Deconvolved SWI phase model of patients with Parkinson disease

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Introduction: Transverse MR relaxation times are a marker of increased iron deposition and therefore a possible indication for Parkinson disease (PD) [1]. In principle, the MR phase image should reflect the magnetic susceptibility of tissues and – hence – iron concentration more directly, but the phase image is actually the convolution of the susceptibility carrying volumes with the typical pattern of a magnetic dipole [2]. This leads to very complex spatial phase patterns especially in the case of intricate geometrical shapes, as e.g. the various nuclei of the basal ganglia. This complicates the definition of regions of interest (ROIs) on phase data itself and ROI definition on magnitude data is undesired due to inclusion of additional effects. In the phase image the nature of the dipolar kernel leads to dramatic phase changes in the vicinity of tissue borders which make the estimated phase value critically dependent on the ROI definition. Here we propose a novel procedure to analyse MR phase images that applies a filtered deconvolution on a group specific phase model to reduce this dipole effect and to simplify ROI definition.

Material and Methods: MRI: T1 weighted and SWI data from 27 Parkinson’s (PD) patients were acquired on a 3 Tesla whole body MR scanner (Siemens, Erlangen, Germany) with a 12 channel head coil. A three-dimensional, fully first-order flow-compensated gradient-echo (SWI) sequence with a TE of 29ms was used for SWI. Other sequence parameters were: TR = 36ms; image-matrix = 256x256 pixel; slices = 176; GRAPPA factor = 2; TA = 17:22 min, resolution = 0.8 mm isotropic. The SWI phase images were filtered using a Homodyne filter with a Gaussian filter kernel corresponding to a fwhm 5mm in image space. T1 weighted imaging parameters were: sagittal MP-RAGE with 208 slices, TR/TE 2300/900/3.59 ms, image-matrix = 320x320, resolution = 0.8mm3; TA = 12:18 minutes.

Results: Fig. 1 shows the performance of deconvolution and the effect of the masking in frequency space. Filtered phase data and deconvolved phase model were compared to magnitude data in Fig. 2. Determined mean phase values and SD for different nuclei are presented in Table 1. Mean phase values for both methods (obtained from model and from individual subject data-sets) are in good agreement but the SD for model analysis is clearly reduced. The values for the RN and the PUT are in good agreement with data from healthy volunteers [4], whereas the phase values for the SN and the GP are roughly doubled which is in line with an increase of iron storage associated with Parkinson disease.

Discussion and Conclusion: This work demonstrates that filtered deconvolution of averaged SWI phase data is possible and leads to a more accurate phase value estimation. Furthermore, phase analysis on a group specific model decreases the tracing effort as only one data set per subject/patient group has to be defined instead of one per subject.

References:
3) G. Grabner et al. MICCAI 2006, volume II : 58–66