# Development of DT-MRI Muscle Fiber Tracking Algorithms

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## Introduction

Diffusion-tensor MRI (DT-MRI) is a promising tool for quantitatively characterizing the striated muscle architecture (1, 2). Muscle DT-MRI fiber tracking as we have described it (2) involves 1) measuring the DT throughout the muscle; 2) defining *a*) a mask of the muscle and *b*) the aponeurosis of fiber insertion (used as the seed surface for fiber tracking); 3) following the path of greatest diffusion without spatial interpolation (streamline tracking); and 4) termination of the fiber tracts when any of the following criteria are met: *a*) angular orientation (θ) between successive points >45°; *b*) FA<0.2; or *c*) reaching edge of the image mask.

Muscle DT-MRI is made challenging, however, by muscle's low $T_2$, low fractional anisotropy (FA), and large diffusivity. In addition, partial volume artifacts make resolving the fiber trajectories around intramuscular fat depositions difficult, creating the need to develop new fiber tracking algorithms. Therefore, the purpose of this study was to use Monte Carlo simulations of model muscles with known muscle architectural patterns to quantify the performance of several novel muscle fiber tracking algorithms. In particular, we consider steps 3 and 4 of the above procedure.

## Methods

*Proposed Algorithms:* First, we compare streamline (SL) tracking with 1) an N-back algorithm, in which the fiber tracking step is calculated as the average of the last three steps in the fiber tract, weighted by distance (3Back); 2) nearest-neighbor interpolation, weighted by distance (NN-D); and 3) nearest neighbor interpolation, weighted by $T_2$-weighted signal (NN-T). We test each of these interpolation schemes using the default stop scheme in which a true condition for any of the three binary arguments listed above (high curvature, excessive FA, or exiting the mask) causes fiber tracking termination (BIN). We compare this to an alternative stop scheme in which linear weighting coefficients are applied to the $T_2$-W signal, FA, and curvature (WEIGHT).

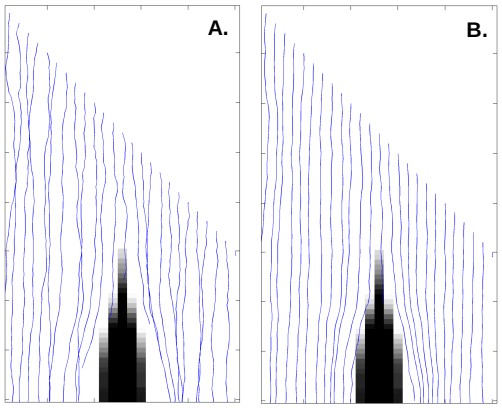


**Figure 1. A**. Sample fiber tracking results, displayed on a $T_2$-weighted image, for BIN/3Back. **B**. Sample fiber tracking for WEIGHT/NN-D.

*Monte Carlo Simulations:* 320 trials (40 for each of the 2×4 stop×interpolation schemes, each at SNR of ~60) were conducted. A model tissue was defined having 1600×500 elements, each representing a 60×60 μm area. A fat infiltrate was generated in the muscle and the adjacent fibers were designed to wrap around it, transitioning to straight fibers on the muscle borders. Muscle elements were defined as having $\lambda_1/\lambda_2/\lambda_3$=2.1/1.6/1.2×$10^{-3}$ $mm^2/s$ and $T_1/T_2$/water proton density (ρ)=1200 ms/35 ms/0.8 AU. Fat elements were defined as having $\lambda_1=\lambda_2=\lambda_3$=0.6×$10^{-3}$ $mm^2/s$ with their eigenvectors randomly oriented and $T_1/T_2/\rho$=500 ms/200 ms/0.1 AU. For each tissue element, the diffusion tensor was calculated. Images were generated at 1.2×1.2 mm in-plane resolution. A fat saturated, $T_2$-weighted image was calculated using TR/TE=5000/45 ms and b=0 $s/mm^2$. After averaging the diffusion tensors for the 400 elements/voxel, diffusion-weighted images were calculated using TR/TE=5000/45 ms and b=500 $s/mm^2$ applied along 10 directions. Two channels of Gaussian noise (1 real, 1 imaginary) were expressed as complex numbers and their magnitude added to the images to create SNR ~60. For each pixel, $\lambda_{1\text{-}3}$ and $\varepsilon_{1\text{-}3}$ were obtained by diagonalizing the DT matrix and magnitude-sorting the eigenvalues.

Fibers were tracked from a hypothetical aponeurosis with the trajectory for each tracking step determined according to the SL, 3Back, NN-D, and NN-T schemes. For 3Back, the trajectory was determined as the distance-weighted average of $\varepsilon_1$ in the current pixel and for the last 3 fiber tracking steps. For NN-D, the fiber trajectory was determined as the distance-weighted average of $\varepsilon_1$ in the current pixel and the 8 neighboring pixels. For NN-T weighting, a $T_2$-W signal weighting statistic (*T*) was calculated such that a pure fat pixel had value of 0 and a pure muscle pixel had a value of 1 and used to weight the average of $\varepsilon_1$ in the current pixel and the 8 neighboring pixels. Fiber stop criteria included either the BIN method or the WEIGHT method, the latter using a score *S*:

$$S = \text{sum}\left( [-(T-1) \quad F \quad C] \cdot \mathbf{W} \right)$$

where *F*=1 if the FA criterion is met and 0 if it is not; C=1 if the curvature criterion is met and 0 if it is not; and **W** is a 1×3 vector of linear weighting coefficients, constrained to sum to 1 and having values of 0.5, 0.1, and 0.4 in this implementation. Fiber tracking terminated if *S*>0.75.

*Data Analysis:* The stop criteria were assessed as follows: by design, 24 of the 25 fiber tracts should have terminated at the muscle border. Therefore, the number of full-length tracts (*N*) was used to assess the stop criteria quality. The interpolation schemes were assessed by calculating the θ for each pair of successive points along tract #24, which was designed to lie entirely in the Y direction. The mean and SD were calculated. The mean values of θ and *N* were compared using the GLM (Stop×Interpolation) with repeated measures and multiple comparisons made using a Bonferroni adjustment.

## Results and Discussion

Figure 1 shows sample fiber tracking results overlaid onto a $T_2$-weighted image for the BIN/3Back and WEIGHT/NN-D conditions. Figure 2 shows the mean values of *N*. *N* was greater ($p$<0.001) for WEIGHT and significantly lower for 3Back than for other interpolation schemes ($p$<0.001). Figure 3 shows the mean values of θ. There was no effect of the stop scheme on θ, but NN-T interpolation resulted in significantly greater values for θ than other interpolation schemes.

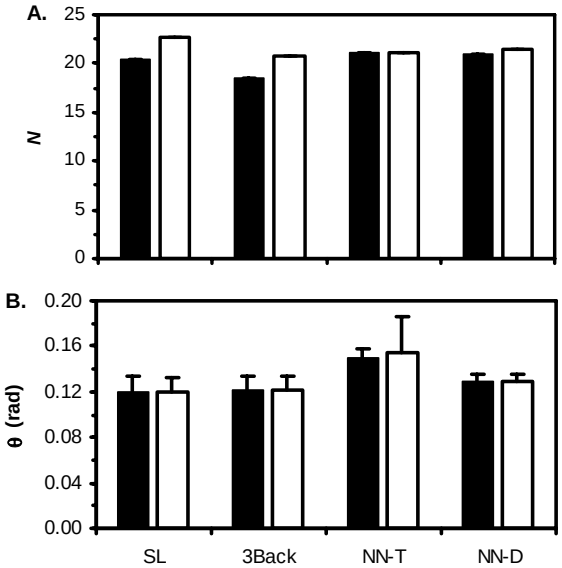


**Figure 2. A.** Mean values for *N* for BIN (black bars) and WEIGHT (open bars). **B.** Mean values for θ for BIN (black bars) and weight (open bars).

## Conclusion

Of the 8 combinations of interpolation/stop schemes, the muscle DT-MRI fiber tracking algorithm that combined NN-D interpolation with weighted stop criteria was best able to track fibers around fat infiltrations under typical SNR conditions.

## References

1. Damon BM, et al. *Magn Reson Med*, **48**:97, 2002.
2. Lansdown DA et al. *J Appl Physiol*, **103** :673, 2007.

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