Pre-Processing Phase: A Quantitative Analysis of Established Methods in SWI

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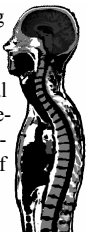
INTRODUCTION – Susceptibility weighted MR phase data provide anatomical contrast complementary to magnitude images [1, 2] by directly reflecting local magnetic field changes. Ambitious approaches for quantitative analysis of phase data were recently published, e.g., evaluation of absolute phase differences [3] or mapping of magnetic susceptibility [4-6]. These methods have interesting applications but are prone to imperfect pre-processing which is required to resolve phase aliasing and suppress strong contributions from air-tissue and bone-tissue interfaces [7,8]. It was described by several groups [3, 8-10] that contrast in pre-processed phase data strongly depends on the chosen filter type and filter parameters. However, the effect of pre-processing on local phase information has not yet been analyzed in-depth since the true local phase is generally unknown. In this contribution we quantitatively analyzed well-established methods for estimation of background field contributions based on a realistic numerical whole-body model. Validity of the results for *in vivo* data was demonstrated based on volunteer data.



MATERIALS AND METHODS

Numerical Model: A detailed numerical anatomical brain model was created from T1-weighted volunteer data (1x1x1 mm^3) via automatic segmentation (FreeSurfer, Athinoula A. Martinos Center for Biomedical Imaging, Massachusetts General Hospital, Charlestown, MA, USA) with manual segmentation of venous vessels. To include field contributions from the torso the brain model was embedded into the skull of a human whole-body model of The Virtual Family (Duke, 1x1x1 mm^3, [11]; Fig. on top right). Reasonable magnetic susceptibilities were assigned to each of the 55 anatomical regions and the field perturbation was computed by fast forward-field calculation [12]. First-order field components were removed from the simulated field to replicate linear shimming. A reference model was generated from brain-tissue compartments of the numerical model (without skull and bone) embedded in parenchyma. As a first approximation this model had no background field contributions (reference model).

Data Acquisition and Pre-Processing: High-resolution volunteer data of the whole brain were acquired from the same volunteer with the ToF-SWI sequence (TE1/TE2/TR/FA=3.42ms/25ms/35ms/15°, voxel-size 0.7x0.7x0.7mm^3, 75% PF in phase and slice encoding direction) [13] on a 3T MR-scanner (Tim Trio, Siemens Medical Solutions) using a 12-channel head-matrix coil. Multi-channel phase images were combined using uniform sensitivity reconstruction [14] and a 3D phase unwrapping algorithm [15] was used to resolve phase aliasing.

Processing: Simulated and measured phase images were corrected using five different methods: a) Homodyne filtering (Hanning width 0.4…35% of matrix size), b) Phase unwrapping + Gaussian high-pass filtering (HPF) (spatial domain FWHM 1…58 voxels), c) Phase unwrapping + 2D polynomial fitting (transversal; order 2…14), d) Phase unwrapping + spherical mean-value estimation (SMVE) [16] (radius/thickness=1…40/1 voxels), and e) an improved geometry dependent artifact correction (GDAC [7]) method [17] + Phase unwrapping + Gaussian HPF (spatial domain FWHM 1…58 voxels). For GDAC the geometry information of the head was obtained from the first echo of the TOF-SWI-dataset.

Analysis: Model data was analyzed by calculation of the Pearson correlation coefficient of the filtered image and the reference model. The analysis was performed in an outer and an inner region of the brain to account for convolution artifacts due to signal voids outside of the brain. For illustration purposes, the mean phase difference of small homogeneous regions in frontal white-matter (WM) and cerebrospinal fluid (CSF) was evaluated. Care was taken that in case of SMVE no convolution artifacts compromised phase values in these regions. Experimental data were analyzed in an inner region with respect to inhomogeneity suppression performance and preservation of local phase differences, which should be maintained as a first approximation. A local differences preservation measure (LDPM; mean Pearson correlation coefficients of the three phase gradient components of the filtered and the original data) and an inhomogeneity measure (IM; standard deviation of the phase in a region of high inhomogeneity normalized by the mean gradient norm; normalization ensures independence from a scale factor) were calculated. An LDPM close to one means local phase information were maintained properly. The IM should be small, but positive.

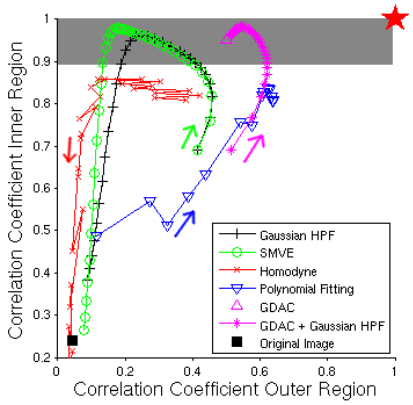


FIG. 1. Correlation coefficient of corrected data and reference model in outer (abscissa) and inner region of the brain (ordinate). The optimal value is marked by a red star. Area of high correlation in inner region is marked by a gray box and directions of increasing filter parameters are denoted by arrows.

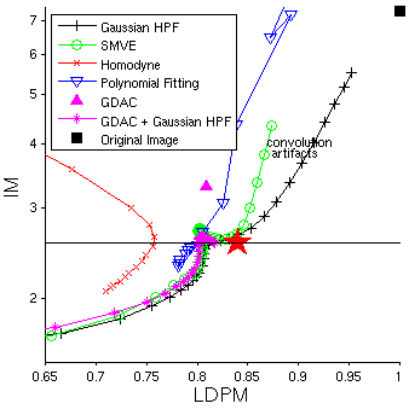


FIG. 2. IM over LDPM of the *in vivo* data. The horizontal black line marks the supposed optimal IM. The best result is marked by a red star.

RESULTS AND DISCUSSION – Results for the model data are depicted in Fig. 1. The overall quality of the local phase significantly depended on the chosen filter-type and filter-parameter. Within the inner region background contributions were estimated very well by SMVE, HPF, GDAC, and GDAC+HPF for certain parameters. However, within the outer region local phase information was highly degraded by all methods; best results were achieved with GDAC and polynomial fitting. Results and conclusions for the *in vivo* data (Fig. 2) are similar indicating that the simulation agrees with the real case. Equal results were also obtained for the model data using the measures IM and LDPM (not shown). All filters but polynomial fitting exhibit a stable region or turning-points at good parameters which may in practice be utilized for determination of good filter parameters. Fig. 3 depicts the absolute phase differences of WM and CSF. Both, absolute phase values and phase differences strongly depend on the chosen filter parameter and significantly differ from the reference value in most cases.

CONCLUSIONS – The results indicate that interpretability of phase data strongly depends on the chosen filter-type, filter-parameter, and region of interest. Significant care has to be taken when analyzing absolute phase values or phase differences (e.g. quantification of magnetic susceptibility) or comparing phase data between different studies.

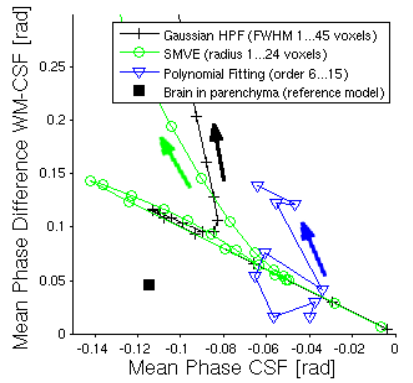


FIG. 3. Phase difference between WM and CSF of model data over phase in CSF region ($B_0 \cdot T_E$=60 ms·T). The reference phase difference is marked by a black square. and directions of increasing filter parameters are denoted by arrows.

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