 55° and 90°, the positive mask provides the maximum contrast. To get the best of both worlds, the triangular mask can be used. In summary, the user is encouraged to try different masks and evaluate the quality of SWI images generated using each mask.
Number of multiplications	4	Sets the number of times the phase mask is multiplied to the original magnitude image. Higher number of multiplications improves venous contrast but also adds noise. Recommended number is 4.
Start Slice for mIP	10	Sets the beginning slice (most inferior) for the stack of images to be used for the mIP.
End Slice for mIP	30	Sets the end slice (most superior) for the mIP.



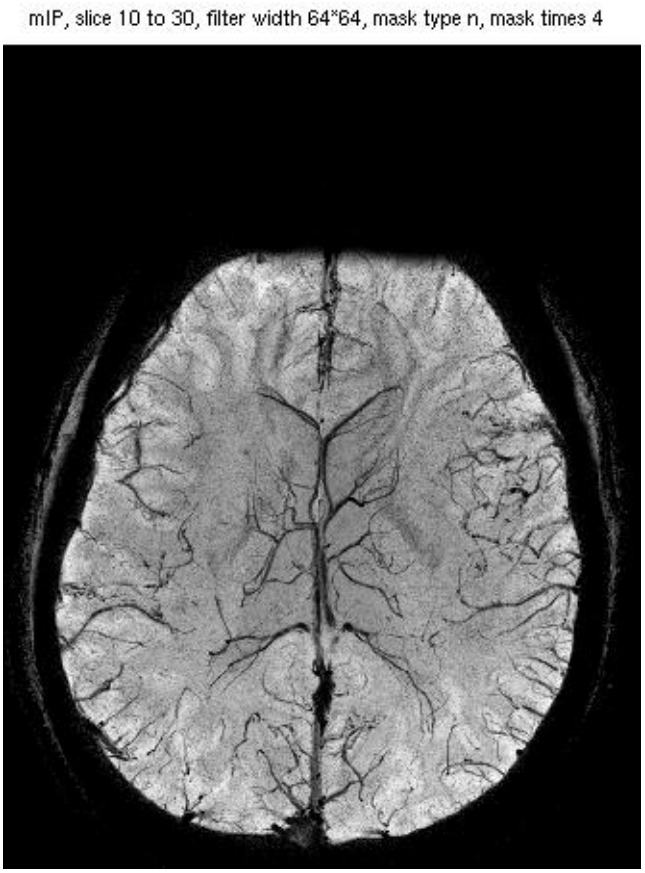
At the end of processing, the MATLAB program returns processed SWI images for each slice and the mIP based on the selected range of slices.

The figure below shows a sample output of the processed SWI images. Images in the left and right columns are before and after processing, respectively. The user can review all slices by scrolling through the window. Based on this initial inspection, the user can readjust the stack of images for creating the mIP.



The images appear to be cropped in the figure above since the scroll arrow was positioned to show two slices but it can be repositioned to show the uncropped image of each slice.

The figure below shows a sample mIP generated by the program. The title displays the range of slices, the size of Hanning filter, the type of mask, and the number of multiplications used to create the mIP.



References

1. Haacke EM et al., AJNR Am J Neuroradiol. 2009 Jan; 30(1):19-30
2. Wang et al., J Magn Reson Imaging. 2000 Nov; 12(5):661-70.
3. Reichenbach JR et al., NMR Biomed. 2001 Nov-Dec; 14(7-8):453-67.

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