Regularized QSM in Seconds

Berkin Bilgic1, Itthi Chatnuntawech1, Audrey P Fan1, and Elfar Adalsteinsson1,2

1EECS, MIT, Cambridge, MA, United States, 2Harvard-MIT Division of Health Sciences and Technology, Cambridge, MA, United States

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

PURPOSE: QSM yields a map of the tissue magnetic susceptibility, \( \chi \), 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 \( F^*DF \phi = \mathbf{f} \), where \( F \) is the Fourier transform, \( D \) is a diagonal matrix with entries \( 1/3 - k_z^2/k^2 \), \( \chi \) is the unknown susceptibility distribution and \( \mathbf{f} \) is the measured tissue phase. Since the kernel \( D \) undersamples the frequency content of \( \chi \) 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: Presented on a numerical phantom with known susceptibility and on in vivo data.

METHODS: \( \ell_2 \)-regularized reconstruction involves the minimization of \( ||F^*DF - \mathbf{f}||^2 + \lambda \cdot ||Gx||^2 \), where \( G = \{G_{\omega}, G_{\alpha}, G_{\gamma}\} \) is the gradient in three dimensions and \( \lambda \) is the regularization parameter. The minimizer \( (F^*DF + \lambda \cdot G \cdot G^{-1}F^*DF) \mathbf{\phi} \) can be computed efficiently given that the matrix inversion is rapidly performed. The gradient along the x-axis can be expressed as \( G_x = F^*E_{\omega}F \), where \( E_{\omega} \) is a diagonal matrix with entries \( E_{\omega}(i,i) = 1 - e^{(2\pi v_{i} x(i)/k_d)} \), which is the k-space representation of the difference operator \( \delta_{\omega} - \delta_{\omega-1} \). Here, \( k_d \) is the k-space index and \( N_{\omega} \) is the matrix size along x, and \( G_{\omega} \) and \( G_{\alpha} \) are similarly defined. With this formulation, a closed-form solution \( \hat{x} = F^*D[W \cdot (E_{\omega}^2 + E_{\alpha}^2 + E_{\gamma}^2) - 1]F \mathbf{\phi} \) 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, \( \chi \) is constant and equal to \( \chi_{\text{gray}} = -0.023, \chi_{\text{CSF}} = -0.018 \) ppm [4]. The field map \( \phi \) (Fig.1a) is computed from the ground truth \( x \) 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. \( \lambda \) 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 \( x \) 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.