

Single-Step QSM with Fast Reconstruction

Berkin Bilgic¹, Christian Langkammer¹, Lawrence L. Wald¹, Kavin Setsompop¹

¹ Martinos Center for Biomedical Imaging, Harvard Medical School & Massachusetts General Hospital, MA, USA;

INTRODUCTION: QSM solves for the magnetic susceptibility that gives rise to subtle changes in the gradient echo (GRE) signal phase. This mapping is made difficult by phase wraps, large background contributions, and the ill-posed linear system that needs to be inverted. Recent contributions in tissue phase estimation and dipole inversion facilitated QSM reconstruction. In particular, SHARP [1] has emerged as an efficient filter for background removal, while MEDI [2] remains an elegant dipole deconvolution method. Combining the two steps directly relate the wrapped phase to the susceptibility [3-5], while obviating the need for SHARP truncation threshold. In this contribution, we extend the single-step approach by: (i) accelerating the reconstruction using preconditioned conjugate gradient (pcg), and (ii) employing variable size SHARP kernels (V-SHARP [6]) to minimize the loss of cortical phase information. This rapid solver takes ~40 seconds to process whole-brain data at 1mm³ resolution, involves a single regularization parameter, and is more successful at mitigating dipole artifacts than our rapid L2-regularized QSM solver [7] (Figs 1&2). Matlab code will be available at <http://www.martinos.org/~berkin>.

METHODS: SHARP [1] recovers the tissue phase ϕ_t from the unwrapped total phase ϕ by solving $MS\phi = MS\phi_t$, where M is a binary mask of reliable phase estimates, and S represents convolution with SHARP kernel. V-SHARP [6] extends this model to reduce the loss of ROI by using multiple kernels of decreasing radius via (i) $\sum_i M_i S_i \phi = \sum_i M_i S_i \phi_t$, and can be efficiently computed in k-space as $S_i = F^{-1} H_i F$, with H_i being the k-space kernel. A truncated inverse of the largest kernel H_1 is employed to solve this singular equation. The susceptibility χ is then found by inverting (ii) $F^{-1} D F \chi = \phi_t$. Using regularization via $\min \|F^{-1} D F \chi - \phi_t\| + \lambda \|W G \chi\|_2^2$ facilitates the deconvolution [4]. Here, W is a weighting mask that prevents smoothing across edges, and G is the 3D gradient operator. We previously proposed a fast solution to this problem using pcg solver [7].

Proposed Single-Step QSM: combines relations (i) & (ii) into $\sum_i M_i S_i \phi = \sum_i M_i S_i F^{-1} D F \chi$. With regularization, we obtain $\min \|\sum_i (M_i F^{-1} H_i D F \chi - M_i F^{-1} H_i \phi)\|_2^2 + \lambda \|W F^{-1} E F \chi\|_2^2$, where E is the gradient operator in k-space. The unwrapped phase ϕ is related to the wrapped phase ϕ_w via the Laplacian (Δ) relation $\phi = \Delta^{-1} \Im(e^{-j\phi_w} \cdot \Delta e^{j\phi_w})$ [3]. Integrating this into the optimization obviates the need for phase unwrapping. We solve the L2-problem using pcg with the preconditioner $(H_1 D)^2 + \lambda E^2$. This relies on the approximation $M_1 \approx W \approx \text{Identity}$, and $M_{i>1} \approx 0$. Since masks for $i > 1$ are all zeros except for a strip of boundary voxels, approximation was seen to be valid in practice and preconditioner provided more than 2-fold speed-up.

Data acquisition: A healthy volunteer was scanned at 7T using Wave-CAIPI [8] accelerated 3D-GRE with 0.5mm isotropic res, FOV=240×192×120, TR/TE=30/20ms, $T_{\text{acq}}=5\text{min}$. The maximum g-factor over the 3D volume at R=3×3 undersampling was $g_{\text{max}}=1.12$, indicating near-perfect parallel imaging reconstruction. A second subject was scanned at 3T using 3D-EPI[9] with 1mm³ res, FOV=230×230×176, TR/TE=69/21ms. R=4-fold GRAPPA was used to minimize distortion, and 4 avg were collected in $T_{\text{acq}}=1\text{min}$.

Data processing: V-SHARP with threshold=0.2 was employed with max kernel diameter of 11mm to generate the tissue phase. This was used as input for the L2-regularized QSM with edge weighting [7]. For comparison, the raw phase data were processed with Single-Step QSM using the same regularization parameter ($\lambda=0.1$ for Wave-CAIPI and $\lambda=0.03$ for 3D-EPI).

RESULTS: Fig1 displays tissue phase, L2-regularized and Single-Step QSM reconstructions at 7T. Processing time for V-SHARP followed by L2-regularized QSM was 2.4 min, while Single-Step mapping took 7.8 min. Fig2 shows 3D-EPI results, where the computation time for V-SHARP and L2-reconstruction was 11 sec, and 40 sec for Single-Step mapping. In both figures, yellow arrows point to regions with residual dipole streaking artifacts in the L2-regularized results and blue arrows indicate regions with imperfect background removal in the Single-Step images.

DISCUSSION: We presented a fast algorithm for Single-Step QSM that involves a single regularization parameter and V-SHARP filtering that is consequently preserving cortical phase information. This was also seen to mitigate the dipole streaking artifacts present in the L2-regularized reconstruction. A limitation of the proposed method is its sensitivity to B0 inhomogeneity, which might be alleviated by increased regularization.

REFERENCES: [1] F Schweser NIMG'12; [2] T Liu MRM'11; [3] K Bredies ISMRM'14; [4] T Liu ISMRM'14; [5] S Sharma ISMRM'14; [6] B Wu MRM'12; [7] B Bilgic MRM'13; [8] B Bilgic ISMRM'14; [9] B Poser NIMG'10.

