Efficient and Automatic Harmonic Field Pre-Filtering For Brain Quantitative Susceptibility Mapping

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INTRODUCTION

Quantitative susceptibility mapping [1-5] has a wide range of biomedical applications, including molecular/cellular imaging, contrast-agent studies, fMRI BOLD quantification, and the assessment of iron overloading and demyelination such as in neurodegenerative and brain vascular diseases. While field maps are dominated by the ~10 ppm air-tissue interface, subtle variations on the order of a fraction of ppm occur in tissue requiring efficient methods to be measured and extracted. Here, a full processing of multi-echo gradient-echo data brain is described to efficiently extract the field inhomogeneities inside the brain while removing background effects. The proposed method couples harmonic filtering [4,6] with the powerful segmentation tools of SPM to extract the brain allowing solving Laplace equation with adequate boundary conditions. Internal field and QSM obtained in vivo at 3T are presented, and compared to R1 (=1/T1) and R2* = (1/T2*) maps.

MATERIAL AND METHODS

In vivo experiments were performed on a clinical 3T Siemens Verio (Siemens Healthcare, Erlangen, Germany) equipped with a 32-channel brain array.

Pulse sequence Two multi-echo 3D spoiled-gradient-recalled (SPGR) images were acquired with the following parameters: TR = 30 ms, TE1/TE8 = 2.67/23.32 ms, FA = 31° (T1-weighted images) and 7° (M0-weighted images), 1.25 mm isotropic voxels. Total acquisition time was 10.5 min.

Field map reconstruction and brain segmentation Combined-coil intensity and phase images were processed using Matlab (The MathWorks, Inc., Natick, MA, USA). Temporal unwrapping among echoes was performed with a FFT along the echo time. Field was then estimated using weighted linear least-squares (WLLS) and an affine model for phase evolution as a function of TE [3]. The sum of square over echoes in the T1-weigthed scan was then used to segment the brain using Statistical Parametric Mapping (SPM) 8 (Wellcome Trust Center for Neuroimaging). The brain mask M was deduced from white and grey matter outputs with dilatation and erosion operations.

Field spatial unwrapping and background filtering were treated simultaneously using Harmonic filtering. The measured field B inside the brain was decomposed as the sum of the internal variations B_{in}, the variations B_{out} induced by external sources and to the mean brain susceptibility B_{mean}. The Laplacians ΔB_{out} and ΔB_{mean} are equal to 0 while $\Delta B=\Delta B_{in}$. Consequently, to isolate B_{in}, ΔB was calculated, appropriately set to 0 at the brain boundaries, and integrated. This was done by solving $\min_{\text{Bin}} \|W_\Delta\ (\Delta B-\Delta B_{in})\|^2$. ΔB was approximated by the spatial calculation [-1 2 -1] for each direction. W_Δ was generated from M error propagation imposing boundary conditions. Unwrapping was included using a modulo function to impose phase gradients to be within]-π, π].

Quantitative susceptibility maps χ were reconstructed using the T1 weighted dataset as spatial priors (3): $\min_\chi \|W\ (\ C\chi - B_{in}/B_0\ )\ \|_2^2 + \alpha^2 \|\ \cancel{M}\chi\ \|_2^2 + \beta^2 \|\ W_g G\chi\ \|_2^2$. The first term is the squared-norm between the measured field B_{in}/B_0 and the fitted ones $C\chi$, where C is the transformation determining the field from χ. The second and third terms are regularization terms on χ and its gradient (G), respectively. The mask M complement $\cancel{M}$ and the T1-w images gradients were used to define spatial priors.

T2* and T1 maps were generated from the same SPGR dataset for comparison. T2* was calculated pixel-wise assuming a mono-exponential decay. T1 maps were calculated using DESPOT1 method [7] with B1+ correction. The spatial distribution of the B1 transmit field (B1+) was evaluated using an optimized version of the actual flip angle imaging (AFI) method [8,9] with the following parameters: FA = 60° (300 μs length hard pulses), TR2 = 5TR1 and TR1+TR2 =100 ms.

RESULTS

Segmentation took ~5 min, internal field calculation ~5 min and QSM reconstruction ~15 min (using MATLAB codes on an Intel core2 Duo CPU@2.4 GHz PC). Internal field was extracted efficiently with removed wrapping and reduced boundary effects (Fig.1). QSM recovers the source of field inhomogeneities and displays large susceptibility values inside iron-rich regions, which correspond to higher R2* regions. χ measured on the putamen, caudate and globus pallidus were +13 ± 17 ppb, +19 ± 17 ppb and +195± 27 ppb, respectively. We also calculated the susceptibility histograms using GW and WM masks. In these regions the values (mean ± std, in ppb) were χ_{GM} = +1 ± 23 and χ_{WM} = -5 ± 20. For comparison, χ on corpus callosum was -15 ± 15 ppb.

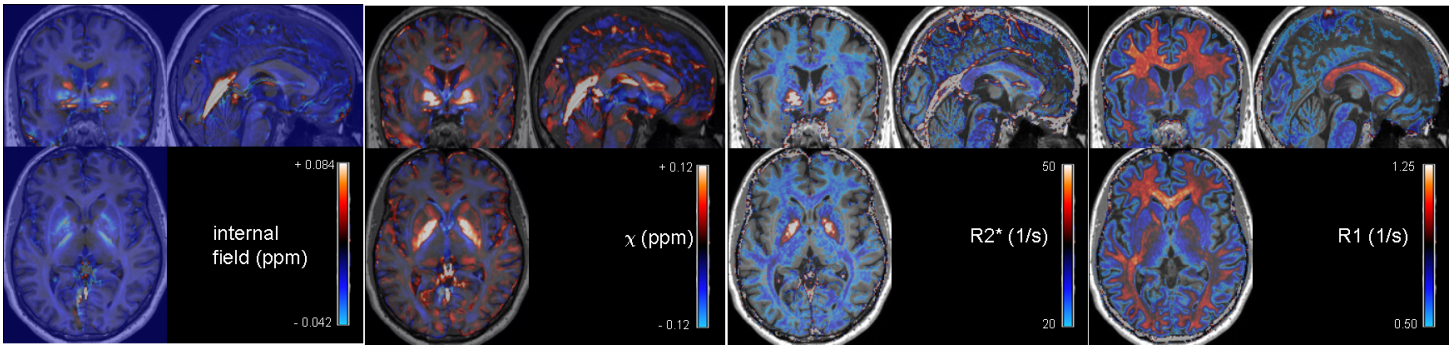

Fig. 1: Multiple views of the internal field, susceptibility, R2* and R1 maps extracted from the 3D SPGR scans overlaid on the T1W images.

DISCUSSION AND CONCLUSION

We have shown that harmonic filtering can be done through a second derivative followed by integration and that field wrapping can be handled in the process simplifying gradient-echo phase processing. The filtering requires the definition of boundaries. To recover internal field within the entire brain, a powerful segmentation tool such as included in SPM can be used to precisely define the brain. This process intrinsically reduces boundary effects that can occur in other filtering methods. Additionally, we have shown that QSM with spatial priors [3] can use anatomical scans separated from field-mapping scans to provide enhanced geometrical information. Using two 3D multi-echo SPGR scans with T1 and M0 contrast, it was possible to extract field, χ, R2* and R1 that are more intrinsic and quantitative tissue properties. Future work will aim at optimizing further acquisition parameters, evaluating reproducibility and obtaining normal and pathological values in neurological diseases. With SPM, it will be possible to process large number of data in an automatic manner.

REFERENCES 1. Kressler et al. IEEE TMI 2009 **2.** Shmueli et al., MRM 2009 **3.** de Rochefort et al., MRM 2010. **4.** Schweser et al., Med Phys 2010, **5.** Wharton et al., 2010, **6.** Li et al., MRM 2001, **7.** Deoni et al., MRM 2004, **8.** Yarnykh et al., MRM 2007, **8.** Nehrke et al., MRM 2009.