Using Track Similarity to Determine Optimum Sequence Parameters for Diffusion Spectrum Imaging

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Abstract

For clinical diffusion spectrum imaging (DSI), fewer diffusion-encoding gradients and lower maximal diffusion-encoding sensitivity (bmax) are needed to reduce scan time and keep the hardware stable. However, aliasing or truncation artifact may become prominent when 3D Fourier transform of the q-space spectral data is performed. The purpose of this study was to determine the optimum sampling scheme for clinical DSI. We used 925 encoding gradients with bmax = 9000 s/mm^2 as the gold standard. Similarity of tractography generated from different sampling schemes to the tractography generated from the gold standard was compared. Using 515 diffusion-encoding gradients and bmax = 6000 s/mm^2 was considered to be the optimum condition for clinical DSI.

Introduction

It has been shown that diffusion spectrum imaging (DSI) has the capacity to resolve complex fiber orientations [1,2], and that tractography based on DSI data can differentiate crossing neural fiber tracts [2,3]. In the clinical setting, however, the maximal diffusion-encoding sensitivity (bmax) and diffusion-encoding gradients are often reduced to keep the hardware stable and scan time acceptable. In this case, 3D Fourier transform of the spectral signal in the q-space is liable to aliasing and truncation artifact, resulting in inaccurate tractography. The purpose of this study, therefore, was to determine the optimum number of diffusion-encoding gradients and the value of bmax for clinical DSI. Tractography results generated from different reduced sampling schemes were compared with the tractography generated from the gold standard. The degree of similarity in tractography was quantified in terms of a similarity index.

Materials and Methods

DSI data were obtained from one healthy volunteer with a 3T MRI system (Trio, Siemens, Erlangen, Germany). A twice-refocused balanced echo diffusion EPI sequence was used to acquire MR diffusion images. Images of DSI were acquired with 925 diffusion-encodings comprising isotropic 3D grid points over the q-space. DSI data were acquired with bmax = 9000 s/mm^2, and TR/TE = 2900/150 ms. In order to implement the tractography, isotropic voxels were obtained by setting in-plane resolution and slice thickness to be 2.7 mm. Fifteen horizontal slices encompassing the middle portion of the brain were acquired. The scan time was less than one hour. DSI analysis was based on the relationship that the echo signal S(q) and the diffusion probability density function P(r) were a Fourier pair, i.e., S(q) = FT{P(r)} [4]. The integration of P(r) r^2 along each radial direction was used to calculate the orientation density function (ODF). The main orientations of the water diffusion were then determined by the local maximum vectors of the ODF [5]. The fiber tracking was based on an automated algorithm that was adapted for DSI data. In the selected seed points, the first three largest ODF vectors of each voxel were used to track. All fiber orientations of the nearest voxels were used to decide the proceeding orientation for the next step. The most coincident orientation which was less than 22° was chosen. The proceeding length of each step was 0.5 voxel. The tracking would stop if there was no coincident orientation in the nearest voxels.

Two different approaches of reduced sampling were studied. The datasets were generated by sub-sampling the original dataset. The first approach consisted of sub-sampled datasets with the same bmax but different reduced samples, the second approach consisted of subsets with the same Δq but different reduced bmax. Tractography with the same seed points was reconstructed from each sampling scheme. The results were compared with the standard tractography generated from the original dataset. To define the track similarity, each track was separated into small segments based on the tracking steps. A unit vector was assigned to each segment according to the orientation of the proceeding orientation. The similarity index of the unit vector $\mathbf{v}_1$ at each step position $\mathbf{p}_1$ with respect to its corresponding vector $\mathbf{v}_2$ at $\mathbf{p}_2$ in the standard tractography was defined as the inner product of $\mathbf{v}_1$ and $\mathbf{v}_2$ divided by the distance between their step positions. The track similarity was obtained by averaging the similarity indices over all the segments in a track. If the length of the two compared tracks differed by more than 20 steps, the similarity was set to 0. Track similarity for each seed point was calculated first and the mean similarity over the total tracks was obtained.

Results

The sampling points in q-space of the original experimental data was shown in Fig. 1, a, the sub-sampled schemes were also shown in b, c, d, e, f and g. Tractography from the original dataset was used as the gold standard (Fig. 2). Six tractography results were generated from the six sub-sampled datasets. The track numbers generated from each dataset were 670, 679, 595, 699, 689 and 660 for b, c, d, e. f and g, respectively, and the mean similarities with respect to the standard tractography were 9.00, 7.78, 4.68, 7.86, 7.16 and 3.47 (x 10^8), respectively. Comparison between schemes b and e, as well as schemes d and g indicated that schemes with higher bmax were relatively better than the schemes with reduced bmax (p = 0.009 and 0.002). However, the difference was not significantly different between schemes c and f (p = 0.12). Among the schemes using a fixed bmax = 9000 s/mm2, similarity increased with the gradient number (Fig. 3). Among the schemes with a fixed Δq and reduced bmax, both e and f had better track similarity than scheme g, but there was no significant difference between schemes e and f (p = 0.066).

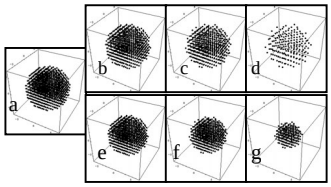

Figure 1. The gold standard is the 925 grid sampling points over the q-space with bmax = 9000 s/mm^2 (a). Schemes b, c and d are the datasets with the same bmax as a, and their sampling numbers in q-space are 691, 515 and 203, respectively. Schemes e, f and g are the interpolated datasets with the same Δq as a. Their sampling numbers are 691, 515 and 203, and bmax are 7250, 6250 and 3250 s/mm^2, respectively.

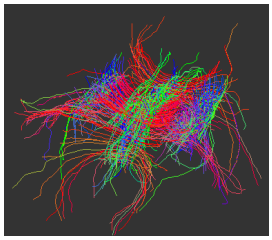

Figure 2. Tractography from the standard DSI dataset with 925 diffusion-encoding gradients and bmax = 9000 s/mm^2 (a in Fig. 2). A total of 667 tracks were generated from 253 seed points. Tract orientation was encoded by 3D color, red in left-right, green in anterior-posterior and blue in top-bottom.

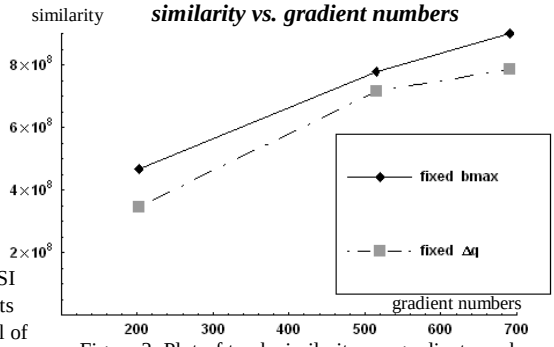

Figure 3. Plot of track similarity vs. gradient numbers using two different sampling approaches: one using fixed bmax and the other using fixed Δq.

Conclusions

In this work, DSI tractography was used to determine optimum sequence parameters for DSI acquisition in the clinical setting. Using 203 diffusion-encoding gradients with bmax = either 3000 or 9000 s/mm^2, the track similarity is approximately 2 folds lower than that reconstructed from 691 encoding gradients. Using 515 diffusion-encoding gradients with bmax = 6000 s/mm^2, the track similarity is only about 10-20 % worse than that reconstructed from 691 encoding gradients. Taking the balance between the scan time, hardware limitation and accuracy of tractography, 515 encoding gradients with bmax of 6000 s/mm^2 is considered to be the optimum condition for clinical DSI.

Reference

[1] Wedeen et al., ISMRM2000, p82. [2] Lin et al., NeuroImage. 19:482-95, 2003. [3] Hagmann et al., ISMRM2004, p62 [4] Kuo et al. ISMRM p1286. [5] Callaghan: Principles of nuclear magnetic resonance microscopy. Oxford Science Publication, 1991.