Fiber tractography is useful for studying a variety of biological phenomena associated with transversely isotropic tissues, in which fibers serve to provide functional strength along a specific axis. One useful application of fiber tractography is finite-element analysis (FEA) studies. Here, we present a method utilizing computational fluid dynamics (CFD) for efficiently determining fiber trajectories in a transversely isotropic material with arbitrary structures of any complexity (such as those determined from biomedical imaging). We demonstrate assignment of fiber directions to FEA mesh by registration with the CFD mesh. Sensitivity analysis on various solver settings, flow characteristics, and material parameters shows less than 2 degrees of average deviation from the nominal fiber vectors if the Reynolds number is 1. INTRODUCTION

As the orientation of the fibers in transversely isotropic biological tissues such as tendon and muscle is critical to their function and adaptation to mechanical stimuli, finite-element models of these tissues require parametrization of the complex trajectories of the fibers. Finite-element models of tissues such as tendon [33], skeletal muscle [4, 24, 7, 8, 30, 32, 14], cardiac muscle [11, 6], ligament [18, 9], vocal cords [1], cartilage [2], heart valves [20], and meniscus [27] must specify a fiber direction vector at each element or node throughout the tissue. Very simple geometries such as rectangles or cylinders can be modeled with global- or circumferentially-defined fiber directions. However, complex geometries are more physiologically relevant and the fiber trajectories are consequently more complicated. This necessitates methods for determining these fiber trajectories in finite-element tissue studies.

Several experimental and computational methods have been previously developed to determine fiber trajectories in transversely isotropic biological tissues, predominantly muscle. Cadaver dissections have been used to reconstruct muscle fiber morphology [16]. This allows direct visualization and determination of fiber trajectories, but the dissection disturbs the in vivo placement of the muscle and is time-consuming. Furthermore, cadaveric muscles do not represent healthy subjects well [12]. Another experimental method to determine fiber trajectories in muscles is MRI diffusion tensor imaging combined with tractography [15]. While this method has the advantage of allowing non-invasive in vivo determination of fiber tracts, the process requires manual selection of regions of interest and is sensitive to noise in the MRI data, resulting in some unrealistic fiber tracts. Another experimental method is ultrasound imaging. This has the advantage of in vivo use, but 2D imaging of muscle [19] cannot reproduce 3D trajectories and 3D imaging [17, 23] can suffer from low spatial resolution of fiber vector maps. One computational method uses interpolated cubic splines to determine fiber trajectories [3]. A template with interpolated fiber arrangements originates as a simple geometry, such as a cube, and is then morphed into physiologically realistic geometries, such as those obtained from MRI data. This method produces realistic fiber trajectories, but requires manual specification of a fiber template and morphing of the template. Another computational method uses a rotation and divergence-free (Laplacian) vector field to automatically determine muscle fascicle tracts in arbitrary muscle shapes [5]. However, the solution is unique, preventing adjustment of the trajectories based on experimental data, and the associated rotation free condition prevents the reproduction of twisting trajectories. A similar technique that formulates a boundary value problem has also been proposed previously [10].
Here, we present a method to determine 3D fiber trajectories in arbitrary structures using computational fluid dynamics. The characteristics of viscous, incompressible fluid flow with the proper boundary conditions help satisfy the observations about fiber trajectories in biological tissues [5]: i) they are coaxially aligned and do not cross each other ii) they do not branch iii) they will not reverse their directions abruptly and iv) they must connect between attachment points. This method is simple and intuitive to implement and enables efficient, robust, and reproducible calculations of fiber trajectories for FEA studies. Another advantage of this method is that the trajectories can be arbitrarily adjusted with flow guides to incorporate experimental data and observations such as twisting. We focus on muscle and tendon tissue, but the method is generalizable to other transversely isotropic tissues such as ligaments or cartilage.

2. METHODS

2.1 Computational fluid dynamics (Figure 1a)

Solid model creation
A variety of methods can be used to reconstruct complex shapes of biological tissues. Common in vivo methods include MRI and ultrasound, while common ex vivo methods include photographs, sectioning, or slicing. These images must be converted to solid models.

Flow guides can be prescribed in the model so that the flow matches specific observations (Figure 2). These surfaces or channels can be specified mathematically or manually within a solid modeling environment to subdivide the solid into separate flow channels.

Boundary conditions and fluid properties
It is necessary to specify where the fibers originate and terminate (Figure 1a). For muscles, this is at the tendinous aponeuroses, which can be located via imaging, cadaveric data, or knowledge of the anatomy. For tendons and ligaments, the origin and termination regions are typically at the ends of their simpler geometries. One region of fiber origin or termination is set to an inlet surface condition (e.g., positive gage pressure, normal flow velocity, or volume flow rate). The other surface is an outlet surface condition with a gage pressure of 0Pa. The other surfaces are specified as slip surfaces that the fluid cannot penetrate. Nominally, we arbitrarily set the inlet pressure to 1Pa and the fluid to be incompressible with a viscosity of 1Pa-s and density of 1g/cm³. This resulted in very low Reynolds numbers (<1) and good convergence.

CFD solver
In the CFD environment, incompressible, laminar, viscous, and steady-state flow are nominally prescribed. These conditions help satisfy the observations about fiber trajectories in biological tissues [5]: i) they are coaxially aligned and do
not cross each other (viscous flow) ii) they do not branch (incompressible flow) iii) they will not reverse their directions abruptly (laminar flow) and iv) they must connect between attachment points (boundary conditions). The simulation is run and the steady-state flow velocity vectors for each mesh node are computed. Fluid streamlines can be visualized within the CFD package.

2.2 FEA fiber mapping (Figure 1b)
Generally, the same solid shape generated from the medical images will be used for both CFD and FEA. Depending on the solid finite element formulation and shape (e.g., tetrahedral, hexahedral, linear, quadratic, cubic), it will be required to specify fiber directions for either single elements [4] or nodes (if the fiber directions need to be interpolated throughout the element [32]). We use a nearest-neighbor algorithm to transfer the fiber directions from the CFD mesh to the FEA mesh (as the meshes may not be identical). That is, for each element or node from the FEA mesh needing a fiber direction, the nearest CFD mesh node is determined and that velocity vector is assigned to the FEA node or element center as the fiber direction vector. ¹

2.3 Sensitivity analysis
We performed sensitivity analysis on different inlet conditions, fluid viscosities, and compressibility. We calculated the average angle deviation of the fiber direction vector from the fiber direction vectors found from our nominal CFD parameter values (1Pa inlet gage pressure, 1Pa-s viscosity, 1g/cm³ density; laminar and incompressible flow) for each node in the FEA mesh.

3. RESULTS

3.1 Iliacus (Figure 2)
The iliacus is a hip flexor muscle that fans broadly. We implemented one curved flow guide and two straight flow guides. The results showed slightly different flow patterns that followed the guides accurately.

3.2 Soft palate muscle complex (Figure 3a)
The soft palate contains several muscles that move and deform the soft palate in speech and swallowing tasks. Some fibers of two of the muscles, the levator veli palatini and the palatopharyngeus, blend inside the soft palate [25]. The results demonstrate these blended fiber trajectories.

3.3 Achilles tendon (Figure 3b)
The Achilles tendon is composed of three distinct fascicles, connecting to the medial gastrocnemius, lateral gastrocnemius, and the soleus muscles. Interestingly, these tendon fascicles exhibit approximately a 90 degree twist from origin to insertion [26, 31]. Flow guides subdivide the whole Achilles tendon image (obtained from MRI) into three twisting compartments. CFD results reproduced the twist for all three compartments.

3.4 Biceps femoris longhead (Figure 3c)
The biceps femoris longhead is a hamstring muscle with a complex three-dimensional morphology. We use an MRI-derived solid model of the muscle [24] and use CFD to calculate realistic fiber trajectories that start at the proximal tendon and end at the distal tendon and these flow patterns are transferred to the FEA mesh. Sensitivity analysis on various solver settings, flow characteristics, and material parameters (Table 1) shows less than 2 degrees of average deviation from the nominal fiber vectors in the FEA mesh if the Reynolds number is <1 and the flow is laminar and incompressible. Reynolds number is calculated using the formula: Re = (ρVd/μ), where ρ is the fluid density, V is the flow velocity, d is the characteristic length scale, and μ is the dynamic viscosity. In this study, we used a characteristic length scale of the muscle’s cross-sectional area, ρ = 1000 kg/m³, V = 1 m/s, and μ = 0.001 Pa·s, resulting in a Reynolds number of 10,000. The high Reynolds number combined with the intricate curvature of the muscle causes turbulent eddies, resulting in unrealistic fiber trajectories for muscle (Figure 3d).

3.5 Adductor Brevis (Figure 4)
The adductor brevis is a thigh adductor that has a smaller origin than the insertion. The fiber trajectories fan out from the origin. A reference vector was reproduced from a previous cadaveric study [29]. In the cadaveric study, the average angle of the fibers from the reference vector (also termed “pennation angle”) was calculated as 6.1 degrees with a standard deviation of 3.1 degrees averaged across 21 cadavers. The average angle of the FEA fiber direction from this reference vector in our study was 6.9 degrees. This represents a close agreement of experimental results with our computational results for fiber direction.

4. DISCUSSION
We have proposed a method using computational fluid dynamics to compute fiber trajectories in transversely isotropic materials of arbitrary complexity and shape. The method leverages the power of CFD solvers and enables efficient fiber mapping of FEA meshes derived from geometries determined with in vivo or ex vivo techniques. For certain tissues with complex fiber trajectories that cannot be feasibly be determined from our procedure, flow guides can easily be implemented to reproduce realistic trajectories (e.g., those determined by cadaveric dissection or diffusion tensor imaging).

Furthermore, this method provides an elegant solution to determining fiber tracts in muscles that have complex attachments, multiple heads, or intertwine with each other. For low Reynolds numbers, the CFD solutions are robust to simulation parameter variations as measured by average angle deviation.

Our quantitative results from the angle of the fibers from the reference vector (pennation angle) in the adductor brevis compared favorably with a cadaveric study [29]. This was a 2D calculation for that study as well as in our study. Many studies report 2D pennation angles, but our study enables the calculation of 3D pennation angles which may prove useful for muscle architecture studies. Future studies can provide additional validation of these measurements in more complex muscles.

¹It can be noted that other least-squares algorithms [13] could also be applied to transfer the fiber directions, but if the CFD mesh is specified to be much finer than the FEA mesh, the errors can be reduced to any desired tolerance using nearest-neighbor methods.
Figure 3. Results. (a) Soft palate muscle complex. Some fibers of two of the muscles, the levator veli palatini and the palatopharyngeus, blend inside the soft palate. The results demonstrate these blended fiber trajectories. (b) Twisting 3-fascicle Achilles tendon results. CFD results reproduced the twist for all three compartments. 5,000 out of 31,125 mesh point vectors shown. (c) Biceps femoris longhead. The CFD solution easily calculates realistic fiber trajectories that start at the proximal tendon and end at the distal tendon and these flow patterns are transferred to the FEA mesh. (d) Laminar, incompressible fluid flow with low Reynolds numbers produces realistic fiber trajectories, while turbulent, compressible airflow with high Reynolds numbers causes turbulent eddies, resulting in unrealistic fiber trajectories.
Table 1. Sensitivity analysis of a variety of CFD conditions. There are less than 2 degrees of average angle deviation from the nominal fiber vectors in the FEA mesh if the Reynolds number is <1 and the flow is laminar and incompressible with our nominal fluid properties (viscosity of 1Pa-s and density of 1g/cm$^3$). Furthermore, the highest average angle deviation results from turbulent, compressible airflow with inlet pressure of 10,000Pa and a Reynolds number around 1,000,000 (Figure 3d).

In spite of the advantages of this method over previous methods, some limitations can be recognized. Validation or calibration with experimental observations of very complex 3D tissue architectures may be difficult. Study-specific sensitivity analyses on boundary conditions, flow guides, and simulation parameters may be desirable in certain cases. Discretization and nearest-neighbor procedures can result in small errors.

Supplementary information, including code, models, demonstration videos, and data, are available online [28].

5. CONCLUSION

As demonstrated by the numerous examples in this study, this method has great potential to enhance and empower future FEA studies on complex, transversely isotropic biological tissues. Future work will also enable the use of this method to conduct in vivo studies of muscle architecture.

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