

Simulated 3D Brain Model to Predict the Phase Behaviour of Brain Geometries

Sagar Buch¹, Saifeng Liu², E. Mark Haacke^{3,4}, and Jaladhar Neelavalli³

¹McMaster University, Hamilton, Ontario, Canada, ²McMaster University, ³The Magnetic Resonance Imaging Institute for Biomedical Research, Detroit, MI, United States, ⁴Wayne State University

Introduction: A 3D simulated model of the brain is created to produce and study phase behavior of the geometries inside the brain and validate the processing techniques currently used on the real MRI phase images. This segmented model of brain structures can be used to create pure phase information used for any type of application regarding the phase images. SWI phase images are very useful in obtaining the anatomical information of the various structures in the brain. These phase images represent the magnetic susceptibility changes among the brain tissue structures. These susceptibility changes are sometimes used to analyze neurodegenerative diseases, like multiple sclerosis, where iron detection correlates with a low signal in the region of interest. This abstract discusses the role of this model in testing various quantification and post-processing techniques, and understanding the phase behavior around various geometries in the brain.

Method: The model includes the structures around basal ganglia (red nucleus, substantia nigra, crus cerebri, thalamus, caudate nucleus, putamen, globus pallidus), vessels, grey matter (GM), white matter (WM) and cerebro-spinal fluid (CSF). Fully velocity compensated, rf spoiled, high resolution, 3D gradient echo SWI-magnitude and phase images, with imaging parameters: TE=18ms, TR=27ms, FA=15°, B₀=3T (Siemens Vario) and 0.5mm isotropic resolution, are used to obtain the structures in basal ganglia region. Susceptibility maps (SMs) of this real data, generated by using the inverse of the Green's function, were used to distinguish the structures from its dipole effect produced in the phase images [1]. For GM, WM and CSF extraction, two double-inversion recovery (DIR) sequences, one with WM suppression (DIR₁: TE=1.46ms, TR=3100ms, 3T) and another with GM and CSF suppression (DIR₂: TE=1.57ms, TR=2800ms, 3T), are used. DIR₂ is used to remove WM efficiently in order to isolate GM and CSF. GM and CSF are separated by using a local thresholding method on DIR₁ to isolate GM and CSF with the help of the intensity difference between them [2]. WM mask is created by subtracting the GM, CSF and basal ganglia structures from the geometry of the whole brain. GM, CSF and WM masks were created with 0.5*0.5*2mm resolution, which is interpolated in k-space (in main field direction) to get (0.5)³ mm data. Validation for the shape and positions of the geometries is done with the help of literature material on anatomy of brain structures to get a symmetrical, more general model, thus, obtaining a 3D matrix of size 512x512x256 [3]. Care was taken to remove any jagged edges, by making the boundary of the geometries more homogeneous, in axial, coronal and sagittal planes to avoid creating unwanted dipole effects. A vessel map is created from SM images of the real SWI phase images and added to the 3D model. The model is used to create a susceptibility distribution mask by giving different susceptibilities to the structures. Susceptibility values (in ppm) used for Fig 1(c) are: red nucleus=0.13, substantia nigra=0.16, crus cerebri=-0.03, thalamus=0.01, caudate nucleus=0.06, putamen=0.09, globus pallidus=0.18, vessels=0.4, GM=0.02, WM=0 and CSF=-0.014 to produce a susceptibility distribution model $[\chi(r)]$. Subsequently, a graphic user interface is created using MATLAB2009a (Mathworks inc.) to be able to assign desired imaging parameters: echo time field strength and resolution to the model, and desired susceptibility values to each aforementioned structure. The phase images are produced by using forward filter $[g(k)=1/3 \cdot k_z^2/k^2]$ where $k^2=k_x^2+k_y^2+k_z^2$ in k-space. The expression of the simulated phase (ϕ) is given as $\phi=-\gamma B_0 TE \cdot FT^{-1}\{FT[\chi(r)] \cdot g(k)\}$ where TE= 20msec, B₀=3T are used. The phase images are collapsed in main field direction (by k-space cropping method) to generate 0.5*0.5*2mm resolution data. High-pass-filter (HP filter) is applied to the original and collapsed phase data to study the effect of HP filtering on the phase information.

Results: The phase images produce the dipole effects around the boundaries of the structures. The real HP filtered phase data is compared with simulated HP filtered phase images (Fig 1(a), 1(b)). Certain structures of basal ganglia like red nucleus show similar results as in the real data. 'Halo' effect that is normally seen around the red nucleus in the real data has been a representative of a capsule body around the boundary of the red nucleus which is the result of the susceptibility difference between red nucleus and its capsule (Fig 2(a), 2(b)), which is also seen outside the red nucleus in simulated phase images (Fig 2(c)). The negative intensity region around the basal ganglia is seen in the HP filtered simulated phase, but is hardly seen in the phase without using HP filter. This region corresponds to the HP filtered real data, where we see a similar ring in the internal capsule region. This model can also be used to produce SMs to quantify the change in the actual chi value given to the structures after using the forward filter, HP filter and inverse of Green's function. The susceptibility for the structures reduces from its actual value after we apply HP filter which can be plotted and used to extrapolate the true susceptibility values for structures.

Discussions and Conclusions: The simulations from the model are helpful in understanding the real data more efficiently. The halo ring seen in simulated phase indicates that this effect might not be due to structural presence of a capsule around the red nucleus but it might be just an artifact caused by the phase behavior outside red nucleus. The decrease in the mean susceptibility value, of approximately normal distribution seen in SMs, inside the geometries after using various HP filter sizes can be plotted and, later, can be used to extrapolate the true susceptibility values for the structures. The phase images created by the model can be used to quantify the true susceptibility of the structures by forward modeling of the simulated phase onto the real phase images with the help of least-square-fitting (LSF) technique, by using different susceptibility values inside the geometries to decide the optimum susceptibility value. Future directions would be being able to use this model to produce phase simulations of the entire brain by adding remaining structures to the model. Also, iron quantification by using the model (or a part of the model) from a real data set will be one of the main future goals. In terms of the simulation, even anomalies like micro-bleeds and lesions can be modeled to understand the phase behavior around them.

References: [1]Haacke et al., JMRI(2010);32:663–676. [2] Sezgin et al., JEI(2004);13(1):146–165. [3] Martin et al., (2003) Neuroanatomy: text and atlas, 3rd Edition (McGraw-Hill).

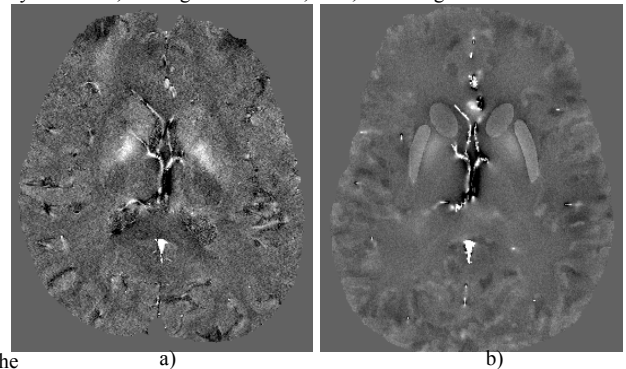


Fig 1: a) Real phase data processed using SHARP (TE=18msec, 3T, (0.5)³ mm resolution. b) Simulated phase produced by using the same parameters as (a).

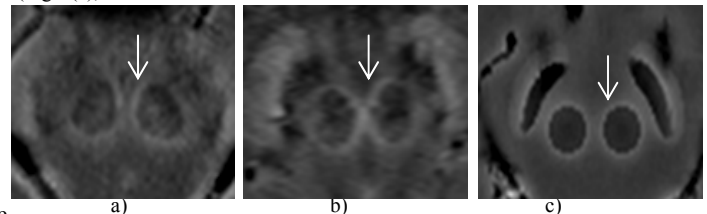


Fig 2: Comparison of the real phase information with simulated model phase profile of rostral mid brain area. a) HP filtered real phase image (TE=20msec, 3T, 0.5*0.5*2mm resolution, HP filter size 64*64), b) Another HP filtered real phase data (TE=20.34msec), c) HP filtered simulated phase data (TE=20msec).