An automated method to optimize the contrast of small structures

R. Chamberlain¹, T. M. Wengenack², J. F. Poduslo², C. R. Jack³, and M. Garwood¹
¹Center for Magnetic Resonance Research, University of Minnesota, Minneapolis, MN, United States, ²Departments of Neurology, Neuroscience, and Biochemistry/Molecular Biology, Mayo Clinic College of Medicine, Rochester, MN, United States, ³Department of Radiology, Mayo Clinic College of Medicine, Rochester, MN, United States

Introduction

Many MRI applications require visualizing structures on the order of a few pixels in size. In these applications the contrast-to-noise ratio of the small structures is more important than the SNR of the image. The CNR can be affected dramatically by the image resolution relative to the size of the structure, but the exact relation of resolution and CNR depends on the specific structure and pulse sequence. This work describes an automated method to optimize the acquired image resolution to obtain the greatest CNR of small structures. It is demonstrated as applied to imaging amyloid plaques in transgenic mouse models of Alzheimer's disease.

Methods

The method requires as input a single data set acquired with the highest resolution practically achievable given experimental constraints. After standard reconstruction of the high resolution data set (1), the plaques can be identified automatically with the following algorithm. The image is divided by the standard deviation of the noise measured outside of the brain, and then a filtered image is generated with a 2D median filter. The original image is subtracted from the filtered image, leaving mainly structures of small size. The magnitude of these points corresponds to the CNR of the structure. A CNR threshold is chosen (4 in this case), which leaves only small structures that are significantly different than the background. The centroid of each remaining structure is recorded as a plaque. These points identified as plaques are used to measure the average plaque CNR for all remaining reconstructions.

To determine the optimal reconstruction, the data set was reconstructed with 15000 resolution combinations. The readout resolution varied between 60 μm and 120 μm. The resolution in the first phase-encoded dimension varied between 48 μm and 110 μm. The resolution in the second phase-encoded dimension varied between 48 μm and 137 μm. Each resolution combination was reconstructed three different ways using: (1) the full Cartesian data, (2) a cylindrical filter on the data where the corners of k-space in the two phase-encoded dimensions were removed, and (3) a spherical filter on the data where all corners were removed. The resulting images were compared by calculating the plaque-to-background contrast for the previously identified plaques throughout the image volume.

Results and Discussion

The cylindrical k-space sampling method consistently gave better plaque CNR than the Cartesian and spherical methods (Fig. 1). The maximum plaque CNR occurred at an image resolution of 71.1 μm x 60 μm x 87.3 μm using the cylindrical sampling method. Our previous studies imaging plaques used an image resolution of 60 μm x 60 μm x 120 μm with a Cartesian sampling method (2), which had a plaque CNR 12% lower than the maximum. Thus, this work offers a significant increase over the current method. This simple optimization algorithm could be applied to any structure that is on the order of a few pixels in size, such as Fe labeled cells, plaques, or small vessels.

![Figure 1: Average plaque CNR as a function of phase-encode resolution.](image)

References


Acknowledgements

Supported by NIH P41 RR008079 and P30 NS057091, the Keck Foundation, and the Minnesota Partnership for Biotechnology and Medical Genomics.