Regularized QSM in Seconds

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TARGET AUDIENCE: Susceptibility Weighted Imaging (SWI) and Quantitative Susceptibility Mapping (QSM) investigators, clinicians.

PURPOSE: QSM yields a map of the tissue magnetic susceptibility, $\boldsymbol{\chi}$, that lends itself to applications such as estimation of tissue iron concentration and venous oxygenation. The mapping requires the solution of an inverse problem of the form $\mathbf{F^H D F}\boldsymbol{\chi} = \boldsymbol{\phi}$, where $\mathbf{F}$ is the Fourier transform, $\mathbf{D}$ is a diagonal matrix with entries $1/3 - k_z^2/k^2$, $\boldsymbol{\chi}$ is the unknown susceptibility distribution and $\boldsymbol{\phi}$ is the measured tissue phase. Since the kernel $\mathbf{D}$ undersamples the frequency content of $\boldsymbol{\chi}$ along a cone in k-space, the inversion is carried out either by using observations at multiple orientations [1], or by regularization with single orientation data [2]. This abstract presents a solution to the regularized QSM formulation that is computed in less than 5 *seconds*, which yields the exact minimizer of the optimization problem unlike time-consuming iterative methods. The proposed method can be coded in a single line of Matlab code. Results are presented on a numerical phantom with known susceptibility and on in vivo data.

METHODS: ℓ_2-regularized reconstruction involves the minimization of $||\mathbf{F^H D F}\boldsymbol{\chi} - \boldsymbol{\phi}||_2^2 + \lambda \cdot ||\mathbf{G}\boldsymbol{\chi}||_2^2$, where $\mathbf{G} = [\mathbf{G_x}; \mathbf{G_y}; \mathbf{G_z}]$ is the gradient in three dimensions and λ is the regularization parameter. The minimizer $(\mathbf{F^H D^2 F} + \lambda \cdot \mathbf{G^H G})^{-1}\mathbf{F^H D F}\boldsymbol{\phi}$ can be computed efficiently given that the matrix inversion is rapidly performed. The gradient along the x-axis can be expressed as $\mathbf{G_x} = \mathbf{F^H E_x F}$, where $\mathbf{E_x}$ is a diagonal matrix with entries $\mathbf{E_x}(i,i) = 1 - e^{(-2\pi\sqrt{-1}k_x(i,i)/N_x)}$, which is the k-space representation of the difference operator $\delta_x - \delta_{x-1}$. Here, k_x is the k-space index and N_x is the matrix size along x, and $\mathbf{G_y}$ and $\mathbf{G_z}$ are similarly defined. With this formulation, a closed-form solution $\tilde{\boldsymbol{\chi}} = \mathbf{F^H D}[\mathbf{D^2} + \lambda \cdot (\mathbf{E_x^2} + \mathbf{E_y^2} + \mathbf{E_z^2})]^{-1}\mathbf{F}\boldsymbol{\phi}$ is obtained. The total cost is two FFTs and multiplication of diagonal matrices. For comparison, the objective function is minimized iteratively using nonlinear conjugate gradient (CG) [3]. 100 CG iterations were used for all results. Experiments were performed on two datasets. The first set is a numerical phantom with 3-compartments (gray and white matter, CSF). Within each compartment, χ is constant and equal to χ_{gray}=–0.023, χ_{white}=0.027, χ_{CSF}=–0.018 ppm [4]. The field map $\boldsymbol{\phi}$ (Fig.1a) is computed from the ground truth $\boldsymbol{\chi}$ map using the forward dipole model and Gaussian noise with peak-SNR = 100 was added, so that the normalized root-mean-square-error (RMSE) of the noisy field map was 5.9% relative to the noise free phase. λ was chosen to minimize the RMSE in the reconstructed $\boldsymbol{\chi}$, and was found to be $\lambda = 2 \cdot 10^{-4}$. The same λ was used for both the closed form and iterative reconstructions. The second dataset is a 3D SPGR on a healthy subject at 1.5T with resolution 0.94×0.94×2.5mm^3 and TR/TE = 58ms/40ms. Background phase (Fig.2a) was removed using dipole fitting [5]. $\lambda = 1.5 \cdot 10^{-2}$ was chosen based on the L-curve heuristic. Data were zero-padded to twice the size to avoid aliasing with circular convolution.

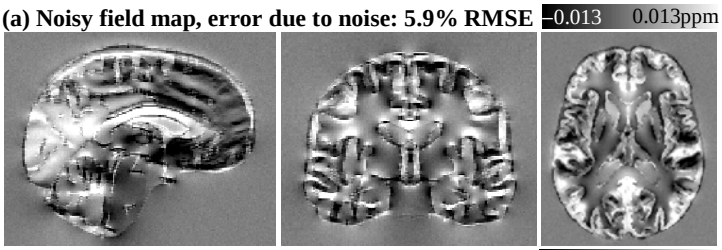
RESULTS: Fig.1 shows closed-form QSM reconstruction and the error relative to the ground-truth $\boldsymbol{\chi}$ for the numerical phantom. Using Matlab running on a standard workstation, the proposed method took 3.3 seconds and yielded 17.4% RMSE, while the iterative algorithm gave 18.0% error in 65 minutes. In vivo reconstruction results are presented in Fig.2, where the processing time was 1.3 seconds for the proposed method and 29 minutes for the iterative CG algorithm. The difference between the closed-form and iterative solutions was computed to be 0.3% RMSE, and is depicted at *250-times* scaling in Fig.2c.

DISCUSSION: The proposed closed-form solution is demonstrated to yield much faster and more accurate results than its iterative counterpart.

CONCLUSION: The presented QSM solver is expected to facilitate online reconstruction of susceptibility maps.

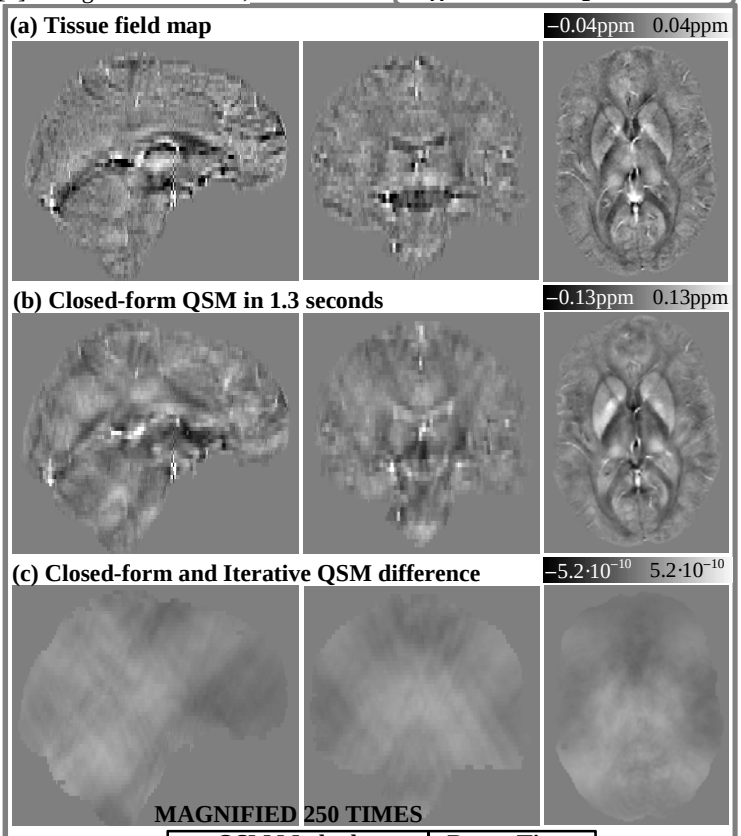
REFERENCES: [1] Liu et al. MRM'09; [2] de Rochefort et al. MRM'10; [3] Lustig et al. MRM'07; [4] Duyn et al. PNAS'07; [5] Liu et al. NMR Biomed'11

Fig.1 Numerical Phantom with 3 compartments



QSM Method	Recon Time	Error relative to true χ
Closed-form (proposed)	3.3 seconds	17.4% RMSE
Iterative (100 iterations)	65 minutes	18.0% RMSE

Fig.2 In Vivo QSM at 1.5T



QSM Method	Recon Time
Closed-form (proposed)	1.3 seconds
Iterative (100 iterations)	29 minutes