Removing Background Phase Variations in Susceptibility Weighted Imaging Using a Fast, Forward-Field Calculation

J. Neelavalli[1], Y-C. N. Cheng[2], J. Jiang[3], and E. M. Haacke[2]

[1]Biomedical Engineering, Wayne State University, Detroit, Michigan, United States, [2]Academic Radiology, Wayne State University, Detroit, Michigan, United States, [3]The MRI Institute for Biomedical Engineering, Detroit, Michigan, United States

Introduction: Susceptibility weighted imaging (SWI) is a powerful clinical tool for studying diseases like multiple sclerosis, stroke, trauma and brain tumors. However, it still suffers from problems caused by rapid phase changes and aliasing near air-tissue interfaces, arising due to background magnetic field inhomogenieties. Usually a high pass (HP) filter is used to remove low spatial frequency phase variations [1]. This however, fails to remove the rapid variations near air-tissue interface. We present here a novel method for removing these background phase effects. This is done by using the structural information of air-tissue interfaces to estimate the geometry induced local field inhomogeneities and the ensuing phase and subtracting it from SWI phase data. The field estimation method we use is a Fourier transform based k-space filter approach [2]. In addition, it has been shown previously by Rauscher et al [3] that first unwrapping original phase followed by HP filtering improves the quality of filtered phase and hence of the processed SWI images. We show that by employing the approach introduced here, the resultant corrected phase images, referred to as, Geometry Dependent Artifact Corrected (GDAC) phase images, can further improve the performance of processing method proposed by Rauscher et al.

Materials And Methods: The induced magnetic field deviation $B_d(r)$ due to air-tissue interface can be calculated through the Fourier transformation of the interface geometry and the tissue susceptibility $\chi(r)$ using $B_d(r) = B_o \cdot FT^{-1}[FT[\chi(r)] \times (1/3 - k_z^2/(k_x^2 + k_y^2 + k_z^2))]$, where B_o is the main magnetic field, FT stands for Fourier transform, and k_x, k_y, k_z, are the k-space coordinates. We obtain geometry information of the object from a fast gradient echo short-TE T1-weighted dataset [5, 6]. Using a measured field map from phase images (from a double echo, gradient echo dataset) and the geometry, we estimate the relevant $\Delta\chi$ values within the structure using a semi-quantitative approach: varying the susceptibility, χ, over a range of values, calculating the difference between predicted field and measured field, and plotting the standard deviation of this remnant field across the assumed χ values. The susceptibility value corresponding to the minimum standard deviation is taken. ***Imaging:*** T1-weighted complex MR data was collected from 3 healthy volunteers (TRs 20, 15, 15ms respectively) at two different echo times, with ΔTE=1ms in volunteers 1 & 2 (TEs 5 and 6ms) and 2ms in volunteer 3 (TEs 7 and 9ms). SWI data was collected at TE=40ms. For both sequences, matrix size was 256x256 and voxel size was 1 x 1 x 2mm. Phase images with an effective echo time of ΔTE were used for estimating difference in susceptibility between mastoid cavity and brain tissue, $\Delta\chi_{mastoid\text{-}tissue}$, and the susceptibility difference between sinuses and brain tissue, $\Delta\chi_{sinus\text{-}tissue}$ for each volunteer. Quantified $\Delta\chi$'s are used to estimate phase at 40ms which was subtracted from the original SWI phase data to produce GDAC (**G**eometry **D**ependent **A**rtifact **C**orrected) phase images. Original and GDAC phase images were then used in conventional SWI processing and also for processing using Rauscher's [3] method. The high pass filter size was 64 x 64 [1].

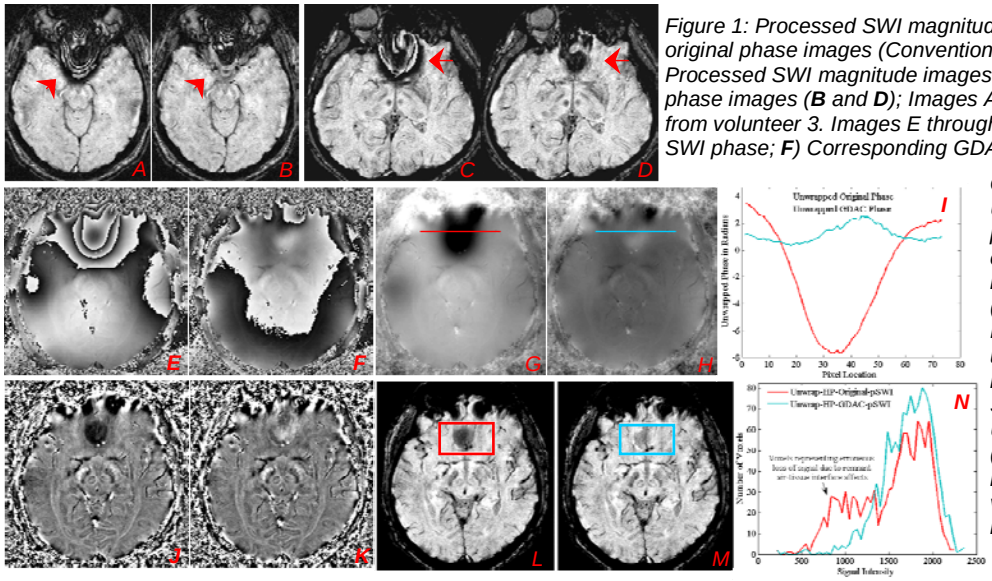

*Figure 1: Processed SWI magnitude images generated using HP filtered original phase images (Conventional SWI Processing) (**A** and **C**); Processed SWI magnitude images generated using HP filtered GDAC phase images (**B** and **D**); Images A&B are from volunteer 2 and C&D are from volunteer 3. Images E through N are from volunteer 1. **E**) Original SWI phase; **F**) Corresponding GDAC phase; **G**) Unwrapped original phase; **H**) Unwrapped GDAC phase; **I**) Profile plot of phase along the indicated red and blue lines on the unwrapped images (G) and (H) respectively; **J**) Result of High pass filtering (G); **K**) Result of High pass filtered (H); **L**) Processed SWI magnitude image generated using unwrapped-HP filtered original phase image(i.e. J); **M**) Corresponding processed SWI magnitude image generated using Unwrapped-HP filtered GDAC phase image (i.e. K); **N**) Histogram plot of the regions marked in (L) and (M) showing the # of voxels erroneously lost when original phase images are used instead of GDAC phase.*

Results: The values obtained for $\Delta\chi_{sinus\text{-}tissue}$ and $\Delta\chi_{mastoid\text{-}tissue}$ are respectively -11ppm, -7ppm (volunteer 1), -13ppm, -7ppm (volunteer 2) and -7ppm, -5ppm (volunteer 3). GDAC phase images were generated after subtracting the estimated phase due to air-tissue interface from the SWI phase data. Figure 1 summarizes the results of using GDAC vs. original SWI phase. Top row images compare the result of conventional SWI processing using original SWI phase and GDAC phase. Significant improvement is seen in all the volunteers when GDAC phase images are used. Middle and bottom row images compare the result of using GDAC phase vs. original phase for Rauscher et al's processing where the phase images are first unwrapped [4] and then high pass filtered for generating the pSWI magnitude. Because most of the rapid phase variation is already removed, the resultant unwrapped-HP filtered GDAC phase (Fig 1K) has much less remnant phase variation than the unwrapped-HP filtered original phase image (Fig 1J). This is reflected in the pSWI magnitude images generated from these filtered phase images (Fig 1 L and M).

Discussion and Conclusion: The ability of the method to successfully remove the rapid aliasing near air-tissue interfaces and generate better SWI images is of utmost importance for studying mid and forebrain regions as well as conditions such as subarachnoid hemorrhages. Although most aliasing is completely removed, the remnant aliasing seen (Fig 1F) could be due to eddy current effects, slightly inaccurate geometry, or error in the quantified $\Delta\chi$ values. The accuracy of $\Delta\chi_{sinus\text{-}tissue}$ and $\Delta\chi_{mastoid\text{-}tissue}$ values also depends upon how well the geometry is represented. However, it is encouraging that despite the possible error in $\Delta\chi$ values, the GDAC phase images still provide much better results compared to using original phase images.

In conclusion, we present here a powerful method for removing background field affects from SWI phase images to produce an artifact free phase and hence better, "cleaner" processed susceptibility weighted images. Furthermore, because most of the phase variation near air-tissue interface is already removed, we show that GDAC phase can enhance the results of other phase unwrapping based SWI processing techniques.

References:1) Haacke et al., MRM, 52:612; 2) Marques et al , Conc in Magn. Reson. MR Eng. 25:65; 3) Rauscher A et al MRI 2008; PMID:18524525; 4) Ghiglia DC et al J Opt Soc Am Optic Image Sci Vis. 11(1):107; 5) Pandian DS et al JMRI;28(3):727 ; 6) Neelavalli J et al Proc. ISMRM 2008 p#3056 and p#3499.