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Polynomial Fitting of DT-MRI Fiber Tracts Allows Accurate Estimation of Muscle Architectural Parameters

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Abstract

Fiber curvature is a functionally significant muscle structural property, but its estimation from diffusion-tensor MRI fiber tracking data may be confounded by noise. The purpose of this study was to investigate the use of polynomial fitting of fiber tracts for improving the accuracy and precision of fiber curvature (κ) measurements. Simulated image datasets were created in order to provide data with known values for κ and pennation angle (θ). Simulations were designed to test the effects of increasing inherent fiber curvature (3.8, 7.9, 11.8, and 15.3 m⁻¹), signal-to-noise ratio (50, 75, 100, and 150), and voxel geometry (13.8 and 27.0 mm³ voxel volume with isotropic resolution; 13.5 mm³ volume with an aspect ratio of 4.0) on κ and θ measurements. In the originally reconstructed tracts, θ was estimated accurately under most curvature and all imaging conditions studied; however, the estimates of κ were imprecise and inaccurate. Fitting the tracts to 2nd order polynomial functions provided accurate and precise estimates of κ for all conditions except very high curvature ($\kappa=15.3$ m⁻¹), while preserving the accuracy of the θ estimates. Similarly, polynomial fitting of *in vivo* fiber tracking data reduced the κ values of fitted tracts from those of unfitted tracts and did not change the θ values. Polynomial fitting of fiber tracts allows accurate estimation of physiologically reasonable values of κ , while preserving the accuracy of θ estimation.

Keywords

diffusion tensor; skeletal muscle; noise; curve fitting; muscle architecture

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1. Introduction

Diffusion-tensor (DT-) MRI-based muscle fiber tracking is a useful tool for characterizing skeletal muscle architecture *in vivo*. Its feasibility and potential for practical application has been demonstrated in animal studies and a wide range of human muscles, including the dorsiflexors, plantarflexors, thigh muscles, forearm, and pelvic floor muscles. Since the method was initially introduced, technical developments have included: using fiber tracking data to calculate pennation angles, fiber tract length, and physiological cross-sectional area; investigating the best practices for data acquisition; implementing denoising procedures; quantitatively assessing tractography outcomes; establishing the within session, within day, and between day repeatability of the diffusion data and the muscle architectural measurements (see also); assessing alternative fiber tracking algorithms, and using DT-MRI data in biomechanics studies. In this work, we continue these technical developments by investigating the best practices for measuring muscle fiber curvature from DT-MRI fiber tracking data, while ensuring that these practices do not alter other important muscle architectural measurements, such as pennation angle.

Curvature is a functionally significant muscle structural property. In muscle fibers, curvature separates the stresses developed by intracellular contractile proteins into normal and tangential components and thus may affect the pathways used for force transmission. Also, muscle architecture-based modeling studies have suggested that fiber curvature influences the magnitude and uniformity of strain development during muscle contraction and leads to intramuscular pressure gradients during contraction, the latter property potentially affecting muscle perfusion patterns. The curvature of entire muscle fascicles has been measured using ultrasound imaging, and curvature has been measured from DT-MRI data for use in fiber tracking and voxel connectivity algorithms and as an inherent property of DT-MRI fiber bundles. However, we are unaware of a previous use of DT-MRI fiber tracking to measure muscle fascicle curvature. The ability to measure fiber curvature accurately in DT-MRI fiber tracts would enable the synthesis of this key muscle architectural property with the data available from other physiological MRI methods, such as arterial spin labeling and spatial tagging, and allow definitive tests of the hypotheses concerning the relationships among muscle fiber curvature, perfusion, and strain.

The focus of this study is on mitigating the effects of image noise and artifacts on muscle pennation angle and curvature measurements. One strategy for reducing the effect of noise on pennation angle measurements is to average the data from the five fiber tract points nearest the seed point of the fiber. The idea underlying this approach is that the position vector between two adjacent fiber tracking points is determined not just by the fiber's true direction, but also by random deviations from the true direction due to noise or artifacts; averaging the data from multiple points cancels or reduces the effects of noise and artifacts on the pennation angle estimates. However, this strategy is likely to be ineffective for fiber curvature estimates, as curvature measurements are based on the orientation difference between two successive points along a curve. In this case, combining the data from multiple fiber tracking points may cause noise-induced errors in the fiber tract direction to propagate, not be cancelled out.

In this study, we examine the impact of noise-induced deviations of muscle DT-MRI fiber tract points from the true fiber tract position on the accuracy and precision of muscle fiber pennation and curvature estimates. We propose polynomial fitting of fiber tracts as a method for reducing these errors and test the hypothesis that this procedure would improve the estimation of muscle fiber curvature, without adversely affecting the pennation angle estimates. We use simulated datasets to show that this is the case, across a wide range of inherent fiber curvature, signal-to-noise ratio (S/N), and voxel dimension conditions. To

demonstrate the utility of this approach, we implement these methods in an *in vivo* fiber tracking dataset.

2. Methods

2.1 Simulation Methods

Formation of and Assumptions Concerning the Model Muscle—To define realistic muscle structures, we digitized a fascicle from a published two dimensional ultrasound image of the human gastrocnemius muscle (Fig. 2 of Reference). To reduce errors associated with hand digitization, this procedure was performed twice. The foot-head direction in the ultrasound image was defined as the Z axis and the anterior-posterior direction was defined as the Y axis. The originally digitized points ranged from 0–18.37 mm and 0–44.06 mm in the Y and Z directions, respectively; to facilitate simulated image formation, the points were scaled to 0–24 mm in the Y dimension and 0–48 mm in the Z dimension. To generate a smooth curve describing this fascicle, the data from the two digitization replicates were combined to form a single dataset. The Y values were fitted as a function of Z to 2nd and 3rd order polynomials. To determine which polynomial order should be used to describe the data, the *F*ratio was calculated to express the improvement in goodness of fit relative to the relative increase in model complexity. The results of this test led us to reject the 3rd order polynomial model and instead use the 2nd order polynomial to fit the digitized data points. We refer to the 2nd order-fitted dataset as the original fascicle (Figure 1). The original model muscle consisted of a series of such fascicles, arranged in parallel arrays along both the Z and X axes.

Design of Simulation Experiments—To test the robustness of the fitting procedures on the estimation of the architectural parameters under a wide range of imaging and muscle structural conditions, we performed three sets of simulations. Image sets were formed having a variety of curvature values, signal-to-noise ratios (S/N), voxel volumes, and voxel aspect ratios (Table 1). In the first set of simulations, we studied datasets having isotropic resolution, voxel volume=13.8 mm³, and S/N ~75, but different inherent fiber curvature values (range 3.8–15.3 m⁻¹) and pennation angles (31.6–47.5°). To increase the fiber curvature, we formed a vector of scaling factors that decreased linearly from an initial value of 1.75 to 1.0. We then performed a pointwise multiplication of the Y values of the original fascicle by the scaling vector. Additional scaling vectors, using initial values of 1.5 and 1.25, were also formed and used to create model muscles with intermediate curvature values. The curvature values are given in Table 1 and the model fascicles are illustrated in Figure 1. The second set of simulations examined datasets having 2.4 mm isotropic resolution (voxel volume=13.8 mm³) and $\kappa=7.9$ m⁻¹, but differing in S/N (range 50–150; see Table 1). The third set of simulations used datasets having different voxel properties: the first dataset tested had $\kappa=7.9$ m⁻¹ and S/N ~75, but 3 mm isotropic resolution. The second dataset had voxel volume 13.5 mm³, $\kappa=7.9$ m⁻¹, and S/N ~75, but an aspect ratio (AR≡slice thickness/in-plane resolution) of 4.0.

In each model, the assumed values for the first, second, and third eigenvalues (λ_1 , λ_2 , and λ_3) of the diffusion tensor, **D**, were 2.0, 1.6, and 1.4×10^{-3} mm²/s, respectively. The formation of the eigenvectors of **D** is described below. The model muscles had a T_2 of 35 ms.

Image Formation—In each voxel, the first eigenvector (e_1) of **D** was formed by evaluating the polynomial defining the original fascicle over the bounds defined by the

voxel dimensions; the mean slope across the voxel ($M_{yz} = \frac{\Delta Y}{\Delta Z}$) was used as the Y component of $\mathbf{e}_1$:

$$\mathbf{e}_1 = \left(\frac{\begin{bmatrix} 0 & M_{yz} & 1 \end{bmatrix}}{\left\| \begin{bmatrix} 0 & M_{yz} & 1 \end{bmatrix} \right\|} \right)^T \quad (1)$$

where the superscript T indicates the transpose operation and the denominator (the vector norm) is used to convert the vector to unit length. The second eigenvector ($\mathbf{e}_2$) was defined as the YZ-plane normal to $\mathbf{e}_1$, and the third eigenvector ($\mathbf{e}_3$) was calculated as $\mathbf{e}_1 \times \mathbf{e}_2$. $\mathbf{D}$ was calculated as:

$$\mathbf{D} = \mathbf{E} \mathbf{\Lambda} \mathbf{E}^T \quad (2)$$

where $\mathbf{E}$ and $\mathbf{\Lambda}$ are the eigenvector and eigenvalue matrices, respectively. Noise-free signals were calculated for T_2 -weighted and diffusion-weighted images. A 3×10 diffusion encoding matrix, $\mathbf{H}$, was defined having 10 evenly distributed diffusion encoding directions. Image signals were calculated assuming a fully longitudinally relaxed condition:

$$S = e^{(-TE/T_2)} \cdot e^{(-b\mathbf{h}^T \mathbf{D} \mathbf{h})}, \quad (3)$$

where the echo time (TE) = 45 ms, the diffusion encoding (b -) value = 0 or 500 s/mm^2 , and $\mathbf{h}$ is a vector corresponding to each column of $\mathbf{H}$. Zero-mean, unit variance, Gaussian-distributed noise was generated in quadrature, scaled to create the S/N values given in Table 1, and added to the noise-free images. The magnitudes of the image signals were taken. For each image set, 1500 independent noise realizations were performed, and the analysis procedures described below were performed each time.

Fiber Tract Generation and Fitting Procedures—In each voxel, $\mathbf{D}$ was calculated by averaging the signals from the voxel plus as many of its 26 nearest neighbors as fell within the image boundaries. This procedure is acceptable in muscle because there is little spatial variation in the orientation of $\mathbf{e}_1$ throughout a muscle. We then performed a weighted least squares fit of the noisy signals to $\mathbf{H}$, as described previously. $\mathbf{D}$ was diagonalized and the eigenvalues were magnitude-sorted. The fractional anisotropy (FA) was calculated using the standard equation. One fiber tract per image set was seeded near the origin and the tract was propagated in the direction of $\mathbf{e}_1$, using a step size equal to the in-plane resolution. The tract was terminated if the FA was < 0.1 or > 0.5 , if the angle formed by two consecutive fiber tracking points was $> 30^\circ$, or if the tract propagated out of the image. Fiber tract positions were converted to distances by multiplying by the image resolution. We refer to these as the raw (originally reconstructed) tracts. Next, the X, Y, and Z positions in the raw tracts were fitted as functions of point number to 2nd order polynomial functions. Examining a wide variety of published muscle ultrasound images revealed that muscle fascicles typically have a single direction of curvature, even in boys with Duchenne muscular dystrophy. Fitting fiber tracts that possess a single curvature direction with polynomial orders higher than two frequently resulted in a hypersensitivity to noise and additional inflections in the fitted tracts (Figure 2). Therefore, a 2nd order polynomial was used in all simulation conditions.

Finally, to generate criterion data that were unaffected by errors such as partial volume artifacts, these procedures were repeated for all of the conditions described in Table 1, except that images were noise-free, the fiber tracking step size was 0.25 times the voxel width, and the 27-voxel averaging procedure was not deemed necessary.

Fiber Tract Structural Characterization—The raw and fitted fiber tracts were analyzed as follows. The fiber tract is defined by the set of points $\mathbf{P} = \{p_1, p_2, p_3 \dots p_N\}$. A position vector, $\vec{\mathbf{p}}_{pn}$, was formed between each successive pair of points $\{p_{(n-1)}, p_n\}$. The length (Δs) of each position vector was calculated using the Pythagorean Theorem and the fiber tract length (L_{ft}) was calculated as their cumulative sum. The pennation angle (θ) was calculated as the arccosine of the dot product of $\vec{\mathbf{p}}$ and a unit vector in the +Z direction. κ was calculated for points $\{p_2 \dots p_{(N-1)}\}$ using a discrete implementation of the Frenet formulas. The discrete implementation was used to allow the possibility of using procedures to smooth or fit fiber tracts that do not result in a continuously differentiable function, such as low pass filtering or piecewise polynomial fitting. The unit tangent vector ($\hat{\mathbf{T}}_{pn}$) between p_n and $p_{(n-1)}$ was calculated as:

$$\hat{\mathbf{T}}_{pn} = \frac{\vec{\mathbf{r}}_{pn} - \vec{\mathbf{r}}_{p_{(n-1)}}}{\|\vec{\mathbf{r}}_{pn} - \vec{\mathbf{r}}_{p_{(n-1)}}\|} \quad (4)$$

where $\vec{\mathbf{r}}_{pn}$ is the position vector between p_1 and p_n . The tangent vector $\hat{\mathbf{T}}_{p_{(n+1)}}$ was also calculated. The spatial rate of change in the two unit tangent vectors, $\frac{\Delta \hat{\mathbf{T}}}{\Delta s}$, was used to calculate the unit normal vector $\hat{\mathbf{N}}$ as:

$$\hat{\mathbf{N}} = \frac{\frac{\Delta \hat{\mathbf{T}}}{\Delta s}}{\left\| \frac{\Delta \hat{\mathbf{T}}}{\Delta s} \right\|} \quad (5)$$

$\frac{\Delta \hat{\mathbf{T}}}{\Delta s} \hat{\mathbf{N}}$ and are related by κ :

$$\frac{\Delta \hat{\mathbf{T}}}{\Delta s} = \kappa \hat{\mathbf{N}} \quad (6)$$

κ was thus calculated using:

$$\hat{\mathbf{N}}^+ \frac{\Delta \hat{\mathbf{T}}}{\Delta s} = \kappa \quad (7)$$

where $\hat{\mathbf{N}}^+$ is the Moore-Penrose pseudoinverse of $\hat{\mathbf{N}}$. The Matlab code used to perform these calculations was verified by generating circular curves having radii of 0.5, 1.0, and 2.0 arbitrary units (AU). The κ values measured for these curves were 2.0 AU^{-1} , 1.0 AU^{-1} , and 0.5 AU^{-1} , respectively.

Analysis of Fiber Tract Population Properties—The following analyses were conducted for the raw and fitted tracts in each image set. The fiber tracts with L_{ft} 80% of the original fascicle's length were identified. For each of these tracts, the mean value of θ over the first 1 cm of the fiber tract was used to represent θ at the point of fiber tract insertion. Also, the mean and 95% confidence interval (95% CI) for κ were determined for the raw and smoothed fiber tracts at 10%, 20%, 30%...80% of L_{ft} for the original fascicle. These were compared to the known values for the tracts generated from the noise-free images.

2.2 In Vivo Implementation

Data Acquisition and Fiber Tracking—To demonstrate the *in vivo* feasibility of DT-MRI-based curvature measurements, a data set from a previously published study was

chosen at random and analyzed. The data acquisition and analysis procedures were presented previously; briefly, the subject provided written informed consent to participate in a study of the repeatability of DT-MRI fiber tracking. DT-MRI and structural images were acquired throughout the entire tibialis anterior (TA) muscle and co-registered; $\mathbf{D}$ was calculated in each voxel by averaging the signals from the voxel plus as many of its 26 nearest neighbors as fell within a hand-defined image mask of the superficial muscle compartment. To define seed points for fiber tracking, a mesh was generated from digitized points representing the TA's central aponeurosis. To smooth this surface, the mesh was generated initially at low density, and the low density mesh was then used to create a final mesh with 3 mm row resolution and 1 mm column resolution at the widest point. Fiber tracking was performed from the points of intersection between the rows and columns of the mesh into the superficial muscle compartment using stop criteria of exiting the image mask, angle difference between two successive points $>30^\circ$, and $FA < 0.1$ or > 0.5 (the raw tracts). The fiber tracking outcome was assessed quantitatively and erroneous results were excluded essentially as described previously, but also taking outlying curvature values into account. Finally, the X, Y, and Z positions of each fiber tract were fitted using the procedures described above.

Fiber Tract Analysis— κ was calculated using Eq. 4–7. θ was calculated essentially as previously described. Briefly, the in-plane and through-plane tangent lines to the seed point were used to calculate the Cartesian equation for the plane tangent to the seed point, and from this equation the normal unit vector to the plane ($\hat{\mathbf{n}}$). Position vectors ($\vec{\mathbf{r}}_n$) were formed between the seed point and each of the first five fiber tracking points. For each point, θ was determined as the arcsine of the dot product of $\vec{\mathbf{r}}_n$ and $\hat{\mathbf{n}}$; the average of all five values was taken. Previously, when determining the tangent lines, we fitted the aponeurosis row and column positions to higher order polynomial functions and used the derivative to calculate the tangent lines. Presently, the tangent lines were calculated using the Cartesian coordinate differences between successive points in the rows and columns of the aponeurosis, smoothed by taking the mean over a 3×3 kernel. This procedure eliminates a problem that we have encountered in subsequently acquired datasets, which is that there may be sufficient curvature in an aponeurosis that there are multiple Y coordinates per X coordinate; of course, such data cannot be fitted to a single mathematical function.

The data from the entire aponeurosis were sampled uniformly by taking the median value for each architectural parameter in every 6 mm (high) $\times$ 3 mm (wide) section of aponeurosis. The values for the raw and smoothed fiber tracts were compared using Bland-Altman procedures. Descriptive statistics include the mean $\pm$ standard deviation (SD). Statistical significance was accepted at $p < 0.05$.

3. Results

3.1 Simulation Data

Curvature and Pennation Estimates with Varying Inherent Fiber Geometries—

Figure 3, Panel A shows the tracking result from the noise-free, $\kappa = 3.8 \text{ m}^{-1}$ condition as the solid black line; a sample raw fiber tract and corresponding fitted fiber tract from an S/N ~ 75 image data set are shown as the gray points and line, respectively. Panels B, C, and D of Figure 3 show the corresponding data for progressively higher curvature conditions.

Figures 4A–D show the κ values from the noise-free dataset as a function of fiber tract length (black lines), the sampled mean and 95% CI's for κ for the raw tracts from the four curvature conditions (gray points and bars), and sampled mean and 95% CI's for κ the fitted tracts from the four curvature conditions (blue points and bars). For the $\kappa = 3.8 \text{ m}^{-1}$ dataset (Figure 4A), the mean values of κ from the raw tracts exceeded those from the noise-free

dataset; and while their 95% CI's included the criterion values from the noise-free dataset, this was only because of the imprecision (large 95% CI's) in the raw tract data. Conversely, the 95% CI's for the fitted tracts were much smaller in magnitude, but still included the criterion values from the noise-free dataset. Similar trends were noted for the $\kappa=7.9 \text{ m}^{-1}$ and 11.8 m^{-1} data (Figures 4B and 4C). For the $\kappa=15.8 \text{ m}^{-1}$ dataset, κ was variably under- or over-estimated in the raw tracts and underestimated in the central portion of the fitted tracts (Figure 4D).

Figure 4E shows the θ data from the noise-free dataset, the raw tracts (mean, 95% CI), and the fitted tracts (mean, 95% CI). For both the raw tracts and the fitted tracts, the 95% CI's included the value from the noise-free dataset in all conditions with $\kappa \leq 11.8 \text{ m}^{-1}$. In the $\kappa=15.3 \text{ m}^{-1}$ condition, the 95% CI for the fitted tracts included the known value from the noise-free dataset; however, this was not true for the raw tracts.

Curvature and Pennation Estimates with Varying S/N—Figure 5, Panel A shows the tracking result from the noise-free, $\kappa=7.8 \text{ m}^{-1}$ curvature condition as the solid black line; a sample raw fiber tract and corresponding fitted fiber tract from the lowest S/N condition (~ 50) are shown as the gray points and line, respectively. Figure 5, Panels B, C, and D show the corresponding data for the S/N=75, 100, and 150 conditions, respectively.

Figure 6 shows the κ values from the noise-free dataset and representative mean and 95% CI's for κ for the raw and fitted tracts from the S/N ~ 50 , ~ 75 , ~ 100 , and ~ 150 conditions (Panels A, B, C and D, respectively). As above, the mean κ values from the raw tracts tended to exceed the known values from the noise-free dataset and have large 95% CI's. The mean κ values from the fitted tracts closely approximated the corresponding values from the noise-free dataset, and had considerably smaller 95% CI's than the mean values of the raw tracts. Figure 6E shows the θ data from the noise-free dataset and the raw and fitted tracts (mean, 95% CI). For both the raw tracts and the fitted tracts, the 95% CI's included the value from the noise-free dataset.

Curvature and Pennation Estimates with Varying Voxel Geometries—Figure 5, Panel E shows the noise-free dataset tracking result from the $\kappa=7.8 \text{ m}^{-1}$ curvature, 3.0 mm isotropic resolution condition as the solid black line; a sample raw fiber tract and corresponding fitted fiber tract from a S/N ~ 75 dataset are shown as the gray points and line, respectively. Figure 5F shows the corresponding data for the voxel volume= 13.5 mm^3 , AR=4.0 condition.

Figure 7, Panel A shows the κ values from the noise-free dataset and representative mean and 95% CI's for κ for the raw and fitted tracts from the $\kappa=7.9 \text{ m}^{-1}$, 2.4 mm isotropic resolution condition. Figures 7B and 7C show the corresponding data from the two altered voxel geometry conditions. Similar trends in the raw and fitted tractography data to those noted previously were observed. Figure 7D shows the θ data from the noise-free dataset, the raw tracts, and the fitted tracts. For both the raw tracts and the fitted tracts, the 95% CI's included the value from the noise-free dataset.

3.2 In Vivo Implementation

Second order polynomial fitting of all of the 758 initially propagated tracts within the *in vivo* fiber tracking dataset required 6 s of additional processing time. Figure 8A shows a sample fiber tract from the *in vivo* dataset before and after the fitting procedure; Figure 8B shows the fitted fiber tracking data. Six hundred and sixty-four of the 758 initial tracts (87.6%) met the quantitative outcome assessment criteria defined for this study. Figure 9A shows a Bland-Altman plot of the θ values from the fitted and raw tracts. The mean value of θ for the fitted tracts ($11.5 \pm 6.9^\circ$) did not differ significantly from the mean value for the raw

tracts ($11.3 \pm 5.9^\circ$) ($p=0.193$). No structure was evident in the Bland-Altman plot for θ (Figure 9A). Figure 9B shows a Bland-Altman plot of the κ measurements. The mean value of κ for the fitted tracts ($6.4 \pm 2.5 \text{ m}^{-1}$) was lower than the mean value for the raw tracts ($12.3 \pm 2.8 \text{ m}^{-1}$) ($p < 0.0001$). The Bland-Altman plot for κ was consistent with this difference in means and revealed no value-dependent variation in the bias between the two methods' estimation of κ (Figure 9B).

4. Discussion

In this work, we have characterized the errors associated with muscle architectural measurements based on DT-MRI fiber tracking and demonstrate that accurate curvature measurements are possible, when polynomial fitting procedures of the tracking data are used. Moreover, the fitting procedure does not adversely affect, and in some cases may improve, the accuracy and precision of the pennation measurements.

4.1 Muscle Architecture Estimation in Raw Fiber Tracts

The first principal finding of this work is that raw (unfitted) muscle DT-MRI fiber tract data allow for accurate pennation angle measurements, but allow neither accurate nor precise curvature measurements. Considering first the pennation data, we found that averaging the data from the 1 cm portion of the fiber tract nearest the seed point results in accurate estimates of θ , even for raw fiber tracts. The only exception to this statement occurred in the high curvature ($\kappa=15.3 \text{ m}^{-1}$)/pennation ($\theta=47.5^\circ$) condition, in which the raw tracking data underestimated the true pennation angle. It should be noted that these curvature and pennation values are larger than the values that have been reported in previous *in vivo* studies; for example, Muramatsu *et al.* reported a whole-fascicle curvature of 11.8 m^{-1} and a pennation angle of $\sim 40^\circ$ during maximal contractions of the gastrocnemius muscle.

In all conditions tested, the magnitudes of the 95%CI's were sufficiently large that they included the known κ values from the tract determined from the noise-free dataset. Certainly, it is reasonable to specify inclusion of the known value within the estimate's 95%CI as a necessary condition for measurement accuracy. However, at least in this case, this condition should not also be interpreted as a sufficient indication of measurement accuracy. For example, in all of the curvature conditions presented in Figure 4, at least one point along the raw tracts had a mean value that was at least two times the corresponding value for tract determined from the noise-free dataset. This was true for all other S/N and voxel geometry values tested (Figures 6 and 7). From these data, it is evident that for any reasonably foreseeable muscle structure or imaging condition, raw DT-MRI fiber tracking data cannot be used to estimate muscle fiber curvature accurately.

The data from the raw fiber tracts support the ideas that fiber tracking points consist of a true position and a noise-induced deviation from this position (the error); that the effects of this error on θ measurements can be cancelled or reduced by averaging multiple data points; and that the error in consecutive points artificially inflates κ estimates. However, we show in the next section that polynomial fitting is an effective means of reducing error in estimating κ .

4.2 Muscle Architecture Estimation in Polynomial-fitted Fiber Tracts

The second principal finding of this work is that polynomial fitting of muscle DT-MRI fiber tract positions allows for accurate curvature measurements of the reconstructed tracts, while preserving the accuracy and improving the precision of pennation angle measurements. For all physiologically likely values of κ ($\kappa \leq 11.8 \text{ m}^{-1}$), the 95%CI's surrounding the mean curvature estimates of the fitted tracts contained the known values from the noise-free dataset and the mean values from the fitted and noise-free dataset differed only slightly

(Figure 4). In conditions of varying S/N, the 95%CI's contained the known values and the mean values from the fitted tracts and the tracts from the noise-free datasets were similar; improved precision (reduced magnitude of the 95%CI's) was noted as a function of increasing S/N. Similar trends in parameter estimation were also noted across all voxel geometry conditions simulated. Notably, the voxel geometry in the AR=4.0 condition matches that of the *in vivo* data. Regarding the pennation data, under all conditions tested, the θ estimates were accurate. This includes the $\kappa=15.3 \text{ m}^{-1}$ condition, the mean θ values from which underestimated the criterion values in the case of the raw tracts. Also, the magnitudes of the 95%CI's were reduced following the fitting procedure.

These findings reflect one of the principal reasons for smoothing or fitting data, which is to reduce the effects of noise while preserving the true structure of the signal; thus improving the estimation of noise-sensitive parameters. Polynomial fitting is an intuitive and frequently used method for this problem. While more sophisticated methods exist, a comparison of these approaches is beyond the scope of this work, since the aim of this study was simply to determine whether or not polynomial curve fitting allows for an accurate and precise estimation of geometric parameters. The results of this study indicate that this is the case, and that polynomial fitting provides sufficient accuracy and precision under expected imaging and muscle architecture conditions.

4.3 In Vivo Implementation

In both the simulation and *in vivo* conditions of this work, a simple averaging of signals from the voxel of interest and maximally 26 nearest neighbors was used to obtain more reliable estimation of muscle fiber directions in the presence of image noise. Certainly, many sophisticated techniques for such purposes have been described in the literature. In a recent skeletal muscle DT-MRI study, for instance, Levin *et al.* employed a technique called Helmholtz–Hodge decomposition and resorted to heavy-duty numerical optimizations to compute a tensor vector field that has an optimal trade-off between consistency among neighboring tensors and fidelity to measured data. Sinha *et al.* used a 3D, iterative log-Euclidean anisotropic filter for image denoising in skeletal muscle DR-MRI data. Evidently, such mathematical maneuvers are very beneficial to vector field estimation and subsequent fiber tracking. However, these benefits may come at the cost of computational complexity, which can hinder the routine use of these methods in practice. The simple averaging procedure that we employed reduced the variability in the estimation of the tensor, at reduced computational expense: there were ~10% reductions in the SD's of the FA values and the angular deviation of $\mathbf{e}_1$ from a unit vector in the imager's +Z direction at the maximum cross-sectional area of the muscle (data not shown) and a >2-fold reduction in the mean κ values of the raw tracts, when comparing tensor calculations based on single voxel data with the 27-voxel averaging procedure. A full comparison of denoising procedures, given the degree of anisotropy and types of partial volume artifacts encountered in skeletal muscle, is warranted.

The motivation for the simulations was, of course, the absence of known values for pennation and curvature in the *in vivo* data; this makes it not possible to conclude that the fitting procedure produces more accurate muscle architecture results than raw tractography data alone. However, comparing the *in vivo* raw and fitted fiber tract data revealed behavior consistent with the simulations, in which such accuracy was demonstrated. As presented in the Results section and shown in Figure 9A, the mean θ estimates for the *in vivo* dataset were not significantly changed by the fitting procedure. Also consistent with the trends in the simulation data, the mean κ estimates were reduced following the fitting procedure (Results and Figure 9B). These findings demonstrate the *in vivo* utility of the fitting approach, and contribute to the likelihood that the architectural parameters derived from the fitted tracts are correct. However, a limitation to the current approach is that it cannot

replace lost data, such as those in which the fiber tracts stopped propagating prematurely, as extrapolating higher order polynomials beyond the last measured data point may result in unrealistic fiber trajectories.

4.4 Conclusions

Polynomial fitting of DT-MRI muscle fiber tracts allows for accurate muscle fiber curvature measurements while preserving the accuracy of pennation angle measurements. The fitting procedure also improves the precision of each measurement. These procedures are feasible for *in vivo* datasets, requiring little computational load over and above that required to compute the diffusion tensors, generate fiber tracts, and quantify their architectural properties.

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Figure 1.

Fascicle geometries used to define the model muscle. The original fascicle ($\kappa=3.8 \text{ m}^{-1}$) was based on a digitized fascicle from a published ultrasound image. The digitized positions were then scaled to permit image resolutions that would allow integer numbers of pixels in the Y and Z directions. The higher curvature fascicles were formed by multiplying the Y positions of the original fascicle by a scaling factor that linearly decreased as a function of Z position.

Figure 2.

Comparison of 2nd and 3rd order polynomial fits to the data. The data are for the same tract as is illustrated in Figure 3A, but the axes have been zoomed for clarity. In both panels, the black lines indicate the tracts from the noise-free dataset, the gray points indicate the raw tracts, and the gray lines indicate the fitted tracts. Panel A shows the 2nd order polynomial fit and Panel B shows the 3rd order polynomial fit to the same data. The 2nd order fit shows a single direction of curvature, while the 3rd order fit shows two directions of curvature with an inflection point centered at Z~0.03 m.

Figure 3. Sample fiber tracking results from the S/N~75, 2.4 mm isotropic resolution, $\kappa=3.8 \text{ m}^{-1}$ (A), 7.9 m^{-1} (B), 11.8 m^{-1} (C), and 15.3 m^{-1} (D) conditions. The black lines represent the fiber tracts generated from noise-free imaging data. The gray points and lines show representative raw and fitted tracking results.

Figure 4.

Curvature and pennation measurements based on raw and fitted fiber tracking data. In Panels A–D, the black lines indicate the data from the noise-free dataset tracts, the gray points and error bars indicate the mean and 95%CI from the raw tracts, and the blue points and error bars indicate the mean and 95%CI from the fitted tracts. All data shown have $S/N \sim 75$ and 2.4 mm isotropic resolution; the four panels indicate the $\kappa = 3.8 \text{ m}^{-1}$ (A), 7.9 m^{-1} (B), 11.8 m^{-1} (C), and 15.3 m^{-1} (D) conditions. Curvature measurements based on raw tracts were inaccurate and imprecise, but the mean θ values from the fitted tracts were accurate and precise for all curvature conditions tested having $\kappa \geq 11.8 \text{ m}^{-1}$. The pennation data are shown in Panel E. Black bars indicate the data from the noise-free dataset, gray bars and lines indicate the mean and 95%CI for the raw tracts, and blue bars and lines indicate the data for the fitted tracts. The mean pennation values determined from the raw tracts were accurate for all conditions with $\kappa \geq 11.8 \text{ m}^{-1}$; the mean values from fitted tracts were accurate under all conditions tested.

Figure 5.

Sample fiber tracking results from the simulation studies in which S/N and voxel geometry were altered. For panels A–D, $\kappa=7.9 \text{ m}^{-1}$ and there was 2.4 mm isotropic resolution. Panels A–D show tracking data from varying S/N levels [50 (A), 75 (B), 100 (C), and 150 (D)]. Also shown are the data from the $\kappa=7.9 \text{ m}^{-1}$, S/N=75, 27 mm³ isotropic resolution condition (E) and the $\kappa=7.9 \text{ m}^{-1}$, S/N=75, 13.5 mm³ AR=4 condition (F). The black lines represent the fiber tracts generated from noise-free imaging data. The gray points and lines show representative raw and fitted tracking results.

Figure 6.

Curvature and pennation measurements based on raw and fitted fiber tracking data. In Panels A–D, the black lines indicate the data from the noise-free dataset, the gray points and error bars indicate the mean and 95%CI from the raw tracts, and the blue points and error bars indicate the mean and 95%CI from the fitted tracts. Data are shown for the $\kappa=7.9 \text{ m}^{-1}$, 2.4 mm isotropic resolution, S/N=50 (A), 75 (B), 100 (C), and 150 (D) conditions. The curvature measurements based on the raw tracts were inaccurate and imprecise, but the data from the fitted tracts was accurate and precise for all conditions tested. The pennation data are shown in Panel E. Black bars indicate the data from the noise-free dataset, gray bars and lines indicate the mean and 95%CI for the raw tracts, and blue bars and lines indicate the data for the fitted tracts. The mean pennation values determined from the raw and fitted tracts were accurate for all conditions tested.

Figure 7.

Curvature and pennation measurements based on raw and fitted fiber tracking data. In Panels A–C, the black lines indicate the data from the noise-free dataset, the gray points and error bars indicate the mean and 95%CI from the raw tracts, and the blue points and error bars indicate the mean and 95%CI from the fitted tracts. Data are shown for the $\kappa=7.9 \text{ m}^{-1}$, $S/N=75$, 2.4 mm isotropic resolution (A), 3.0 mm isotropic resolution (B), and 1.5×1.5×6.0 mm resolution (C) conditions. Curvature measurements based on raw tracts were inaccurate and imprecise, but the data from the fitted tracts was accurate and precise for all conditions tested. The pennation data are shown in Panel E. Black bars indicate the data from the noise-free dataset, gray bars and lines indicate the mean and 95%CI for the raw tracts, and blue bars and lines indicate the data for the fitted tracts. The mean pennation values determined from the raw and fitted tracts were accurate for all conditions tested.

Figure 8.

In vivo implementation of the fitting procedures. Panel A shows a sample tract, with gray points indicating the raw tract and the blue line indicating the fitted tract. Panel B shows the fitted tracts only from the entire dataset. In B, tract colors are randomly varied and the color variations are intended only to produce contrast. The axis labels refer to positions along the foot-head (F-H), left-right (L-R), and anterior-posterior (A-P) axes.

Figure 9.

Bland-Altman analysis of the *in vivo* pennation (A) and curvature (B) measurements. The mean value of θ for the fitted tracts ($11.9 \pm 6.9^\circ$) did not differ significantly from the mean value for the raw tracts ($11.3 \pm 5.9^\circ$) ($p=0.193$). The mean value of κ for the fitted tracts ($6.4 \pm 2.5 \text{ m}^{-1}$) was lower than the mean value for the raw tracts ($12.3 \pm 2.8 \text{ m}^{-1}$) ($p<0.0001$). The Bland-Altman plot for κ demonstrates this difference in means and reveals that the bias between the two methods is consistent across all values of κ .

Design of simulated data sets. The Voxel Properties columns give the in-plane resolution and slice thickness, voxel volume, and aspect ratio (AR) of each data set. The Known Architecture columns give the mean curvature and pennation angle of the fiber tract determined from the noise-free dataset. The S/N was calculated for the non-diffusion-weighted images; the mean±standard deviation are given for all of the noise realizations in which the tract met the >80% L_H length criterion. Finally, the number of tracts meeting the >80% L_H length criterion is presented. Major divisions within the table are used to show the designs of the simulation experiments intended to test the effects of inherent fiber geometry, image S/N, and voxel geometry on the ability of the smoothing procedure to estimate muscle architectural properties accurately. Cells with bold type are used to highlight the values of the parameters altered in each experiment.

Table 1

Property Examined	Known Architecture		Voxel Properties				Number of Tracts with $L_H > 80\%$
	k (m ⁻¹)	θ (°)	Realized S/N	In-plane (mm)	Slice Thickness (mm)	Volume (mm ³)	Aspect Ratio
Inherent Curvature	3.8	31.6	75.7±10.3	2.4×2.4	2.4	13.8	1.0
	7.9	37.0	75.8±10.5	2.4×2.4	2.4	13.8	1.0
	11.8	42.4	75.2±10.4	2.4×2.4	2.4	13.8	1.0
	15.3	47.5	75.7±10.5	2.4×2.4	2.4	13.8	1.0
S/N	7.9	37.0	51.0±7.1	2.4×2.4	2.4	13.8	1.0
	7.9	37.0	75.8±10.5	2.4×2.4	2.4	13.8	1.0
	7.9	37.0	101.0±14.3	2.4×2.4	2.4	13.8	1.0
	7.9	37.0	149.5±22.0	2.4×2.4	2.4	13.8	1.0
Voxel Dimensions	7.9	37.0	75.8±10.5	2.4×2.4	2.4	13.8	1.0
	7.9	36.5	76.1±12.1	3.0×3.0	3.0	27.0	1.0
	7.8	37.5	74.7±8.3	1.5×1.5	6.0	13.5	4.0