Constrained Spectroscopic Imaging with Hard and Soft Anatomical Boundary Constraints

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INTRODUCTION

Although MRSI is a powerful tool for biochemical imaging, its practical utility has been rather limited because of poor spatial resolution and signal-to-noise ratio. Great effort has been made to address this problem over the last two decades, resulting in a range of promising methods, one of which is anatomically-constrained spectroscopic imaging [1-3]. An existing challenge with anatomically-constrained spectroscopic imaging lies in how to handle exact and uncertain boundary constraints so that the uncertain edges won't create "false" edges in the resulting metabolic maps, as may be the case with some of the earlier methods. The proposed method provides an effective way to address this issue by incorporating the exact boundaries into the basis functions of a spatial-spectral model, and uncertain boundary constraints into a regularizing penalty function.

PROPOSED METHOD

The proposed method involves collecting an anatomical image along with a conventional MRSI dataset. Boundary information is extracted from the anatomical image and is divided into two groups: known boundaries and uncertain boundaries. Known boundaries are those certain to exist in the metabolite image, such as support boundaries and boundaries between very different tissue types. These edges are enforced in a strong way as *hard* mathematical constraints. Uncertain boundaries are those that are present in the water proton image, but may or may not exist in the metabolite maps. These uncertain edges are enforced in a *soft* way as described below.

In image reconstruction, we use the generalized series [2] to model the spatial distribution for each spectral frequency component: $\rho(\mathbf{x}, f) = C(\mathbf{x}, f) \sum_n c_n e^{i2\pi \mathbf{k}_n \cdot \mathbf{x}}$, where $C(\mathbf{x}, f)$ is a constraint function. Hard boundary constraints are directly incorporated into $C(\mathbf{x}, f)$, as is done in GSLIM [2]. In the original GSLIM, $C(\mathbf{x}, f)$ absorbs all of the given boundary constraints, which can be problematic for uncertain edges. For the proposed method, uncertain boundary constraints are incorporated into the process of determining the coefficients c_n through a regularizing penalty function, $U(\rho)$. Specifically, the optimal series coefficients are determined by solving $\arg\min_{\mathbf{c}} \|\mathbf{Hc} - \mathbf{d}\|_2^2 + U(\rho)$, where the first term measures data consistency, and the second term is the penalty function. In the proposed method, the penalty function discourages non-smooth behavior but preserves edge structures, and has the specific form $\sum_n \sum_{i \in \partial_n} w_{n,i} |\rho_n - \rho_i|$, where the inner summation is over the neighbors of voxel ρ_n. Soft constraints are incorporated through the weights, $w_{n,i}$, such that spatial variations in reconstructed metabolite maps are not penalized as much near the uncertain boundaries [4].

RESULTS

Experimental CSI data (TE/TR = 25/1800ms, 9 x 9 mm inplane resolution, a 15mm-thick slice, spatial-spectral matrix size 34x34x256) were obtained on a 1.5T Vision (Siemens) system. We also acquired 5 high-resolution anatomical slices (thickness of 3 mm each) of the same region, which were used to identify image boundaries. Figure 1(a) shows the full-data reconstruction of a frequency corresponding to the NAA peak. While NAA does not exist in the skull, no spectral fitting has been applied, and the signal that still appears is leakage from the lipid peak. To test the proposed algorithm, only 16×16 k-space samples were retained. Figure 1(b) shows the zero-padded reconstruction, and 1(c) shows the generalized series reconstruction with hard and soft edges and 64×64 basis functions. The hard edge structures are shown in 1(d), and all imposed edge structures are shown in 1(e).

(a) Full Data FT (34x34 encodings) (b) Zero-Padded FT (16 x 16 encodings) (c) Proposed Technique (16 x 16 encodings) (d) Hard edge map (e) Overall edge map
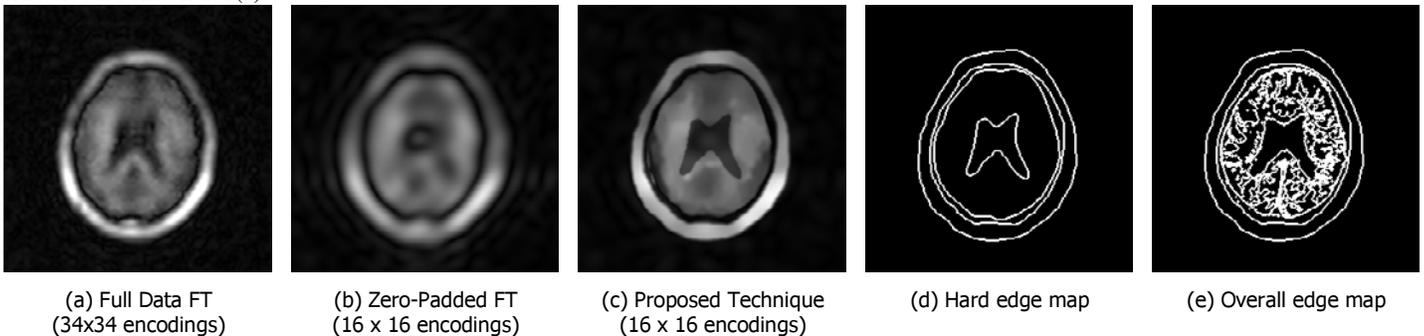
Figure 1. Reconstruction results for experimental dataset

CONCLUSION

This paper addresses the image reconstruction problem in MR spectroscopic imaging experiments where noisy, limited Fourier data are often collected due to temporal constraints. A parametric method is proposed which is capable of incorporating exact and uncertain boundary constraints. Experimental results show that the technique can generate metabolic images with much higher spatial resolution than the conventional Fourier method and other existing constrained reconstruction methods.

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