Jeffrey Tsao, Paul C. Lauterbur

Biomedical Magnetic Resonance Laboratory, Center for Biophysics and Computational Biology. University of Illinois at Urbana-Champaign 61801, USA

INTRODUCTION

MR Imaging or MR Spectroscopic Imaging (MRSI) of metabolites has long been a challenging task. The low concentrations of metabolites often necessitate increasing the number of signal averages and concomitantly sacrificing spatial resolution in order to acquire data within a reasonable time frame.

Over the past decade, various methods have been proposed to improve spatial resolution by incorporating prior information in terms of geometric constraints (e.g. regions that are reasonably homogeneous, or spatial support of the object). These methods can dramatically improve the reconstruction when the constraints are valid, but may cause significant artifacts when the constraints are violated.

On a case-by-case basis, the performance of different reconstruction methods can be quite variable, making it difficult to rely on a single method. A pragmatic approach is to allow the user to try quickly different reconstruction algorithms and test a number of "what-if" scenarios with various reconstruction options. To this end, we have examined a number of promising algorithms¹⁻⁷, and developed a software package called "Visual GSLIM", which encapsulates the salient features of these algorithms into a common framework.

METHODS

Visual GSLIM provides a graphical user interface for data manipulation, reconstruction, and visualization of results. It is written as a module in Matlab 5 (The Mathworks, Inc., Natick, MA). The source code of Visual GSLIM is available upon request from Jeffrey Tsao (jtsao@bmrl.med.uiuc.edu).

Data Requirements: Visual GSLIM requires two data sets: 1) a low-resolution MRSI data set, and 2) a high-resolution compartment image, with compartment labels denoting relatively homogeneous regions within the image. Both data sets may have up to three spatial dimensions. For the MRSI data, the number of points along the spectroscopic dimension is arbitrary, but the data are assumed to have at most one spectroscopic dimension. If there is more than one spectroscopic dimension, the data along the spectroscopic dimensions can be stretched out (i.e. rasterized) into a single dimension for subsequent processing.

Processing: Data processing is divided into three stages (see Figure): **Stage 1 - Spectroscopic Localization by IMaging (SLIM)**¹

A SLIM analysis¹ is applied to the MRSI data and the compartment image to derive the "average" compartmental signals. These compartmental signals are combined with the compartment image to generate a synthetic spectroscopic image, referred to as the SLIM image. The SLIM image is equivalent to the true image if the underlying compartmental assumptions are correct (i.e. the compartment image accurately depicts the homogeneous regions within the image). Any violations of the assumptions are manifested as discrepancies between the k-space data of the SLIM image and the actual MRSI data. These discrepancies are rectified in Stage 3.

Stage 2 - Optional Noise Reduction by Data Blending

When the signal to noise is low, the measured MRSI data may be unreliable. Visual GSLIM offers the option to blend the measured MRSI data with the k-space data of the SLIM image, with the degree of blending being controlled by a filter. Blending helps to reduce noise in the measured MRSI data, albeit at the risk of increasing reliance on the accuracy of the prior information. Blending is justifiable because the SLIM image represents the best estimate of the true image based on the available prior information.

Stage 3 - Generalized SLIM (GSLIM)²

GSLIM² combines SLIM (i.e. Stage 1) with additional mechanisms to reconcile errors in the underlying compartmental assumptions. In many ways, GSLIM is similar to some dynamic imaging approaches in which a high-resolution reference image is first acquired, followed by a series of low-resolution dynamic updates. In the present context, the SLIM image can be regarded as the reference image, while the MRSI data serve as a dynamic data set.

Visual GSLIM offers four algorithms for his processing stage: ^① Reduced-encoding Imaging by Generalized-series Reconstruction (RIGR)³, ^② keyhole⁴⁻⁵, ^③ Iterative Compartment Smoothing (ICS), and ^④ modified Improvement of Keyhole Effect (IKE)⁶. The details of the RIGR and keyhole algorithms are found elsewhere³⁻⁵. In ICS (similar to Ref. 7), the algorithm iterates between two steps until convergence. The first step is a keyhole data replacement. The second step involves anisotropic diffusion to smooth the signal variations within each compartment. In modified IKE, the algorithm is identical to the original implementation⁶, except that data blending is achieved by the approach in Stage 2 in order to avoid any line-to-line discontinuities in k-space.



DISCUSSIONS AND CONCLUSIONS

Visual GSLIM is a software system for reconstructing high-resolution spectroscopic images from low-resolution data by using prior geometric information. Its visual interface allows the user to test and compare various reconstruction algorithms quickly.

In combining various algorithms into the same software package, we have identified three important stages in the reconstruction process, facilitating a more systematic comparison among different reconstruction schemes.

REFERENCES

- 1. Hu X, et al. Magn Reson Med. 8:314-422. 1988.
- 2. Liang ZP, Lauterbur PC. IEEE Trans Med Imag. 10:132-137. 1991.
- 3. Liang ZP, Lauterbur PC. IEEE Trans Med Imag. 13:677-686. 1994.
- 4. Jones RA, et al. Magn Reson Med. 29:830-834. 1993.
- 5. Van Vaals JJ, et al. J Magn Reson Imag. 3:671-675. 1993.
- 6. Oesterle C, Hennig J. Magn Reson Med. 39:244-250. 1998.
- 7. Hu X, Stillman AE. IEEE Trans Med Imag. 10:290-294. 1991.

ACKNOWLEDGEMENTS

This work was supported by Biomedical Research Technology Grant PHS 5 P41 RR05964. We would like to thank Prof. Joan Dawson, Prof. Zhi-Pei Liang and Dr. Chris Hess for valuable discussions, Dr. Joe Kmiecik for the gerbil brain data, and Dr. Victor Schepkin and Sherrie Frydenger for the human leg data.



