SCP Solver for Nonlinear Quantitative Susceptibility Mapping

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Introduction

Magnetic resonance imaging (MRI) is inherently sensitive to changes in tissue magnetic susceptibility. Changes in tissue magnetic susceptibility result in a shift in the phase of the MR signal. The relationship between the phase of the image and the tissue magnetic susceptibility can be described as $Ax = b$, where $A \in \mathbb{R}^{m \times n}$ is a known Toeplitz matrix, $x \in \mathbb{R}^n$ is a vector of magnetic susceptibilities and $b \in \mathbb{R}^m$ is a vector of phase angles. Calculating quantitative susceptibility maps (QSM) from the MR image with proper regularization would give researchers a noninvasive method for studying neurodegenerative diseases.

Common Formulation

Since $A$ contains low singular values, direct inversion of $A$ results in amplification of noise and artifacts in the reconstructed image. Therefore, a regularization scheme is needed to calculate the susceptibility maps. The most common QSM formulation employs a $l_2$ norm penalty on the gradient of the image. However, this formulation encourages a piecewise linear solution which obscures fine tissue detail that are of interest in studying diseases such as multiple sclerosis.

Our Formulation

We impose a total variation norm based constraint to improve retention of fine tissue structures compared to the $l_2$ norm constraint in the standard formulation. We also formulate the relationship between susceptibility and phase shift as a nonconvex, complex relation by taking the pointwise exponential of $iAx$ and $ib$. This complex formulation has been shown to improve robustness to errors in the phase map.

 SCP Algorithm

We implemented a Sequential Convex Program (SCP) to solve our problem in MATLAB. Our solver takes advantage of the Toeplitz structure of $A$, and an affine relaxation of the nonconvex problem in order to achieve fast convergence.

Given

- $x^0$: initial guess
- $\lambda^0$: initial Lagrange multiplier

repeat until convergence

1. minimize $\nabla f(x^k)^T p + \lambda^k p^T p$
   subject to $c(x^k) + \lambda^k \nabla c(x^k)^T p \geq 0$
2. Compute step size $\alpha$ by backtracking line search.
3. Update $x^{k+1} := x^k + \alpha p^*$, $\lambda^{k+1} := \lambda^k$, $k := k + 1$.

return $x$.

In step 2, the QP was solved using a quasi-Newton method with limited memory BFGS by approximating the constraint with a log-barrier function.

Algorithm Performance

Quantitative susceptibility maps were calculated from a MR data set acquired on a 7T system. The dimension of the image was $280 \times 280 \times 170$ voxels with $0.5 \times 0.5 \times 0.75$ mm resolution. The SCP was solved on the Sherlock computing cluster, which uses an Intel(R) Xeon(R) CPU E5-2650 v2 @ 2.60GHz with 24 GB of RAM in 9 minutes and 36 seconds. This represents a substantial speedup over the current solver for the nonconvex QSM formulation as shown in Figure 1 below.

Results

Figure 2: Solution using SQP solver on nonconvex formulation showing reduced artifacts with good detail retention.

Figure 3: The nonconvex formulation with a total variation based constraint shows improved tissue detail retention and artifact suppression compared to the popular $l_2$ norm and direct inversion methods.

Conclusion

Our SCP implementation for solving the nonconvex QSM formulation represents a significant increase in speed over current methods. In addition, the total variation norm-based constraint limits image artifacts while retaining tissue detail better than the current $l_2$ norm or direct inversion methods. More work is needed to validate data and performance on pathological tissue.

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