Quantitative Susceptibility Mapping with a Combination of Different Regularization Parameters

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Target Audience: Researchers and clinicians working with or interested in quantitative susceptibility mapping (QSM).

Background/Purpose:

The accurate estimation of tissue magnetic susceptibility could provide useful information for diagnosis such as iron contents or blood oxygen saturation. QSM based on regularization approaches produces susceptibility maps with low noise and artifact [1-4]. However, these methods cannot estimate tissue susceptibility with complete accuracy [1,2]. One cause of this problem is that the regularization parameter λ has a trade-off between accuracy and precision. For example, in L1-norm regularization [4], a susceptibility map calculated by small λ has high accuracy but low precision. On the other hand, a susceptibility map calculated by large λ has high precision but low accuracy. In this study, to resolve this trade-off and achieve a susceptibility map with high accuracy and high precision, a method is proposed for QSM with a combination of different regularization parameters. To evaluate the usefulness of the proposed method, a numerical simulation based on a COSMOS reconstructed susceptibility map was used to compare both the accuracy and the precision of susceptibility maps calculated by conventional and proposed methods.

Methods:

Proposed method The k-space was divided into three domains (low-frequency (L) domain, high-frequency (H) domain, and magic-angle (M) domain as shown in Fig. 1) and susceptibility maps calculated by different regularization parameters λ were applied to each domain. To overcome the trade-off between accuracy and precision, susceptibility maps calculated by different λ were applied to different frequency domains in k-space. A susceptibility map with small λ (λ=10^{-5}) was applied in L domain, in which the information of tissue susceptibility exists, and a susceptibility map with large λ (λ=10^{-3}) was applied in H domain, in which the information of tissue susceptibility does not exist. Moreover, to improve the accuracy, edge information of a susceptibility map calculated by large λ (λ=10^{-4}) was applied to M domain referring to the formulation shown in [2,3]. The susceptibility maps applied in L and H domains were calculated by the L1-norm regularization [4], and the susceptibility map applied in M domain as edge information was calculated by the L1-norm regularization of image gradients [5]. The mean value of weight W in the fidelity term [1,4,5] were set to 1 in this paper. The boundary threshold a_{th} between L domain and M domain is defined by $a_{th} = |1/3 - k^2/k_z^2|$, and the boundary threshold k_{th} between L domain and H domain is defined by $k_{th} = |k|$.

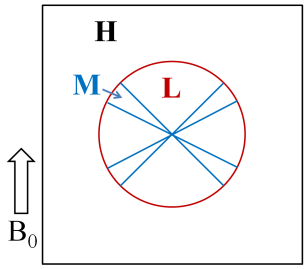

Figure 1. Schematic view of k-space division in proposed method.

Evaluation The usefulness of the proposed method was evaluated by comparing the conventional and the proposed methods using a numerical simulation based on a COSMOS reconstructed susceptibility model. The conventional methods were MEDI [1] and TKD [6]. <Simulation model> Head-image experiments involving healthy volunteers were performed to make a model susceptibility map. The experiments were performed on a 1.2T open-type MRI scanner, and a model susceptibility map was calculated by the COSMOS method [7] (the head position was rotated by 60°, 0°, and -45° around the body axis). The model susceptibility map is shown in Fig. 3(A). <Simulation procedure> The phase images were simulated from the model susceptibility map by the method of Marques and Bowtell [8], and Gaussian noise was added to real and imaginary parts. Susceptibility maps were calculated by using MEDI, TKD, and the proposed method. The regularization parameter λ of MEDI [1] was set to $10^{3.5}$, and the truncation value of TKD [6] was set to 10. <Evaluation> Accuracy, precision, and artifacts of the conventional and the proposed methods were compared. Accuracy was defined by relative errors of susceptibility in iron deposited tissues. The relative errors e were calculated using mean true susceptibility χ_t and mean calculated susceptibility χ_c in the ROIs as $e = |\chi_t - \chi_c| / \chi_t$. Tissues are left and right caudate nucleus (LCN and RCN, respectively), left and right globus pallidus (LGP and RGP, respectively), left and right substantia nigra (LSN and RSN, respectively), and internal cerebral vein (V). Precision was evaluated by standard deviation of susceptibilities of the white matter region. Artifacts were evaluated visually.

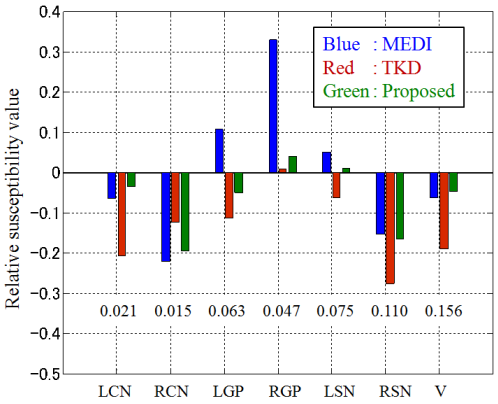

Figure 2. Comparison of relative susceptibility value calculated by MEDI (blue), TKD (red), and proposed method (green). Values below bars indicate mean true susceptibility χ_t in each ROI.

Results and Discussion:

As shown in Fig. 2, the relative errors of the proposed method are smaller than those of MEDI and TKD in many tissues. The mean relative errors of all tissues of MEDI, TKD, and the proposed method are 0.14, 0.14, and 0.077, respectively. The standard deviation of susceptibilities of white matter of MEDI, TKD, and the proposed method are 0.047, 0.079, and 0.054, respectively. These results show the accuracy of the proposed method is higher than that of the conventional methods and the precision of the proposed method is comparable to or higher than that of the conventional methods. The possible reason for this is that the proposed methods overcome the tradeoff between accuracy and precision by applying different λ to different k-space domains and improve the accuracy by using relatively correct spatial priors. As shown by the arrows in Fig. 3 (C), streaking artifacts are seen in the susceptibility map by TKD that are not seen in the susceptibility maps by MEDI and the proposed method.

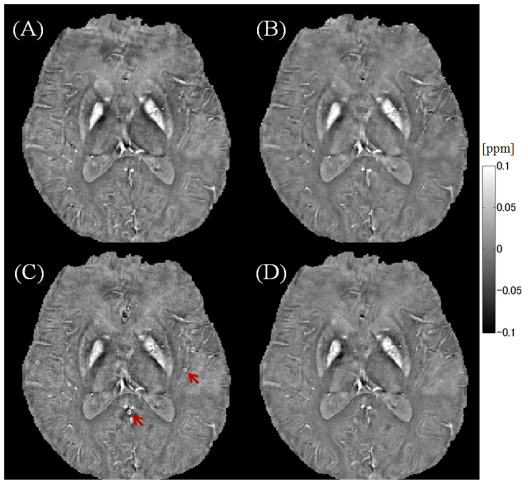

Figure 3. Model susceptibility map (A) and calculated susceptibility map by MEDI (B), TKD (C), and proposed method (D).

Conclusion:

A method was proposed for QSM with a combination of different regularization parameters. The numerical simulation suggests that the accuracy and the precision of the proposed method are comparable to or higher than those of the conventional methods.

References:

[1] Liu et al. MRM 2011;66(3):777 [2] Schweser et al. Neuroimage 2012; 62(3):2083 [3] Wu et al. MRM 2012; 67(1): 137 [4] Kressler et al. IEEE TMI 2010; 29(2):273 [5] Bilgic et al. NeuroImage 2012; 59(3):2625 [6] Shmueli et al. MRM 2009; 62:1510 [7] Liu et al. MRM 2009; 61(1):196 [8] Marques and Bowtell, Concepts MR PartB 2005; 25(1):65