Enhancing K-Space Methods for Quantitative Susceptibility Mapping by Exploiting Consistency in Cone Data

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INTRODUCTION: Quantitative susceptibility mapping (QSM) requires solving a magnetic field-to-susceptibility inverse problem through dipole deconvolution. The k-space methods based on kernel division in Fourier space are usually computationally efficient and easy to implement (1-4). However, the k-space methods usually produce results with streaking, as they provide erroneous susceptibility energy in the zero-cone region of the dipole kernel. Here, we aim to improve the results of k-space methods by constraining the error energy in the cone region through prior information related to the underlying susceptibility distribution. We show that this method is effective in suppressing streaking artifacts and retaining quantitative accuracy in phantom experiment and in vivo data.

THEORY: We utilize two observations: 1) the number of useful unknowns in susceptibility χ, i.e. non-zero elements, may be drastically reduced by applying a sparsifying transform, ∇, and 2) a large portion of k-space is faithfully reconstructed in the trusted region, or non-cone region, $T: |1/3 - k_z^2/k^2| > th$ (th is a threshold value). These two observations can be formulate into Eq. (1), where χ_0 is an initial result from a k-space method, F is the Fourier transformation, ∇^+denotes the Moore-Penrose pseudoinverse of ∇, U is a diagonal matrix having non-zero elements at locations corresponding to edge elements, and w represents unknown strengths at those locations. Once w is solved from Eq. (1), an edge matched susceptibility map χ_{em} is obtained through Eq. (2), which is then combined with χ_0 to compensate for the loss of information in the cone region. Since this method exploits data consistency in the cone region, we term this method Consistency in Cone Data (CCD).

$$TF\chi_0 = TF\nabla^+ Uw \quad (1)$$

$$\chi_{em} = \nabla^+ Uw \quad (2)$$

$$\chi^* = F^{-1}\left[\frac{1}{\frac{1}{D}+D}\left(\frac{1}{D}F\chi_{em} + DF\chi_0\right)\right] = F^{-1}\left[\frac{1}{\alpha + D^2}(\alpha F\chi_{em} + D^2 F\chi_0)\right] \quad (3)$$

METHODS: The phantom experimental data and in vivo datasets were downloaded from the online QSM repository (http://weill.cornell.edu/mri/QSM/Online.zip). The phantom is 130x130x116 with 1mm isotropic voxels. The in vivo data is 256x256x146 with .9375x.9375x1 voxels. In the CCD implementation, U was determined by applying the gradient operator to the tissue field obtained from Projection onto Dipole Fields (PDF) (5). The normal equation of Eq. (1) was solved using the conjugate gradient (CG) method. The CG iterations terminated when the energy of the residual was smaller than 1% of the energy of measurement. After w was determined, the corresponding edge matched susceptibility map χ_{em} was combined with χ_0 in Fourier space with Eq. (3), where D is the dipole kernel, and α is a parameter that determines the influence of χ_{em} on the final solution. Here, the threshold value was chose to be .15 to generate T, and α is .1. The accuracy of CCD was evaluated by comparing the slope and R^2 of the initial results of k-space method to the results after CCD enhancement with respect to the COSMOS result. Since COSMOS uses data acquired from multiple orientations, its susceptibility value in anisotropic white matters might be different from that of the k-space methods, which use data acquired from a single orientation. Therefore the slopes and R^2 were fitted only in grey matters. We chose two representative k-space methods, TKD method (4) and LSQR method (1), to evaluate the effectiveness of CCD.

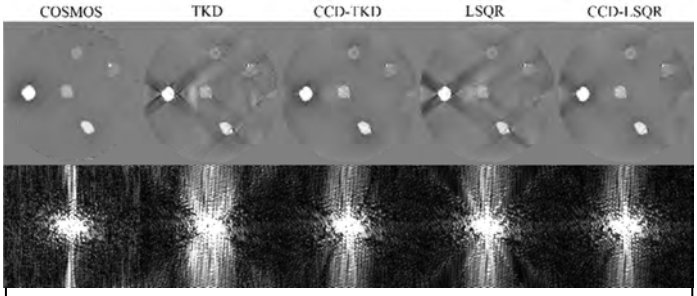

Figure 1. Results on a gadolinium phantom. The top row shows the axial view in image space. The bottom row shows the corresponding k-space view.

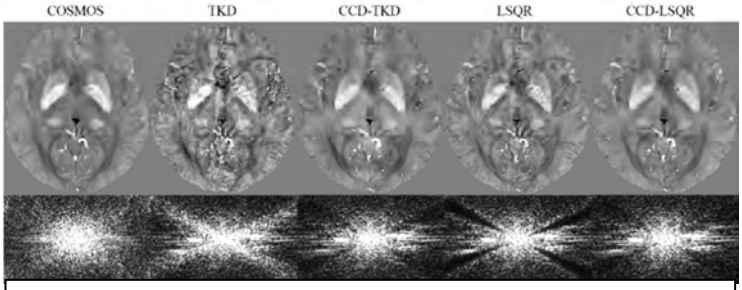

Figure 2. Results on an in vivo human brain. The top row shows the axial view in image space. The bottom row shows the corresponding k-space view.

RESULTS: Results are shown in Figs. 1&2. Streaking artifacts seen in the TKD and LSQR reconstructions were suppressed by applying CCD. In the gadolinium phantom, the slope and R^2 are .77 and 39 for TKD, .82 and .55 for CCD-TKD, .69 and .42 for LSQR, and .77 and .53 for CCD-LSQR. In the *in vivo* human brain, the slope and R^2 are 1.10 and .32 for TKD, 1.10 and .49 for CCD-TKD, .95 and .46 for LSQR, and 1.01 and .53 for CCD-LSQR. In the phantom, the computation time is .5 seconds for TKD, 30 seconds for LSQR, and 56 seconds for CCD. In the brain, the computation time is 2.3 seconds for TKD, 189 seconds for LSQR, and 275 seconds for CCD.

DISSCUSSION: Fundamentally, CCD attempts to enforce consistency in data fitting with all available known information. In k-space, the data fitting is forced to be consistent with measured MRI data in the trusted region according to the dipole. In image space, the data fitting is forced to be consistent with structural information of the susceptibility. The data fitting is iteratively solved using CG. A few iterations are sufficient to converge to a good solution, avoiding long calculation time. This is because when solving for $A = xb$ with CG, the direction with large eigenvalues of A are prefertially search first from the properties of the Krylov subspace. Here, by modeling the susceptibility in the gradient domain where uniform regions have small values in U, search directions that tend to introduce variations in uniform regions are visited later. Therefore, early termination actually helped with the solution. In the future, wavelet sparsifiers may also be used for CCD. The CCD method can be further extended for general MRI and CT reconstruction to remove non-local image artifacts in undersampled data.

CONCLUSIONS: We presented a consistency in cone data (CCD) method to remove streaking artifacts in the results of k-space methods according to known structurral inforamation. The results in phantom and human data demonstrated that CCD can effectively remove streaking artifacts, and properly recover data in the dipole zero-cone region.

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