3-D *Tomographic* Reconstruction of the Average Propagator from Diffusion-Weighted MR Data

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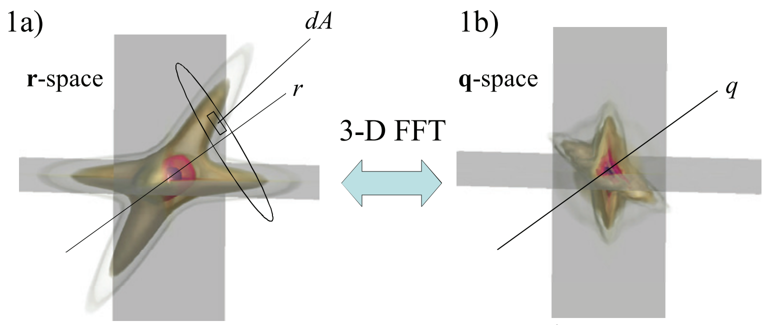
Introduction

The measurement of the 3-D “average propagator”, $p(\mathbf{r})$, from diffusion-weighted (DW) NMR or MRI data has been a “holy grail” in materials science and biomedicine, as $p(\mathbf{r})$ provides detailed microstructural information, particularly about restriction. While Callaghan proposed a 3-D Fourier Transform relationship between $p(\mathbf{r})$ and the DW signal attenuation, $E(\mathbf{q})$ [1], using it to measure $p(\mathbf{r})$ from $E(\mathbf{q})$ data is not feasible biologically or clinically, owing to the staggering amount of DW data required.

To address this problem, we propose using computed tomography (CT) principles to reconstruct $p(\mathbf{r})$ from $E(\mathbf{q})$ data. Moreover, by employing information about known properties of $E(\mathbf{q})$ and $p(\mathbf{r})$, our CT reconstruction algorithms can be performed efficiently using many fewer DW $E(\mathbf{q})$ data points than conventional 3-D q-space MRI [1] or Diffusion Spectrum Imaging (DSI) [2] require.

Algorithm

As shown in Fig. 1, $E(\mathbf{q})$, measured along a ray in **q**-space, q, is the 1-D Fourier Transform of $p_m(r)$, the marginal probability density function of $p(\mathbf{r})$, which is obtained by projecting $p(\mathbf{r})$ along the corresponding ray in (displacement) **r**-space, r. CT reconstruction can then be used to estimate $p(\mathbf{r})$ from different projections, $p_m(r)$, by inverting the 3-D Radon Transform shown in Fig. 1. We propose using the Gerchberg and Papoulis (G-P) iterative procedure, originally developed for the 2-D [3] and 3-D ray transforms [4]. While iterating between **q**- and **r**-space, *a priori* information about the properties of $E(\mathbf{q})$, $p(\mathbf{r})$, and $p_m(r)$ can be applied as constraints.

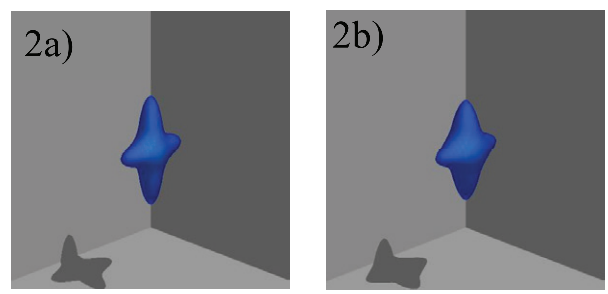


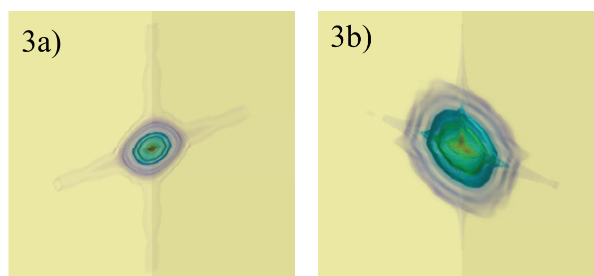
$$p_m(r) = \iint p(x,y,z)\,dA$$

3-D Radon Transform

$$E(q) = \int p_m(r)\, e^{-2\pi i q r}\, dr$$

1-D Fourier Transform





To test our modified G-P algorithm, numerical simulations were performed. In Fig. 2a, the exact $p(\mathbf{r})$ is shown as an iso-surface. In Fig. 2b, $E(\mathbf{q})$ rays with only 13x13 polar and azimuthal angles and 9 radial points (1,521 total points) were sufficient to reconstruct $p(\mathbf{r})$ faithfully. Two constraints were applied during the iterative procedure: positiveness of $p(\mathbf{r})$ and smoothness of $E(\mathbf{q})$ (i.e., Tikhonov regularization). Only four iterations were required to reconstruct $p(\mathbf{r})$ with an RMS error = 22%.

In Fig. 3a, we reconstructed $p(\mathbf{r})$ from one voxel of experimental DWI data obtained from excised spinal cord using 31 gradient directions, each with 16 radial points in **q**-space (496 total points). Fig.3b shows the full restoration of the real part of $E(\mathbf{q})$.

Discussion and Conclusion

In considering the novelty of this new approach, it is important to distinguish it from “tensor tomography” [5], in which the diffusion tensor field is reconstructed from DWI data by integrating signal intensities along rays within the imaging volume. Our CT reconstruction of $p(\mathbf{r})$ is performed using $E(\mathbf{q})$ data obtained within *each voxel*. Our approach also differs from q-ball MRI [6], which only reconstructs orientational features of $p(\mathbf{r})$ by using $E(\mathbf{q})$ data acquired on a sphere in **q**-space. We use $E(\mathbf{q})$ data obtained throughout **q**-space to reconstruct the *entire* average propagator, $p(\mathbf{r})$.

References

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